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中国生态学学会微生物生态专业委员会学术年会
暨全球华人学者环境科技前沿论坛

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论 文 集

2023年8月14日-17日
中国 • 哈尔滨

全国生态日

十四届全国人大常委会第三次会议28日表决通过决定，将8月15日设立为全国生态日。2023年中国生态学学会微生物生态专业委员会学术年会暨全球华人学者环境科技前沿论坛借此契机召开，以实际行动践行习近平生态文明思想，深化习近平生态文明思想传播，为全面推进美丽中国建设，加快推进人与自然和谐共生的现代化贡献出“环境人”的一份力。

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摘要集

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大会报告

气溶胶暴露健康效应智能化探测与早期预警

要茂盛 [1*]

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摘要

气溶胶暴露能造成多种疾病，甚至死亡。气溶胶种类繁多，包括生物与化学物质。病原体气溶胶常常被稀释，浓缩富集与检测存在极大挑战。此外，气溶胶暴露无声无息，防不胜防。该报告主要围绕气溶胶的浓缩富集、监测以及健康效应，讨论基于芯片、细胞、动物以及人体的气溶胶的实时探测。同时，以新冠病毒气溶胶的监测为例讨论相关的挑战。该报告还讨论来自中国的 31 个主要城市的大气颗粒物的毒性，包括其组分差别等，并通过酵母菌、大鼠以及人体的暴露，研究生命体系释放的挥发性有机物以及其它气体标志物来实时探测气溶胶暴露的健康效应。此外，以内毒素为例研究污染物暴露后，生命体系释放挥发性有机物的规律。最后，本报告将探讨利用大鼠来监测空气毒性的相关工作，同时阐述人体呼出气气体标志物在新冠肺炎的测试应用，以及作为人体疾病“烟雾报警器”的可能性。

关键词：气溶胶暴露；智能化探测；疾病早期检测；挥发性有机物；呼出气气体标志物

微生物氧化氨产生氮气的一种新途径—Dirammox

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摘要

微生物是自然界中氮素生物地球化学循环的重要驱动者。报告简要回顾总结生物脱氮和微生物氧化氨过程，重点介绍微生物氧化氨产生氮气的新进展，包括一种氨氧化新途径 Dirammox 的发现和研究过程，介绍参与 Dirammox 的微生物多样性、基因和酶等。

关键词：生物脱氮；微生物氨氧化；Dirammox；氮素生物地球化学循环

从 RACS-Seq/Culture 到 FISH-RACS-Seq：“物种-代谢功能”双靶向性的单细胞全基因组技术服务微生物组机制研究和资源挖掘

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摘要

微生物生态学的本质问题之一是“Who is doing, What, and Why?”。为了在生命的单元尺度和进化的单位水平回答这个问题，单细胞中心和青岛星赛生物合作，基于拉曼组/元拉曼组原理，开发了单细胞拉曼分选耦合测序/培养系统（RACS-Seq/Culture）、高通量流式拉曼分选仪（FlowRACS）等拉曼组仪器平台，能针对复杂微生物组样品建立“代谢表型组-基因组-培养组”在单细胞精度的关联。该平台实现了：（1）免荧光标记、高通量、活体、全景式的单细胞代谢表型组（代谢活力、底物利用、产物合成、环境应激等）测量；（2）针对目标代谢功能细胞，“所见即所得”（RACS）或高通量（FlowRACS）的单细胞代谢功能分选；（3）针对分选出的功能细胞，精确到 1 个细菌细胞、覆盖度可超 99%的全基因组测序；（4）针对分选出的功能细胞，并行化的单细胞培养（RACS-Culture）从而获得功能菌剂（益生菌、耐药菌等）。在此基础上，我们最新建立了 FISH-RACS-Seq 技术，针对复杂环境样品，实现了同时针对“目标物种”和“目标代谢功能”、双靶向性的单细胞分选并耦合全基因组测序。虽然元基因组关联分析能发现大量“目标物种”，但其原位代谢功能与全基因组往往难以验证，因此 FISH-RACS-Seq 为突破这一瓶颈问题提供了一个广谱适用的解决方案。总之，拉曼组仪器平台实现了“原位代谢功能”、“物种”或“物种+代谢”靶向性的单细胞多组学解析，有望成为新一代的微生物生态学研究和微生物资源挖掘装备体系。

长期滞留和消毒引发的饮用水中睡美人细菌赋存与抗性传播风险

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摘要

保障饮用水的微生物安全是供水安全最基本的要求之一。但水传病原菌（Waterborne Pathogens，WPs）在饮用水消毒及输送过程中有可能进入有活性但不可培养（Viable But Non-Culturable，VBNC，亦称“睡美人”状态）的休眠状态，从而在管网长期赋存、耐受各种环境压力、逃避标准方法检测，是威胁水质微生物安全的重大隐患。本研究针对上述问题的研究表明：（1）长期滞留可导致饮用水中可培养细菌污染严重，最高超标 100 倍以上；Legionella pneumophilia，Salmonella spp.，Enterococcus faecalis 等典型 WPs 被 PMA-qPCR 法高频检出，主要以 VBNC 形态长期赋存于供水管网；（2）发现氧化消毒诱导的 VBNC 型 E. coli 存在抗生素广谱性抗性特征和促进抗性基因（Antibiotics Resistance Genes，ARGs）接合性水平转移的滞后性抗性风险；提出外排泵系统增强和氧化应激效应对于 VBNC 型病原菌形成抗性风险中的关键作用；（3）探讨 UV/氯组合工艺对环境水样中病原菌及其 VBNC 状态的控制潜力，其对 VBNC 型病原菌及 ARGs 的去除效果较传统工艺更强，但实际水环境中细菌初始浓度高和水质条件会加速氯的衰减而影响协同消毒效果，Acinetobacter 和 Mycobacteria 等氯抗性细菌（Chlorine Resistant Bacteria，CRB）会成为 UV/氯组合工艺消毒后的优势菌群。本研究结果表明，应完善供水的微生物安全评价体系和提高消毒工艺效能，并将 VBNC 型病原菌作为一种新型的微生物污染物加以控制。

关键字：饮用水消毒；病原菌；活的不可培养状态；抗性；微生物控制

Occurrence and risk of ARGs spreading of the sleeping beauty bacteria in drinking water induced by long-term stagnation and disinfection

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Abstract:

Ensuring the microbiological safety of drinking water is one of the fundamental requirements for water supply safety. However, waterborne pathogens (WPs) have the potential to enter a dormant state known as viable but non-culturable (VBNC), also known as the "Sleeping Beauty" state, during the disinfection and distribution processes of drinking water. In this state, they can persist in the distribution network for a long time, tolerate various environmental pressures, and evade detection by standard methods, posing a significant hidden risk to the microbiological safety of water quality.

This study on the above-mentioned issues has shown the following: (1) Long-term stagnation can lead to severe contamination of culturable bacteria in drinking water, exceeding the standard by more than 100 times. Typical WPs such as Legionella pneumophila, Salmonella spp., and Enterococcus faecalis were frequently detected using PMA-qPCR, and they mainly persist in the water supply network in VBNC state. (2) It was found that VBNC E. coli induced by oxidative disinfection exhibited broad-spectrum antibiotic resistance and a delayed resistance risk in promoting horizontal transfer of antibiotic resistance genes (ARGs). The enhanced efflux pumping system and oxidative stress were identified as key factors in the formation of resistance risk in VBNC pathogens. (3) The control potential of the UV/chlorine combination process on pathogenic bacteria and their VBNC state in environmental water samples was explored. It showed stronger removal effects on VBNC pathogens and ARGs compared to traditional processes. However, high initial bacterial concentrations and water quality conditions in actual water environments can accelerate chlorine decay and affect the synergistic disinfection effect. Chlorine-resistant bacteria (CRB) such as Acinetobacter and Mycobacteria become dominant bacterial populations after UV/chlorine combination disinfection.

The above results indicate the need to improve the microbial safety assessment system for water supply, enhance the efficiency of disinfection processes, and consider VBNC pathogens as emerging microbiological contamination that needs to be controlled.

Keywords: Drinking water disinfection; Pathogens; Viable but non-culturable state; Resistance; Microorganism control

氮循环合成微生物群落多样性与功能及生态位分化机制

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摘要

微生物驱动的氮循环发挥重要的生态系统功能，而合成微生物生态学通过改变微生物群落组成而增强其生态系统功能和稳定性。氮循环是生物圈内最基本的物质循环之一，我们利用遗传背景清晰的微生物菌株构建了氮循环合成微生物群落，探索了微生物群落多样性与功能和生态位分化机制。首先，合成反硝化群落结果表明微生物群落多样性与功能（生长和反硝化速率）具有正相关关系，而长期实验室进化可降低微生物间的竞争从而增强生态系统功能；同时，物种多样性高的合成群落具有较强的群落功能与稳定性。其次，通过合成硝化微生物群落探索了全程硝化细菌(Comammox)、氨氧化古菌(AOA)、氨氧化细菌(AOB)及亚硝酸盐氧化菌(NOB)对铵浓度的生态位分化机制。进一步研究将利用现有微生物资源与模型预测，聚焦微生物相互作用及其机制，推动环境微生物组工程的发展。

关键词：氮循环；合成微生物生态学；合成反硝化群落；合成硝化群落；生态系统功能

Biophotoelectrochemistry: An emerging frontier for channeling photoelectric effect into darkness zone of soil and sediments

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Abstract

Solar energy captured by photosynthetic plants in the photic zone is recognized as the main driver for the formation of organic matter utilized by soil communities. However, the contribution of organic transformation to the linkage of solar energy and microbial metabolism of soils is reduced when the vadose zone is saturated. Different from the conventional biophotoelectrochemistry via photosynthesis with phytoplankton during the periodic saturation of soils, recent studies suggest that non-phototrophic microorganisms in soils and sediments are able to conduct the light-dependent metabolism to sustain their functionality with photosensitizers under illumination. These interactions and processes utilize long-distance electron transfer networks to interconnect diverse electron transfer chains that channel photoexcited electrons into the opaque zone for soil communities. Such an emerging process not only makes for better understanding the biogeochemical process such as the carbon sequestration and mitigation in soil, but also shows great potential for the environmental treatment such as the bioremediation of contaminated soil. Therefore, we suggest here that the biophotoelectrochemistry via photoelectric effect can have significant, heretofore unappreciated values in theory and practical application.

Keywords: Biophotoelectrochemistry; Electron transfer; Light-dependent metabolism; Soil; Photoelectric effect

根瘤菌适应性演化过程中转座元件群落的生态位分化

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摘要

根瘤菌-豆科植物共生固氮是效率最高的生物固氮类型，在全球氮素循环和国家减施化肥战略中发挥着重要作用。但是，商业根瘤菌剂的接种效果会受到作物品种、土壤条件与田间管理措施的显著影响——如何获得广谱抗逆高效根瘤菌是菌剂产品迭代研发的核心内容。针对耐盐碱的广宿主费氏中华根瘤菌，我们发现长链群体感应信号分子可增强根瘤菌向植物根表的迁移与定殖能力（ISME J 2023a）；可转座插入序列在三型分泌系统及其效应蛋白 NopP 编码基因的插入突变介导了不匹配菌株共生匹配性的快速适应性演化（mSystems 2021; ISME J 2018）；趋同演化的外源基因沉默蛋白 MucR 在结瘤固氮功能与根瘤菌底盘适配优化中发挥了全局调控作用（Nucleic Acids Research 2022; ISME J 2022; mBio 2021）；进一步基于生态学共性原理构建了细胞内“同质园”，利用实验进化与分子生物学方法发现外源基因在多复制子根瘤菌底盘的突变频率依赖外源基因的 GC 含量及其所在的复制子，这种突变频率的差异主要是由不同转座元件的生态位分化造成的——其中外源基因沉默蛋白 MucR 在转座元件群落的生态位分化中扮演了重要角色（ISME J 2023b）。这些工作为我们系统理解根瘤菌定殖根表、侵染、结瘤固氮过程的生态与演化机制，以及广谱抗逆高效根瘤菌菌种的合成生物学创制提供了有益参考。

关键词：根瘤菌；结瘤；固氮；匹配性；演化

未培养古菌新类群及微生物代谢互作关系

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摘要

近年来，古菌研究得到了越来越多的关注。古菌是生命之树上的第三大生命形式，具有与真核生物相似的遗传系统。然而，由于古菌基因组和菌株缺乏，我们对古菌的生理生态功能了解不足。因此，本研究以“古菌的生理生态功能及其演化机制”为主题，采用多学科交叉技术，从古菌的物种多样性、物质代谢潜能以及与细菌的代谢互作机制三个方向展开研究。

在古菌的物种多样性方面，通过大规模的样品采集和宏基因组分析，我们发现了 7 个古菌新门，其中一个新门被命名为悟空古菌。与其他阿斯加德古菌不同，悟空古菌是一种严格厌氧自养微生物，其代谢功能与其他古菌有明显差异。此外，我们还建立了首个阿斯加德古菌功能基因库，其中包含了 1.4 万多个功能蛋白基因。针对乌斯古菌，我们将其划分为 10 个亚群，其中乌斯古菌 J 亚群具有不依赖宿主的独立代谢能力。通过基因家族进化史的分析，我们发现细菌在乌斯古菌的代谢模式演化中起着重要作用。这一发现改变了人们对乌斯古菌只能进行代谢共生的认识。

考虑到古菌具有代谢共生特性，我们推测微生物在原位环境中可能存在复杂的代谢互作关系。因此，我们分析了深圳福田红树林沉积物中的微生物基因组和转录组数据，重构了微生物的代谢互作网络。通过复杂网络降维方法构建了微生物活性功能模块，发现表层微生物主要参与固碳、硝酸盐还原和硫酸盐还原，而底层微生物主要参与降解复杂有机碳。此外，我们还发现存在一个微生物驱动的有机碳从表层向底层输送、降解和埋藏的路径。

综上所述，本研究对于古菌的生理生态功能及其与微生物的代谢互作关系进行了深入的研究。这些研究结果对于理解地球生命起源和演化具有重要意义，并对环境保护和生物技术等领域具有潜在应用价值。

关键词：微生物生态学；古菌；生理生态功能；演化机制；代谢互作关系

绿色农业中新污染物传播的生物健康风险

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摘要

广泛使用兽用抗生素已经导致动物粪便中抗生素浓度的积累。在有机农业生产过程中，将动物粪便作为土壤有机肥料可能会引发抗生素等新污染物在环境中的广泛传播，其中伴生的生物健康风险对全球公共卫生构成了重大威胁。因此，深入研究环境中抗生素、雌激素、抗生素抗性基因等新污染物的传播特征和生态效应对于应对和阻控环境中的生物传播风险具有重要意义。本研究采集了北京郊区五个生猪养殖场中的粪肥和堆肥，以及施用了堆肥的农田土壤及对照土壤。研究发现，在这一潜在环境传播链中，抗生素、雌激素、微生物物种与功能基因的变化特征及其生态效应均发生了明显变化。抗生素浓度在环境传播过程中减少了 10-1000 倍。粪肥和堆肥中的病原微生物、毒力基因、抗生素抗性基因和病毒基因的相对丰度显著高于堆肥施用土壤，揭示了病原菌的传播风险。此外，相较于土壤，粪肥和堆肥样品中病毒与抗生素抗性基因之间的关联更加紧密，表明有机肥施用将会增强病毒介导的抗性基因传播。本研究表明，绿色农业中有机肥的使用引发新污染物传播及生态健康风险。因此，有必要规范有机肥的管理和使用，并进一步开发新污染物环境传播的阻控技术。

关键词：环境新污染物；抗生素抗性基因；雌激素；生态健康风险

单细胞表型检测与精准分选前沿技术—功能微生物筛选新策略

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摘要

自然界中存在着数量巨大的难培养微生物，被称为微生物界的“暗物质”，它们中存在着数量可观的具有疾病治疗、环境净化等作用的功能微生物。宏基因组学能够揭示微生物群落的多样性和复杂性，但无法定义或验证复杂微生物群落中个体成员的作用。完全破译特定微生物在复杂群落中的作用，并将其功能表型与基因组联系起来仍然非常困难。相较而言，单细胞技术可逐一表征微生物菌株在群落中的特性，进行多维度、跨尺度的微生物研究，为难培养微生物资源的研究与开发提供了一种新策略。

环境样本通常杂质较多，生物种类繁多，大小形态各异，还有一些内生菌丰度比较低。由于土壤介质的复杂性，对如何获得土壤微生物单细胞提出了挑战。单细胞显微拉曼光谱技术具有无损、快速、免培养、高灵敏度与高空间分辨率等特点，在微生物鉴别中具有重要作用。而可视化单细胞精准分选系统与单细胞表征及下一代测序技术相结合，可以排除环境和宿主干扰，定位和分离目标细胞，推进复杂环境下微生物生态、菌群互作、代谢机制及功能研究。

本文中我们将介绍微生物单细胞研究的整体方案，包括目标类群的富集、表型靶向微生物宏基因分析、功能微生物多模态识别、微生物单细胞的可视化精准分离、微生物单细胞培养组学等。应用这一体系，成功地从土壤样品中免标记、非破坏性地识别并分离出一系列功能菌株，并实现单个微生物的基因组测序与培养，为微生物生态、功能菌筛选、未培养微生物研究等提供有力工具。

关键词：微生物单细胞可视化分选；功能微生物筛选；深度学习；拉曼光谱识别

气候变化下高寒草地土壤微生物介导的碳周转

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摘要

作为地球第三极，青藏高原是全球生态环境变化的指示器和调节器。草地是青藏高原面积最大的生态系统类型，气候变化下发生巨大变化，对其碳固持与碳汇功能产生重大影响，关乎到国家生态安全屏障建设与“碳达峰碳中和”目标的实现。区域尺度上，冷湿条件下的草地土壤表层具有更高的碳密度，很大程度上源自微生物介导的碳周转过程在低温条件下受限。然而，微生物的温度适应性能在一定程度上调节土壤碳周转速率，例如在通透性差的高寒湿地土壤中，甲烷微生物具有独特的冷适应特征，介导了高效的甲烷代谢速率。此外，微生物与植物的互馈对土壤碳循环具有重要意义。两者通过对营养获取的竞争与合作同时影响源自植物的土壤碳输入和微生物介导的碳周转，进而影响草地土壤碳库的储量及其稳定性。

关键词：微生物生态学；青藏高原；碳库稳定性；碳输入；碳周转

降解水污染物的非均相还原催化剂

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摘要

2023 年实施的新版《生活饮用水卫生标准》包括了高氯酸盐、氯酸盐等一系列有害含氧负离子污染物，但针对这些污染物的化学处理方法研究并不多。我们长期致力于开发相关的还原催化剂，将金属的选取和应用扩展到元素周期表的第 5，6，7，8 族。这些金属在水-催化剂界面表现出独特的化学机制和优异的催化活性，并将非均相催化剂对 pH 值的依赖从酸性拓展到中性。本报告将对这一方向进行简要的总结和展望。

Effects of non-antibiotic and antibiotic co-exposure on the development and propagation of antibiotic resistance in *E. coli* populations

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Abstract

Antimicrobial resistance is one major threat to public health around the world. The minimum selection concentration of antibiotics could be much lower than the minimum inhibitory concentration, imposing risks of antibiotic resistance development in environmentally relevant conditions. Antibiotics often coexist with non-antibiotic micropollutants in many environments during water and biosolids reuse applications. How the non-antibiotics at environmental levels would affect the selection and dissemination of antibiotic resistance was largely unknown. This presentation will summarize our recent studies on the development, propagation, and transmission of antibiotic resistance in E. coli populations exposed to antibiotics and non-antibiotic micropollutants. We demonstrated the synergistic effect of the pesticide and antibiotic co-exposure on stimulating the emergence of antibiotic resistance in the tested E. coli populations, whereas pharmaceuticals did not show such synergistic effects. Moreover, the synergistic effect seemed more specific to E. coli strains, including the pathogenic ones. Evolutionary trajectories revealed distinct target mutations conferring the much stronger phenotypic resistance, which commonly emerged in several E. coli strains coexposed to pesticides and antibiotics. Those could be complementary biomarkers indicative of antibiotic resistance levels in the environment. The growth fitness of the evolved resistant mutants under different environmental conditions could be used to predict their abilities to survive and thrive in changing environments.

Dry Well Performance Analysis: Efficiency of Stormwater Capture and Emerging Contaminants Removal

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Abstract

Dry wells are vadose zone infiltration systems that are increasingly being used in the US to collect urban surface runoff and recharge groundwater. Compared with other stormwater infiltration systems, dry wells have a smaller footprint, and lower capital, operating, and maintenance costs. Thus, they are an important part of future urban water infrastructure for the beneficial use of urban stormwater. However, research on dry well performance is limited. The infiltration capacity of dry wells under current and future climate conditions remains unclear, and concerns have been raised about potential groundwater contamination caused by dry wells. Considering these inadequacies, this study investigates the performance of several existing dry wells in the City of Los Angeles and designs and tests cost-effective treatment systems for these dry wells. A field monitoring program is first designed and implemented. Both stormwater quantity data (i.e., urban runoff flow rates) and quality data (i.e., concentration profile of nine hydrophilic organic compounds from the curb to dry well primary chambers) are collected from five rainfall events. The quantity results are used for the calibration and verification of the hydraulic model developed in the next step, while the quality results illustrate the importance of the development of stormwater treatment systems for dry wells. Next, the stormwater capture efficiency of dry wells is estimated based on a hydraulic model for different climate conditions and dry well designs. It is shown that dry wells are effective during droughts, but the increased frequency of intense storm events results in less capture efficiency. However, building multiple dry wells in sequence for a large catchment area can improve capture efficiency. Lastly, four stormwater treatment systems (e.g., biochar filter, regenerated activated carbon filter, UV-AOP + biochar filter, UV-AOP + regenerated activated carbon filter) are constructed and tested for the removal of hydrophilic contaminants of

emerging concerns (CECs) in urban runoff. The results show that large grain size biochar and regenerated activated carbon are cost-effective materials for stormwater treatment. The addition of a UV-AOP system can significantly increase the removal efficiency of most CECs and thus prolong the life span of carbon filters. The results of this study will provide a better understanding of the potential for widely employing dry well systems as infiltration practices to improve stormwater runoff management while minimizing the risk of possible groundwater contamination.

一、微生物生态学理论与方法

微生物组学支持的土壤碳氮过程机制探讨与耦合模拟

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摘要

基于微生物休眠-激活机制，开发了耦合微生物-酶功能群的土壤生物地球化学模型 MEND（Microbial-ENzyme Decomposition），其主要特点包括：（i）考虑微生物休眠-激活机制；（ii）耦合多个酶功能组动态竞争机制的碳氮转化过程；（iii）可测量的土壤有机质库分类（颗粒态、矿物结合态、溶解态等），避免了传统土壤库（如快速、慢速、被动库等）难以实际测量的缺点;（iv）考虑土壤有机碳的物理化学保护机制（矿化物结合态；吸附-反吸附）;（v）考虑碳同位素模拟。通过模型-实验整合分析，探索了将微生物数据(尤其是微生物组学数据)与生物地球化学循环机制与模拟结合的思路和方法，通过对温带草地生态系统 7 年野外增温实验数据分析与模拟结果表明，在传统土壤呼吸数据基础上，首次采用酶/基因功能组（如氧化酶和水解酶）丰度随时间变化的趋势来约束生态系统模型中的酶动力学，能有效降低模型参数的不确定性，揭示了土壤微生物异养呼吸对增温的持续适应性机制有助于减少土壤 CO_2 排放。MEND 模型还被成功地应用于历经 12 年的 BioCON (Biodiversity, CO_2, and N deposition)草地野外试验率定和验证，表明在自然氮沉降（aN）下，酶/基因功能组对 CO_2 浓度升高的正响应高于在氮肥添加（eN）情形下的正响应，其结果与实验观测一致；并揭示 CO_2 浓度升高在低氮条件下对异养和总土壤呼吸具有更显著的影响。这些生态系统尺度的实验-模型整合研究为深入理解“气候变化-水循环-微生物调控碳氮循环”之间的关系提供了机制解释和定量描述。

关键词：微生物生态学；土壤碳氮循环；酶功能群；生物地球化学模型；耦合模拟

定量微生物个体氮素利用的方法优化与应用

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摘要

微生物是生物地球化学循环的引擎。理解和预测生物地球化学循环对人类活动和气候变化的响应需要原位定量微生物个体的功能。近年来，科学家采用定量稳定同位素探针技术（quantitative stable isotope probing, qSIP）定量微生物个体对碳和水的利用研究取得了很好的进展，但受限于 ^{15}N 标记后核酸密度变化比核酸被 ^{13}C 或 ^{18}O 标记后的密度变化小，采用 qSIP 定量微生物个体对氮素的利用难度较大。而且，这种 ^{15}N 标记后引起的核酸密度变化容易被试验误差掩盖。传统超高速离心后的密度梯度液体分层为单管逐层进行，后分层的样品密度梯度逐渐缩小，不同密度核酸沿密度梯度分开的距离逐渐缩小，特别是当离心样品较多时，实验时间延长，前后样品分离效果的差异显著增加。为此，我们设计了多通道超高速离心液体分层仪，以达到快速、同时对超高速离心后所有样品管里液体一次性进行分层的目的。运用的结果显示，该方法能消除同一批离心分层样品间由于分层时间拉长导致的实验误差，还能达到不同样品每一层密度的一致性，当固定离心结束和分层开始之间的时间，改方法还能实现不同批次离心样品之间的一致性，使 qSIP 技术标准化，便于跨实验室结果的比较。同时，我们还设计了一个离心管可以离心两个样品的方法，真正达到事半功倍，节省试验成本，提高效率。

将该方法用于研究 ^{13}C 秸秆碳利用和 ^{15}N 氮素微生物固定，我们发现微生物个体对碳和氮的利用能够得到很好定量，微生物个体对秸秆碳和土壤氮的利用均不是等同的，与其种属关系紧密联系。而且，微生物对秸秆碳和土壤氮的利用高度相关，呈现紧密的碳氮耦合关系。说明我们的方法为微生物个体氮素利用定量提供了良好的途径。

关键词：微生物个体；qSIP；稳定同位素；定量；超高速离心

预测微生物代谢相互作用的纳什均衡

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摘要

微生物代谢相互作用对生态系统、人类健康和生物技术过程产生深远影响。然而，实验上测量这些相互作用仍然是一个难题。因此构建数学模型来研究微生物间的相互作用变得至关重要。传统的生态模型通常缺乏代谢层面的具体信息，所以代谢网络模型被寄予了厚望。然而，现有用于预测微生物群落代谢的算法通常带有‘强制利他’设定的约束条件和目标函数（显性或隐性的）。这种设定会导致某些微生物在满足自身需求之前，通过输出代谢产物的方式满足其他微生物的需求，以最大化群体目标函数。纳什均衡被认为是预测微生物代谢互作的生物学第一性原理，但包含“强制利他”设定的算法所得到预测结果无法保证是纳什均衡的，导致了预测结果与实验结果相比存在巨大误差。这种‘强制利他’设定广泛存在于以往的算法中。作者开发了一个不包含‘强制利他’设定的算法，名为‘NECom’，用来预测微生物间的代谢互作。

NECom 的内层问题体现了进化的基本原理，而外层则寻找纳什均衡。作者使用 NECom 成功预测了多种经典的博弈模型，如囚徒困境、合作模型以及雪堆博弈模型。预测结果可以解释微生物有时为何不选择合作，尽管合作会带来互赢互利；为什么有些时候微生物选择分泌代谢产物，尽管这样做会消耗自身的资源；以及合作的微生物成员和不劳而获的微生物成员是如何可以共存的。随后，利用 NECom 对一个微藻-酵母混养体系进行了深入分析，结果显示 NECom 在没有特设参数和任何拟合训练下能够捕获实验数据所揭示的趋势。基于 3221 组生长速率实验数据的分析表明，对比与包含‘强制’利他约束的代表性算法 Joint-FBA 相比，NECom 对莱茵衣藻和酿酒酵母生长速率的预测误差（RSME）分别降低了 63.5%和 81.7%。最后 NECom 的预测结果阐明了衣藻-酵母系统稳定特性的形成机制，为理性设计稳定的人工菌群提供了帮助。

关键词：微生物代谢互作预测；纳什均衡；代谢网络模型；算法

网络分析解析复杂微生物群落的互作关系

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摘要

微生物群落生物多样性高，物种相互作用复杂。针对复杂微生物群落内微生物物种间的相互作用或共存模式，我们开发了微生物组学数据网络分析平台 iNAP，用于解析复杂微生物群落的物种共存及潜在的互作关系。iNAP 平台包括两套独立的分析流程，即分子生态网络分析流程 MENAP 和跨域物种生态网络分析流程 IDENAP，分别用于单一类群和两个物种类群的物种互作解析，涵盖了基于随机矩阵理论 RMT 的相关性方法、SparCC、eLSA 和 SPIEC-EASI 等多种物种互作统计方法，网络分析模块主要有分子生态网络的拓扑学属性、节点属性、模块化属性、环境因子分析和模块特征基因分析等，近期已增加 iDIRECT 和稳定性分析方法。iNAP 网络分析平台，可以分析细菌、古细菌、真菌、原生动物、植物等微生物群落内部以及跨营养级物种之间的共存关系，已得到广泛应用。（1）用于解析群落恢复力机制，发现生物膜内优势物种地杆菌与甲烷短杆菌之间的种间竞争关系，可能是影响群落恢复力的内在机制。（2）在区域尺度构建的植物-微生物的跨域生态网络，呈现高连接度、嵌套性、物种不对称性和模块化分布等网络拓朴结构属性，与特定植物（辽东栎）共存的微生物类群在多个局部的生态网络中比较一致。（3）通过构建的原核生物与原生动物丝足虫之间的共现网络结果，发现了土壤质地对于玉米根际核心微生物群落构建的重要影响。（4）利用宏基因组学数据，构建共现网络和代谢互补网络，发现热泉微生物的代谢互补潜力在高温下更强。iNAP 网络分析平台（http://mem.rcees.ac.cn:8081），免费开放注册，操作简单，无需生物信息学知识和编程技能，可以助力科研人员快速方便的完成微生物组学数据的网络分析。

关键词：微生物生态学；网络分析；网络稳定性；代谢网络

海洋微生物群落构建机制

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Abstract

Understanding and quantifying the relative importance of ecological processes that contribute to the assembly of communities across space and time are primary goals of microbial ecology. In the past few years, we revealed marine microbial community assembly with special emphasis on cell size, life strategy, metabolic activity, relative abundance, and domain-level difference. Most recently, we focused on bacterial community assembly in the Pearl River–South China Sea Continuum (PSC). Along this river–sea continuum, bacteria are directionally dispersed by water flow while being exposed to strong environmental gradients. To test the contrasting mechanisms that potentially govern metacommunity dynamics, namely homogenizing dispersal and selection, we characterized the total (16S rRNA gene) and putatively active (16S rRNA transcript) bacterial communities in the PSC, during the wet (summer) and dry (winter) seasons using high-throughput sequencing. We found that selection was more important than homogenizing dispersal in both the total and active fractions of bacterial communities. Specifically, homogeneous selection was prevalent in both total and active bacterial communities in two seasons, which was primarily due to the bacterial communities' large phylogenetic extent (associated with rarity) and our fine-spatial sampling design. In summary, our (previous plus recent) work sheds novel insights into marine microbial community assembly from multiple aspects.

Keywords: Microbial ecology; Spatial pattern; Ecological process; Community assembly

Development and application of high accuracy functional gene database

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Abstract

High throughput profiling of microbial functional traits involved in various biogeochemical cycling pathways using shotgun metagenomic sequencing has been routinely applied in microbial ecology and environmental science. Gene families of interest were extracted and analyzed based on functional profiles by searching shotgun metagenomes against public databases. However, critical issues exist in applying public databases for specific processes such as B_{12} biosynthesis pathways. We developed a curated functional gene database termed VB$_{12}$Path for accurate metagenomic profiling of B_{12} biosynthesis gene families of microbial communities in complex environments. VB$_{12}$Path contains a total of 60 B_{12} synthesis gene families, aiming to provide accurate functional and taxonomic profiles of B_{12} synthesis pathways for shotgun metagenomes and minimize false positive assignments. In addition, the performance of assembly-based (single-sample and multi-sample assembly) and read-based (merged reads and raw data) data processing approaches in data analyses and result interpretation was compared using the developed functional gene databases from both technical and biological/ecological perspectives. As a result, multi-sample assembly provided the most amount of usable information for targeted functional traits, at high cost of computational cost and running time. Single-sample assembly and read-based analysis were comparable in obtaining usable information, but the former was much more time and resource consuming. Critically, different approaches introduced much stronger variations in microbial profiles than biological differences. However, community level differences between the two sampling sites could be consistently observed despite the approaches being used. In choosing an appropriate approach, researchers shall balance the trade-offs between multiple factors, including the scientific question, the amount of usable information, computational resources, and time cost. This study is expected to provide valuable technical insights and guidelines for the various approaches used for metagenomic data analysis.

Keywords: Functional gene database; B_{12} synthesis; Metagenomic profiling; Biogeochemical cycling

复合缓释碳源材料调控奥奈达希瓦氏菌 *Shewanella oneidensis* MR-1 还原脱氯的机制研究

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摘要

氯代烯烃（Chlorinated ethenes, CEs）是地下水中常见的有机污染物，电子供体的可利用性被认为是 CEs 生物降解的关键控制因素。然而，目前很少有研究从电子转移的角度解析不同碳源材料与功能微生物还原脱氯代谢机制的适应性。本研究以天然高分子材料为原料，以纳米零价铁（Nano zero-valent-iron, nZVI）为还原剂，腐殖酸（Humic acid, HA）为电子介体构建了复合缓释碳源材料。在还原脱氯的过程中，综合评价了复合缓释碳源材料对奥奈达希瓦氏菌 *Shewanella oneidensis* MR-1（MR-1）代谢机制的影响。结果表明，在复合缓释碳源存在的情况下，超过 86.3-99.6%（500μmol）的 CEs 污染物在 60 天的试验周期内被去除。此外，nZVI 克服了大分子碳源物质水解的限速步骤，并将挥发性脂肪酸（Volatile fatty acids, VFAs）的产量提高了 2.6-7.2 倍。电子转移能力测试（Electron transfer capacity, ETC）表明，富含醌官能团的 HA 具有较强的电子接受能力，在加速电子转移方面发挥着重要作用。同时，HA 通过刺激小分子组分的产生增强了菌株 MR-1 的代谢活性，进而促进了 CEs 的还原脱氯。转录组结果表明，在复合缓释碳源材料的作用下，与脂肪酸生物合成（超过 1296%）和糖酵解/糖异生（超过 4453%）有关的关键功能基因显著上调。更重要的是，参与细胞外电子转移（Extracellular electron transfer, EET）、碳水化合物摄取和脂肪酸生物合成的关键功能酶基因在复合缓释碳源材料的作用下显著富集，证实了 MR-1 的代谢模式可以受电子供体的定向调控。这一创新发现为复合缓释碳源材料调控细菌-环境动态的相互作用提供了新的见解。

关键词：氯代烯烃；复合缓释碳源材料；奥奈达希瓦氏菌；细胞外电子转移

生物多样性对土壤生态系统功能和稳定性的影响及其机制

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摘要

在全球气候变化和生物多样性丧失的背景下，认识生物多样性与生态系统功能和稳定性的关系及其相关调控机制，有助于预测未来环境变化对生态系统及其功能的影响，制定有效的生物多样性保护策略。目前研究多重点关注地上生态系统中植物多样性与生产力及其稳定性的关系，对土壤生态系统及其功能和稳定性的研究较少。土壤微生物高度多样，是土壤生态系统重要的功能主体，并且与地上植物间存在紧密的联系。我们近期重点探究了土壤微生物群落与生态系统功能的关系，以及环境变化下地上植物多样性和丛枝菌根真菌对土壤生态系统稳定性的调控作用。相关结果揭示群落功能冗余对土壤微生物多样性与生态系统功能关系的负向调节作用，以及植物多样性和丛枝菌根真菌对土壤微生物群落干旱抗性、入侵抗性、群落恢复能力的正向调节作用，这与植物多样性和丛枝菌根真菌所调控的土壤养分含量和扰动适应性菌群的增加有关。上述研究结果对于理解土壤微生物群落与生态系统功能的关系以及土壤生态系统对环境变化的响应与调控机制具有重要科学意义。

关键词： 多样性-功能关系；地上-地下关系；群落稳定性；功能冗余；菌根真菌

全蛋白组结构预测重建古菌细菌共同祖先代谢

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摘要

以现有生命追溯并重建演化过程和早期生命形式是研究生命起源和演化的一种重要思路。通常，研究者会基于基因组比较来推测早期生命的代谢特征，但高可变的基因组往往难以清晰地揭示演化脉络和模式。本研究首次建立了基于高通量深度学习技术的全蛋白组结构预测，对深海热液来源的具有相似代谢功能和生态位的古老的超嗜热古菌和嗜热细菌的代表菌株进行研究。对序列、结构、功能三方面进行比较分析，发现蛋白的起源和演化不是孤立的而是以代谢模块为单位，并通过结构的保守性重构了古菌细菌共同祖先的保守代谢特征。出人意料的是，这些共同祖先的保守代谢模块与已实验证实的前生命化学反应高度重合，这使得由现有生命重建共同祖先的逆推过程与从非生命化学反应到生化反应的正推过程出现了交汇，侧面证明了全蛋白组结构预测获得的保守代谢模块绝非巧合。这一方法为祖先代谢重建和生命起源研究提供一种新的研究思路，展示了蛋白质结构组在研究生命起源、环境与生命协同演化中的重要应用前景。

关键词：蛋白结构组；高通量蛋白结构预测；早期生命过程；共同祖先代谢重建；微生物与环境协同演化；微生物生态

膜表面生物层形成机制与控制

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摘要

膜法水处理技术在出水水质和占地等方面有着其他传统污水处理工艺无法比拟的优势，因此，其能在全球范围内得以广泛应用。但，其也存在诸多不足，例如，膜表面生物层的形成，即膜污染，导致频繁清洗，并由此带来了运行不稳定、能耗高、膜更换等弊端，是制约其稳定运行的主要问题之一。“膜污染物来源多（生物大分子、微生物）及其动态演变（膜截留、微生物代谢与互作）”和“化学清洗与膜材料稳定之间的矛盾”是困扰膜法水处理技术运行的关键。膜污染机制不明确是限制膜污染控制以及膜工艺应用的主要瓶颈。为探明膜表面生物层的形成机制，本团队借助蛋白质组学的表征和相似性分析，明确了不同膜污染阶段中微生物胞外聚合物（EPS）和溶解性微生物产物（SMP）的贡献规律；借助纯菌分离和培养的研究方法，发现了 EPS 中的 α-1,4 糖苷键和酰胺 II 键在膜污染中的重要作用，首次明确报道了糖醛酸和 O-乙酰基对 EPS 凝胶特性及其膜污染重要性；采用生态零模型发现了膜表面生物层的组装规律，膜污染过程与微生物组装的随机性和确定性相关；进一步，通过靶向混菌实验，揭示了物种之间形成生物层的“红皇后和黑皇后”效应，阐明了菌种来源和基质浓度等对生物层中微生物相互作用的影响机制；研究发现了不同粒径污泥形成生物层的规律，这在一定程度上解释了膜污染过程中跨膜压差（TMP）跳跃这一现象。TMP 跳跃本质上是生物层内层微生物活性衰减并释放大量 EPS 和 SMP 所致。基于以上发现，本团队提出一种以低浓度营养液反洗以维持膜表面生物层活性的新方法，构建膜表面活性动态层，通过膜表面生物层的有效控制，在极大延缓膜污染的同时规避了化学清洗导致的膜破坏效应，保证了膜材料的长期稳定性。

关键词：膜污染；生物层；微生态；膜污染控制

可视化的电化学活性菌分离利用基于凝胶化电极的电化学平板

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摘要

电化学平板，将电化学培养和细菌平板分离相结合，被认为是一种有效和有前景的电化学活性菌（EAB）筛选分离技术。然而，在前期研究报道中，电化学平板的菌落形成过程缓慢且不可见，菌落观察依赖染色。为了解决这一问题，本研究设计了一种新型的凝胶化电极，实现了在电化学平板中快速形成可观察到的菌落。利用基于凝胶化电极的电化学平板，分离得到两株新的 EAB，分别为 *Pseudomonas monteilii*、*Rhodococcus qingshengii*。这两株 EAB 具有良好的正向胞外电子传递能力，能够利用短链脂肪酸和糖类产电。同时，这两株 EAB 也具有良好的反向胞外电子传递能力，能够直接利用电能还原二甲基亚砜（DMSO）、三甲基胺 N-氧化物（TMAO）和富马酸（Fumarate）。这两株 EAB 的胞外电子传递机制包括直接电子传递和间接电子传递，电子中介体的添加能够明显促进电子传递效率。本研究实现了利用电化学-平板筛选得到可见的单菌落，为筛选分离 EAB 提供了技术支撑。

关键词：电化学活性菌；电化学平板；凝胶化电极；菌株筛选；产电性能

ONT-based Metagenomic Study on High-altitude Permafrost and Glacier Aquatic Microbiome

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Abstract

We applied on-site MinION sequencing on the microbiome of high-altitude permafrost in Qilian Mountain (4000m altitude) China. ONT-based long-read metagenomics enabled an effective alternative to NGS-assembly and binning in revealing the ecological function of important microbial populations at genome-level resolution. A Frame-shift correction based ONT reads annotation tool FUNpore was developed. The post-correction long-reads showed encouraging precision and recall in functional prediction. Compared to frozen permafrost soil, the thawed soil showed higher transcriptional activity in denitrification which may lead to the discernible N_2O release in summer. In contrast methane release from thawed permafrost seems of less concern as very active aerobic methane oxidation by *Methylomonas* was observed in the topsoil and methane generation cannot be detected in batch tests with elevated temperature. Meanwhile putative human pathogens were detected in the glacier melting water indicating water safety concern for direct drink.

Keywords: Nanopore sequencing; Permafrost; metagenomics

二、微生物-环境相互作用

甲酸强化的短程反硝化-厌氧氨氧化协同脱氮

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摘要

厌氧氨氧化(Anammox)作为一种新型自养脱氮工艺，能有效降低曝气能耗及碳源，对实践污水碳中和具有重要意义。厌氧氨氧化工艺常面临出水硝氮较高的问题，而短程反硝化作用可以利用有机碳源作为电子供体消耗部分硝氮，产生的亚硝氮还可以促进厌氧氨氧化作用。目前以乙酸钠作为碳源，可以实现短程反硝化耦合厌氧氨氧化（Partial denitrification and anammox，PD-A）协同脱氮，但面临污泥产量过高，泥龄变短导致厌氧氨氧化菌加速流失的问题。有文献报道，甲酸作碳源时异养反硝化菌的细胞产率低于乙酸作碳源，同时甲酸也是厌氧氨氧化菌生长必需的中间产物。甲酸可由有机物发酵生产，是一种新型清洁可再生资源，未来作为储氢载体的应用前景广阔。因此，甲酸可能替代乙酸钠成为 PD-A 工艺更理想的碳源并得到规模化应用。

本文旨在研究甲酸作为碳源强化短程反硝化耦合厌氧氨氧化的脱氮效能、群落特征及代谢互作关系。通过运行实验室颗粒污泥厌氧氨氧化反应器，利用宏基因组学、15N 同位素示踪等手段，1）表征甲酸对短程反硝化耦合厌氧氨氧化工艺脱氮效能及污泥性状的影响；2）分析甲酸强化下短程反硝化耦合厌氧氨氧化的微生物群落演替特征；3）揭示甲酸强化下短程反硝化菌和厌氧氨氧化菌的代谢互作机制。本研究将为厌氧氨氧化工艺出水水质提升、减污降碳提供理论支撑。

关键词：短程反硝化；厌氧氨氧化；宏基因组；甲酸

微纳塑料对污泥厌氧发酵微生物组重塑机制

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摘要

在全球范围内，微塑料（MPs）在生态系统中的积累和污染引起越来越多的关注，这是由于其对水生生物和人类的不利环境影响和毒理学风险导致的。微塑料通常被定义为直径小于 5 毫米的塑料碎片。一般来说，广义的 MPs 可进一步分为纳米塑料（NPs）（<1000nm）和微米塑料（1μm-5mm）。值得注意的是，与 MPs 相比，NPs 由于其显著增强的性能、反应性和影响可能会引发更严重的环境问题。污水处理厂是天然环境中微塑料的重要来源。值得注意的是，废水中超过 98%的微塑料被截留在废弃活性污泥（WAS）中，而并非直接排放至水生生态系统。因此，WAS 中的微塑料污染及其潜在的生态健康风险是迫切需要解决的问题。厌氧消化（AD）由于其成本效益高及能量的可回收性被认为是最有效的污泥处理方法之一。多项研究表明，污泥中聚乙烯（polyethylene, PE）、聚对苯二甲酸乙二醇酯（polyethylene terephthalate, PET）和聚氯乙烯（polyvinyl chloride, PVC）MPs 的存在通过释放有毒化学污染物或诱导的不平衡的氧化应激反应对污泥 AD 关键微生物产生有害影响，从而抑制污泥的发酵性能，尤其会抑制甲烷的产生。研究表明 MPs 对微藻生长抑制、基因表达、光合作用和氧化应激的影响可能与 MPs 的大小、表面特征、浓度甚至暴露时间有关。在污泥的 AD 期间，NPs 对微生物的毒性作用机制尚不清楚。因此，本研究综合性地评价了 PSNPs 对污泥 AD 性能的影响。

关键词：微塑料；纳米塑料；污泥；厌氧发酵；基因芯片

Polystyrene Nanoplastics Shape Microbiome and Functional Metabolism in Anaerobic Digestion

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Abstract

Nanoplastics (NPs) and microplastics (MPs) are ubiquitous in the natural environment, social production, and life. However, our understanding of the effects of NPs and MPs on shaping the microbiome and functional metabolism of anaerobic microorganisms is limited. We investigated the response of core microbiomes and functional genes to polystyrene (PS) NPs and MPs exposure in a representative anaerobic micro-ecosystem of waste activated sludge. Independent anaerobic digestion (AD) experiment indicated that PS nanobeads suppressed acidogenesis by inhibiting the activity of acetate kinase, and subsequently reduced methane production. Our findings confirmed that MPs (1 and 10 μm) had no perceptible effect on methane production, yet 50 nm NPs resulted in a 15.5% decrease in methane yield, perhaps driven by the behavior of dominant genera *Sulfurovum*, *Candidatus* Methanofastidiosum, and *Methanobacterium*. Assays revealed that NPs contributed to the simplest network assemblies in bacterial communities, contrary to empirical networks in archaeal communities.

Keywords: Microplastics; Anaerobic microorganisms; Methanogenesis; Waste activated sludge; Community network

抗氧化节杆菌 QL17 应对氧化胁迫的防御机制研究

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摘要

强辐射地区的土壤，在阳光辐照时会产生大量活性氧类自由基，对生存于其中的微生物形成高强度氧化胁迫，使得生存于其中的微生物体内积累大量的超氧离子或过氧化物，抑制其生长或直接造成其死亡。因此，强辐射环境下的微生物大多具有较强的抗氧化能力，这类微生物可能具有特殊的氧化胁迫防御机制。东绒布冰川位于珠穆朗玛峰北坡海拔 6300m 处，由于该地区海拔高、空气稀薄、大气洁净以及地理纬度低等独特的自然地理条件使该地区形成强氧化环境，蕴藏着丰富的菌种资源，是研究生物体对极端环境适应性的重要场所。因此，通过对该生境中微生物的氧化胁迫防御机制研究，可为冰川地区抗氧化资源的开发以及氧化损伤的抗性修复资源提供科学依据和理论支持。本研究从珠穆朗玛峰北坡东绒布冰川冰碛物中筛选分离得到了 1 株能够分泌胞外水溶性蓝色素的节杆菌属新种——抗氧化节杆菌 QL17（*Arthrobacter antioxidans* QL17）。研究发现，该菌株对 H_2O_2 具有很强的耐受性，最高能够耐受 400 mM H_2O_2 溶液（存活率为 71.5%）。对抗氧化节杆菌 QL17 进一步通过重离子束诱变得到了蓝色素产量有显著差异的 2 个突变株（M157 和 M186），其中 M157 的蓝色素产量是野生型菌株的 1.46 倍，而 M186 丧失了蓝色素的产生能力。通过对野生型菌株和突变株的 H_2O_2 耐受性实验分析发现，野生型菌株及其突变株对 H_2O_2 的耐受性具有显著性差异，其中 M157、wt 和 M186 对 H_2O_2 的最高耐受能力分别为 600mM、400mM、300mM。进一步通过全基因组和转录组联合分析，在菌株 QL17 中注释到了 1 条非核糖体肽生物合成基因簇（cluster7），该基因簇中所涉及的 27 个基因中有 18 个基因在菌株 QL17、M157 以及 M186 的表达量有显著性差异，而该基因簇中的非核糖体肽关键合成酶基因 gene3529 是菌株 QL17 特有的。研究结果表明，菌株 QL17 的产蓝色素能力增强了该菌株的抗氧化能力，推测 cluster7 基因簇负责菌株 QL17 蓝色素的生物合成。

关键词：东绒布冰川；冰碛物；抗氧化节杆菌；重离子束诱变；天然蓝色素

湿地芦苇根际锰氧化物与微生物的相互作用及其净水机制

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摘要

污染去除是湿地的重要生态功能之一。芦苇作为常见的湿地植物，广泛应用于人工湿地污水尾水处理系统中，其根际微生物以及生物锰氧化物（BMO）在污染去除过程中扮演着重要角色。但是 BMO 在芦苇根际中的富集情况及其对根际微生物群落结构和功能的影响，尤其对污染降解相关功能影响，尚缺乏深入探究。本论文以湿地植物芦苇根际 BMO 为研究对象，涉及自然湿地和人工湿地，结合工程实际和实验室实验，研究 BMO 与湿地微生物群落的相互作用及其对净水效能的提升。

本研究首先通过对全国范围内 17 块代表性自然湿地进行采样分析，结果表明，相较于非根际，芦苇根际能够富集 1.012～10.54 倍的锰氧化物；通过宏基因组测序，发现芦苇根际能够富集特定类型的锰氧化菌，如含有锰氧化基因 cueO 的 Enterobacteriaceae；冗余分析显示，芦苇根际富集的锰氧化物可解释 5.28%的微生物群落结构差异，其中，通过解析与锰氧化物含量具有显著相关性的根际核心微生物的功能发现，芦苇根际的锰氧化物具有增强土壤碳氮循环和降低健康风险的潜在生态功能；对 6 块长期稳定运行的人工湿地的分析显示，锰氧化物作为微生物结构和功能的重要环境驱动因子，其含量与氨氧化菌丰度之间存在显著线性相关性（$R = 0.61$），同时锰氧化菌与完全氨氧化菌（Comammox Nitrospira）之间也具有潜在的共存关系。为了验证相关性结论在实际工程中的应用可行性，搭建填加锰砂的中试人工湿地，并在一年的连续监测中观测到锰砂能提升平均 23.34%的氨氮去除率并显著富集氨氧化功能基因 amoA；通过识别在锰强化型人工湿地显著富集的微生物，发现部分微生物具有降解微量有机污染物的潜能。搭建实验室规模的人工湿地探究填加锰砂对微量有机污染物生物转化过程的影响，结果表明，人工湿地中填加锰砂能够分别提升阿替洛尔、阿特拉津和磺胺甲恶唑 13.16%、8.48%和 6.27%的平均去除率。进一步结合宏基因组测序和微量有机污染物中间产物测定，发现填加锰砂的人工湿地可以有效强化这三种微量有机物污染物的生物降解，并且这些具有微量有机污染物降解功能的微生物广泛存在于实际工程人工湿地中。

关键词：湿地；芦苇；锰氧化物；宏基因组；生物强化

Electric-Inducive Microbial Interactions in a Thermophilic Anaerobic Digester Revealed by High-Throughput Sequencing of Micron-Scale Single Flocs

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摘要

尽管导电材料已被证明能够通过改变微生物间的相互作用来提高厌氧消化(AD)的效率，但在高温条件下的相互作用关系尚未被研究。为了确定高温厌氧消化(TAD)微生物组中真正的物种-物种之间的关联，以及揭示碳布(CC)添加的影响，我们从实验室规模的高温厌氧消化反应器中随机分离了微米级(40-70μm)的单颗粒。结果表明，添加碳布不仅显著提高了甲烷产量，还增加了基质中群落的空间异质性。加入碳布后，Pseudomonadaceae 明显从基质向生物膜转移，表现出显著的生物膜形成能力。此外，Clostridium 和 Thermotogaceae 在 TAD 菌群的基质和生物膜中紧密聚集并稳定共存，这可能与它们独特的胞外糖代谢方式有关。最后，还发现了 Syntrophomonas 与反硝化菌 Rhodocyclaceae 之间的相互作用，在这些物种的细胞膜上，呼吸相关电子转移基因(cystic-c, complex III)的上调表明了反硝化途径与通过直接种间电子转移(DIET)的乙酸盐氧化的潜在耦合。这些发现为导电材料如何促进高温消化性能提供了见解，并为改善生物处理系统的群落监测开辟了道路。

关键词：厌氧消化；高温；微米尺度；碳布；微生物互作

Rhizosphere soil bacterial and fungal communities vary with soil properties and plant functional traits in an alpine grassland

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Abstract

Rhizosphere soil contain tens of thousands of microorganisms that are critical to plant growth and health. Both plant functional traits and soil properties influence the composition and structure of rhizosphere soil microbial communities. However, we still known little about their importance in explaining the composition and structure of rhizosphere microbiome, especially in natural grassland ecosystems. Here, we explored how plant functional traits and soil properties influence plant rhizosphere soil bacterial and fungal communities in an alpine grassland from Hebei Province, China. We found that soil water content (SWC) was the main soil property affecting rhizosphere soil bacterial and fungal diversity. The distance-based redundancy analysis of the forward-selected plant functional traits and soil properties variables explained almost 20% and 21% of the variation in the composition of bacterial and fungal communities. Plant functional traits (percent of R^2 explained: 56%) contribute more to variation in bacterial community composition than soil properties (percent of R^2 explained: 44%), and soil properties (percent of R^2 explained: 67%) contribute more to variation in fungal community composition than plant functional traits (percent of R^2 explained: 33%). SWC and root depth were the strongest soil properties and plant functional traits that restricted the composition of bacterial and fungal communities, respectively. These results suggested that soil properties and plant functional traits have differently importance in shaping rhizosphere soil bacterial and fungal communities.

Keywords: Alpine grassland; Community composition; Microbial diversity; Plant functional traits; Rhizosphere soil; Soil properties

光催化耦合厌氧氨氧化强化脱氮及基于 cbb3 型细胞色素 c 氧化酶的厌氧氨氧化菌有氧呼吸模式

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摘要

本研究通过耦合光催化剂 g-C_3N_4 纳米颗粒，创新性在厌氧氨氧化体系中引入光生电子。耦合体系实现了 94.25%的高脱氮效率，这突破了厌氧氨氧化化学计量所规定的 89%的生化极限。光生电子通过强化关键酶（NIR、HZS 和 WLP 相关蛋白）来促进 anammox 代谢活性，并增强藻类卡尔文循环以触发藻类快速富集，从而形成厌氧氨氧化-藻类协同的多途径脱氮过程。更为重要地是，本研究首次发现并报道了 cbb3 型细胞色素 c 氧化酶在 anammox 菌中的同源表达，这赋予其有氧呼吸能力，并使它们成为藻类光合放氧下高 DO 环境（7.9-19.8mg/L）中的主要耗氧者。此外，光生电子选择性地将 cb1 复合物和 cbb3 型细胞色素 c 氧化酶作为激活位点，同时调动 RegA/B 调节系统以激活 cbb3 型细胞色素 c 氧化酶的表达。cbb3 型细胞色素 c 氧化酶大量消耗胞内活性氧合成底物（氧气）从而阻断厌氧氨氧化中的氧化应激现象，这优化了厌氧氨氧化细菌的环境敏感性并保持其高代谢活性。本研究扩展了对厌氧氨氧化细菌生理特性的理解，并为应用太阳能增强废水处理开辟道路。

关键词：厌氧氨氧化；光生电子；强化脱氮；太阳能；多组学技术

Experimental evolution reveals environmental stress adaptation mechanisms in bacteria

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Abstract

Microbial experimental evolution uses background-known microorganisms to understand evolutionary adaptation and underlying mechanisms with microbial populations and communities, bringing a great power and precision to study microbial ecology and evolutionary biology. We evolved model sulfate-reducing bacteria (*Desulfovibrio vulgaris* Hildenborough, DvH) and synthetic denitrification *Shewanella* communities (SDCs) under nitrate stress to explore the stress adaptation mechanisms. Nitrate-evolved (EN) DvH populations and SDCs increased nitrate tolerance. For EN DvH populations, whole genome resequencing identified 109 new mutations in 44 genes of 12 evolved populations, among which six functional gene groups were discovered with high mutation frequencies at the population level. We observed a high frequency of nonsense or frameshift mutations in nitrosative stress response genes (DVU2543, DVU2547 and DVU2548), nitrogen regulatory protein C family genes

(DVU2394-2396, DVU2402 and DVU2405), and nitrate cluster (DVU0246-0249 and DVU0251). Mutations in those gene groups could increase nitrate tolerance through regulating energy metabolism, barring entry of nitrate into cells, altering cell membrane characteristics or conferring growth advantages at the stationary phase. For EN SDCs, microbial richness had a significantly positive ($p < 0.05$) correlation with functions, while such relationships were dynamic as they were significantly positive at early stages, of the experimental evolution, and became insignificant ($p > 0.05$) at later stages. Also, we found that SDCs functions generally increased along the experimental evolution, but the community function increased more at a low richness level than at a high richness level. Further analysis of biodiversity effects revealed that low-richness SDCs became more complementary than high-richness SDCs as they evolved, thus positive BEF relationships could be largely attributed to complementary effects. This study advances our understanding of environmental stress adaptation in microbial systems, providing important implications for linking genotypes with phenotypes in microorganisms and biodiversity protection.

Keywords: Experimental evolution; Sulfate-reducing bacteria; Synthetic denitrification *Shewanella* community; Environmental stress

Long-term elevated precipitation induces grassland soil carbon loss via microbe-plant–soil interplay

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Abstract

Global climate models predict that the frequency and intensity of precipitation events will increase in many regions across the world. However, the biosphere-climate feedback to elevated precipitation (eP) remains elusive. Here, we report a study on one of the longest field experiments assessing the effects of eP, alone or in combination with other climate change drivers such as elevated CO_2 (eCO_2), warming and nitrogen deposition. Soil total carbon (C) decreased after a decade of eP treatment, while plant root production decreased after 2 years. To explain this asynchrony, we found that the relative abundances of fungal genes associated with chitin and protein degradation increased and were positively correlated with bacteriophage genes, suggesting a potential viral shunt in C degradation. In addition, eP increased the relative abundances of microbial stress tolerance genes, which are essential for coping with environmental stressors. Microbial responses to eP were phylogenetically conserved. The effects of eP on soil total C, root production, and microbes were interactively affected by eCO_2. Collectively, we demonstrate that long-term eP induces soil C loss, owing to changes in microbial community composition, functional traits, root production, and soil moisture. Our study unveils an important, previously unknown biosphere-climate feedback in Mediterranean-type water-limited ecosystems, namely how eP induces soil C loss via microbe-plant–soil interplay.

Keywords: Elevated precipitation; Microbial functional trait; Resource acquisition; Soil carbon loss; Viral shunt

Mechanistic insight into reductive dechlorination in *Shewanella oneidensis* MR-1 assisted by physiological suitability electron donor

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Abstract

The research into the biostimulation of reductive dehalogenation has already made significant progress. However, few studies have attempted to determine whether additional carbon source materials match the metabolic mechanism of functional microorganisms, particularly from the perspective of electron transfer chain. In the present study, the effectiveness of bioreactive carbon source materials coupled with metabolic mode of *Shewanella oneidensis* MR-1 (MR-1) was comprehensively evaluated in the reductive dechlorination using natural polymer materials as feedstock. The results showed that humic acid (HA) can promote the reductive dechlorination of chlorinated ethenes (CEs) by increasing the content of propionic acid in volatile fatty acids (VFAs) with slowly generate electrons. The addition of nanoscale zero-valent iron (nZVI) overcome the hydrolysis limiting-rate step of macromolecular substances and improved the meanwhile VFAs production. Transcriptome analysis revealed that the key functional enzymes genes of extracellular electron transfer (EET) transmission, carbohydrate uptake and fatty acid biosynthesis, was significantly enriched under the action of carbon source materials, confirmed that the metabolic mode of MR-1 can be directionally regulated by electron donors. Moreover, the high expression of malate synthase genes resulting in significant differences in tetrachloroethylene (PCE) and trichloroethylene (TCE) degradation efficiencies. Electron transfer capacity (ETC) revealed that the HA rich in quinones functional groups plays an important role to accelerated the transfer of electrons by having strong electronic acceptance. This innovative discovery can be used to facilitate a predictive understanding of halide-bioremediation at contaminated sites.

Keywords: Natural polymer materials; Chlorinated ethenes; *Shewanella oneidensis* MR-1; Reductive dichlorination; Electron transfer chain

切萨皮克湾微生物群落对养分输入的响应

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摘要

频繁人类活动导致的养分积累对海湾生态系统的功能具有显著影响。分布广泛、功能多样、适应性强并对环境变化敏感的微生物群落是反映海湾生态功能的重要指标。以切萨皮克湾（美国第一大海湾）为研究对象，本研究探索了养分积累对微生物群落的生态效应及其潜在驱动因素。随机森林模型表明干流潮汐区（重要得分均值：0.94）是研究微生物群落对养分输入响应的理想区域；分子生态网络表明 Proteobacteria、Actinobacteriota、Cyanobacteria、Bacteroidota、Planctomycetota、Errucomicrobiota 和 Bdellovibrionota 等优势门类（4.62–15.80%）是微生物群落生态网络中的关键类群（度≤8）。零模型（β_{NTI}：-11.05–15.27，R_{Cbray}：-0.75–1）和 Sloan 模型（R^2：0.77、迁移率：0.02）表明随机过程在群落组装中发挥着重要作用。基于抗性基因和毒力因子的投影寻踪回归模型表明干流中游水质造成的潜在生态风险较高（投影≤32）。梯度提升回归模型表明硝酸氮、亚硝酸氮、正磷酸盐、透明度、盐度和温度是影响微生物群落的关键环境因子（重要得分≥2.5）。自 1984 年到 2022 年间，切萨皮克湾的养分表现出显著的空间差异（Z 得分：0.67–43.09，P＜0.05），硫酸盐（平均值±标准差：195.3±266.4mg L^{-1}）是主要的养分。Mann-Kendall 趋势检验检测到亚硝酸盐、溶解有机氮和总氮等养分浓度随时间的显著增加（斜率>0，P<0.05）。源解析表明，在过去的 38 年里，与人类活动相关的养分输入源（如化肥使用和污水排放）对养分积累的贡献显著增加（非潮汐区：61.90–85.08%，潮汐区：85.38–95.56%）。综上，频繁的人类活动促进了切萨皮克湾养分积累的时空动态演变，导致切萨皮克湾水质显著变化，并影响微生物群落的多样性、组装和功能。本研究为海湾生态系统的生态建设和可持续发展提供了科学依据。

关键词：微生物群落；养分积累；源解析；海湾生态系统

长期土壤增温增加了 K-策略微生物的比例并提高了微生物的碳分解潜力

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摘要

土壤微生物是调节陆地碳循环的基础。气候变暖对土壤微生物群落的干扰可能会对陆地生态系统碳循环产生重要影响。然而，长期变暖对亚热带森林土壤微生物群落的影响和微生物介导的碳损失仍不清楚。我们在亚热带森林地区开展了一项为期 7 年的野外土壤增温实验，研究增温对土壤微生物群落结构、碳循环相关代谢功能和微生物呼吸速率的影响。结果表明，细菌和真菌群落的 α-多样性在土壤增温 2°C 和 5°C 时 C 尤其是（增温 5°C）显著下降。增温下微生物 K-策略者与 r-策略者的比例显著增加，表明长期土壤增温增强了 K-策略微生物的优势地位。此外，长期增温还增加了碳循环相关基因（如碳降解）的相对丰度和酶活性，这两者都与 K-策略微生物与 r-策略微生物的比例呈显著正相关。长期土壤增温下这些群落策略和代谢功能的变化使微生物的碳分解潜力增强，从而解释了 2°C 和 5°C 增温后土壤有机碳的显著降低（9%-18%）和土壤微生物呼吸速率的显著增加（31%-58%）。这些结果为长期变暖对亚热带森林土壤微生物群落变化和微生物介导的土壤碳反应过程的影响提供了预测性理解。

关键词：土壤增温；微生物群落；K-策略者；碳分解；微生物呼吸

Methane supply drives prokaryotic community assembly and networks at cold seeps of the South China Sea

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Abstract

Marine cold seeps are unique chemosynthetic habitats fueled by deeply sourced hydrocarbonrich fluids discharged at the seafloor. Through oxidizing methane and other hydrocarbons, microorganisms inhabiting cold seeps supply subsurface-derived energy to higher trophic levels, sustaining highly productive oases of life in the deep sea. Despite the central role of microbiota in mediating biogeochemical cycles, factors that govern the assembly and network of prokaryotic communities in cold seeps remain poorly understood. Here we analyzed geochemical and microbiological profiles of 11 different sediment cores from two spatially distant cold seeps of the South China Sea. We show that prokaryotic communities belonging to the same methane supply regimes (high-methane-supply, low-methane-supply, and nonseep sediments) had a highly similar community structure, regardless of geographical location, seep-associated biota (mussel, clam, microbial mat), and sediment depth. Methane supply appeared to drive the niche partitioning of anaerobic methanotrophic archaea (ANME) at the regional scale, with ANME-1 accounting for >60% sequence abundance of ANME in the high-methane-supply sediments, while ANME-2 dominated (>90%) the low-methanesupply sediments. Increasing methane supply enhanced the contribution of environmental selection but lessened the contributions of dispersal limitation and drift to overall community assembly. High-methane-supply, moreover, promoted a more tightly connected, positive correlations dominated, and less stable prokaryotic network. Together these results provide a potential new framework for understanding the niches and network interplays of prokaryotic communities across different methane seepage regimes in cold-seep sediments.

Keywords: Cold seeps; Community assembly; Marine sediments; Methane supply; Methanotrophic microbiome; Network

三、微生物与宿主相互作用

肠道微生物-鱼类-环境互作机制

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摘要

脊椎动物从水生到陆生进化是生命演化史上一次质的飞跃，其“登陆”事件发生在硬骨鱼类。然而，鱼类成功“登陆”并非独立完成，因为任何一个动物个体都是与其共生微生物组成的“共生功能体”，其基因组既包括动物基因组，也包括与动物共生微生物的基因组，总称为“全基因组”。动物基因组比较保守，所以进化通常很缓慢；而微生物基因组能很快适应环境而改变。有研究表明，核心肠道微生物能在动物体内延续成百上千代，其基因组的快速演变可能帮助“共生功能体”适应环境变化，为动物基因组进化争取必要时间。因此，动物成功从水生到陆生进化离不开共进化的肠道微生物。然而，肠道微生物与动物的协同进化机制仍不清楚，这方面研究的主要困难在于动物(尤其是鱼类)多样性高，生活在同一环境的各种动物肠道微生物进入环境后相互之间，以及与动物和环境间互作关系错综复杂。因此，解析“肠道微生物-动物-环境”互作是揭示肠道微生物和动物协同进化机制的关键。我们以脊椎动物中从水生到陆生进化过程扮演最为关键“登陆”角色的硬骨鱼类为研究对象，围绕“肠道微生物-鱼类-环境”互作机制和在共进化过程的耦合效应进行了一系列研究。取得的主要成果包括：(1)提出以鱼类肠道为“岛屿”模型，揭示了肠道微生物形成和演替规律，发现肠道微生物主要受宿主发育影响，决定性过程贡献随发育减弱，但稳定性随宿主发育增强；(2)解析了肠道微生物对鱼类关键功能的调节途径，发现肠道微生物通过脂多糖途径加重草鱼炎症反应；并率先基于宏基因组构建了草鱼肠道微生物代谢通路；(3)阐明了肠道微生物-鱼类-环境以关键生源要素循环为核心的互作，发现养殖生态系统微型生物、鱼类、环境间若干耦合效应和调控机制。这不仅为揭示动物演化规律和多样性维持机制提供了新依据，还为动物适应未来变化的演变提供重要启示。

关键词： 鱼类；肠道微生物；共进化；环境调控；互作机制

海洋细菌与典型海洋无脊椎动物附着互作研究

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摘要

在海洋生态系统中，许多海洋无脊椎动物都具有浮游—底栖生活阶段，浮游幼虫的附着是其生活史的关键一环，其附着的成功与否直接决定着生活史能否顺利完成。海洋环境中，海洋微生物被膜广泛存在于水下基质表面，是海洋细菌在海洋各种生境存在的主要方式，有效介导诸多海洋无脊椎动物幼虫附着过程。尽管这种现象在海洋中广泛存在，但对其机制知之甚少。我们以典型海洋无脊椎动物贻贝为研究对象，查明了浅海和深海等不同生境海洋细菌对幼虫附着的诱导作用，提取和纯化了介导幼虫附着的细菌胞外多糖、胞外脂类、胞外蛋白等化学信号物质，开展了胞外多糖、胞外脂类、胞外蛋白等生物合成途径的解析，提出了细菌的酪氨酸代谢、胞外多糖、脂类以及胞外蛋白途径调控贻贝幼虫附着模型，确定了海洋细菌通过第二信使 c-di-GMP 在贻贝幼虫附着过程中的关键作用。我们的研究结果为海洋细菌调控海洋无脊椎动物幼虫附着机制解析提供新的思路。

关键词：海洋无脊椎动物；海洋化学生态学；海洋细菌；幼虫附着；天然化学信号

人工湿地对昼夜交替及根系泌氧的响应：性能和微生物机制

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摘要

人工湿地作为一种基于自然的污水处理系统，与自然环境保持着物质和能量的持续交换。根际是根系周围的动态区域，是研究植物与根际微生物相互作用的关键界面。光照条件可驱动植物生长和微生物代谢活性发生节律性变化，调控植物和微生物之间的相互作用，进而影响人工湿地的污染物处理效能。因此，探究植物和微生物相互作用对光照的响应机制将有助于加深根际在污染物去除中的作用的认识。本研究探究了昼夜交替对人工湿地根际微生物群落的影响。结果表明，在人工湿地稳定运行时，其内部环境存在动态交替机制，本研究显示的核心微生物群落、微生物代谢活性和污染物去除的节律性变化验证了这一机制。结果表明，微生物对污染物的去除(如总氮)在白天条件下比在夜间条件下高 1.31 倍。随着昼夜节律进化的根际核心微生物类群(如 *Chloroflexus* 和 *Beijerinckia*)主要与碳、氮、磷和能量代谢有关，夜间平均相对丰度较低。尽管白天也观察到较高的微生物代谢活性，但夜间条件下与碳和氮代谢功能相关的基因水平较高。结构方程模型 (SEM) 分析进一步表明，环境因素在驱动微生物去除污染物过程中具有显著影响，微生物群落在夜间对污染物去除的促进作用大于白天。此外，植物与微生物之间复杂的相互作用构成了人工湿地去除污染物的基础。植物通过光合作用向根际分泌氧气，根系泌氧(ROL)对功能微生物的活性和丰度起着关键作用。然而，垂直空间尺度下 ROL 对微生物群落生态位分化的影响却鲜有研究。本研究结果表明，ROL 随深度降低，促进了根际微生态系统的氧化还原。上层高水平的 ROL 可支持好氧菌(*Haliangium*)的供氧，促进 COD(60%)和 NH_4^+-N(50%)的去除，而下层反硝化菌(如 *Hydrogenophaga* 和 *Ralstonia*)和甲烷氧化菌(*Methanobaterium*)的富集可促进反硝化作用。功能预测结果进一步证实，在根际氧浓度梯度的作用下，根际中催化硝化和反硝化过程的基因丰度分别在上层和底

层显著增强。这将有助于进一步揭示根际效应，提高对人工湿地污染物去除机制的认识。综上所述，本研究可为人工湿地中植物与微生物的相互作用提供见解，并为人工湿地的设计和运行提供科学的指导。

关键词：人工湿地；昼夜交替；根系泌氧；污染物去除；微生物群落

微生物介导的气生根-黏液固氮功能与稳态维持机制

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摘要

微生物可以直接或间接与植物互作以促进宿主植物的生长和胁迫耐受力，这些微生物统称为植物微生物组（也被称为植物的第二基因组）。虽然学界已经认识到这些微生物塑造了宿主植物的个体性状和适应性，但它们如何发挥功能并维持其内部稳态在很大程度上未被探索。我们以蔓性野牡丹(*Heterotis rotundifolia*)为研究对象，明确了微生物组介导的气生根-黏液微环境的固氮功能及其稳态维持机制。我们发现气生根黏液富含各类初级代谢物（如碳水化合物）和高丰度固氮细菌，氮同位素标记实验、15N 自然丰度和植物基因表达分析表明：气生根黏液中细菌可以固定空气中氮素并促进植物生长（生物固氮量高达 54.8%）。我们进一步在黏液中发现了一种被宿主“招募”的“友好”真菌 F-XTBG8(*Chaetomella raphigera)*能够维持黏液微生物稳态。该菌具有广谱的抗菌活性，抑制环境中的微生物但选择性地允许固氮菌生长。本研究发现了气生根-黏液的固氮功能和关键的“友好”真菌，为根系生物学功能和微生境稳态维持提供了新的见解。

关键词：根际生态；微生物稳态维持；固氮菌；黏液微环境；友好真菌

Microbiota-mediated nitrogen fixation and microhabitat homeostasis in aerial root-mucilage

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Abstract

Plants sustain intimate relationships with diverse microbes. Though it is well-recognized that these plant-associated microbiota shape individual performance and fitness of host plants, but much remains to be explored regarding how they exert their function and maintain their homeostasis. Here, using pink lady (*Heterotis rotundifolia*) as a study plant, we investigated the phenomenon of microbiota-mediated nitrogen fixation, and elucidated how this process is steadily maintained in the root mucilage microhabitat. Metabolite and microbiota profiling showed that the aerial root mucilage is enriched in carbohydrates and diazotrophic bacteria. Nitrogen isotope-labelling experiments, 15N natural abundance and gene expression analysis indicated that the aerial root-mucilage microbiota could fix atmospheric nitrogen to support plant growth. While the aerial root mucilage is a hotspot of nutrients, we did not observe high abundance of other environmental and pathogenic microbes inside. We further identified a fungus isolate in mucilage that has shown broad-spectrum antimicrobial activities, but solely allows the growth of diazotrophic bacteria. This “friendly” fungus may be the key driver to maintain nitrogen fixation function in the mucilage microhabitat. The discovery of new biological function and mucilage-habitat “friendly” fungi provides insights into microbial homeostasis maintenance of microenvironmental function and rhizosphere ecology.

Keywords: Rhizosphere ecology; Mucilage microhabitat; Diazotroph; Friendly microbe; Microbial homeostasis

Differentiated responses of the phyllosphere microbiome of the yellowhorn tree to precipitation and temperature regimes across Northern China

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Abstract

As an ephemeral and oligotrophic environment, the phyllosphere harbors many highly diverse microorganisms. Importantly, it is known that their colonization of plant leaf surfaces is considerably influenced by a few abiotic factors related to climatic conditions. Yet how the dynamics of phyllosphere microbiome assembly are shaped by detailed climatological elements, such as various bioclimatic variables, remains poorly understood. Using high-throughput 16S rRNA gene amplicon sequencing technology, we analyzed the bacterial communities inhabiting the leaf surfaces of an oilseed tree, yellowhorn (*Xanthoceras sorbifolium*), grown at four sites (Yinchuan, Otogqianqi, Tongliao, and Zhangwu) whose climatic status differs in northern China. We found that the yellowhorn phyllosphere's bacterial community was generally dominated by four phyla: Proteobacteria, Firmicutes, Actinobacteria, and Bacteroidetes. Nevertheless, bacterial community composition differed significantly among the four sampled site regions, indicating the possible impact of climatological factors upon the phyllosphere microbiome. Interestingly, we also noted that the α-diversities of phyllosphere microbiota showed strong positive or negative correlation with 13 bioclimatic factors (including 7 precipitation factors and 6 temperature factors). Furthermore, the relative abundances of 55 amplicon sequence variants (ASVs), including three ASVs representing two keystone taxa (the genera *Curtobacteriu*m and *Streptomyces*), exhibited significant yet contrary responses to the precipitation and temperature climatic variables. That pattern was consistent with all ASVs' trends of possessing opposite correlations to those two parameter classes. In addition, the total number of links and nodes, which conveys community network complexity, increased with rising values of most temperature variables. Besides that, stronger positive associations were found between average clustering coefficient and most precipitation variables. Altogether, these results suggest the yellowhorn phyllosphere microbiome is capable of responding to variation in rainfall and temperature regimes in distinctive ways. Our findings provide detailed information regarding how the structure of yellowhorn phyllosphere microbiota is possibly regulated by precipitation as well as temperature in tandem, which could elucidate the role played by climate in microbiome assembly on plant leaf surfaces.

Keywords: Yellowhorn; Phyllosphere microbiome; Climate factors; Community composition, Microbial networks; Keystone taxa

根际噬菌体-宿主病原菌互作驱动作物健康

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摘要

由土传病原菌引起的土壤生物障碍不仅导致粮食减产，还因病原菌携带高风险的抗生素抗性基因而威胁一体化健康（One health），成为农业、环境和公共卫生领域共同关注的问题。滥用农药和抗生素所带来的病原菌耐药性、土壤微生态失衡等环境健康风险加剧成为国际共识，亟需建立阻控土壤病原菌的新理论和新技术。如何生态靶向消减土壤病原菌，修复和提升土壤生态系统功能，是环境地球科学领域的国际前沿热点和国家重大战略需求。噬菌体是地球上丰度最高、种类最多的专性侵染细菌/古菌的病毒，其通过特异性与宿主细菌互作在调节地球生态系统物质循环和能量流动等方面发挥关键作用。因具有靶向性强、裂解效率高、对环境微生态扰动小等优势。以土壤青枯菌生物障碍为对象，基于宏基因组测序，解析了根际噬菌体组-病原青枯菌互作特征，并建立了全国青枯菌专性噬菌体资源库；从生态进化学角度阐明噬菌体侵染削弱宿主病原菌竞争致病能力、定向调控根际微生态的作用机制；最后提出通过优化噬菌体施用方法，提升噬菌体消减土壤生物障碍效率的策略，相关研究为建立完善噬菌体靶向消减土壤生物障碍的微生态疗法提供了理论和技术体系。

关键词：微生物生态学；噬菌体；病原菌；实验进化学；权衡

Rhizosphere Bacteriophage-Host Pathogen Interactions Drive Crop Health

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Abstract

The soil-borne disease not only leads to reduced crop yields but also pose a threat to the One Health, becoming a shared concern in the fields of agriculture, environment, and public health. The escalating environmental health risks such as pathogen resistance and soil microecological imbalance resulting from the misuse of pesticides and antibiotics have become an international consensus, necessitating the establishment of new theories and technologies to control soil-borne pathogens. The ecological targeting and reduction of soil-borne pathogens, as well as the restoration and enhancement of soil ecosystem functions, have become the forefront of research in the field of environmental earth sciences and a major strategic requirement for the country. Bacteriophages, viruses that infect and replicate within bacteria and archaea, are the most abundant and diverse group of specialized viruses on Earth. They play a critical role in regulating material cycles and energy flow in the Earth's ecosystems through specific interactions with their bacterial hosts. Bacteriophages have advantages such as strong targeting, high lytic efficiency, and minimal disturbance to environmental microecology. In this study, using metagenomic sequencing, the interaction characteristics between the rhizosphere bacteriophage community and the pathogenic bacteria of bacterial wilt were analyzed, and a national bacteriophage resource library for *Ralstonia solanacearum* was established. The study elucidated the mechanisms by which bacteriophage infection weakens the competitive and pathogenic abilities of the host pathogenic bacteria and selectively regulates rhizosphere microecology from an ecological evolutionary perspective. Finally, strategies to enhance the efficiency of bacteriophage-mediated reduction of soil-borne pathogens were proposed through optimizing bacteriophage application methods. This research provides a theoretical and technical framework for the establishment and improvement of bacteriophage-based targeted therapies for soil-borne pathogens.

Keywords: Microbial ecology; Bacteriophages; Pathogen; Experimental evolution; Trade-offs

文蛤体内弧菌与共生菌群互作关系及其抗性演化规律研究

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摘要

文蛤是我国沿海滩涂养殖的重要经济贝类，然而弧菌性疾病作为最为常见并且导致文蛤死亡最为严重的疾病之一，已成为制约文蛤养殖产业发展的瓶颈问题之一。因此，探究文蛤弧菌病的流行暴发机制是病害防治的关键。本研究采用高通量测序方法对文蛤体内细菌群落进行分析，结果表明变形杆菌在文蛤体内细菌群落中占主导地位（50%），弧菌是夏季文蛤肝胰腺的优势菌属之一。alpha 多样性在夏季达到最高值。采用可培养方法从文蛤体内共分离出 19 种 73 株弧菌，优势菌种包括地中海弧菌（19%）、哈维氏弧菌（11%）、溶藻弧菌（10%）和副溶血弧菌（8%）。不同龄期文蛤体内细菌群落结构存在差异，同一龄期文蛤体内细菌群落结构存在季节差异。文蛤体内的弧菌丰度、可培养细菌总数均与水温呈正相关（$p < 0.05$）。夏季文蛤体内弧菌丰度最高。与其他龄期文蛤相比，3 龄文蛤体内弧菌种类和丰度最高。不同龄期弧菌抗生素抗性指数（ARI）值在 0.13 至 0.18 之间，3 龄文蛤弧菌的 ARI 值高于其他龄期文蛤。耐药性弧菌中已检测到对重金属（包括 Cd、Zn 和 Cu）的抗性。本文研究表明虽然文蛤栖息地蛤蜊岗受抗生素污染较少，但文蛤体内致病性弧菌的耐药性状况十分严重，弧菌携带的抗生素抗性基因与重金属抗性基因之间具有相关性。

关键词：文蛤；弧菌；共生菌群；抗性演化

微生物组的群落构建、稳态维持与植物的营养和健康

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摘要

植物微生物组对宿主的营养吸收、生长发育和环境适应至关重要，被称为植物的“第二基因组”。传统的微生物组学研究主要是基于细菌 16S 核糖体基因的高通量测序,获得微生物组的相对丰度结构组成，但忽视了样本中微生物的绝对丰度。基于定量微生物组技术，我们建立了植物根际微生物群落的“扩增—选择”组装模型，揭示了丛枝菌根共生与根瘤共生在植物根际层面的协同进化机制。基于多组学联动技术，我们提出了植物“农业精准微生物组”概念，并将菌群稳态失调和双生病毒侵染与大豆重大病害“症青”的发生建立关联，为微生物菌肥的精准施控及农作物病原的快速鉴定提供了范例。

关键词：植物微生物组；定量微生物组学；群落构建机制；菌群稳态

不同类群浮游动物附着细菌群落结构及其生态意义

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摘要

动物的生长和发育等很大程度上受到其附着细菌的影响，因此动物与细菌之间的交互研究受到越来越多的关注。其中，针对简单生物模型，例如无脊椎动物和低等脊椎动物等，产生了一系列重要的宿主—微生物交互理论。然而，对于湖泊中广泛存在的无脊椎动物类群—浮游动物，其附着细菌的群落结构及其多样性特征研究仍然是有限的。实际上，同其他动物类似，浮游动物体表和体内（肠道等）也附着着丰富的菌群。本文通过对不同浮游动物类群附着细菌的广泛调查，确定了各类菌群群落组成、多样性以及潜在功能。研究发现，对于滤食性甲壳浮游动物—枝角类，其附着细菌变化范围较大。不同地区或不同湖泊的大型溞、裸腹溞附着细菌均差异较大。而具有选择性捕食策略的桡足类，即使其所处环境空间距离超过 2500km，其附着细菌仍表现出较为相似的特征，且不受特定的环境因子影响。即甲壳类浮游动物中，桡足类与细菌之间存在较为稳定的联系。本文从浮游动物的角度，为宿主—微生物相互作用提供了新的思路。

关键词：宿主；微生物；生态联系；湖泊

马铃薯疮痂病发生与防治的土壤微生态机制研究

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摘要

疾病发生是由病原菌引起的多个共生微生物、宿主和环境相互作用的结果。马铃薯疮痂病是由生痂链霉菌引起的世界性顽固病害，然而土壤微生物组与疮痂病的关系依然研究不足。我们选取发病较重和发病较轻的植株，通过高通量测序、宏基因组等方法对马铃薯生活区域（薯表土、根际土、根区土）和非生长区域（垄沟土）进行了检测，发现薯块表层微环境与疮痂病发生紧密相关。发病轻的薯表土病原菌和细菌丰度较低、细菌多样性较高、菌群共存网络较复杂。我们在疮痂病发病程度、病原链霉菌绝对丰度、毒素基因 *txtAB* 拷贝数三个层面上分析了薯表土细菌与疮痂病的关系，结果显示 *Stenotrophomonas*、*Variovorax* 和 *Agrobacterium* 等 17 个菌属与疮痂病存在显著正相关，*Geobacillus*、*Curtobacterium* 和 unclassified *Geodermatophilaceae* 等 11 个菌属与疮痂病存在显著负相关。我们对宏基因组数据进行了 KEGG 功能注释，对差异 KO 分别进行 KEGG 通路富集分析。结果显示氮代谢、ABC 转运器、细菌分泌系统、类固醇生物合成等代谢通路显著富集在发病重薯表土中；而一些抗生素生物合成途径显著富集在发病轻薯表土中。我们进一步在山东区域内四块具有显著差异土壤和气候条件的地块进行了检测，分析在区域尺度下土壤病原菌丰度、细菌群落和理化特征对疮痂病发病程度的解释率。结果显示，土壤群落对疮痂病发病程度的解释率最高，其次是土壤理化，而病原菌丰度最低。土体土和薯表土关联分析揭示，土体土引发疮痂病主要是通过塑造薯表菌群环境而非单纯提供病原菌。我们以马铃薯表皮为样，分离出 420 株菌株。以组学分析为指导，选择出与病原菌显著相关的菌株，检验其对病原菌生长和毒力的影响。结果显示，分离到的一些 *Chryseobacterium*、*Stenotrophomonas*、*Sphingobacterium*、*Flavobacterium* 和 *Microbacterium* 等菌株能显著抑制病原菌的生长和/或缓解病原菌对植物幼苗生长的毒害作用。为解析生防菌株如何调节土壤菌群从而减轻病害，我们通过栽培实验对侧孢短芽孢杆菌 *Brevibacillus laterosporus* BL12 进行了分析。结果显示，该菌株能成功在根际和薯表定植，能够抑制疮痂病链霉菌的丰度。我们通过 MENA 网络

分析，发现该菌株能成为菌群内的关键（Keystone）微生物。相关性分析揭示，该菌株与一些微生物显著相关，包括 *Pseudomonas*、*Microbacterium*、*Nocardioides* 等，这些微生物被报道也具有生防功能。可见，生防菌株 *B. laterosporus* BL12 能够稳定定植并发挥效果可能源于其成为了菌群的关键微生物，该菌株不仅能抑制病原菌，而且能招募其他微生物共同防治疮痂病。

关键词：马铃薯疮痂病；土壤微生物组；群落组成和功能；生防菌株

盐碱胁迫对紫花苜蓿根际土壤微生物群落的影响研究

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摘要

盐碱胁迫是威胁土壤生产力的主要非生物胁迫因素之一，给作物的生长带来极大的负面影响。植物根际土壤微生物在帮助植物抵抗环境胁迫和促进植物生长等方面的作用已经有所报道。但是，目前关于盐碱胁迫对紫花苜蓿根际土壤微生物群落的多样性、组成及功能的影响仍鲜有报道。本研究分析了不同浓度盐碱胁迫对紫花苜蓿生长的影响，利用 Biolog-Ecoplate、16S rRNA/ITS 基因高通量测序和宏基因组测序技术揭示了紫花苜蓿根际土壤微生物群落的多样性、组成和功能的改变。生物量测定结果表明，低浓度盐碱胁迫促进了紫花苜蓿的生长，而高浓度盐碱胁迫显著降低了紫花苜蓿的生长及叶片叶绿素含量。Biolog-Ecoplate 结果表明，低浓度盐碱胁迫提高了紫花苜蓿根际土壤微生物对不同碳源利用的代谢活性和功能多样性，高浓度盐碱胁迫则降低了相应的功能多样性。高通量测序结果表明，低浓度盐碱胁迫显著提高了根际土壤微生物群落的多样性，一部分有益于植物生长且具有帮助植物抵抗非生物胁迫能力的关键微生物类群在根际土壤中显著富集，如：鞘氨醇单胞菌属（*Sphingomonas*）和木霉菌属（*Trichoderma*）；高浓度盐碱胁迫显著降低了根际土壤微生物群落的多样性和丰富度，且假单胞菌属（*Pseudomonas*）等在内的一部分有益关键微生物类群的相对丰度显著降低。宏基因组测序结果发现，高浓度盐碱胁迫致使紫花苜蓿根际土壤中一部分与促进植物生长及帮助植物应对逆境胁迫的相关功能基因丰度呈下降趋势，如：氨基酸转运和代谢、碳水化合物转运和代谢以及氨基酸的生物合成等；而低浓度盐碱胁迫下一部分相关的有益功能基因丰度在根际土壤中有所提高。根际土壤微生物群落的多样性、组成和功能的改变可能是不同浓度盐碱胁迫下紫花苜蓿生长发生变化的原因之一。

关键词：盐碱胁迫；紫花苜蓿；Biolog-Ecoplate 分析；16S rRNA/ITS 基因高通量测序；宏基因组测序

活性污泥群落网络运动规律研究：从生态相理论到应用

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摘要

活性污泥是应用最广泛的污水生物处理工艺，它利用污泥群落中不同功能微生物的代谢以去除污水中的各类污染物。然而，污泥群落微生物以一种非线性的方式相互影响彼此并构成一个动态的互作网络，进而决定了污泥群落的组装和性能。因此，系统研究活性污泥群落网络的运动规律对我们挖掘微生物群落的代谢潜能和开发新型污水生物处理工艺具有重要意义。本研究立足于宏观生态学的生态相理论，采用 16S rRNA 高通量测序、生态相空间概念及其相关机器学习算法解析了实际污水处理厂活性污泥的物种相互作用的波动过程。我们借鉴了前人相空间法、集合平均和空间收敛交叉映射等思想，开发出一种新型的离散流形局部加权拟合模型。我们从统计学角度探究了微生物种间关系波动性的内在机制，并识别出群落中目标微生物的天生合作者和竞争者。此外，利用一种深度强化学习网络节点算法分析了活性污泥群落动态网络的可控性问题。在此基础上，根据局部加权拟合模型的预测结果提出并模拟验证了一种针对动态网络的新型靶向控制策略，即利用群落目标微生物的天生合作者或竞争者靶向促进或抑制其活性，以实现特定的微生物系统功能。我们利用上述框架预测了实际污水处理厂活性污泥工艺和实验室规模厌氧氨氧化反应器的潜在靶向控制策略，并发现预测结果与前人的实验结果相吻合。我们相信，生态相理论为活性污泥等微生物群落生态研究提供了新的视角，并将在微生物群落工程化应用的发展中扮演重要的角色。

关键词：活性污泥群落网络；种间关系波动性；生态相；机器学习算法；靶向控制

塑料降解超级蠕虫(*zoophobas atratus*)肠道微生物组对微塑料和抗生素的生态稳健性和适应性

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摘要

目前，石油基塑料的有效生物降解已成为一个世界性的难题。已有研究表明，一些昆虫幼虫能够快速摄取和生物降解塑料，但幼虫肠道微生物组对微塑料（MPs）的生态适应性仍有待研究。本研究描述了塑料降解超级蠕虫：大麦虫（*Zoophobas atratus*）对五种最常用石油基微塑料（MPs）的生物降解及肠道微生物组对微塑料（MPs）和抗生素的生态稳健性和适应性。MPs 在幼虫肠道内的平均分子量的变化、含氧特征峰增加、以及代谢中间体的出现，证明了所有 MPs 的解聚和生物降解。大麦虫对 5 种 MPs 的消化表现出广泛的适应性，而抗生素的补充影响了幼虫的存活率和 MPs 的降解。喂食 MPs 的幼虫肠道微生物组与同时喂食 MPs 和抗生素的幼虫肠道微生物组不同，表明抗生素的补充在很大程度上塑造了肠道微生物组的组成。此外，喂食 MPs 的幼虫肠道微生物组的网络复杂性和稳定性高于同时喂食 MPs 和抗生素的幼虫，这表明肠道微生物组的生态稳健性保证了幼虫对不同 MPs 的功能适应性。此外，Mantel 试验表明，肠道微生物群落组成与塑料降解水平、抗生素暴露和幼虫存活率有明显关系。这一发现为昆虫肠道微生物组对不同 MPs 的自适应性提供了新的见解。

关键词：微塑料；抗生素；*Zoophobas atratus*；肠道微生物组；生态稳健性

四、病原微生物检测与健康风险

新型复合消毒剂 GD 胁迫对畜禽养殖废水生物处理系统微生物生态的影响及机理

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摘要

戊二醛和二癸基二甲基溴化铵(GD)是一种畜禽养殖生产中广泛使用的新型复合消毒剂，用于非洲猪瘟(ASF)防控。然而，残留的 GD 对来自污水处理厂活性污泥微生物生态的影响仍然是未知的。本研究建立了七个模拟系统，研究了不同浓度 GD 对污水处理厂的影响，揭示了不同浓度 GD 对污水处理厂微生态反应的潜在机制。氮和碳的去除率均随 GD 浓度的增加而降低，氮代谢受到更明显的抑制，但这种抑制随胁迫时间的增加而减弱。当暴露于小于 1 mg/L 的 GD 时，微生物激活其 SoxRS 系统以促进 ATP 合成和电子转移，从而通过产生少量的 ROS 来支持 GD 的水解和流出。ROS 的过量产生导致抗氧化剂和脱氮酶活性的降低，并且当暴露于高于 1 mg/L 的 GD 时，孔蛋白基因的上调增加了 GD 进入细胞内空间的风险。一些反硝化菌通过抗性及其糖代谢和氮同化的基本能力而存活。值得注意的是，低浓度的消毒剂可促进多种抗性基因(尤其是氨基糖苷类)在微生物间的垂直和水平转移，这不仅会增加反硝化菌的适应能力，还会增加对生态系统的风险。因此，针对 ASF 消毒剂对生态和健康的风险以及新冠肺炎疫情消毒剂残留的影响应得到更多的关注。

关键词：复合消毒剂；畜禽养殖废水；污泥微生态；脱氮途径

From air to airway: Dynamics and risk of inhalable bacteria in municipal solid waste treatment systems

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Abstract

The Municipal solid waste treatment (MSWT) system emits cocktails of microorganisms that jeopardize environmental and public health. However, the dynamics and risk of airborne microbiota associated with MSWT are poorly understood. Here, we analyzed the bacterial community of inhalable air particulates (PM10, n = 71) and the potentially exposed on-site workers' throat swabs (n = 30) along with waste treatment chain in Shanghai, the largest city of China. Overall, the airborne bacteria varied largely in composition and abundance during the treatment ($P < 0.05$), especially in winter. Compared to the air conditions, MSWT-sources that contributed 15 ~ 70% of airborne bacteria more heavily influenced the PM10-laden bacterial communities (PLS-SEM, $\beta = 0.40$, $P < 0.05$). Moreover, our year-span analysis found PM10 as an important media spreading pathogens (104 ~ 108 copies/day) into on-site workers. The machine-learning identified Lactobacillus and Streptococcus as pharynx-niched featured biomarker in summer and Rhodococcus and Capnocytophaga in winter (RandomForest, ntree = 500, mtry = 10, cross = 10, OOB = 0%), which closely related to their airborne counterparts (Procrustes test, $P < 0.05$), suggesting that MSWT a dynamic hotspot of airborne bacteria with the pronounced inhalable risks to the neighboring communities.

Keywords: Air PM_{10}; Airborne pathogens; Human airway; Inhalable risks; Municipal solid waste treatment

严寒地区细颗粒物化学组分对微生物气溶胶特征的影响研究

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摘要

气溶胶对病毒和细菌的传播已经通过科学研究得以证实。人们逐渐意识到大气环境中微生物污染的严重性，对于大气细颗粒物及微生物气溶胶特征的研究存在着重大国家战略需求。严寒地区独特的地理位置造成了特有的气候条件和微生物群落特征。本研究以严寒地区的气候特征参数为影响因子，对大气细颗粒物（$PM_{2.5}$）的理化特征及其微生物组分特征开展了规律性研究；通过不同温度梯度微生物气溶胶的表征，研究细颗粒物化学组分对其附着微生物多样性的影响规律。具体研究内容包括低温环境中大气细颗粒物微生物群落结构特征研究，气象因素及大气污染物对微生物气溶胶组分特征的影响研究和大气颗粒物化学组分对微生物气溶胶组分特征的影响研究。

冬季选取 5 个温度梯度（-25℃~-20℃，-20℃~-15℃，-15℃~-10℃，-10℃~-5℃，-5℃~0℃）采集空气颗粒物样品，基于 16S 和 ITS 测序分析微生物物种多样性指数，主要包括 Chao 指数，ACE 指数，Richness 指数，Shannon 指数，Pielou 指数和 Simpson 指数。结果表明，细菌的 Shannon 指数和 Pielou 指数显著高于真菌，即细菌的群落丰度和多样性均高于真菌，在空气原核生物中占主导地位。细菌和真菌群落的 Chao 指数和 ACE 指数随温度变化趋势基本一致，呈现出以-15℃~-10℃温度区间内群落丰度最高；同时 Shannon 指数与 Simpson 指数在该温度区间分别呈相对最高和最低水平，进一步印证了在此温度区间微生物群落的高生物多样性。PM2.5 浓度和 Simpson 指数之间存在显著负相关关系，说明采样期间细颗粒物浓度越高群落物种多样性越高；PM2.5 浓度和 Order，Family 之间有着显著的正相关关系，说明细颗粒物浓度越高群落物种丰度越高。细颗粒物中的碳质组分和水溶性离子与细菌群落各分类水平上物种数目的相关性高于与细菌微生物多样性指数的相关性。Phylum（门）和 Class（纲）与镁、钙离子呈正相关关系，Order（目）与镁离子呈正相关关系；Cr、Se 和 Ba 与细菌群落的相关性高于其它元素，其中 Cr 与群落丰富度呈负相关，Se 和 Ba 与群落丰富度呈正相关。真菌微生物群落与无机元素整体相关性高于细菌群落。

关键词：严寒；低温梯度；微生物气溶胶；细颗粒物化学特征；微生物群落

活性污泥过程中微生物密度依赖的病毒动态和低活性的温和噬菌体

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摘要

噬菌体是废水处理系统中最丰富的微生物，其生态行为知之甚少，尤其是温带噬菌体。我们使用耦合的污泥宏基因组和病毒组学分析研究了实验室规模的活性污泥反应器中裂解性和温和性噬菌体的时间动态。发现所鉴定的溶源性片段(原噬菌体)广泛分布于重建的宏基因组拼装基因组中(61.7%，$n = 227$)。然而，只有 12.3%的原噬菌体经历了溶源-裂解转换，原噬菌体对游离病毒群落的丰度贡献仅为 0.02-0.3%，表明温和噬菌体的活性较低。虽然污泥群落在反应器运行期间发生了显著变化，但没有检测到大量的原噬菌体诱导事件。统计分析显示，污泥浓度与游离病毒和温和噬菌体群落之间有很强的相关性，表明污泥微生物群中的微生物密度依赖病毒动力学。

关键词：病毒；温和噬菌体；宏基因组学；活性污泥过程

Microbial density-dependent viral dynamics and low activity of temperate phages in the activated sludge process

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Abstract

The ecological behavior of bacteriophages (phages), the most abundant biological entity in wastewater treatment systems, is poorly understood, especially that of temperate phages. Here, the temporal dynamics of lytic and temperate phages in a laboratory-scale activated sludge reactor with a sludge bulking issue was investigated using coupled sludge metagenomic and viromic analyses. The lysogenic fragments (prophages) identified were widely distributed in the reconstructed metagenome-assembled genomes (61.7%, n = 227). However, only 12.3% of the identified prophages experienced lysogenic-lytic switching, and the abundance contribution of prophages to free virus communities was only 0.02–0.3%, indicating low activity of temperate phages. Although the sludge community changed dramatically during reactor operation, no massive prophage induction events were detected. Statistical analyses showed strong correlations between sludge concentration and free virus and temperate phage communities, suggesting microbial density-dependent virus dynamics in the sludge microbiota.

Keywords: Viruses; Temperate phages; Metagenomics; Activated sludge process

全球土壤致病菌和抗性基因的生物复合污染特征与地理分布格局

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摘要

大量抗生素残留引起的环境压力，加速抗生素抗性基因(ARGs)的富集和传播，从而对公共卫生构成严重威胁。尽管土壤中 ARGs 的发生、分布和驱动因素得到了广泛研究，但在全球尺度上对土壤致病菌和 ARG 的生物复合污染知之甚少。本研究从全球土壤宏基因组序列中组装了高质量 contigs，鉴定出 407 种至少含有一个 ARG 的致病菌(ARG-carrying pathogens; APs)。这些 APs 在 1443 个土壤样本中被检测出，占所有 1643 个样品的 87.8%(检出率)。具体地，农业土壤的 APs 丰富度(中位数为 20)高于非农业生态系统；与大肠杆菌属 Escherichia、肠杆菌属 Enterobacter、链球菌属 Streptococcus 和肠球菌属 Enterococcus 等临床相关的 APs 在农业土壤中流行率较高。从农业土壤中检测到的 APs 倾向于与多重耐药基因和 bacA 基因共存。此外，在未来气候情景下，冰川和苔原地区的 APs 丰富度将会增加，而农业用地中 APs 丰富度也将发生大幅变化，一些农业地区的 APs 丰富度增加幅度最大。总之，这些结果有助于理解 APs 全球分布及其对气候和土地利用变化响应，这也将积极推动“一体化健康”倡议的发展。

关键词：全球尺度；土壤；致病菌；抗生素抗性基因；耐药致病菌

城市家居环境食物腐败的微生物安全

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摘要

食物腐败和浪费是全球性的大问题，据联合国粮食及农业组织（FAO）统计数据显示，全球近三分之一的食物被浪费。其中，由细菌、真菌、霉菌等多种微生物引发的食物腐败是主要原因之一。腐败微生物不仅使食物的颜色、口感、及气味发生变化，更重要的是食物富含的营养物质和水分利于病原微生物的滋生，造成毒力因子或真菌毒素的富集，对人类健康构成严重威胁。本文研究四种典型的中国烹饪食物（红烧肉、清蒸鱼、炒青菜和米饭），分别在家居环境（夏季室温 28℃和 4℃冰箱冷藏条件）存储 0-30 天，利用高通量芯片结合 Illumina 测序技术监测微生物群落、抗性基因（ARGs）及病原菌的动态变化。结果发现，室温条件仅存储 1 天，在三种食物类型（肉、鱼、菜）中检测到 10^8-10^{10} copies/g 的 ARGs 及 4 种病原菌。随着存储时间的延长（5-10 天后），ARGs 丰度显著提高。此外，肺炎克雷伯菌（*Klebsiella pneumoniae*）在这三种食物均检测到，且持久留存于整个存储时期。相较于其它食物类型，米饭腐败的速度最慢（3 天后发生）、ARGs 的丰度（10^7-10^8 copies/g）最低，鱼类是最高的。然而，冰箱冷藏条件下，腐败食物检测的抗性基因种类和丰度均低于室温条件，但仍检测到 4 种病原菌及若干致病真菌。此外，随着冷藏时间延长，ARGs 丰度显著增加。特别是清蒸鱼，仅 3 天就显著提高，比蔬菜和肉类快（10 天后），表明其微生物风险最高。通过网络共现性分析发现，潜在病原菌可能是多个 ARGs 的宿主，暗示多重耐药菌的威胁。本研究结果强调，常用的家居食物存储方法，不管是室温还是冰箱冷藏的食物腐败过程，均存在不容忽视的微生物风险，对于提高城市居家环境的微生物安全意识具有重要意义。

关键词：食物腐败；食物存储；抗性基因；病原菌；微生物安全

Construction and application of the Chinese local *Salmonella* genome database version 2 based on "One Health" strategy

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Abstract

Foodborne *Salmonella* infection remains a major public health concern worldwide. With rising antimicrobial resistance, genomic surveillance is key to tracking outbreaks and monitoring transmission, but there is no comprehensive national surveillance scheme for *Salmonella* involving humans, food, animals, and the environment in China. Moreover, the association between antimicrobial resistance and climate, social and economic factors has rarely been investigated. Here, we sequence 1962 *Salmonella* isolates and add 6187 publicly available genomes to build a Chinese local *Salmonella* genome database version 2 (CLSGDB v2) representing 30 Chinese provinces, covering 1905–2022. Using the CLSGDB v2, we mapped the landscape and spatiotemporal dynamics of antimicrobial resistance markers, virulome, and mobilome in Salmonella. We identified 317 *mcr* positive and 745 azithromycin resistance genes positive *Salmonella* isolates out of 7997 isolates. We further uncovered the geographic distribution veil of *mcr-1*, *fosA7*, *fosA3*, *mph(A)*, and $bla_{\text{CTX-M-55}}$ genes in China, all of them resistant to the critically important antimicrobials including colistin, fosfomycin, azithromycin, and the 3rd-generation-cephalosporins. Interestingly, economic, climatic, and social factors can drive the rise of antimicrobial resistance was observed. Finally, we release the CLSGDB v2 as an open-access database and thus can assist surveillance studies tracking 164 Salmonella enterica serovars and 295 sequence types across the globe.

Keywords: One Health; *Salmonella* genomics; Antimicrobial resistance; Public health; Antibiotic resistance gene

真菌毒素污染微生态效应及控制

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摘要

土壤共生微生物对于植物的适应性至关重要，对植物健康和产量能产生重要影响。由多种真菌产生的生物毒素是威胁农产品和食品质量安全的重要影响因素，这些毒素具有极强的生物毒性和致癌性。农产品中存在的产毒真菌主要来源于土壤环境和田间生产活动，产毒真菌同寄主植物、共生微生物和土壤生态环境关系密切。土壤生态环境显著受到生态区域和地势的影响，不同生态条件下的土壤环境如何影响花生产毒真菌及核心共生微生物的装配进程，如何影响产毒真菌同共生微生物种群结构、功能的相互关系并不是完全的清楚。这里我们评估了不同地势生境下花生土壤的理化性质，分析了不同地势生境下荚果及荚果际真菌微生物区系、结构特征和装配进程，发现了核心共生真菌种群对花生荚果内及荚果际产毒真菌种群动态和富集的影响，明确了生态环境和土壤理化性质对核心共生真菌区系及产毒真菌种群关系和装配的调控作用。利用宏基因和宏转录组技术分析了不同生态环境土壤中同共生真菌的功能基因和代谢通路，揭示了他们在花生的富集和表达，明确了关键功能基因和通路同产毒真菌及其毒素的关系，发现了土壤理化性质对功能基因组和代谢通路的调控。另外，通过宏代谢技术，我们发现了同产毒真菌富集程度密切相关的关键代谢物质，分析了土壤理化性质对产毒真菌和关键代谢物质的影响。我们的研究表明不同土壤生态环境显著影响花生真菌微生物的装配进程、产毒真菌的富集程度、功能基因和通路及其代谢产物的差异，调控他们之间的关系，影响植物的健康成长和农产品的质量安全。这为我们研究农产品真菌毒素污染预警和科学防控发现一个新的思路和视角。

关键词：土壤微生态；真菌毒素；环境条件；调控作用

冰核微生物在大气降水中的作用研究进展

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摘要

生物气溶胶作为气溶胶的重要组成部分，因其能传播疾病,引发疫情,其健康效应一直备受科学界关注。从 20 世纪 50 年代法国气象学家 Soulage 首次发现生物冰核至 70 年代早期分离鉴定出冰核活性细菌（可以在-10℃以上较温暖的温度条件下催化液滴产生冰核），到 1982 年英国科学家 Sands 最早提出细菌有可能影响降水并提出了“生物降水假说”，从此国际上开启生物冰核对大气降水影响的研究序幕。尽管以 *Pseudomonas syringae* 为代表的高效生物冰核，可以在-1℃引起水滴冻结是当前已被发现的高效冰核中冰核活性最高的冰核微生物。当年由于缺乏交叉学科人才，使得生物气溶胶的气候效应直至新世纪以来，国际上有关微生物作为大气冰核和云凝结核在气候变化过程中的作用影响才再次吸引了众多的不同学科领域的科学家们的关注，成为新兴的综合性交叉前沿科学研究领域。而自然界中能具有高效冰核的微生物种类和数量极为有限，这样就引发了有关生物冰核在降水过程中贡献大小的争议，双方各持己见，都在寻找各自的证据。在此国际学术背景下，中国科学院大学资环学院杜睿课题组，自 2008 年以来在国内开启了生物冰核在大气降水中的作用研究新方向,目前已累计获得四项相关的国家面上基金项目的资助。本文主要回顾与展望最近十余年来在大气降水中冰核微生物的分布与特征以及新发现的新型高效冰核物质。

关键词：微生物；冰核；大气降水；新型高效冰核

季节水文动态调控水生抗生素抗性组的赋存方式

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摘要

抗生素抗性基因（ARGs）在环境中的传播扩散潜在威胁环境生态安全和居民健康。深层水库具有鲜明的夏季分层、冬季混合的季节性水文条件变化的特点。然而，有关这一水文过程引发的环境变化对 ARGs 赋存方式，如颗粒附着态（>3μm,以下简称附着态）和浮游态（0.22μm-3μm）ARGs 的影响还知之甚少。本研究采用高通量定量 PCR 和多元统计技术，深入研究了闽江水口水库中附着态与浮游态 ARGs 的季节演变规律及其调控机制，并引入颗粒附着指数解析了水文动态对 ARGs 赋存方式的影响。研究结果表明，共有 23 种和 16 种 ARG 亚型分别偏好附着态和浮游态的赋存方式（保守型 ARGs），而有 94 种 ARG 亚型无赋存（方式）偏好性（非保守型 ARGs）。值得注意的是，保守型 ARGs 在分层期趋于消失，且总 ARGs 及多个 ARGs 类型表现出由混合期的附着态向分层期的浮游态的转变趋势。ARGs-细菌 OTUs 共现网络分析表明，浮游态网络中浮游态保守型 ARGs-OTUs 的关联度显著高于其在附着态网络，而附着态网络中附着态保守型 ARGs-OTUs 的关联度显著高于其在浮游态网络，说明赋存方式是影响保守型 ARGs 传播扩散的重要因素之一。PLS-PM 模型分析表明，与浮游态 ARGs 相比，移动遗传元件（MGEs）是影响附着态和浮游态 ARGs 相对丰度，以及 ARGs 赋存方式的关键因子。然而，季节水文动态导致的温度、溶氧变化，可通过影响 MGEs 和细菌群落的赋存方式，间接驱动 ARGs 赋存方式的转变。这种转变可能会影响 ARGs 的赋存特征。以上研究结果为我们深入认识水库分层-混合的季节性水文过程对水体 ARGs 赋存方式的影响提供了科学依据。

关键词：抗生素抗性基因；浮游态；颗粒附着态；季节性分层；水库

长期连续递增毒性冲击对微生物电化学系统产电和群落结构的影响

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摘要

以电化学活性微生物（EAB）为核心的微生物电化学系统（MES）在污水处理领域具有良好的应用前景。前期研究仅报道了水体中急性毒性污染物能够抑制 EAB 活性、降低 EAB 丰度，进而损害 MES 的产电性能，但 EAB 对毒性污染物的适应性还尚未见报道。本研究中，我们首次报道了 EAB 能够对急性毒性污染物适应性地调整群落结构，使得 MES 在高毒性暴露条件下维持稳定的产电。本研究选择了 2 种急性毒性污染物（$HgSO_4$ 和 CH_2Cl_2），探究了 MES 在长期、连续、递增的毒性暴露条件下产电和群落结构的变化。结果表明：在毒性暴露的初期，随着毒性污染物浓度提高，MES 的产电被明显抑制，1.5 mg/L $HgSO_4$ 和 10 mg/L CH_2Cl_2 对 MES 的电流抑制率分别达到了 13.0% 和 19.6%；随着暴露时间的延长，两种 MES 的抗性均明显提高，毒性污染物对 MES 产电的抑制作用逐渐消失，两种 MES 最高可以抵抗 12mg/L $HgSO_4$ 和 240mg/L CH_2Cl_2 的高毒性，且产电性能几乎不受影响；长期毒性暴露导致 MES 的微生物群落结构发生了适应性改变，丰度最高的 2 种产电菌中，Geomonas 丰度明显升高而 Geobacter 丰度明显下降。而且，这两种菌的总丰度，这也基本上是产电菌 Geobacteraceae 的丰度，在经历毒性暴露后丰度基本未变。因此，本研究初步表明，Geomonas 具有比 Geobacter 更高的毒性污染物抗性，同时 MES 能够对有毒环境适应性地调节 Geomonas 和 Geobacter 的比例，以提高自身抗性并维持稳定的产电。本研究为 MES 应用于高浓度污染物及有毒废水处理提供了基本数据。

关键词：微生物电化学系统；电化学活性微生物；毒性污染物；群落结构；地杆菌科

Microbiome and antibiotic resistome in bioelectrochemical toilets for onsite treatment of fecal sludge

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Abstract

Fecal sludge (FS) is a mixture of human feces and urine in onsite sanitation systems, which contains a high concentration of organics, nitrogen, phosphorus and pathogens. There are certain health and safety risks associated with the transportation and treatment of fecal sludge. To treat the fecal sludge safely and efficiently, we developed bioelectrochemical toilets (BETs) for the onsite treatment of human excrement. Compared with the open-circuit bioelectrochemical toilets (OC-BETs), BETs had higher removal rates of total organic carbon, total nitrogen, and total phosphorus. Microbiome analysis indicated dominant populations were affiliated with electroactive bacteria The species co-occurrence network showed that the biofilm microbiome of electrodes in the BETs had more complex correlations than that in the OC-BETs. Compared with the initial samples, the relative abundance (gene copy number normalized to the gene copy number of 16S rRNA) of antibiotic resistance genes (ARGs) in both BETs and OC-BETs decreased, and the removal rate of BETs was higher than OC-BETs. BET offers a promising and innovative solution for in situ treatment of fecal sludge. Its independent operation from the sewage system makes it ideal for remote and off-grid areas where establishing traditional sewage infrastructure is challenging or costly.

Keywords: Bioelectrochemical toilet; Onsite treatment; Fecal sludge; Microbiome; Antibiotic resistance genes

炎症性微生物和基因可作为帕金森病的潜在生物标志物

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摘要

帕金森病（PD）是当今世界第二大神经退行性疾病，给我们的社会带来了严重的经济和医疗负担。近年来越来越多的证据表明，肠道微生物组可能影响 PD，但 PD 的发病机制尚不清楚。此外，目前 PD 的诊断可能是不准确和昂贵的。本研究通过对公开数据（16S rRNA 基因 2269 份样本，霰弹枪宏基因组 236 份样本）和自己收集的数据（16S rRNA 基因 90 份样本，霰弹枪宏基因组 16 份样本）进行分析，旨在揭示 PD 与肠道微生物组的关系，建立 PD 预测模型。结果表明，PD 组潜在的促炎细菌、基因和代谢通路的相对丰度显著升高，而潜在的抗炎细菌、基因和代谢通路的相对丰度显著降低。这些变化可能导致潜在的抗炎物质（短链脂肪酸）的减少和潜在的促炎物质（脂多糖、硫化氢和谷氨酸）的增加。值得注意的是，16S rRNA 基因和宏基因组分析结果一致表明 PD 中有 5 个丰度减少的属（*Roseburia*, *Faecalibacterium*, *Blautia*, *Lachnospira* 和 *Prevotella*）和 5 个丰度增加的属（*Streptococcus*, *Bifidobacterium*, *Lactobacillus*, *Akkermansia* 和 *Desulfovibrio*）。*Desulfovibrio* 的丰度与帕金森病的严重程度正相关。此外，基于与炎症相关的 11 个属（准确度 ＞80%）或 6 个基因（准确度 ＞90%）的随机森林模型能够较好的预测帕金森病。最后，我们提出了一种可能的机制来解释炎症导致 PD 的发病机制。我们的研究结果为基于炎症的 PD 的预测和治疗提供了进一步的见解。

关键词：帕金森病；肠道微生物组；炎症；机器学习；生物标志物

复杂性生殖道感染的精准检测

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摘要

生殖道微生态是指女性生殖道微生物与宿主、环境之间构成的相互协调、相互制约的生态系统，健康的生殖道微生态在维护女性生殖道健康过程中起到至关重要的作用。生殖道感染是由细菌、病毒、衣原体、假丝酵母菌、滴虫、支原体等病原体的侵袭导致女性常见病。临床上几类经典的阴道感染分别是：滴虫性阴道炎 TV、细菌性阴道病 BV、真菌感染 VVC 和需氧菌性阴道炎 AV。高通量测序在生殖道感染诊断和治疗过程中扮演着十分重要的角色。传统宏基因组高通量测序对生殖道微生态中的白色念珠菌等真菌的检出率很低（~30%），特别是针对一些混合感染样本，白色念珠菌的丰度很低，再加上真菌难以破壁，极易造成漏检。为了改善提取效率，在传统提取裂解液裂解的基础上加入研磨珠进行机械裂解，以提高真菌的破壁效率，有效增大白色念珠菌的检出率，结合自主研发的微量建库试剂盒及高准确性的测序平台，对临床上 VVC 和一些混合感染鉴定及耐药基因识别效果显著。本研究测试了 13 例临床样本（包括一些单纯性真菌感染），结果显示微生态宏基因组测序对真菌感染识别准确性可达到 100%，且结合生殖道微生态耐药基因识别结果可以对生殖道感染治疗提供相应参考。

高通量测序技术的飞速发展和测序成本的显著下降，极大地加快了阴道微生态相关研究。目前生殖道感染的最大的问题是混合感染性、反复感染，揭示这些疾病的致病机理往往需要挖掘微生物表达的功能基因。生殖道微生态宏基因组研究可以识别单纯性感染、混合性感染和反复感染，将生殖道感染的诊治从单纯的抗菌治疗转向靶向性抗菌、修复生殖道微生态的新阶段。

关键词：生殖道微生态；宏基因组；高通量测序；真菌感染

Inflammatory microbes and genes as potential biomarkers of Parkinson’s disease

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Abstract

As the second-largest neurodegenerative disease in the world, Parkinson's disease (PD) has brought a severe economic and medical burden to our society. Growing evidence in recent years suggests that the gut microbiome may influence PD, but the exact pathogenesis of PD remains unclear. Additionally, the current diagnosis of PD could be inaccurate and expensive. In this study, we analyzed public data (2269 samples by 16S rRNA gene and 236 samples by shotgun metagenomics) and data collected by ourselves (90 samples by 16S rRNA gene and 16 samples by shotgun metagenomics), aiming to reveal the connection between PD and gut microbiome and establish a model to predict PD. The results showed that the relative abundances of potential pro-inflammatory bacteria, genes and pathways were significantly increased in PD, while potential anti-inflammatory bacteria, genes and pathways were significantly decreased. These changes may lead to a decrease in potential anti-inflammatory substances (short-chain fatty acids) and an increase in potential pro-inflammatory substances (lipopolysaccharides, hydrogen sulfide and glutamate). Notably, the results of 16S rRNA gene and shotgun metagenomic analysis have consistently identified five decreased genera (*Roseburia*, *Faecalibacterium*, *Blautia*, *Lachnospira* and *Prevotella*) and five increased genera (*Streptococcus*, *Bifidobacterium*, *Lactobacillus*, *Akkermansia* and *Desulfovibrio*) in PD. *Desulfovibrio* was positively correlated with disease severity. Furthermore, random forest models performed well for PD prediction based on 11 genera (accuracy > 80%) or 6 genes (accuracy > 90%) related to inflammation. Finally, a possible mechanism was presented to explain the pathogenesis of inflammation leading to PD. Our results provided further insights into the prediction and treatment of PD based on inflammation.

Keywords: Parkinson's disease; Gut microbiome; Inflammation; Machine learning; Biomarker

五、自然和人工生态系统微生物过程

水源水库微生物组与水质调控

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摘要

湖库中的微生物数量众多且种类丰富，是湖库水体中食物链和食物网的基础部分，驱动着湖库水体地球元素循环，其分解代谢功能与水体水质安全有着密切关联。湖库功能微生物研究对更好地维护湖库水体水质安全具有深远意义。水库修建使流水环境转为静水环境，在夏秋之际，表层水温升高，在表层形成暖而轻水层，冷而重水层分布在库底，形成“热分层结构”。水体热分层演替过程中，微生物对水体环境改变产生响应，其中优势菌群及功能微生物通过代谢影响水质，即微生物种群和环境的耦合会消除部分污染物。此外，人类活动造成水体氮素过量会诱发水体富营养化。富营养化对水质、饮用水供应产生严重威胁。水库氮素循环受到 *nirS* 型反硝化细菌调控，*nirS* 型反硝化细菌与水源水质偶联可以揭示水库氮污染迁移转化进程。因此加强对湖库中 *nirS* 型反硝化细菌研究，对于阐明微生物群落与水环境关系有重要意义。

对不同污染程度水库沉积物细菌群落代谢特征进行了探究。结果显示随着污染程度加深，沉积物中微生物活性明显提高；且在不同营养化程度水体中细菌和真菌群落结构有明显差异。就热分层期对水源水质及细菌和真菌群落结构垂向分布存在明显差异。此外，对好氧层 *nirS* 型反硝化菌群进行研究。好氧层中 *nirS* 型反硝化菌群高通量测序显示：水库存在大量未分类 *nirS* 型好氧反硝化细菌；八月份优势菌属为副球菌属。在水源水中筛选出高效脱氮细菌 *Paracoccus versutus* KS293、真菌 *Hanseniaspora uvarum* KPL108 和好氧反硝化菌群。菌株 KS293 在不同条件下菌株生长及脱氮除碳能力结果显示 KS293 在好氧条件下对脱氮除碳能力高于厌氧条件。此外，*nirS*、*narG*、*nosZ* 在好氧脱氮过程中丰度明显高于厌氧脱氮过程；对 KPL108 应用 ^{13}C 同位素标记进行碳源代谢通路研究，显示磷酸戊糖途径和 TCA 循环是菌株碳代谢主要通路。菌群中 *Bacillus subtilis*, *Pseudomonas stutzeri*, *Rhodococcus* sp.是优势菌属，它们在培养过程中具有高于 99%硝氮去除能力。

关键词：水源水库；热分层；功能微生物；好氧反硝化；代谢通路

长期增温背景下高寒草地土壤碳库变化及微生物机制

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摘要

阐明生态群落的组织结构和时空演替对气候变化的响应规律是生态学研究的核心问题之一。生态群落中物种的相互作用对于群落组织结构和系统功能极为重要，但是对于气候变化如何影响生态群落的相互作用网络这一问题缺乏深入的研究。本研究利用高通量测序分析了美国中部大平原草地生态系统 2009-2014 连续六年的增温（+3℃），降水减半(-50%), 降水倍增(+100%) 以及年度刈割收获植物的单因子和交互作用处理下收集的 264 个土壤样品，研究土壤细菌群落在不同气候变化条件下的相互作用网络的演替变化。结果表明，增温是驱动土壤细菌多样性，群落结构和相互作用网络随时间演替变化最重要的气候因子。增温强烈地促进了土壤细菌群落网络体系结构的时间演替，包括网络大小、连通性、平均度、连接度、相对模块性等 （速率是非增温条件下的 1.8-5.8 倍, $r^2=0.582-0.938$, $p<=0.048$）。多种理论和经验分析表明增温条件下细菌群落相互作用网络对于物种丢失、群落变动、外界干扰、时间变异表现出更强的抗性。进一步分析发现，网络的稳健性与网络的平均度、平均聚簇系数和相对模块性显著相关（r2=0.61-0.89, p<=0.05），表明网络的复杂性显著影响了群落的稳定性。

关键词：微生物群落；相互作用网络；稳定性；气候变暖

Climate warming enhances microbial network complexity and stability

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Abstract

Unravelling the relationships between network complexity and stability under changing climate is a challenging topic in theoretical ecology that remains understudied in the field of microbial ecology. Here, we examined the effects of long-term experimental warming on the complexity and stability of molecular ecological networks in grassland soil microbial communities. Warming significantly increased network complexity, including network size, connectivity, connectance, average clustering coefficient, relative modularity and number of keystone species, as compared with the ambient control. Molecular ecological networks under warming became significantly more robust, with network stability strongly correlated with network complexity, supporting the central ecological belief that complexity begets stability. Furthermore, warming significantly strengthened the relationships of network structure to community functional potentials and key ecosystem functioning. These results indicate that preserving microbial ‘interactions’ is critical for ecosystem management and for projecting ecological consequences of future climate warming.

Keywords: Microbial community; Network complexity; Community stability; Climate warming

产甲烷古菌变身食甲烷生长的生理生态学研究

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摘要

厌氧生物圈的产甲烷古菌与甲烷氧化古菌是大气甲烷最主要的“源”与“汇”，二者的产甲烷与食甲烷功能在调控全球甲烷收支平衡与减缓温室效应方面扮演着重要角色。目前，虽然对产甲烷古菌生长代谢机理的认识已较为深入，但甲烷氧化古菌由于生长缓慢、无纯菌分离，严重阻碍了利用生物化学、遗传学等手段对于食甲烷生长代谢机理的研究。本研究首次发现了与甲烷氧化古菌亲缘关系较近的两株从海底沉积物中分离的模式产甲烷古菌 *Methanosarcina acetivorans* 与 *Methanococcoides orientis* 具有以甲烷作为唯一碳源和能源的食甲烷生长代谢功能，该功能需要耦合胞外三价铁或腐植酸的还原，甲烷最终被不完全氧化为乙酸与/或甲酸等产物。本研究通过测定食甲烷生长过程中所积累的生物量、甲烷氧化量、三价铁还原量、乙酸与/或甲酸的生成量，精准计算了 *M. acetivorans* 与 *M. orientis* 所进行甲烷转化的化学计量数与热力学自由能，并基于 *M. acetivorans* 与 *M. orientis* 完备的基因组注释信息，合理推断了截止目前最详细的甲烷厌氧氧化代谢途径，进一步证实了长期存在的科学假设，即甲烷厌氧氧化是通过逆转产甲烷代谢途径实现的。本研究不仅建立了研究食甲烷生长代谢分子机制的理想平台，而且对于进一步认识由产甲烷古菌与甲烷氧化古菌所介导的影响地球气候的甲烷循环过程具有重要科学价值。

关键词：产甲烷古菌；甲烷厌氧氧化；甲烷循环；温室气体；厌氧生态系统

厌氧污泥颗粒化过程的多策略——基于群落演替和相互作用关系的新发现

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摘要

基于厌氧颗粒污泥的污水处理工艺，具有有机负荷率高、污泥沉降性能好、耐有机负荷冲击、能耗低和碳足迹小的突出优势，自上世纪 70 年代问世以来，已被广泛应用于各类有机废水的处理。厌氧颗粒污泥是多种微生物在协同或拮抗作用下，为整体利益而形成的微生物聚集体，关键物种在此过程中起重要作用。借助 16S rRNA 的分子生物学技术和微传感器，学者初步解析了不同生境的微生物在厌氧颗粒污泥中形成的层状结构：Chloroflexi 和 Betaproteobacteria 在颗粒的外壳中占主导地位，产乙酸产甲烷菌 Methanosaeta 为颗粒的内核，中间以厚壁菌门为主。尽管取得了上述进展，但厌氧污泥造粒过程中不同微生物之间的互作关系及形成层状结构的机制尚不明确。因此，本论文旨在阐明不同微生物在厌氧污泥颗粒化过程的多种策略，并重点关注 AHL 介导的群体感应。研究基于实验室 UASB 反应器，进水为合成废水，反应器运行中持续监测污泥 AHL 和 EPS 的组成和浓度、污泥颗粒大小和微生物群落结构，通过微生物群落结构与多种环境变量的相关性分析、分子生态网络结构的演替、功能基因的预测和解析，揭示微生物在厌氧污泥颗粒化过程的多策略。微生物群落演替及其与环境变量的相关性表明，厌氧污泥颗粒化过程可分为四个阶段：即选择、成核、扩张和成熟。在这一过程中，趋化吸引和鞭毛运动是驱动微生物聚集的主要策略。cGMP 和 cAMP 信号通路参与了丝状菌 Euryachaeota 和 Chloroflexi 作为颗粒内核的组装，而群体感应和 N-聚糖生物合成介导了颗粒成熟前的快速膨胀。在污泥造粒过程中，系统发育分子生态网络的演替主要由微生物之间的对抗或竞争作用主导，并主要由低丰度（<1%）菌群驱动。

关键词：系统发育分子生态网络；厌氧颗粒污泥；群体感应；趋化吸引

红树林温室气体排放通量的季节变化及其调控机理

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摘要

红树林湿地分布在热带、亚热带河口地区，具有重要的生态系统服务功能，如维持生物多样性、净化环境、为动植物提供栖息地及维持海岸带生态平衡等。红树植物可以通过光合作用固定大气二氧化碳，然后作为有机物埋藏在土壤中几十年到几百年；被掩埋的碳被称为蓝碳。尽管红树林提供了高的碳储量，但其广泛的缺氧土壤条件也使其成为二氧化碳(CO_2)、甲烷(CH_4)等温室气体的重要来源，并降低了其碳汇的贡献。温室气体通量受微生物代谢过程驱动，随环境变化以及微生物群落组成呈现时间和空间变异性。如甲烷生成和消耗由产甲烷古菌和甲烷氧化菌进行。虽然甲烷转化的微生物过程已经被很好地理解，但复杂的野外生态系统中涉及的微生物生态学还远没有那么清楚。因此，我们的研究目的是揭示红树林自然生态系统中，温室气体排放通量的调控机理。

我们的采样地点位于深圳市福田红树林，共设置 6 个采样位点：红树林湿地内部 3 个样点、近海滩涂 3 个样点。采样时间自 2021 年 3 月到 2022 年 1 月，共采集 66 个样品。测定了环境参数：温度、pH、盐度、营养盐浓度，发现总氮、总碳、总有机碳在红树林样点>滩涂样点，再次证明红树林具有固碳和储碳的生态功能。测定了温室气体通量，发现 CO_2 和 CH_4 温室气体的排放通量在夏秋季>冬春季，而盐度是显著预测因子，盐度与温室气体排放通量存在显著负相关。测定了微生物的 16S 的高通量测序，发现总体微生物和甲烷代谢功能微生物，夏秋季和冬春季显著不同，受到总碳/总氮/总有机碳和 pH 的调控。

我们也测定了红树林及滩涂春夏秋冬 4 个季度的宏基因组和宏转录组的数据。通过宏基因组学的分析，获得了多个类群的产甲烷古菌的基因组和甲烷氧化菌的基因组。系统发育学分析显示产甲烷古菌分别属于 Methanofastidiosales、甲烷马赛球菌目、甲烷八叠球菌目、甲烷微菌目。甲烷氧化菌属于厌氧甲烷氧化微生物（ANME）和 Gamma 变形菌。Methanofastidiosales 和甲烷马赛球菌目的相对丰度在秋季显著高于其他季节，可能解释了秋季甲烷排放通量较高；甲烷氧化菌在红树林显著高于滩涂，可能解释了红树林甲烷排放通量较低。

关键词：微生物生态学；红树林；甲烷；宏基因组；宏转录组

典型温带河口沉积物中碳循环关键过程微生物驱动机制

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摘要

选取辽河口和鸭绿江口表层沉积物作为研究对象，解析沉积物中碳循环功能微生物的群落结构及其环境和空间影响因子，并探究河口沉积物中碳循环的转录学证据，解析群落组成和功能活性表达的关系。结果显示，在辽河和鸭绿江河口的表层沉积物中 5 个碳固定关键功能基因平均丰度呈现出 *acl*B>*cbb*L>*cbb*M>*hcd*>*acc*A 的趋势。鸭绿江河口含 *cbb*L 基因和 *acc*A 基因固碳微生物丰度和多样性高于辽河口。与环境因子相比，空间因子对含 *cbb*L 和 *acc*A 基因固碳微生物群落结构的影响更大。辽河口和鸭绿江口含 *cbb*L 基因固碳微生物中化能异养过程是两个河口含 *cbb*L 基因微生物主要的代谢模式。含 *acc*A 基因固碳微生物主要的代谢模式是化能异养和需氧化能异养型过程。鸭绿江口沉积物中功能基因表达活性呈现出 *cbb*L>*cbb*M> *acl*B>*hcd*>*acc*A 趋势，其中 *cbb*L、*cbb*M 和 *acl*B 均呈现远岸最低的趋势，而 *hcd* 和 *acc*A 则呈现出远岸最高的趋势。宏转录组证明与碳循环相关的 GO 功能在离岸不同距离沉积物中表达均存在显著差异，其中，碳固定功能基因呈现远岸最高的趋势。鸭绿江口沉积物环境中的微生物功能基因在 COG 中注释到 22 个分类功能，其中能量产生和转换功能最高。KEGG 中功能注释到 12 条二级代谢通路和 6 个一级代谢通路；河口沉积物环境中的微生物编码 CBMs 的基因的表达量最高。注释到 2 条碳固定相关路径。近岸和中间、远岸沉积物环境中微生物基因表达差异显著。本研究为减污降碳提供重要依据，对践行陆海统筹减排增汇方案具有重要意义。

关键词：河口；固碳微生物；功能基因；碳循环；丰度；转录活性；宏转录组

小幅盐度变化改变了城市水库微型真核浮游生物的群落构建和共存网络

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摘要

微型浮游生物是水库生态系统的重要组成部分，具有极高的多样性，在元素循环和生态系统稳定性维持中发挥关键作用。在气候变化和人为活动等多重压力下，内陆淡水水体盐碱化现象日益增加，淡水水生生物生长、发育甚至繁殖已受到不同程度的不利影响。因此，保护淡水生物多样性已成为全球面临的挑战之一。当前，需要更全面深入地了解水库微型浮游生物群落多样性如何适应环境因素的干扰。本研究通过调查中国亚热带城市水库（杏林湾水库），使用高通量测序技术和生态统计方法，在连续 13 个月高分辨率时间序列中研究了微型真核浮游生物多样性、群落构建和网络稳定性对小幅盐度变化的响应。结果发现，与其他因素相比，盐度与微型真核浮游生物群落结构的相关性更为显著。水体盐度的小幅增加显著改变了水库微型真核浮游生物群落组成，并导致生物多样性显著降低。此外，盐度通过调控确定性和随机性生态过程之间的平衡塑造了群落构建，且随着盐度的上升，确定性过程越来越重要。更重要的是，核心浮游生物子网络在低盐度水平较为稳定，而卫星浮游生物子网络在中/高盐度水平具有较高的稳定性。我们的研究结果为城市内陆水体浮游生物生态学以及盐度变化对微生物群落构建的影响提供了新见解。

关键词：亚热带水库；浮游生物；群落构建；网络稳定性

干旱影响亚热带森林甲烷汇的微生物过程

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摘要

大气甲烷（CH_4）是仅次于二氧化碳（CO_2）第二大温室气体，贡献大约 25%的全球温室效应。森林是最大的陆地生态系统甲烷汇，但干旱对森林 CH_4 汇的影响及其内在的微生物机制仍所知甚少。此外，我们对干旱胁迫下森林汇的研究进行了全球荟萃分析，发现干旱对亚热带森林汇的影响几乎未见报道。

基于此，我们对干旱胁迫下亚热带森林 CH_4 汇进行了为期 3 年的原位观测，发现干旱显著增加了土壤 CH_4 汇，但干旱并没有明显改变甲烷氧化菌潜在活性与多度；宏基因组测序分析发现干旱也没有明显改变甲烷氧化菌群落组成。通过 ^{13}C-CH_4 标记结合宏基因组分析，我们发现活跃的甲烷氧化群落以 *Methylosinus* 属为主。结构方程模型分析表明，干旱的直接途径（如土壤通气性的增加）超过了干旱引起的间接途径（如甲烷氧化菌群落结构和多样性），从而驱动了亚热带森林 CH_4 汇。

我们的工作在国际上较早的深入探究了干旱对亚热带森林 CH_4 汇的影响及其驱动机制，为准确模拟未来干旱情景下森林 CH_4 汇的变化提供了理论依据。

关键词：干旱；甲烷氧化菌；同位素分析；宏基因组分析；亚热带森林

侧流与主流污水脱氮过程中厌氧甲烷氧化耦合厌氧氨氧化颗粒污泥中微生物响应特征深度解析

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摘要

反硝化厌氧甲烷氧化（n-DAMO）耦合厌氧氨氧化（Anammox）颗粒污泥工艺是一种能高效地同时去除废水中的氮素和溶解性甲烷的绿色低碳生物技术。然而，迄今为止对颗粒污泥中 n-DAMO 和 Anammox 功能微生物之间在不同运行条件下的代谢交互作用仍缺乏深入了解，严重制约了该项技术的发展。为了填补这一空白，本研究设计了三个独立的膜颗粒污泥反应器（MGSRs），分别基于颗粒系统处理不同类型的含氮废水。通过宏基因组和宏转录组学分析，我们首次深入洞察了颗粒污泥中 n-DAMO 和 Anammox 之间的交互作用。n-DAMO 群落在侧流条件下从 *Candidatus* Methanoperedens 向 *Candidatus* Methylomirabilis 呈现明显的种群转变。相对丰度为 25.2%的 *Candidatus* Methanoperedens 在侧流条件下发挥了主要脱氮作用，表现出 *mcrA* 和 *narG* 的高表达活性，对硝酸盐还原和甲烷氧化起到了重要作用。*Candidatus* Methylomirabilis 在主流条件下占据了微生物群落中的主导地位，相对丰度达 32.1%，*pmoA* 和 *hao* 的高表达活性支持了这一结果。此外，对比侧流与主流的颗粒污泥微生物群落结构还观察到了 Anammox 种群从 *Candidatus* Kuenenia 向 *Candidatus* Brocadia 的转变过程。*Candidatus* Kuenenia 和 *Candidatus* Brocadia 菌株共同完成厌氧氨氧化过程，关键功能基因 *hdh* 和 *hzs* 的高表达量与群落结构一致。推测 *Candidatus* Methylomirabilis 菌株被在主流条件下可以通过 *pMMO* 进行氨氧化。这些发现揭示了 n-DAMO 和 Anammox 微生物的交互作用和生态位差异，为 n-DAMO）耦合 Anammox 颗粒污泥技术的推广和发展提供了科学支撑。

关键词：反硝化厌氧甲烷氧化；厌氧氨氧化；颗粒污泥；脱氮

沼渣生物有机肥的开发与应用

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摘要

随着我国沼气工程的大力发展，产生了大量的厌氧消化残余物——沼渣和沼液，它们具有营养成分丰富，养分全面等优点，是一种优良的有机肥原料。沼渣的资源化利用，能更加全面发挥沼气工程的生态环保效益和社会效益。常见处理沼渣的方式是经过简单堆沤后直接施入农田，对作物有较好的促生作用。目前，关于沼渣资源化利用的研究主要集中在肥效方面，对沼渣结合植物促生菌菌剂制成沼渣生物有机肥，评价其促生提质的研究还较少。本研究采用牛粪/秸秆为原料厌氧发酵的沼渣作为基质，接种固氮、溶磷、溶钾、产嗜铁素的 PGPR 复合菌剂，制备成沼渣生物有机肥。将不同用量的沼渣生物有机肥施加于大田鲜食玉米，通过评估玉米产量、籽粒品质、口感，探究沼渣生物有机肥的最佳菌株组合、沼渣/复合菌株配比及施肥量。田间实验结果表明，溶磷(*Priestia megaterium*)菌、解钾菌(*Pseudomonas adaceae*)、固氮菌(*Pantoea dispersa*)、产嗜铁素菌(*Pseudomonas moraviensis*)以 1:1:1:1 的浓度比接种于沼渣后制备成的生物有机肥（A2），A2 以 3.5 t/hm^2（R2）水平的施用量（R2A2）做基肥施用于鲜食玉米，生长 99 d 时鲜食玉米农艺性状指标较 CK 有显著提高，如株高平均达到了 2.44 m，平均根活力 8.02 mg/g/h，单株产量平均达到了 0.1598 kg/株；其品质指标，如籽粒可溶性糖提高了 31.56%，淀粉含量提高了 55.51%；口感指标的品尝鉴定总分达到了 93.7，等级评定达到了一级，经主成分分析，各品质指标均与口感呈正相关。沼渣生物有机肥（A2）能够通过提高农艺指数和品质促进鲜食玉米生长，并改良口感，是一种有效的化肥替代品，沼渣生物有机肥的开发将大大推动生态农业的健康发展。

关键词：沼渣；PGPR；生物有机肥；鲜食玉米；促生提质

宏基因组学揭示微生物电化学滤池脱氮除锰的微生物组响应

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摘要

自养生物滤池被广泛用于去除地下水中的锰和氨氮，但电化学系统对其的影响尚不清晰。本文构建了一种新型的石墨电极锰砂自养微生物电化学滤池（MEF），探讨了电化学效应对自养生物滤池性能的影响。结果表明，电化学效应有助于提高自养生物滤池的处理性能和耐冲击能力。在 20 mg/L 1,4-二恶烷暴露条件下，MEF 对锰和氨氮的去除率分别为 94.72%和 27.27%，而普通生物滤池的去除率为 88.76%和 0%。生物滤池的主导菌种为自养硝化细菌 *Nitrospira deluvii* 和 *Nitrospira moscoviensis*,，它们在 MEF 中的相对丰度分别为 2.70-3.21%和 0.42-1.43%。电化学系统被发现可以增强与碳和氮固定相关的基因表达，从而缓解自养生物过滤器在贫养条件下运行的脆弱性。锰的生物氧化依赖于多铜氧化酶基因 *mmcO*，系统中锰的还原可能驱动亚硝酸盐的非生物氧化。这些发现为在贫营养条件下实际应用中调节和增强生物过滤器过程提供了有价值的见解。

关键词：微生物电化学滤池；地下水；宏基因组；锰；氨氮

Metagenomic unravels the microbiome response of microbial electrochemical filter for manganese and ammonia removal

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Abstract

Autotrophic biofilters are widely used for the removal of manganese and ammonia nitrogen from groundwater, but the understanding of the impact of electrochemical systems on them is still insufficient. Here, a novel manganese sand autotrophic microbial electrochemical filter (MEF) with graphite electrodes was constructed to explore the influence of electrochemical effects on the performance of autotrophic biofilter. The results showed that electrochemical effects serve to enhance the treatment performance and the resilience of the autotrophic biofilter. The MEF achieved the removal rates of manganese and ammonia nitrogen of 94.72% and 27.27% under 20 mg/L 1,4-dioxane exposure, respectively, while the ordinary biofilter had 88.76% and 0%. The biofilters were dominated by autotrophic nitrifying bacteria *Nitrospira deluvii* and *Nitrospira moscoviensis*, which possessed a higher relative abundance of 2.70-3.21% and 0.42-1.43% in the MEF. The electrochemical system was found to enhance gene expression associated with carbon and nitrogen fixation, thereby mitigating the vulnerability of autotrophic biofilters to oligotrophic conditions. The biological oxidation of manganese depended on the multicopper oxidase gene *mmcO*, and the reduction of manganese in the system may drive the abiotic oxidation of nitrite. These findings provide valuable insights into the regulation and enhancement of biofilter processes in practical application under oligotrophic conditions.

Keywords: Microbial electrochemical filter; Groundwater; Metagenomics; Manganese; Ammonium

原始和光老化微塑料暴露对微藻生长的影响

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摘要

近年来，微塑料污染已成为全球环境面临的重要挑战。微塑料在水体中的广泛分布对生态系统和生物多样性造成了严重威胁。然而，值得关注的是，当微塑料颗粒暴露在自然光照下时，紫外线的辐射会引发一系列复杂的化学反应。这包括微塑料表面的氧化和降解，导致微塑料分子链的断裂以及官能团的重新组合，从而使得微塑料的表面形貌和化学性质发生显著变化。在水生生态系统中，微藻扮演着重要的角色，作为原始生产者，其生理反应对整个食物链的稳定和生态平衡至关重要。尽管微藻是生态系统的关键成员，然而对其对原始和光老化微塑料的生理反应了解还相对有限。初步研究发现，微藻对原始微塑料和光老化微塑料表现出截然不同的生理反应。原始微塑料的存在可能干扰微藻的生长和光合作用，对其生理机能造成不利影响。而光老化微塑料，由于经历了漫长的环境暴露，可能导致微藻产生更为复杂的应激反应，进而影响微藻的生理代谢途径。通过对微藻与原始和光老化微塑料相互作用的深入研究，我们可以为应对微塑料污染提供科学依据和解决方案，以保护水生生态系统的健康和生物多样性的持续发展。

关键词：微藻；微塑料污染；光老化；生理反应

稻田土壤中的塑料际是微生物汞甲基化的热区

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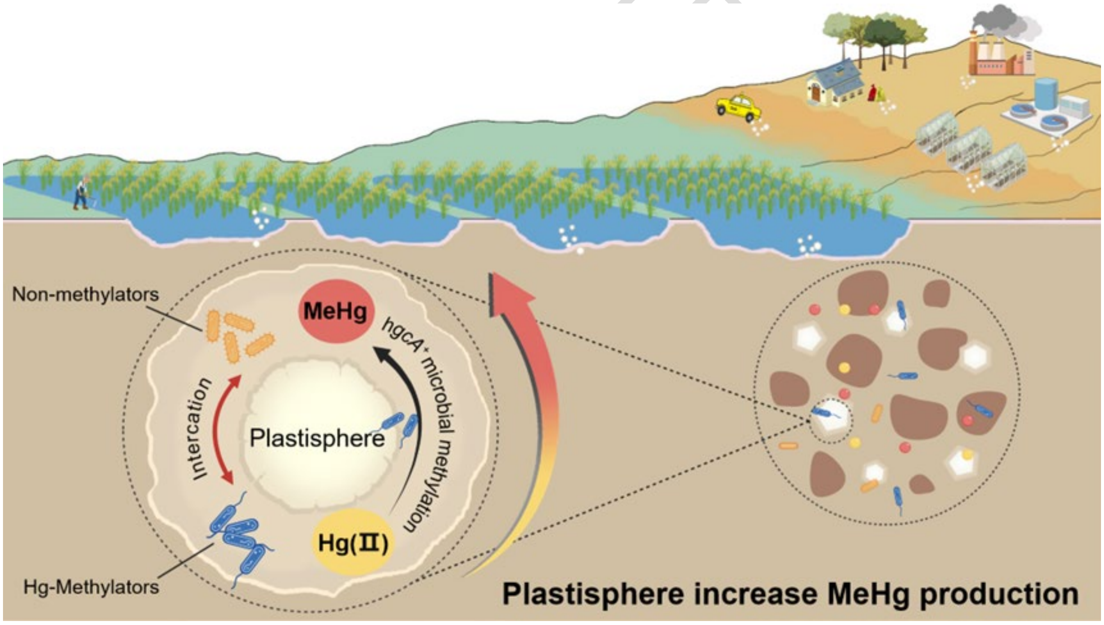
摘要

微塑料(MPs)作为一种新兴污染物在农业生态系统中广泛积累，并对生物地球化学过程产生重要影响。然而，水稻土中 MPs 如何影响汞(Hg)向神经毒性甲基汞(MeHg)的转化仍然知之甚少。本研究以中国两种典型水稻土(即黄壤和红壤)为研究对象，研究了 MPs 对汞甲基化的影响及相关微生物群落。结果表明，在两种水稻土中，MPs 的添加均显著提高了 MeHg 的生成，这可能由于塑料际比周围大块土存在更高的汞甲基化潜能。汞甲基化微生物组成在塑料际和大块土中存在显著差异，黄壤中的 *Geobacterales* 和红壤中的 *Methanomicrobia* 在塑性际中占比高于大块土。此外，还发现非汞甲基化微生物和汞甲基化微生物在塑料际中的联系相比于大块土壤更为紧密。塑料际和大块土中截然不同的汞甲基化潜能可能归因于这些微生物的差异。这些结果表明塑料际是 MeHg 产生的独特生境，并为农业土壤中 MPs 积累的环境风险提供了新的认识。

关键词：微塑料；塑料际；甲基汞；汞甲基化微生物



六、污染物降解微生物组学

联用多维组学技术解译氯霉素类污染物生物转化机制研究

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摘要

氯霉素是一种广谱抗生素，其在人类医疗、畜禽和水产养殖等方面的持续使用，促使其残留物不断释放到环境中，对生态系统的稳定性造成了干扰，促进了抗生素耐药基因产生和传播。目前人们对于微生物如何协同合作实现氯霉素生物降解及其生物转化途径仍然缺乏全面深入的认识。针对上述研究空白，本团队利用多维组学（（宏）基因组、宏转录组、蛋白组）结合微生物纯培养的方法，系统阐释了活性污泥菌群生物降解氯霉素的新机制。该项研究通过宏基因组和基因组分析揭示了氯霉素降解菌群的群落结构和基因组特征；发现群落中的关键功能细菌首先将氯霉素的 C1-OH 和 C3-OH 基团氧化、C3 异构化和 C3-OH 基团乙酰化，氯霉素的氧化产物、异构化产物和乙酰化产物经过一系列转化后裂解为对硝基苯甲酸（PNB）和 2,2-二氯乙酸（DCA），最终这两种产物被群落中的其它成员完全矿化利用；Sphingomonas、Caballeronia、Cupriavidus 三个关键菌属之间的协同合作实现了氯霉素的高度矿化和生物解毒；挖掘了参与氯霉素代谢的关键酶，包括氯霉素氧化酶 capO、乙酰基转移酶 catB 等。本研究为高浓度氯霉素废水（如制药废水、畜禽废水等）的强化生物处理提供了良好的菌株和酶资源。

关键词：多组学；抗生素；生物转化；代谢途径；菌株互作

土壤汞的微生物转化与生态效应

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摘要

环境中的某些厌氧微生物可将无机汞转化为强效生物累积性神经毒性甲基汞(MeHg)。土壤是各种厌氧微生物的重要场所；然而，对河岸带湿地土壤中与汞甲基化相关的微生物群落和影响因素知之甚少。本研究采集了中国典型河岸带湿地土壤，利用宏基因组分析来研究分析了的甲基化微生物汞的多样性和分布特征，并阐明汞甲基化微生物与环境参数之间的潜在关联。结果表明，Deltaproteobacteria、Syntropicales、Desulfuromonadales 和 Anaerolineales 是携带 hgcA 基因的主要汞甲基化微生类群，并且底部沉积物中 hgcA 基因的丰度总体高于表层沉积物。根据随机森林分析表明，浮霉菌是甲基汞积累的重要预测因子。进一步相关分析表明，MeHg 浓度与沉积物中有机质(OM)的相关性最强，表明 OM 可能通过影响湿地沉积物中与 Hg 甲基化相关的微生物群落的生长和代谢来影响 MeHg 的产生。此外，hgcA 的相对丰度与 Fe 含量呈显着正相关，而与沙土含量呈负相关。粘土含量较高的沉积物通常具有较高的 hgcA 丰度。此外，我们从 148 个重建的宏基因组组装基因组(MAG)中鉴定出 10 个含有 hgcA 基因的 MAG。我们的研究结果为中国河流湿地汞甲基化微生物的分布和环境驱动因素提供了新的见解。

关键词：微生物生态学；健康；绿色

柴达木沙漠链霉菌 S10^{T} 活性天然产物挖掘及其生物合成机制研究

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摘要

天然产物及其类似物是重要的药物来源。普通环境来源的天然产物发现已进入瓶颈期；由于极端环境微生物特殊的基因类型、生理机制及代谢产物，具有极大的应用价值，因此极端环境微生物是新型天然产物发现的重要资源。随着宏基因组技术和基因编辑技术的发展，极端环境微生物中的活性天然产物资源挖掘成为新的研究热点。我国西北沙漠中含有较丰富的链霉菌资源，其中的活性天然产物资源一直未深入挖掘。本研究以从柴达木盆地的沙漠样品中分离得到的一株柴达木沙漠链霉菌 S10^{T}（*Streptomyces qaidamensis* S10^{T}）作为研究对象，通过菌株基因组测序，分析了其次级代谢产物的合成能力及潜在活性，通过 in-frame 法敲除了与抑菌活性相关的 8 个基因簇，发现 ΔC27 基因敲除突变株的抑菌活性与野生型相比明显降低，证明了基因簇 C27 所合成的产物对于 S10^{T} 的抑菌活性十分重要。挖掘到的两种活性天然产物阿糖腺苷和 differolide，并探究了 differolide 的生物合成途径，证实了该化合物是由一个聚酮类化合物基因簇负责合成。随后又通过重离子诱变和致病菌共培养的方式诱导其沉默基因簇的表达，并分离了一个新的化合物。

关键词：柴达木沙漠链霉菌 S10^{T}；基因组挖掘；天然产物；生物合成；沉默基因簇激活

锑和砷污染对芒根际细菌、古菌、真菌群落碳矿化和硝化作用的协同影响

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摘要

由于环境中重金属的持久性和生物毒性，研究其对土壤微生物群落的影响受到广泛关注。然而，锑和砷污染如何协同影响植物根际微生物驱动的生态过程尚不清楚。本文研究了锑和砷污染对先锋植物（芒）根际微生物群落驱动的碳氮循环的协同效应。与低污染（LC）组相比，高污染（HC）组中锑和砷浓度，总碳含量显著升高（$P<0.05$），而有效磷、与碳和氮代谢相关酶活性、碳矿化和硝化潜力均显著降低（$P<0.05$）。多重变量分析显示，土壤 pH 和可利用磷是影响微生物群落结构和装配的主要因素，而锑和砷污染通常降低了微生物 α-多样性和种间相互作用。随机森林分析（RF）表明，微生物关键类群能较好地预测土壤碳矿化和硝化作用。偏最小二乘路径模型（PLS-PM）证明，锑和砷污染通过影响土壤微生物生物量、α-多样性和土壤酶活性来降低碳矿化和硝化作用。本研究阐明了锑和砷污染通过阻碍微生物功能特性，影响根际土壤碳氮循环，对促进重金属污染环境微生物-植物的可持续修复具有重要意义。

关键词：锑矿山；根际微生物；关键类群；碳矿化；硝化作用

Linking biodiversity and ecological function through extensive microeukaryotic movement across different habitats in six urban parks

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Abstract

Urban parks have become important hot spots for human recreational activity. Microeukaryotes are ubiquitous and connected between different ecosystem components, which play substantial ecological roles in the urban environment, maintaining ecosystem services. However, the connectivity of microeukaryotes in various habitats, and the impact of their movement on biodiversity and ecological functions in urban ecosystems remain largely uncharacterized. In this study, we conducted a field survey of microeukaryotes in five different habitats, viz. moss, soil, tree hole, pond sediment, and water in six urban parks. Results showed that there were significant differences in taxonomic and phylogenetic diversities, as well as metabolic flexibility among habitats. Both deterministic and stochastic processes were determined to be very important in shaping the microeukaryotic community assembly within a habitat, whereas deterministic dispersal limitation leads to community turnover across habitats. Notably, extensive migrations of microeukaryotes across urban park habitats were uncovered. Microeukaryotic movement facilitates the spread of microbes, and any habitat in urban parks has the potential to be an important source of microeukaryotes, consequently contributing to biodiversity maintenance. Opisthokonta was the main group moving between habitats, among which soil and water displayed the most active communication. Saprotrophs and symbiotrophs generally moved in all types of habitats, while pathotrophs were frequently observed traveling between moss, tree hole, and water, suggesting discrepant ecological functionality.

Additionally, high-throughput sequencing was applied to target both V4 and V9 regions of 18S rRNA gene to better understand the overall microeukaryotic diversity and movement profile. Our analysis demonstrated that the V4 region was more accurate than the V9 region in some specific groups (e.g., testate amoeba), and primer pairs greater influenced the results in aquatic compared to terrestrial ecosystems. Our results highlight important microeukaryotic movement or connectivity across different habitats in supporting biodiversity and ecosystem functioning.

Keywords: Urban greenspace; Microeukaryote; Niche; Connectivity; Movement ecology; Fungal guild; One Health

微生物在多种重金属污染环境中的协同解毒机制

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摘要

重金属砷、镉、铬广泛分布于土壤环境中，重金属的过度积累能够引起土壤理化性质和生态结构的变化，威胁民众健康。微生物对重金属的解毒作用（砷氧化、铬还原和镉钝化）在其生存和污染环境的修复中起着至关重要的作用。本课题组在一株具有砷氧化和铬还原能力的肠杆菌 Z1 中发现了一种新型的氧化还原酶 NemA，该蛋白受到有机三价砷及六价铬的诱导。异源表达 NemA 能够提高大肠杆菌对有机三价砷及六价铬的抗性，且 NemA 能够将高毒性的有机三价砷氧化为低毒性的有机五价砷，同时将高毒性的六价铬还原为低毒性的三价铬。在砷与铬共同存在的条件下，NemA 砷氧化速率具有显著的提升，表明 NemA 能够将电子从有机三价砷传递给六价铬，从而完成两种高毒性重金属的协同解毒。此外，该基因上游的调控蛋白 NemR 通过 21 位、106 位和 116 位半胱氨酸识别有机三价砷信号，进而调控 *nemA* 基因的转录表达。NemAR 为首次报道的对砷和铬协同解毒的系统，驱动微生物协同解毒环境中的砷和铬。

生物被膜吸附是微生物钝化环境中镉的主要机制，然而在镉铬共存的环境中，铬能够抑制微生物生物被膜的产生。贪铜菌 MP-37 为一株具有协同钝化镉和还原铬的细菌，该细菌在不同重金属条件下表现出了不同的镉钝化表型：在镉单独存在的环境中，其通过生物被膜钝化镉；在镉和铬共同存在的环境中，细菌可通过生物被膜和胞外分泌物两种方式同时钝化镉。研究发现该细菌 GlyI 蛋白受到铬的诱导而上调表达，GlyI 蛋白为细菌中甲基乙二醛解毒系统，可将甲基乙二醛分解生成乳酸，从而缓解细胞内的氧化压力。GlyI 蛋白过表达能够降低胞内甲基乙二醛的含量，提高胞外分泌物钝化镉的比例。此外，通过添加 GlyI 系统的产物乳酸，同样能够增加细菌胞外分泌物钝化镉的比例。本研究揭示了微生物在镉铬共污染环境中的镉钝化新机制，即在生物被膜被铬抑制情况下，激活甲基乙二醛解毒系统驱动甲基乙二醛的清除和镉离子的胞外钝化。

关键词：重金属；砷氧化；铬还原；镉钝化；转录调控；生物修复

大麦虫取食降解泡沫塑料与消化道功能菌群和消化酶活性响应

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摘要

塑料因具有质轻、韧性强、耐腐蚀等优点而被广泛使用。但是，由于塑料属于高分子聚合物，化学稳定性强，很难自然分解，而在环境中形成长期污染。可以取食降解塑料的昆虫幼虫的发现，给塑料的生物降解提供了新的思路。为了揭示大麦虫（*Zophobas atratus*）可取食降解塑料类型以及与塑料消耗相关的潜在变化，使用聚苯乙烯（PS）、聚乙烯（PE）和聚氨酯（PU）泡沫三种塑料作为唯一饲料，以麸皮为对照，喂养大麦虫幼虫 35 天。与对照相比，PS 或 PU 喂养的幼虫存活率为 100%，PE 喂养和饥饿的幼虫存活率分别降低了 81.67%和 65%。塑料喂养组和饥饿组的幼虫体重均下降。PS、PE 和 PU 的消耗率分别为 1.41、0.30 mg/d/larva 和 0.74mg/d/larva。利用衰减全反射傅里叶变换红外光谱（ATR-FTIR）、差示扫描量热仪和热重分析（DSC-TGA）分析表明，与塑料原料相比，排泄物中的官能团和热稳定性发生了变化，表明塑料发生了部分氧化和降解。肠道消化酶活性测定显示，所有塑料喂养组的蛋白酶活性都有所增加。肠道微生物群落相对丰度变化明显，所有塑料喂养组的 *Enterococcus* 丰度增加，PE 组的 *Citrobacter* 丰度增加，PS 组的 *Dysgonomonas* 和 *Sphingobacterium* 丰度增加，PU 组的 *Mangrovibacter* 丰度增加。其中，后 3 属为首次报道。总之，研究结果表明大麦虫幼虫可以有效降解 PS 和 PU 泡沫塑料，塑料降解与肠道菌群和消化酶活性相关。

关键词：塑料生物降解；Zophbas atratus；泡沫塑料；消化道功能菌群；消化酶活性

地膜源微塑料残留对黑土微生物群落功能的影响机制研究

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摘要

微塑料通常指粒径小于5mm的塑料纤维、碎片或颗粒等，其广泛分布与急剧增加已成为全球性环境污染热点问题。微塑料在土壤中长期残留不但破坏土壤结构完整性，还会改变土壤微生物群落及功能，进而影响土壤质量与作物健康。然而，黑土微生物组对微塑料残留的响应机制尚不清晰。为此，我们采用室内微宇宙模拟培养实验体系结合二代测序技术，研究传统（聚乙烯，PE-MP）和生物可降解（聚乳酸-己二酸对苯二甲酸丁二醇酯，BMP）微塑料残留对黑土微生物组的影响特征。结果发现，两种微塑料残留时间是驱动黑土微生物群落分布的主导因素。当微塑料浓度超过1%时，土壤微生物多样性开始显著下降，且BMP对微生物群落结构的影响更为显著。与土壤相比，微塑料圈，尤其是BMP富集大量特异性微生物，促进土壤氮代谢过程。PE-MP显著富集放线菌而BMP增加了变形菌丰度，其中*Ramlibacter*主导了BMP与PE-MP微塑料圈中多条氮代谢途径差异。利用binning技术拼接获得的高质量基因组中bin115，bin53和bin26都分类为*Ramlibacter*，且它们的丰度在BMP圈上最高。这3个新型基因组携带了调控氮降解、氮固定和同化硝酸盐还原代谢路径的多个拷贝基因，这些代谢路径共同指向于铵态氮的生成。通过测定土壤含氮养分发现BMP残留土壤中的铵态氮含量的确高于CK和PE-MP土壤。本研究揭示出生物可降解地膜源微塑料较传统地膜显著改变土壤微生物群落且促进土壤有效氮素累积，为推进传统地膜的减量与替代提供微生物学理论依据。

关键词：东北黑土；地膜源微塑料；土壤微生物；宏基因组

活性污泥系统中塑料圈的抗性组赋存特征及其生物降解特性研究

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摘要

塑料污染已成为威胁生态安全与人类健康的全球性挑战。在环境中塑料在多重因素作用下易分解成为粒径更小的微塑料（Microplastics, MPs）。MPs 体积小、比表面积大，可富集多种抗生素抗性基因（Antibiotic Resistance Genes, ARGs）。在污水处理活性污泥系统中，有关 MPs 表面生物膜（微塑料圈）抗性组赋存特征、赋存菌群与 ARGs 互作关系等仍有待进一步研究。活性污泥菌群对多种持久性有机污染物具有一定的降解能力，因此挖掘当中降解塑料的潜在功能菌群资源具有重要意义。本研究以活性污泥系统为研究对象，采用宏基因组学探究了 MPs 在四环素和铜离子选择压力下的 ARGs 赋存特征，并揭示微塑料圈菌群与 ARGs 的联系。结果表明，MPs 对 ARGs 具有选择性富集作用，相比活性污泥菌群，微塑料圈菌群与 ARGs 联系和相关性更强，且携带更多的 ARGs 潜在宿主。此外，以聚乙烯（Polyethylene, PE）MPs 作为唯一碳源，对活性污泥菌群进行富集，发现 PE 薄膜重量出现明显损失、疏水性下降、表面形成活性官能团（羰基、羟基和醚键），表明 PE 被生物降解。同时，基于 HPLC-MS 分析的代谢组学表明以 PE 为碳源的实验组代谢产物谱显著区别于对照组，进一步证实了菌群对 PE 的降解作用。随后，通过宏基因组分箱技术发现 PE 塑料的解聚可能由多种细菌协同完成。研究结果有助于评估污水处理系统中微塑料圈赋存的 ARGs 和潜在致病菌对生态环境的潜在风险，并为挖掘活性污泥菌群降解塑料的潜能奠定理论基础。

关键词：活性污泥；微塑料；抗生素抗性基因；生物降解；聚乙烯

Biodegradation mechanism of recalcitrant microplastics by larvae of *Tenebrio molitor*

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Abstract

Plastics are considered the most common and versatile materials of the modern age, but their recalcitrant nature and deterioration product, microplastics (MPs) are causing great environmental problems. The traditional technique for their decomposition potentially leads to severe environmental and health concerns. Recently, the biodegradation of some recalcitrant plastics by the larva of *Tenebrio molito*r L. (mealworm) has been reported. Its short-term behavior and potential in MPs degradation were extensively studied, but its mechanism remained largely unknown. In this study, we investigated the long-term effects of MPs feeding on survival, growth and development by extending the studied period to over 400 days. Its mechanism in PS and PE degradation was studied by RNA sequencing and transcriptome analysis. KEGG mapping revealed that mealworms act as downstream decomposers in plastic depolymerization and that fatty acid degradation pathway plays important roles in intermediates digestion. In addition, functional depolymerases probably acted on the distal backbone and produce shorter linear chains that contained ≤16 C atoms. The intermediates of PS degradation are expected to be further decomposed by mealworms as xenobiotics. This study provided a preliminary understanding of MPs degradation mechanism by mealworms.

Keywords: Plastic degradation; Microplastics; Mealworm; Transcriptome analysis; Fatty acid degradation

水环境中可生物降解塑料的微生物定殖特征及降解机制解析

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摘要

塑料制品的广泛使用导致其废弃物不断进入环境并持久存在，从而并对生态系统产生不利影响。可降解塑料作为石油基塑料（不可降解塑料）的主要替代物，其在自然水环境中的微生物定殖特征及降解机制研究较为缺乏。基于此，本研究以 PVC，PS 和 PP 等不可降解塑料为对照，探究了自然水环境中典型可生物降解塑料聚己二酸对苯二甲酸丁二醇酯/聚乳酸/淀粉混合塑料（PBAT-H）和聚乳酸（PLA）的降解特征。研究发现可生物降解塑料 PBAT-H 和 PLA 具有更高的降解率，其在 58 d 后表面破碎呈现絮状化，降解率最高可达 17.05%。塑料表面疏水性减弱，粗糙度增加，最大粗糙度分别为初始的 3.97 和 2.83 倍。水环境中塑料表面会形成生物膜，宏基因组学结果显示塑料表面定殖了塑料降解相关微生物且存在乳酸、对苯二甲酸、酯酶和水解酶代谢相关的基因，该结果表明塑料表面生物膜具有驱动 PBAT-H 和 PLA 降解的潜力。进一步的模拟实验分析了泥水冲刷的非生物因素和微生物作用的生物因素对降解效果的贡献。结果表明，驱动 PLA 和 PBAT-H 表面特性改变并发生降解的主要因素分别为泥水冲刷和生物作用，且泥水冲刷和生物联合作用时两种塑料降解效果最佳。降解 60 d 后，PBAT-H 和 PLA 的质量损失分别为 37.51%和 10.72%，表面最大粗糙度增加为初始的 2.24 和 3.41 倍，水接触角降至 82.6675°和 80.5725°。基于 ^{13}C 的同位素分馏进一步证实了生物降解作用的贡献，且 PLA 和 PBAT-H 的降解过程中伴随着塑料低聚物（如乳酸三聚体、PBAT 低聚物）和添加剂（如邻苯二甲酸酯）的释放。宏基因组分析结果表明体系中存在塑料低聚物和添加剂降解相关的微生物和功能基因，证实了水环境中可生物降解塑料在生物作用下发生酯键断裂、聚合度降低、产物和添加剂溶出等过程，且泥水冲刷对生物降解过程具有促进作用。研究结果对于明确可降解塑料的环境行为和降解特征具有重要意义。

关键词：可生物降解塑料；水环境；降解特征；降解机制；生物强化降解

Characterization of microbial colonization and degradation mechanism of biodegradable plastics in the aquatic environment

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Abstract

The widespread use of plastic products has resulted in the continuous entry and persistence of plastic waste into the environment, which in turn has a negative impact on the ecosystem. Biodegradable plastics act as the major alternative to petroleum-based plastics (non-degradable plastics), and the relevant research on the microbial colonization characteristics and degradation mechanisms in natural aquatic environments were insufficient. This study investigated the degradation characteristics of typical biodegradable plastics, polybutylene terephthalate adipate/polylactic acid/starch hybrid (PBAT-H) and polylactic acid (PLA), in natural aqueous environments using non-biodegradable plastics, such as PVC, PS, and PP, as control. It was found that the biodegradable plastics PBAT-H and PLA had higher degradation rates, and their surfaces were broken up and showed flocculation after 58 d, with degradation rates up to 17.05%. The hydrophobicity of the plastic surface was weakened and the roughness increased, with the maximum roughness being 3.97 and 2.83 times of the initial one, respectively. Biofilms were formed on the plastic surface in the aqueous environment, and the metagenomics results showed that the plastic surface was colonized by plastic degradation-related microorganisms and the presence of genes related to the metabolism of lactic acid, terephthalic acid, esterase, and hydrolase, which indicated that the biofilm on the plastic surface had the potential to drive the degradation of PBAT-H and PLA. Further simulation experiments analyzed the contribution of abiotic factors of mud and water washout and biotic factors of microbial action to the degradation effect. The results showed that the main factors driving the change in surface properties and degradation of PLA and PBAT-H were mud-water scouring and biological action, respectively, and the best degradation of both plastics was achieved with the combined effect of mud-water scouring and biological action. After 60 d of degradation, the mass loss of PBAT-H and PLA was 37.51% and 10.72%, respectively, the maximum surface roughness increased to 2.24 and 3.41 times of the initial one, and the water contact angle decreased to 82.6675° and 80.5725°. The contribution of biodegradation was further confirmed by 13C-based isotopic fractionation and the degradation of PLA and PBAT-H was accompanied by the release of plastic oligomers (e.g., lactic acid trimers, PBAT oligomers) and additives (e.g., phthalates). The results of metagenomic analysis indicated the presence of microorganisms and functional genes related to the degradation of plastic oligomers and additives in the system, confirming that biodegradable plastics in the aqueous environment undergo the processes of ester bond breaking, polymerization reduction, and the leaching of products and additives under the biological action, and that mud and water flushing has a facilitating effect on the biodegradation process. The results of the study are of great significance in clarifying the environmental behavior and degradation characteristics of biodegradable plastics.

Keywords: Biodegradable plastics; Water environment; Degradation characteristics; Degradation mechanism

Plastisphere Community: The Formation and Ecological Processes

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Abstract

The gradual accumulation of microplastics has aroused increasing concern for the unique niche, termed ‘plastisphere’. As research so far has focused on their characteristics in aquatic ecosystems, our understanding of the colonization and assembly of the attached bacterial communities on microplastics in soil ecosystems remains poor. Here, we aimed to characterize the plastisphere microbiome of two types of microplastics (polylactic acid (PLA) and polyethylene (PE) differing in their biodegradability in two different soils. After incubation for 60 days, considerably lower alpha diversity of bacterial community was observed on the microplastic surfaces, and prominent divergences occurred in the microbial community compositions between the plastisphere and the bulk soil. The temperature, rather than polymer type, significantly induced the differences between the plastisphere communities. The ribosomal RNA gene operon (rrn) copy numbers were significantly higher in the PLA plastisphere, suggesting potential degradation. The co-occurrence network analysis showed that the PE plastisphere exhibited greater network complexity and stronger stability than those in the PLA plastisphere. The stochasticity ratio indicated the remarkable importance of stochastic process on community assembly in PE and PLA plastispheres, while the null model analysis showed the non-negligible roles of deterministic processes in shaping the plastisphere communities. Higher contributions of homogenous selection in PLA plastisphere were observed in comparison with PE plastisphere, which were probably attributed to the selective pressure induced by microplastic degradation. Our findings enhance our mechanistic understanding of the diversity patterns and assembly processes of plastisphere in soil environments, and have important implications for microbial ecology and microplastic risk assessment.

Keywords: Electroactive biofilm; Metatranscriptome; Extracellular electron transfer; Low temperature

研究生论坛

微/纳米塑料对 SBR 中活性污泥脱氮效能及抗性基因赋存影响的研究

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摘要

微塑料(MPs)、纳塑料(NPs)和抗生素抗性基因(ARGs)是污水处理厂中频繁检出的新兴污染物。然而，鲜有研究对比分析 MPs 和 NPs 对活性污泥脱氮效能及 ARGs 传播扩散的影响。本研究旨在探究 MPs 和 NPs 对序批式反应器中活性污泥脱氮效能及 ARGs 赋存的影响和机制。结果表明，MPs（10 μg/L 和 1000 μg/L）和低浓度 NPs（10 μg/L）对和活性污泥脱氮效能没有影响，高浓度 NPs（1000 μg/L）使 NH_4^+-N 去除率降低 24.48% 并导致 NO_3^--N 和 NO_2^--N 积累。机制分析表明 NPs 对活性污泥具有毒性作用，表现为促进了活性氧生成和乳酸脱氢酶释放，并进一步导致了硝化菌和反硝化菌的相对丰度降低，这些负面影响伴随着硝化（*amoA* 和 *nxrA*）和反硝化（*narG*、*nirK* 和 *nirS*）功能基因丰度下降，最终抑制了活性污泥的脱氮效能。此外，MPs 和 NPs 显著促进了四环素抗性基因(TRGs)的扩增，其中主要促进了外排泵和酶修饰机制 TRG 的增值。同时，MPs 和 NPs 增加了多重耐药基因和移动基因元件(MGEs)的传播风险。相关性分析显示，ARGs 与 MGEs (*intI1* 和 *intI2*)之间无显著相关性，但 MPs 和 NPs 的添加显著增加了 ARGs 潜在宿主的丰度，说明 MPs 和 NPs 胁迫下促进 ARGs 增殖的主要因素不是基因水平转移，而是微生物群落结构的改变。以上结果表明应关注污水处理厂中 MPs 和 NPs 带来的环境健康风险。

关键词：微塑料；纳塑料；活性污泥脱氮；抗性基因

单双季种植模式对不同粒径团聚体中细菌和真菌群落构建与共现网络的影响

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摘要

作为微生物生存和活动的主要场所，土壤团聚体结构的改变不仅直接影响微生物群落，且会造成土壤养分循环的差异，进而改变生态系统服务。了解微生物对不同农业管理和土壤团聚体的响应对于生态学研究很重要。然而，耕作模式不同导致的土壤团聚体中微生物群落构建的差异及其驱动因素尚不清晰。本研究以鄱阳湖围垦 60 年的水稻田为研究对象，探究了单季/双季水稻种植模式下不同粒径团聚体（散土，>5mm; 2-5mm; 0.25-2mm; <0.25mm）中土壤团聚体微生物群落构建过程和相互作用的动态。结果表明双季种植模式有助于增加稻田土壤养分和团聚体稳定性，提高土壤微生物多样性和活性，有利于微生物功能发挥。两种水稻种植模式下，细菌群落构建以随机性过程为主，真菌群落构建以确定性过程为主。随着团聚体粒径降低，选择作用在细菌群落构建中的作用不断增加；随机性过程对真菌群落构建的影响增强。总氮和总磷驱动了稻田土壤细菌群落构建过程。真菌群落构建主要受到总磷和总有机碳的调控。此外，我们发现从大团聚体到下小团聚体，微生物网络复杂性和稳定性降低，微生物相互作用减小。以上结果强调了鄱阳湖湿地围垦后单/双季水稻种植显著改变了土壤团聚体结构和稳定性，且不同水稻种植模式下，不同粒径团聚体中土壤养分的变化驱动了微生物群落构建过程差异，加深了对湿地围垦为水稻田后土壤变化情况的认识，为湿地合理管理与利用提供支持。

关键词：土壤团聚体；单季/双季水稻种植；群落构建；共现网络；湿地围垦

温度对不同抗生素浓度暴露下 *E. coli* 抗性演化规律的影响

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摘要

全球变暖步伐加快，可能对环境安全和人类健康产生严重威胁，但其对细菌抗生素抗性的影响规律目前还不清楚。通过研究在 22、27、32、37 及 42°C 下，*E. coli* 面对浓度逐步升高的氨苄西林和加替沙星时的表型和基因型变化，以了解不同温度下致病菌接触环境水平抗生素时的抗性演化规律。研究发现，进化后（约 400 代）*E. coli* 的最低抑菌浓度（minimum inhibitory concentrations, MICs）增加了 4～323 倍。即使是未添加抗生素的 *E. coli*，其 MICs 最高也增加了 80 倍，出现在 27 和 32°C 中。温度对 MICs 的影响与 *E. coli* 的耐受性、细胞膜通透性、活性氧水平、突变率和 ß-内酰胺酶含量相关。不同温度下，相同抗生素水平对 *E. coli* 的抑制效果也存在差异，以 32°C 最优。*marA* 和 *rpoS* 为主的全局调控因子，热休克基因 *groEL* 和 *htpG*，以及铁转运调控因子在转录水平上的上调有助于菌株应对抗生素和温度的单独及联合胁迫。全基因组测序揭示了不同温度下抗性进化的特异性和一般性遗传变化。各个温度下 *E. coli* 的逐步突变主要集中在增强外排上，膜通透性的降低和抗生素靶位点的改变分别倾向于低温和高温。在重复试验中，可再次获得同类型突变。最后通过不同温度中进化后 *E. coli* 的适应度代价、抗性持久性以及生长曲线，评估全球变暖所带来的抗生素抗性风险。

关键词：抗生素抗性；全球变暖；环境浓度；基因突变

微塑料污染对微生物组的生态影响研究综述

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摘要

微塑料(microplastics, MPs，尺寸< 5 mm)碎片作为一类新兴污染物，广泛分布于环境和有机体中，因其粒径较小、稳定性较好、生物降解较难等特点，正受到越来越多的关注。微生物群落在生物地球化学循环中起着至关重要的作用，迄今为止，关于微塑料对微生物群落影响的研究很少。鉴于微生物组的重要性以及科学界对潜在微生物生态风险研究的呼声，预计相关研究将在未来几年蓬勃发展。本文拟对水生、土壤环境中微塑料对微生物组污染的研究现状进行综述。本综述的目的是：1)总结土壤中 MPs 的丰度、来源和性质；2)重点分析 MPs 污染物对陆地土壤系统微生物群落（细菌、真菌和原生生物）的污染机制；3)探讨 MPs 对水生环境中微生物组的生态效应；4）讨论生物可降解微塑料与微生物组群落组成、多样性相互作用的研究现状。本篇综述使生态学家、微生物学家、环境学家和政策制定者更好地理解微塑料污染，增加对土壤 MPs 污染的整体认识，突出了未来的重点研究领域，强调了 MPs 与微生物组的相关性及其对微生物群落生态平衡所构成的潜在威胁。

关键词：微生物生态学；微塑料污染；塑料降解；生态效应

宏基因组分析揭示了微生物驱动的全球内陆水磷循环

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摘要

微生物在磷（P）循环和 P 生物有效性中发挥着至关重要的作用。然而，尽管许多研究关注微生物介导的土壤 P 循环，但水体微生物 P 循环的潜力研究相对较少。本研究中，我们全球内陆水体的宏基因组测序数据集进行分析，探索微生物在全球内陆水体中参与磷循环的潜力，以及调查不同栖息地之间的潜力差异。研究发现，嘌呤和嘧啶代谢是调控水体磷循环动态的主要磷代谢途径。值得注意的是，氧化磷酸化和糖磷酸戊糖途径是河流和湖泊中的关键途径。相反，运输体和双组分系统是水库和饮用水中的 P 循环做出贡献的主要代谢途径。磷溶解微生物（PSMs）作为驱动全球土壤 P 循环的重要类群，同样广泛分布于各种水体生境中，这表明它们在水生态系统中的重要生物地球化学作用。在内陆水体中，具有溶解无机磷潜力（$\mathrm{PSM^{I}}$）的 PSMs 数量超过了能矿化磷酸酯（$\mathrm{PSM^{Pe}}$）和磷酸盐（$\mathrm{PSM^{Ph}}$）的 PSMs，在所有研究的水生生境中都存在类似趋势，这表明在水生态系统中，无机磷溶解可能是一个更关键的 P 循环过程。有趣的是，$\mathrm{PSM^{I\&Pe\&Ph}}$ 占所有 PSMs 总丰度的 16.9%，其中绝大部分属于变形菌门（80.2%），这表明变形菌门在内陆水生栖息地中是重要的 PSMs，并在促进 P 循环中发挥着重要作用。本研究为了解微生物在水生态系统中的磷循环作用提供了新的见解，这对于理解和管理这些环境中的养分动态可能具有潜在的影响。

关键词：内陆水体；磷（P）循环；磷代谢；溶磷微生物（PSMs）

Microbially-driven global inland water phosphorus cycling as revealed by metagenomic analysis

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Abstract

Microorganisms play crucial roles in phosphorus (P) turnover and P bioavailability. However, such understanding mainly focused on microbial-mediated P-cycling in soils, there are many fewer studies on water microbial P-cycling. In this study, we analyzed a global inland water metagenome sequencing dataset to explore the potential of microorganisms in P-cycling across different habitats. We found that purine and pyrimidine metabolism were the prominent P metabolic pathways in regulating the P-cycling in aquatic systems. Notably, oxidative phosphorylation and the pentose phosphate pathway were identified as key pathways in rivers and lakes, distinguishing them from other habitats. Conversely, transporters and two-component systems were found to be the primary metabolic pathways contributing to P-cycling in reservoirs and drinking water. Phosphorus-solubilizing microorganisms (PSMs), vital taxa that drive global soil P turnover, were found to be ubiquitously distributed across diverse water habitats. This underscores their significant biogeochemical role in aquatic ecosystems. PSMs of inland water with the potential to solubilize inorganic phosphate (PSM^{I}) outnumbered those capable of mineralizing phosphate esters (PSM^{Pe}) and phosphonates (PSM^{Ph}) across all the investigated aquatic habitats. This suggests that inorganic phosphate solubilization may be a more critical process for P-cycling in aquatic ecosystems. Interestingly, $\text{PSM}^{\text{I\&Pe\&Ph}}$ account for 16.9% of the total abundance of all PSMs, with the majority affiliated with the phylum of Proteobacteria (80.2%). Thus, Proteobacteria are important PSMs in inland water and play a vital role in facilitating P-cycling. Our study provides novel insights into the role of microorganisms in phosphorus cycling in aquatic systems, with potential implications for understanding and managing nutrient dynamics in these environments.

Keywords: Inland water; Phosphorus cycling; Phosphorus metabolism; Phosphorus-solubilizing microorganisms

海洋细菌胞外多糖可拉酸对厚壳贻贝附着的影响

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摘要

海洋细菌通常会以生物被膜的形式广泛存在于海洋中，生物被膜上存在复杂的水溶性胞外产物及表面特征性物质，这些化学信号能够诱导贻贝的附着。可拉酸（Colanic Acid）是一种主要的细菌胞外多糖，它既可以作为组成成分在细菌生物被膜形成过程中发挥重要作用，又可以以胞外多糖的形式作用于宿主生物。本研究通过提取纯化海洋细菌多糖可拉酸，构建可拉酸生物合成基因 *wcaJ* 缺失突变菌株 Δ*wcaJ*，探究可拉酸在海洋细菌生物被膜形成及诱导厚壳贻贝附着的作用。结果表明，从一种广泛存在的近海细菌海假交替单胞菌 *Pseudoalteromonas marina* ECSMB14103 中提取纯化出的可拉酸可以诱导厚壳贻贝稚贝的附着。与野生型相比，Δ*wcaJ* 细菌的运动性增强，生物被膜膜厚和细菌密度减少、胞外多糖及蛋白的含量降低，对厚壳贻贝稚贝附着的诱导活性显著降低。加入提取纯化后的可拉酸共同孵育，Δ*wcaJ* 生物被膜诱导活性显著提高，胞外多糖和蛋白含量显著回升。此外，厚壳贻贝完成附着变态的生理过程后，在二次附着阶段主要附着器官为足丝，为探究可拉酸在厚壳贻贝二次附着过程中的影响，本研究将提纯后的可拉酸稀释注射至厚壳贻贝体内，利用实时荧光定量 PCR 对贻贝足中足丝蛋白基因表达的变化进行了探究。发现可拉酸对厚壳贻贝不同的足丝蛋白起调控作用，增强贻贝的二次附着能力。综上，本研究为细菌生物被膜及厚壳贻贝附着变态之间的分子相互作用提供了新颖的见解，对探究可拉酸及其基因对生物被膜形成及厚壳贻贝附着调控机制提供了一定的理论基础。

关键词：可拉酸；*wcaJ*；生物被膜；厚壳贻贝；附着

Influence of Polymer Size on Polystyrene Biodegradation in Mealworms (Tenebrio molitor): Responses of Depolymerization Pattern, Gut Microbiome, and Metabolome to Polymers with Low to Ultra-High Molecular Weight

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Abstract

Biodegradation of polystyrene (PS) in mealworms has been identified with commercial PS foams. However, there is currently limited understanding of the influence of molecular weight (MW) on insect-mediated plastic biodegradation and the corresponding responses of mealworms. In this study, we provided the results of PS biodegradation, gut microbiome, and metabolome by feeding mealworms with high purity PS microplastics with a wide variety of MW. Over 24 days, mealworms fed with 0.20 g of PS showed decreasing removal of 74.1 ± 1.7%, 64.1 ± 1.6%, 64.4 ± 4.0%, 73.5 ± 0.9%, 60.6 ± 2.6%, and 39.7 ± 4.3% for PS polymers with respective weight-average molecular weight (M_w) of 6.70, 29.17, 88.63, 192.9, 612.2, and 1,346 kDa. The mealworms degraded most PS polymers via broad depolymerization but ultra-high MW PS via limited-extent depolymerization. The gut microbiome was strongly associated with the biodegradation, but that with low and medium MW PS was significantly distinct from that with ultra-high MW PS. Metabolomic analysis indicated that PS biodegradation reprogramed the metabolome and caused intestinal dysbiosis depending on MW. Our findings demonstrate that mealworms alter their gut microbiome and intestinal metabolic pathways in response to *in vivo* biodegradation of PS polymers of various MW.

Keywords: Polystyrene; Molecular weight; Biodegradation; Mealworms; Gut microbiome; Metabolome

Functional Traits Resolve Mechanisms Governing the Assembly and Distribution of Nitrogen-Cycling Microbial Communities in the Global Ocean

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Abstract

Microorganisms drive much of the marine nitrogen (N) cycle, which jointly controls the primary production in the global ocean. However, our understanding of the microbial communities driving the global ocean N cycle remains fragmented. Focusing on "who is doing what, where, and how?", this study draws a clear picture describing the global biogeography of marine N-cycling microbial communities by utilizing the Tara Oceans shotgun metagenomes. The marine N-cycling communities are highly variable taxonomically but relatively even at the functional trait level, showing clear functional redundancy properties. The functional traits and taxonomic groups are shaped by the same set of geo-environmental factors, among which, depth is the major factor impacting marine N-cycling communities, differentiating mesopelagic from epipelagic communities. Latitudinal diversity gradients and distance-decay relationships are observed for taxonomic groups, but rarely or weakly for functional traits. The composition of functional traits is strongly deterministic as revealed by null model analysis, while a higher degree of stochasticity is observed for taxonomic composition. Integrating multiple lines of evidence, in addition to drawing a biogeographic picture of marine N-cycling communities, this study also demonstrated an essential microbial ecological theory—determinism governs the assembly of microbial communities performing essential biogeochemical processes; the environment selects functional traits rather than taxonomic groups; functional redundancy underlies stochastic taxonomic community assembly.

Keywords: Marine nitrogen cycle; Functional traits; Diversity patterns; Community assembly; Stochasticity; Functional redundancy

反硝化菌外泌体产生及其功能的环境调控机制

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摘要

现有研究表明所有可培养细胞均可产生外泌体（Extracellular vesicles，EVs），其广泛存在于体液和自然环境中，并具有多种多样的功能。因此，细胞产生 EVs 以实现特定功能可能是生命过程普遍存在的一种基本机制。由于不同的外泌体产生机制使得环境中存在丰富多样的外泌体类型，并在这些微生物主导的生态系统中发挥着不同的生态作用。本研究以典型的反硝化细菌铜绿假单胞菌（*Pseudomonas aeruginosa* PA01）为研究材料，探索反硝化过程中的关键环境调控因子（氧气，硝酸盐浓度）对外泌体的产生、大小以及潜在功能的影响。我们发现在好氧和厌氧条件下，*P. aeruginosa* 产生外泌体的产率和丰度存在显着差异，其中外泌体的产率在好氧条件下显著高于厌氧条件。此外，厌氧条件下 *P. aeruginosa* 释放的外泌体的大小随生长周期显著增大，同时外泌体的产量与添加的硝酸盐浓度显著正相关。外泌体蛋白质组学分析表明，环境因子影响了 *P. aeruginosa* 外泌体运输的蛋白质组成和功能。在好氧条件下 *P. aeruginosa* 外泌体介导的细菌毒力和致病性增强，而当补充硝酸盐时，*P. aeruginosa* 外泌体中检测到了完整的反硝化途径的蛋白，推测反硝化细菌产生的外泌体参与了反硝化过程。本研究揭示了反硝化菌培养细胞外泌体在不同环境条件下的特征，并深入探讨了反硝化菌外泌体的潜在功能，这对于理解反硝化微生物群落外泌体参与的生态作用和生物地球化学循环至关重要。

关键词：反硝化；外泌体；蛋白质组学；铜绿假单胞菌（*Pseudomonas aeruginosa*）

低温好氧颗粒污泥信号分子调控机制及强化策略研究

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摘要

好氧颗粒污泥技术（AGS）是一种微生物在好氧条件下自固定化形成的具有紧实颗粒状结构的微生物聚集体，有研究表示，通过控制反应器运行条件 10°C 可以培养出好氧颗粒污泥，然而这种不利的生长条件使得颗粒在形成过程中的耗时较长且形成颗粒不稳定极易解体，因此需要对低温好氧颗粒污泥系统启动及稳定运行过程中的机制进行进一步的明确。以常温及低温条件的快速启动和变温运行过程中的好氧颗粒污泥系统的为研究对象，结合污泥形成特征分析、高效液相色谱仪检测、高通量测序技术等检测分析方法，考察常温和低温下恒温启动，变温运行过程中好氧颗粒污泥的理化性质、污染物处理效能、胞外聚合物含量组成成分、QS 系统中 AHL 信号分子、DSF 信号分子、c-di-GMP 信号分子与 EPS 浓度及成分的变化规律，并将其与颗粒污泥系统中的微生物群落组成的变化规律相结合，得出好氧颗粒污泥形成及运行的微生物学机制，解析各信号分子浓度对 EPS 分泌形成的影响，得出在这一过程中的关键节点、形成一种有效促进而非抑制的信号分子指导思路，从而得出常温、低温以及变温情况下颗粒产生的生物学机制。

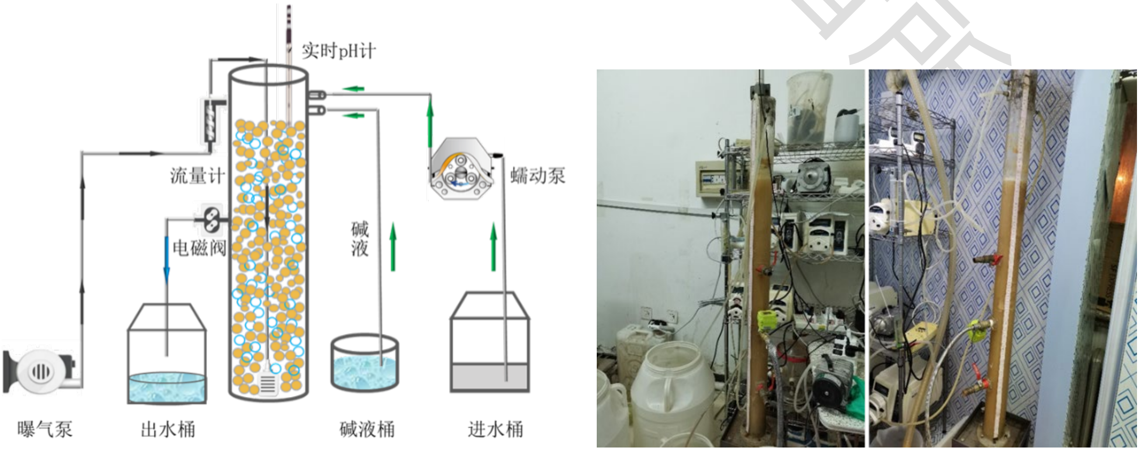

图 1 反应器组装示意图

关键词：低温条件；好氧颗粒污泥；信号分子；胞外聚合物（EPS）

海假交替单胞菌 *Pseudoalteromonas marina* 外膜蛋白调控因子通过调控外膜蛋白 OmpW 诱导厚壳贻贝附着

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摘要

厚壳贻贝（*Mytilus coruscus*） 由于其独特的附着生活方式会形成生物污损，但同时它也是我国重要的经济贝类。前期许多研究表明，海洋细菌形成的生物被膜能够作为外源化学信号影响海洋无脊椎动物的附着。海假交替单胞菌 *Pseudoalteromonas marina* 是存在于厚壳贻贝生活海域的优势菌，其生物被膜被证实可以稳定诱导厚壳贻贝稚贝附着，但具体诱导机制尚不明确。外膜蛋白 (OMP) 是广泛存在于革兰氏阴性菌中的生物被膜基质，能够介导细菌和宿主之间的黏附作用，目前它在细菌生物被膜调控海洋无脊椎动物附着中的作用尚不清楚。本研究选取厚壳贻贝作为模式生物，通过构建 OMP 家族相关基因缺失菌株、外源添加重组外膜蛋白 OmpW 诱导稚贝附着等实验，探究外膜蛋白调控厚壳贻贝附着的机制。结果表明，外膜蛋白调控因子 *ompR* 基因缺失菌株形成的生物被膜诱导稚贝附着率显著降低（$P<0.05$），Δ*ompR* 生物被膜中可拉酸等胞外多糖含量明显减少（$P<0.05$），同时发现 *ΔompR* 的外膜蛋白基因 *ompW* 表达水平降低，OmpW 蛋白含量显著减少。*ompW* 基因的缺失导致菌体内中第二信使 c-di-GMP 含量降低，细菌运动性增强，生物被膜密度、厚度以及可拉酸含量显著降低（$P<0.05$），并且对厚壳贻贝的附着诱导率减少 38.33%。分别添加重组蛋白 OmpW 至 Δ*ompR* 与 Δ*ompW* 共培养形成的生物被膜，其生物被膜的诱导附着率均恢复至野生菌水平，同时可拉酸等胞外多糖也得到了上调。

综上所述，外膜蛋白调控因子 *ompR* 能够通过调控外膜蛋白 OmpW 含量介导可拉酸等胞外多糖的分泌，从而调控生物被膜诱导厚壳贻贝附着。本研究为细菌生物被膜调控海洋无脊椎动物附着变态作用机制提供参考依据，同时为海洋细菌与宿主之间相互作用的研究提供新思路。

关键词：外膜蛋白 OmpW；生物被膜；厚壳贻贝；附着

耐 Cr(VI)微生物的筛选及其对 Cr(VI)的转化作用

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摘要

铬(VI)因其强毒性而引起的环境污染问题日益突出，在众多修复技术中，微生物修复技术处理铬污染场地具有应用潜力。因此筛选出能适应铬污染场地环境且具有高效转化还原 Cr(VI)能力的菌株尤为重要。本研究从受铬污染的蟒河水体-沉积物中分离筛选的 Cr(VI)高效还原菌，对菌株进行分子生物学鉴定，并探究了菌株对 Cr(VI)的转化还原能力。结果表明，菌株 P18、P20 具耐受 Cr(VI)浓度为 1000mg/L 的能力且生长良好。经分子生物学鉴定，菌株 P18 为 *Trichoderma yunnanense*，菌株 P20 为 *Fusarium annulatum*。通过测定外源添加不同浓度 Cr(VI)、不同培养时间条件下菌株对 Cr(VI)的转化还原能力，结果表明，在培养 120h 内，菌株 *Trichoderma yunnanense*、*Fusarium annulatum* 在 100mg/L Cr(VI)浓度下 Cr(VI)去除率可达 79.4%、63.48%；在 200mg/L Cr(VI)浓度下 Cr(VI)去除率可达 55.2%、33.66%；在 500mg/L Cr(VI)浓度下 Cr(VI)去除率可达 23.42%、22.41%。且培养上清中残留 Cr(VI)的降低伴随着 Cr(III)的增加，在 120h、100mg/L Cr(VI)浓度条件下菌株 *Trichoderma yunnanense*、*Fusarium annulatum* 上清 Cr(III)占比为 73.55%、63.48%；通过对 100mg/L Cr(VI)浓度下菌体生物量与上清 Cr(III)占比进行相关性分析，*Trichoderma yunnanense*、*Fusarium annulatum* 生物量与上清 Cr(III)占比 R^2 分别为 0.886、0.948，P 值分别为 0.019、0.004，均呈显著正相关关系，菌株存在对 Cr(VI)的转化作用。本研究分离筛选出得到的 *Trichoderma yunnanense*、*Fusarium annulatum* 为潜在的可用于铬污染微生物修复的候选菌株。

关键词：铬污染；Cr(VI)转化；*Trichoderma yunnanense*；*Fusarium annulatu*

Bacteria rather than fungi mediate the chemodiversity of dissolved organic matter in a mudflat intertidal zone

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Abstract

Dissolved organic matter (DOM) in natural ecosystems is intimately associated with microbial communities. However, it remains unclear whether the diversity patterns followed by microbes can be transmitted to DOM compounds. Considering the structural properties of DOM compounds and the roles of microbes in ecosystems, we hypothesized that bacteria tended to be more closely associated with DOM compounds than fungi. To test the above hypothesis and bridge this knowledge gap, the diversity patterns and ecological processes for the DOM compounds, and the bacterial and fungal communities in a mudflat intertidal zone were comparatively investigated. As a result, spatial scaling patterns followed by microbes, including the diversity-area and distance-decay relationships, were also observed for DOM compounds. Lipid-like and aliphatic-like molecules comprised the major DOM compounds associated with environmental factors. Both the alpha- and beta-chemodiversity of DOM compounds were significantly associated with the diversity of bacterial communities, but not fungal communities. Co-occurrence ecological network analysis suggested that DOM compounds were more frequently associated with bacteria than fungi. Further, consistent community assembly patterns were observed for DOM and bacterial communities, but not fungal communities. Integrating multiple lines of evidence, this study demonstrated that bacteria rather than fungi mediated the chemodiversity of DOM in the mudflat intertidal zone. This study elucidates the spatial patterns of complex dissolved organic matter (DOM) pools in the intertidal ecosystem, shedding light on the intricate relationship between DOM compounds and bacterial communities.

Keywords: Dissolved organic matter; Microbial communities; Spatial scaling; Stochasticity analyses; Ecological networks

外源供氢强化污水污泥厌氧消化原位沼气提纯

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摘要

原位沼气提纯已被认为是实现二氧化碳捕获和高效资源利用的一种很有前途的方法。最近的研究表明外源供氢可以用于强化沼气提纯。然而，外源氢气供应对原位沼气升提纯的影响仍知之甚少。本研究旨在研究直接和间接外源氢气供应对原位沼气提纯的影响，并阐明其潜在的机制。试验结果表明，在外源氢气供应条件下甲烷生产和沼气提纯效率显著提高。具体而言，在批量试验中，添加 10 g/L 粗零价产生最高的累积甲烷产量（286.4 mL/g-VS）和最高的甲烷含量（95.5%），与不添加零价铁相比，分别增加了 2.2 倍和 1.5 倍。在半连续运行试验中，使用中空纤维进行氢气扩散的加氢反应器提高了甲烷的产生速率（52.0 mL/g-VS），而由加零价铁反应器的结果表明，较低的氢气量更有利于甲烷的纯化（92.0%）。进一步分析得到，外源氢气供应通过增强水解、产乙酸和氢营养产甲烷过程促进甲烷的产生和沼气的提纯，这与微生物群落分析的结果一致。这些发现为污泥厌氧消化过程中外源氢气供应对原位沼气提纯的影响提供了宝贵的见解，为未来制定旨在提高甲烷产量和废物源沼气提纯的战略提供了指导。

关键词：厌氧消化；原位沼气提纯；氢气；零价铁

Enhanced *in-situ* biogas upgrading with exogenous hydrogen supply during anaerobic digestion of sewage sludge

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Abstract

In-situ biogas upgrading has been proposed as a promising approach to achieve carbon dioxide capture and efficient resource utilization. Recent investigations have highlighted that exogenous hydrogen is available to drive biogas purification. However, the impact of exogenous hydrogen supply on *in-situ* biogas upgrading remains poorly understood. This study aims to investigate the effects of direct and indirect hydrogen supply on *in-situ* biogas upgrading and elucidate the potential underlying mechanisms. The experimental findings demonstrate a significant enhancement in methane production efficiency and biogas upgrading through exogenous hydrogen supply. Specifically, batch tests showed that adding 10 g/L coarse zero valent iron (ZVI) yielded the highest cumulative methane yield (286.4 mL/g-VS) and methane content (95.5%), representing a 2.2-fold and 1.5-fold increase, respectively, compared to the absence of ZVI. In semi-continuous tests, the implementation of hollow fiber for hydrogen diffusion leads to an increased methane production rate (52.0 mL/g-VS), while the addition of ZVI revealed that lower hydrogen amounts are more favorable for methane purification (92.0%). Further analysis reveals that exogenous hydrogen supply promotes methane production and biogas upgrading by enhancing hydrolysis, acetogenesis, and hydrogenotrophic methanogenesis, which is consistent with the results obtained from the microbial community analysis. These findings provide valuable insights into the impact of exogenous hydrogen supply on *in-situ* biogas upgrading during anaerobic digestion of sewage sludge, offering guidance for the development of strategies aimed at enhancing methane production and biogas upgrading from waste sources in the future.

Keywords: Anaerobic digestion; *In-situ* biogas upgrading; Hydrogen; Zero valent iron

富营养化改变浮游细菌-浮游植物群落结构及其与 CH_4、CO_2 的耦合关系

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摘要

大气中 CH_4 和 CO_2 的迅速增加是全球变暖的主要原因之一。人工水库在许多方面不同于自然系统，这可能会改变这些系统的 CH_4 和 CO_2 排放。此外，水库的建设改变了水体的营养状态，破坏了原有的生态平衡，改变了微生物数量、结构以及各种相关的环境因素。然而，浮游植物-细菌相互作用强度对不同营养级水体中 CH_4 和 CO_2 的影响尚不清楚。本研究利用 16S rRNA 和 23S rRNA 对长江上游 TGR、XLD、XJB、SZT、XB 等 5 个不同营养级典型水库中的浮游细菌和浮游植物群落进行样品测序分析。结果表明，营养程度越高，浮游细菌和浮游植物的 α 多样性越低。贫营养和中营养水体中浮游细菌和浮游植物的 α 多样性影响 CH_4 和 CO_2 浓度。随着浮游生物微生物 α-多样性的增加，水体中 CH_4 的浓度有增加的趋势，造成这种现象的原因可能与微生物对碳的利用有关。共现性网络分析表明，网络密度、聚类系数和网络复杂度随着营养水平的增加而增加，表明微生物相互作用的变化与富营养化有关。随机森林模型分析表明，TSI、DOC、DO、POC 和 N/P 是影响浮游植物-细菌相互作用强度的最重要因素。进一步相关分析发现，CH_4、CO_2 与 TSI、DOC、DO、POC、N/P 显着相关，间接表明营养水平的变化会影响浮游植物-细菌相互作用，进而影响 CO_2、CH_4。此外，结构方程模型还表明浮游植物-细菌相互作用与 CH_4/CO_2 比之间存在直接因果关系。通过揭示不同营养水平水库浮游植物和细菌的群落多样性、群落结构及相互作用，探讨水库浮游植物-细菌群落与 CH_4 和 CO_2 浓度的关系，为阐明长江上游典型水库 CH_4 和 CO_2 汇的微生物驱动机制奠定了理论基础。

关键词：浮游细菌；浮游植物；CH_4；CO_2；藻-菌互作

外源电子强化高底物浓度厌氧发酵产氢同步产丁醇

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摘要

氢气被认为是最清洁的能源，具有密度低和热值高等优势。此外生物丁醇也是一种极具潜力的新型生物液体燃料，被认为是最适合代替汽油的可再生能源。本研究针对目前厌氧发酵产氢系统中底物浓度低，容积产气率不高的问题，探究了高底物浓度条件下厌氧发酵产氢的可行性，在此基础上考察了外源电子对高浓度底物厌氧发酵产氢及产丁醇的促进作用。结果表明，底物浓度升高到 50 g/L 时，单位容积产氢量和丁醇浓度都显著提高，进行能源回收分析发现，底物浓度 50 g/L 时的能源回收效率达到最高。初始底物浓度 50 g/L 时物种多样性高于其他组，且群落分布均匀度高于其他组，这可能也是其具有良好的产氢气和丁醇能力的原因之一。结合产物得率和能源回收效率分析，确定最佳底物浓度为 50 g/L，在此基础上对发酵体系添加外源电子中性红和甲基紫精。添加中性红和甲基紫精后发酵末端的氢气和丁醇产率相比空白对照均有所提升，丁醇在发酵末端挥发性有机物中的占比也明显提高。通过对醇脱氢酶、乙酸激酶和丁酸激酶的测定发现，外源电子对醇脱氢酶、乙酰激酶和丁酰激酶的表达具有促进作用。

关键词：底物浓度；氢气；丁醇；外源电子；调控

悬浮污泥微生物群落功能和构建过程的电选择机制

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摘要

弱电介入型水解酸化工艺被证明能够有效提升难生物降解工业废水预处理效能。然而，弱电介入对悬浮污泥微生物群落功能和构建过程的影响知之甚少。我们使用 16S rRNA 基因和宏基因组测序，研究了弱电介入对悬浮污泥微生物群落结构、功能、构建过程和微生物相互作用的选择机制。与传统水解酸化相比，弱电介入提升了模式污染物（含硝基偶氮有机物茜素黄 R）的生物转化效率。弱电介入显著改变了悬浮污泥微生物群落结构和功能基因组成，脱色功能菌属和电活性菌属被显著富集；发酵菌属与脱色功能菌属和电活性菌属之间的相互作用更多，而不同发酵菌属之间的相互作用更少；弱电介入下编码偶氮/硝基还原酶的基因以及参与偶氮染料转化的氧化还原中介体（例如泛醌）生物合成基因在脱色功能菌属中显著富集。确定性过程在弱电介入的微生物群落构建过程中相对重要性更高，且脱色功能菌属和电活性菌属的构建主要受确定性过程主导，发酵菌属受随机性过程主导。这项研究为弱电介入对悬浮污泥微生物群落功能和构建过程的影响提供了新见解，并为调控水处理工程系统中污泥微生物组提供了新策略。

关键词：水解酸化；弱电介入；微生物群落构建；微生物互作；功能基因

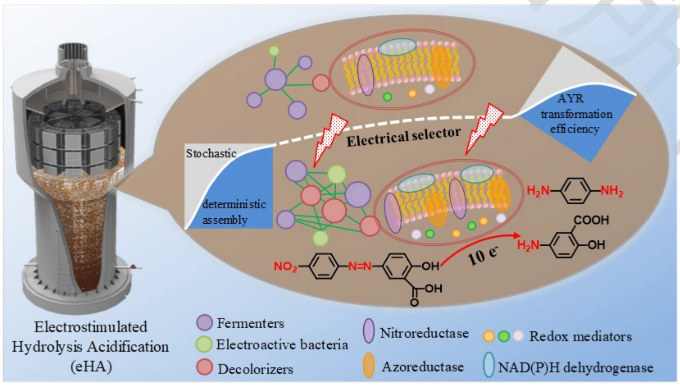

图1 污泥菌群功能与构建过程的电选择机制模型

近海潮间带木质素降解细菌群落的结构及功能特征

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摘要

挖掘海洋生态系统的固碳储碳潜力，提升海洋碳汇能力，能够助力实现“碳中和”的目标。微型生物所驱动的代谢活动是海洋碳汇的重要组成部分，而陆源有机碳在海洋中的转化过程目前仍是一个“谜”。本研究中，我们通过四种不同类型的木质素底物在近海潮间带进行了为期一年半的原位富集。结合扩增子和宏基因组学鉴定和表征了近海潮间带环境下参与不同类型木质素底物降解细菌群落的结构及功能特征。结果表明，确定性（时间、底物）始终主导着近海潮间带环境中木质素降解细菌群落的结构组成，且富集时长对于群落结构的影响高于不同类型底物的影响。随着富集时长的增加，群落中物种的均匀度逐渐增加，参与木质素降解细菌群落成员间的互作也变得更加紧密。尽管不同底物间群落结构差异显著，但杨木、松木底物所富集群落结构的相似度始终较高，我们将在官能团水平上进一步解析其群落结构相似性的原因。我们也观察到，在底物所富集的群落中可能存在着两个菌群，分别参与纤维素、半纤维素降解和木质素降解，且两个群落间存在一定的协同效应。进一步研究中，我们将结合宏基因组学，对参与纤维素、半纤维素、木质素降解的功能基因进行探究，解析两个群落是如何作用，从而共同完成底物降解。本研究有助于理解木质素在海洋生态系统中的降解和转化过程，弥补微生物因素在海洋（近海水圈生境）碳循环模式构建中的缺失。

关键词：近海潮间带；木质素；降解；细菌群落；功能基因

污水厂中多重耐药菌的筛选及耐药基因转移机制的研究

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摘要

抗生素是一种具有杀菌、抑菌和促生长功效的物质，生产方便、效能显著，广泛应用于医疗和畜牧领域。我国抗生素的使用量常位居世界前列，但抗生素的实际利用率有限，部分抗生素随着人类和动物的生命活动进入到环境中造成选择性压力，使得环境中的微生物出现耐药性，导致耐药基因的富集。耐药基因可复制、可转移，威胁到人类健康和环境安全。为了解析我国北方污水厂中多重耐药菌中耐药基因的接合转移机制，从哈尔滨市某污水厂中筛选出能发生接合作用的多重耐药菌，通过药敏试验和全基因组测序，全面解析菌株生物学特征，进一步从基因组层面探究耐药基因转移机制。为今后微生物耐药问题的治理提供理论基础和数据支持。

关键词：污水厂；多重耐药菌；转移机制；全基因组测序

Screening of multidrug resistant bacteria and Study on the mechanism of drug resistance gene transfer in sewage treatment plan

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Abstract

Antibiotics are substances with sterilization, bacteriostasis and growth promoting effects. They are widely used in the fields of medical treatment and animal husbandry. The use of antibiotics in China is often in the forefront of the world, but the actual utilization rate of antibiotics is limited. Some antibiotics enter the environment with the life activities of human and animals, causing selective pressure, making microorganisms in the environment resistant to drugs and leading to the enrichment of drug-resistant genes. Drug resistance genes can be replicated and transferred, threatening human health and environmental safety. In order to analyze the conjugation and transfer mechanism of drug-resistant genes in multidrug-resistant bacteria in sewage plants in northern China, multidrug-resistant bacteria capable of conjugation were screened from a sewage plant in Harbin. Through drug sensitivity test and whole genome sequencing, the biological characteristics of the strains were comprehensively analyzed, and the mechanism of drug-resistant gene transfer was further explored from the genomic level. To provide theoretical basis and data support for the treatment of microbial drug resistance in the future

Keywords: Sewage plant; Multidrug-resistant bacteria; Transfer mechanism; Whole genome sequencing technology

蜜蜂肠道菌群的宿主与地理分异机制研究

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摘要

蜜蜂作为传粉者和产蜜者，具有重要的生态价值和经济价值。肠道菌群在维持宿主健康和环境适应性方面具有重要作用。但是，蜜蜂肠道菌群的大尺度空间分异规律及菌群构建的生态过程机制尚不清楚。该研究对我国 1000 公里范围内的两种蜜蜂（中蜂、意蜂）的肠道菌群进行了高通量测序分析，探究了蜜蜂肠道菌群的宿主格局和地理格局，区分了不同生态过程（均质选择、异化选择、均质扩散、扩散限制和随机漂变）在塑造这种格局上的相对作用。研究发现中蜂和意蜂的肠道菌群显著不同，这种格局是由宿主与肠道菌群长期共进化形成的种间扩散限制导致。均质选择作用在意蜂肠道菌群构建上起主导作用（图 3），这使意蜂具有比中蜂更多样且更稳定的肠道菌群。大尺度下蜜蜂肠道菌群呈明显的地理分异规律，表现为显著的 alpha 多样性随纬度降低以及群落相似性随距离衰减的关系模式。这种地理格局的形成是由随机漂变，而非异化选择或扩散限制主导。该研究揭示了宿主和地理因素改变群落构建过程进而塑造特异的蜜蜂肠道菌群格局的生态规律，为理解蜜蜂肠道菌群的形成、发展和进化提供了理论基础。

关键词：肠道微生物；蜜蜂；宿主；地理环境；群落构建过程

大型海藻凋落过程微生物驱动的碳汇形成机制

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摘要

大型海藻是重要的蓝碳，因其碳汇潜能大而被广泛关注，但不同类型大型海藻生态系统碳汇途径及其微生物驱动机制不清楚。本研究以海藻凋落期大型海藻恢复区（北海涠洲岛）和大型海藻栽培区（汕头南澳岛）为对象，通过对海藻区和无海藻对照区海水和沉积物样品分析，结合室内模拟验证实验，以期揭示大型海藻系统微生物驱动的碳汇形成机制。碳组分分析结果表明，大型海藻栽培区海水中 DOC 含量显著高于海藻恢复区；虽然两种不同大型海藻系统海水 DOC 含量与对照区无显著差异，但沉积物中 TC、SOC 及 DOC 含量显著高于无海藻对照区。基于 16S rRNA 基因扩增子测序，海藻区域微生物多样性更高，且海藻栽培区微生物群落 α 多样性、稳定性和网络复杂度均显著高于恢复区。分子生态网络分析表明 *Thermoanaerobacteraceae*、*Nitrosococcaceae* 和 *Desulfobulbaceae* 是决定海藻生态系统微生物群落生态网络的关键类群，分别参与厌氧发酵、厌氧氨氧化和硫酸盐还原过程。进而对 42 个沉积物样品的宏基因组测序分析得到 854 个宏基因组组装基因组（MAGs），基于 dbCAN 数据库注释了所有基因组草图和 MAGs 中的碳水化合物活性酶（CAZyme）基因，发现 *Vibrionaceae*，*Xenococcaceae*，*Nitrosopumilacea* 具有最高比例的糖苷水解酶（GH）、碳水化合物酯酶（CE）、碳水化合物结合模块（CBM）、辅助活性酶（AA）和多糖裂解酶（PL）。而且，多糖代谢途径可以决定大型海藻分解过程中多糖的存在形式。总而言之，大型海藻凋落后主要通过沉积物碳储存途径增加海洋碳汇。进而我们正在通过室内模拟实验，对碳同位素标记海藻碳汇途径和微生物驱动机制进行进一步验证。因此，本研究将为大型海藻向沉积物储碳并形成碳汇的微生物驱动机制提供新见解。

关键词：碳代谢；大型海藻；微生物群落；碳汇途径

锑污染环境微生物驱动的溶磷和抗锑机制

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摘要

微生物在重金属污染土壤中的磷（P）循环和 P 生物可利用性增加中起着关键作用。然而，微生物驱动的 P 循环过程及其对重金属污染物的抗性机制尚不清楚。我们以世界上最大的锑（Sb）矿区——中国锡矿山为对象，从不同污染程度区域的水平和垂直两个维度采集土壤样品，通过测定土壤理化性质及相关磷酸酶活性，结合微生物组 16S rRNA 基因扩增子和宏基因组测序分析，解析了锑污染土壤磷循环微生物群落，揭示了微生物驱动的磷循环机制和抗锑策略。我们发现土壤中的总 Sb 含量和 pH 是影响细菌群落多样性、结构和 P 循环特性的主要因素。携带编码葡萄糖酸酶的 *gcd* 基因的细菌与无机磷（Pi）溶解紧密相关，并显著增强土壤中 P 的生物可利用性。共获得 106 个几乎完整的细菌宏基因组组装基因组（MAGs），其中 60.4%携带了 *gcd* 基因。携带 *gcd* 基因的细菌又普遍存在由 *pit* 或 *pstSCAB* 编码的 Pi 转运系统，携带 *gcd* 基因细菌中有 43.8%的细菌也携带编码 Sb 外排泵的 *acr3* 基因。对 *acr3* 基因的系统发育和潜在水平基因转移（HGT）分析表明，Sb 外排是一种主要的的抗锑机制，并且两个携带 *gcd* 基因的 MAGs 可能通过 HGT 获得 *acr3* 基因。综上，Sb 外排可以增强矿区土壤中溶磷菌的磷循环和重金属抗性。本研究不仅拓展了对土壤磷循环微生物的生态功能的认知，也可为有效管理和修复重金属污染土壤提供了新依据。

关键词：锑污染；磷循环微生物；宏基因组学；溶磷菌；锑抗性

典型农牧交错带三种植被类型土壤微生物特征及影响因素

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摘要

本研究利用 Illumina MiSeq 高通量测序技术，分析典型农牧交错带——张家口屯垦林场三种典型植被恢复模式(天然草地、樟子松 *pinus sylvestris var. mongolica* 人工林和杨树 *populus spp.*人工林)土壤细菌和真菌群落组成及多样性，并探究其与土壤环境因子的相关性。测序结果表明，放线菌门、酸杆菌门和变形菌门是土壤主要的细菌群落，担子菌门和子囊菌门为主要的土壤真菌群落。α 多样性分析结果表明：三种植被恢复模式土壤细菌 shannon 和 chao 指数无显著差异，草地真菌 shannon 指数和 chao 指数均极显著高于杨树，草地真菌 shannon 指数显著高于樟子松。β 多样性分析结果显示：三种植被恢复模式土壤细菌群落组成差异不显著（P=0.229），而土壤真菌群落组成差异显著(P=0.001)。冗余分析发现粉粒是细菌群落结构的重要驱动因素，而土壤有机碳、全氮、SOC/TN 和黏粒是真菌群落结构的重要驱动因素。综上所述，植被类型对土壤真菌的影响较大，对土壤细菌的影响较弱。研究结果可为半干旱农牧交错生态脆弱区的生态恢复提供理论依据及技术支撑。

关键词：植被恢复；高通量测序；微生物多样性；人工林

Structural characteristics and influencing factors of soil microbial community in three types vegetation restoration in Zhangjiakou area

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Abstract

Illumina MiSeq high-throughput sequencing techniques were used to analyze the soil bacterial and fungal community of three vegetation restoration types (natural grassland, pinus sylvestris var. mongolica plantation, and populus spp. plantation) within a typical agro-pastoral zone – Zhangjiakou Tunken Forest, and correlation between these communities and soil environmental factors was explored. The sequencing results indicated that Actinobacteria, Acidobacteriota, and Proteobacteria were the dominant bacterial communities, whereas Basidiomycota and Ascomycota were the main fungal communities. The α-diversity analysis revealed no significant difference in the Shannon and Chao indices of soil bacteria among the three vegetation restoration modes. However, the Shannon and Chao indices of grass fungi were both very significantly higher than those of populus, and the Shannon index of grassland fungi was significantly higher than that of pinus. The β-diversity analysis indicated a significant difference in the composition of soil fungal communities (*P*=0.001), while no significant difference was observed in the composition of soil bacterial communities among the three vegetation restoration patterns (*P*=0.229). Redundancy analysis demonstrated that meal particles played a crucial role in shaping bacterial community structure, while soil organic carbon, total nitrogen, SOC/TN ratio, and mucilage were influential factors in fungal community structure. In conclusion, vegetation type exhibited a stronger influence on soil fungi and a weaker influence on soil bacteria. These findings offer theoretical bases and technical supports for ecological restoration in semi-arid agro-pastoral ecologically fragile regions.

Keywords: Vegetation restoration; High-throughput sequencing; Microbial diversity; Plantation forestry

黄河河南段沉积物中三唑类杀菌剂耐药性研究

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摘要

近年来，病原真菌的抗药性水平持续上升，在临床和农业领域引发了严重的后果。在临床实践中，病原真菌的耐药性导致了药物疗效的降低、失效甚至患者死亡；在农业生产中，病原真菌的耐药性导致全球范围内超过 20%的粮食作物减产，对人类社会的健康发展构成了严重威胁。河南作为农业及人口大省，三唑类杀菌剂被广泛应用于农业生产，每年使用农药 14 万余吨。其间杀菌剂的大量使用、耐药真菌的流行是否会导致黄河河南段沉积物中的耐药真菌的出现，目前未见报道。本研究以黄河河南段沉积物的 13 个样本点（干流：孟津到陈桥 5 个，支流：伊洛河与沁河各 3 个，入河口 2 个）为对象，通过药敏平板培养-菌落计数法、分子生物学鉴定，对三唑类杀菌剂耐药真菌在沉积物中的赋存特征进行研究。结果表明，三唑类杀菌剂（戊唑醇、腈菌唑、三唑酮）的耐药比例为 10-20%，远低于非三唑类杀菌剂（嘧菌酯、多菌灵）的 60-100%。沁河入河口（71.95%）与伊洛河入河口（47.87%）、花园口（31.13%）的三唑类耐药比例均值远高于其它位置，且分离得到的对单一杀菌剂耐药的真菌（均 200 株以上）及多重耐药真菌（均 60 株左右）也表现同样特征。单一三唑类杀菌剂耐药真菌中，36.1-41.4%的菌株对 3 种三唑类杀菌剂都表现耐药性，18-26.8%同时对 5 种杀菌剂表现耐药性。通过 ITS 鉴定，得到 6 种主要的多重耐药真菌属：*Meyerozyma* spp.、*Clonostachys* spp.、*Trichoderma* spp.、*Parasarocladium* spp.、*Fusarium* spp.、*Aspergillus* spp.。本研究为黄河沉积物中的耐药真菌及其带来的健康风险提供了数据支持，进一步分析了黄河流域真菌群落的耐药情况，为黄河微生态研究提供了理论依据，并提示了其可能对人类社会存在潜在风险。

关键词：黄河沉积物；三唑类杀菌剂；耐药比例；多重耐药真菌

绿肥不同施肥模式对农田土壤微生物群落以及土壤改良的影响

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摘要

目前，由于大量使用化肥，特别是不合理使用，造成农田污染，农田质量下降，土壤硬化等问题，导致越来越严重的环境问题。绿肥是作物轮作休耕，提高耕地质量，减少化肥施用的重要技术手段。本研究在十年玉米种植试验田中，分别施用不同绿肥（甜豌豆，麻豌豆）和采取不同的施用方式（根茬和压青）处理模式下，研究对根际土壤微生物群落和土壤改良的影响，阐明土壤微生物参与不同处理下玉米和绿肥产量以及土壤改良作用机理。我们发现微生物系统发育被分为四个主要的生态群，其中包含一定比例的快速生长群、营养群和潜在的植物病原体。相比于单作，间作不同绿肥并施用不同施肥方式改变土壤微生物的群落变化，养分含量和养分利用率有所提高，潜在致病菌的相对丰度降低，丛枝菌根真菌（AMF）的相丰度增加。硝态氮，铵态氮，速效钾和 PH 跟微生物群落变化呈显著性相关。我们的工作表明，间作绿肥对土壤微生物和土壤改良的响应在在很大程度上调节了农田土壤土壤质量和微生物群落，并表明操纵这些微生物系统类型可能为维持田间生产力提供一个可持续的解决方案。

关键词：绿肥；土壤微生物群落；间作；土壤改良

一株新根瘤菌 Neorhizobium glycine EC2-8 及其应用

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摘要

根瘤菌能侵染豆科植物并与之形成共生结瘤固氮体系，其固氮量占到生物固氮总量的 60%以上。生物固氮作用可减少化学氮肥的施用，降低氮肥过量施用造成的土壤无机氮素累积、土壤酸碱失衡、水体富营养化等风险，促进并提高农田生态系统的健康发展。因此，筛选具有高效结瘤固氮能力的根瘤菌既可以丰富国际根瘤菌菌种资源库、又能为研发商用根瘤菌菌剂提供候选菌株，减少化肥的施用，实现农业绿色发展。在本研究中，我们从大豆根瘤内分离纯化获得一株根瘤菌。通过对菌株进行形态特征、生理生化检测和系统发育分析，确定其为隶属于 *Neorhizobium* sp.（新根瘤菌属）的一个根瘤菌新种，并将其命名为 EC2-8。与亲缘关系最相近的菌株 *Neorhizobium tomejilense* T17_20$^{\mathrm{T}}$ 的 16S rRNA 基因相似性为 98.57%。回接实验表明，菌株 EC2-8 能够侵染大豆根部并形成有效根瘤，还可明显增加大豆根长、根表面积和根体积，以及地上鲜重和干重。通过与优良的大豆根瘤菌 USDA110 进行比较，发现菌株 EC2-8 在根瘤数目、地上干重方面，与 USDA110 表现相当，具有非常可观的开发前景。

关键词：新根瘤菌；大豆；结瘤；共生

土壤功能菌株的环境调控影响农田土壤氧化亚氮排放差异的探究

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摘要

农田土壤的氮循环网络中，多种氮转化途径共同参与维持土壤中整体的氮平衡，部分氮转化途径如反硝化、硝化、硝酸盐异化还原为铵（DNRA）等会产生气态氮化物 N_2O、N_2 释放到大气中。N_2O 是一种强效的温室气体，其增温潜势是 CO_2 约 300 倍，并且参与对平流层臭氧层的破坏。全球农田氮素每年输入总量高达 2 亿吨，而较低的氮素利用率和氮素流失导致水体富营养化、土壤酸化、温室效应、生物多样性减少等问题。因此如何调控农田土壤氮循环从而更有效利用氮素、减少温室气体 N_2O 排放是目前亟待解决的问题。本实验室前期研究发现，采集自我国黑龙江省的黑土和河北省的潮土的氮转化效率、N_2O 排放量之间存在明显差异。为了探究两种土壤氮转化效率和 N_2O 排放差异的微生物机制，本研究设置不同培养条件，从黑土和潮土中共分离筛选得到 893 株菌株，包括黑土中 3 门 22 属 306 菌株，潮土中 3 门 33 属 336 菌株。通过 16S rRNA 基因测序鉴定分离株分类地位，包括黑土和潮土中的优势属 *Lysobacter*、*Ensifer*、*Castellaniella*、*Streptomyces*、*Bacillus*、*Nocardiodes* 等。检验不同分离株的反硝化以及 DNRA 途径相关功能基因组成，初步筛选到分离株 16 属 35 株携带 *narG* 基因、4 属 13 株携带 *nirS* 基因，8 属 38 株携带 *nirK* 基因，16 属 59 株携带 *nosZ* 基因，以及 5 属 7 株携带 *nrfA* 基因。进一步通过功能表型验证，得到土壤中关键的氮转化功能分离株，包括黑土中 7 属 150 株和潮土中 7 属 154 株。探究碳源、氮源、O_2 等不同环境因素对土壤关键分离株的影响，为减少温室气体排放和土壤氮损失的微生物机制提供直接依据，为今后开展广泛和深入的研究提供一定的理论基础，这对于减轻环境污染和促进农业可持续发展有着重大的意义。

关键词：氮转化途径；黑土；潮土；N_2O；氮转化功能菌株

河口红树林湿地微生物驱动的甲烷氮硫循环及其耦合机制

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摘要

微生物驱动的甲烷循环是影响全球变暖的重要过程。作为滨海典型的蓝碳生态系统，河口红树林湿地具有生物多样性高、环境多变、好氧厌氧交替，多种电子受体共存等特色，是重要的碳汇和甲烷排放源。然而红树林湿地微生物驱动的甲烷氮硫循环耦合机制及其对缓解全球变暖的贡献还没有清晰的认识。鉴于现有公共数据库对于分析甲烷循环微生物群落存在局限性，我们首先构建了高效准确的甲烷循环功能基因数据库（MCycDB），包含了 298 个甲烷循环功能基因并覆盖 10 条甲烷代谢通路。与已知数据库（arCOG, COG, eggNOG, KEGG）相比，MCycDB 对于分析宏基因组中甲烷循环微生物群落具有高度的特异性、覆盖度和准确性。基于构建的数据库，本研究进一步利用宏基因组测序方法研究了红树林沉积物甲烷、氮和硫循环基因/途径的垂直分布规律及其潜在的耦合机制。结果表明不同深度的红树林沉积物微生物驱动的甲烷氮硫循环过程存在明显差异，pH 和酸可挥发性硫化物（AVS）等环境因子驱动了不同代谢过程的垂直分布规律，其中 AVS 可能是影响红树林沉积物硫氧化和反硝化的关键电子供体。参与硫氧化和反硝化过程的关键基因在浅层 (0-15 cm) 丰度相对较高，主要由硫氧化驱动的反硝化菌介导，其中 *Burkholderiales* 在耦合这两个过程中起重要作用。参与硫还原和产甲烷过程的关键基因在中层 (15-30 cm) 和深层 (30-100 cm) 丰度较高。硫酸盐还原菌 (SRB) 可以通过直接电子转移或零价硫与甲烷厌氧氧化菌(ANME) 建立共生关系，从而促进产甲烷菌和 SRB 在中层和深层的共存。研究强调了硫氧化耦合反硝化过程对 N_2O 排放的重要作用，以及红树林沉积物深层的 ANME 和 SRB 耦合的新机制。这项研究对于预测环境和全球变化背景下的生态系统功能具有重要意义。

关键词：甲烷循环数据库（MCycDB）；红树林沉积物；宏基因组分析；甲烷/氮/硫循环过程耦合机制

城市湖泊水环境因子与抗生素对细菌群落的影响

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摘要

抗生素可以通过影响天然微生物群落和对环境微生物施加选择性压力来干扰生物系统。城市湖泊与人类活动密切相关，本研究选取西安市 3 种不同类型的城市湖泊。结合基本水质指标、抗生素赋存状态、细菌群落及其潜在代谢功能，使用 Spearman 相关系数和冗余分析探究其相互之间的关系，进一步探讨环境因子和抗生素对细菌群落结构的影响机制。研究表明，OFX、ETM 和 RTM 是西安市湖泊的主要抗生素类型，抗生素生态风险较低，3 个湖泊的抗生素赋存状况存在明显的聚类；Proteobacteria 是最为丰富的细菌，每个湖泊都有其特有的优势细菌，细菌受不同来水水源、污染源、周边环境的影响；统计分析得出 pH 和氮营养盐是影响细菌群落的最关键环境因子（$P<0.01$），TCs 和 LMs 是对细菌群落影响显著的抗生素（$P<0.05$）；抗生素对 3 个城市湖泊的细菌多样性、群落结构和潜在代谢功能的影响小于环境因子。这些结果有助于明确抗生素作为环境中新兴污染物的对细菌群落的影响机制，为城市湖泊水环境保护提供理论支持。

湖泊铁氧化耦合硝酸盐还原过程活性、产物及驱动微生物

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摘要

铁氧化耦合硝酸盐还原微生物过程（Iron oxidation coupled nitrate reduction, NRFO）被发现至今已有二十余年，但是目前除了 KS 富集物外，没有被严格证明自养的 NRFO 菌株(Bryce et al., 2018)。且由于亚铁可以与氮氧化物进行化学反应，使得 NRFO 的过程机理仍不清楚。原位研究中发现铁的存在有利于硝酸盐的铵化途径（Dissimilatory nitrate reduction to ammonia, DNRA）而抑制反硝化途径，但富集培养体系或混合营养型的 NRFO 菌株只进行反硝化而非 DNRA(Robertson et al., 2017)，相互矛盾的结果使得 NRFO 的过程产物仍有待研究。

本研究对位于中国东部平原的洪泽湖和南四湖进行采样，设计了短期培养和长期培养两组实验，分别研究 NRFO 过程中的生物和非生物作用、NRFO 生物作用下的硝酸盐还原产物及驱动微生物。短期培养实验结果说明：硝酸盐几乎不与亚铁发生化学反应，但亚硝酸盐可以被亚铁化学性还原。化学反应的亚硝酸盐还原速率不足生物反应的 25%，NRFO 生物作用占洪泽湖硝酸盐还原总量的 30%-49%、南四湖的 6%-27%。

长期培养实验设置加铁组和对照组，每次向培养体系添加 1 mM 硝酸盐，当硝酸盐被完全消耗后再输入 1 mM 硝酸盐。在 540 天的培养过程中，洪泽湖培养体系共输入 17 次硝酸盐，南四湖培养体系共输入 19 次硝酸盐。自第四次硝酸盐输入起，加铁组的硝酸盐还原速率明显高出对照组。^{13}C-NaHCO$_3$ 标记实验中发现：21 天标记培养后，加铁组有机碳中的 δ^{13}C 在洪泽湖和南四湖中分别增加了 25.1‰、47.5‰，而对照组中只增加了 1.9‰、4.4‰，这证明了加铁组中自养 NRFO 功能菌的作用。利用 ^{15}N-NaNO$_3$ 示踪，研究了培养体系中反硝化、DNRA 和厌氧氨氧化的过程速率。结果表明：长期加铁后反硝化和 DNRA 过程速率均增加，厌氧氨氧化速率基本不变，说明铁的长期输入会同时促进硝酸盐转为铵盐和氮素气体。基于宏基因组测序结果，分析了长期培养过程中反硝化标志基因 *nirK*、*nirS* 和 DNRA 标志基因 *nirB*、*nrfA* 的群落结构。结果表明已被报道的 NRFO 菌 *Sideroxydans lithotrophicus*、*Azospira oryzae* 存在于 *nirS* 群落中，*Pseudogulbenkiania* sp.、*Thiobacillus denitrificans* 存在于 *nirB* 群落中。这些菌多属于 *nirS*

和 *nirB* 系统发育树中的 *Betaproteobacteria* 簇，同时 16S rRNA 分析结果也发现了 *Betaproteobacteria* 的大量增长，说明 *Betaproteobacteria* 可能是湖泊 NRFO 过程的主要驱动微生物。

关键词：铁氧化耦合硝酸盐还原；湖泊；反硝化；DNRA；*Betaproteobacteria*

Quorum sensing stimulates direct interspecies electron transfer in anaerobic methane production

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Abstract

Direct interspecies electron transfer (DIET) provides an innovative way to achieve efficient methanogenesis, and this study proposes a new approach to regulate DIET pathway by enhancing quorum sensing (QS). Based on long-term reactor performance, QS enhancement achieved more vigorous methanogenesis, with 98.7% COD removal efficiency at 14 kg COD/m3·d organic load. In the control system, the methanogenesis failure occurred at the accumulated acetate of 7420 mg COD/L and lowered pH of 6.04, and much lower COD removal of 41.9% was observed. The more significant DIET in QS-enhancing system was supported by the stronger intertwinement and higher fluorescence intensity of the DIETers. Specifically, the expression of e-pili and the c-Cyts cytochrome secretion related genes was effectively promoted by 12.7- and 10.3-fold upon QS enhancement. Moreover, QS enhancement also improved the energy production capability, with the increase of F-type ATPase and V/A-type ATPase expression by 6.3- and 4.2-fold, and this effect provided more energy for e-pili and c-Cyts cytochrome secretion. From the perspective of community structure, QS enhancement increased the abundance of typical DIETers, i.e., Methanosaeta and Geobacter, from 54.3% and 17.6% in the control to 63.0% and 33.8% accordingly. Furthermore, the expression of carbon dioxide reduction and alcohol dehydrogenation genes was also observed to increase by 0.6- and 7.1-fold. Taken together, this study indicates the positive effects of QS chemicals to stimulate DIET, and advances the understanding of the DIET methanogenesis in involved in environments such as anaerobic digesters and sediments.

Keywords: Electroactive biofilm; Metatranscriptome; Extracellular electron transfer; Low temperature

藏东南微生物多样性的海拔梯度格局及其与土壤呼吸的关系

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摘要

青藏高原东南部的横断山脉地区是世界重要的生物多样性热区，其跨度极大的海拔落差提供了丰富的生态系统类型和生物多样性梯度。对该地区而言，土壤微生物作为土壤碳功能的主要驱动者，其生态功能关系（Biodiversity-ecosystem functioning）一直缺乏详细的评估。本研究通过采样一条横断山脉地区的典型海拔梯度带（853-4,420 米），揭示了该地区土壤中细菌与真菌多样性的空间格局，并进一步分析了它们与土壤呼吸（Rs）之间的关系。我们发现细菌与真菌的 β 多样性与 Rs 呈现出稳定的正相关关系，同向扩散和扩散限制两种随机性生态过程也对 Rs 有显著影响。该研究从机制上揭示了全新的基于微生物 β 多样性为生物多样性与生态系统功能关系，对微生物多样性的保护与开发提供了新的视角。

关键词：藏东南；微生物多样性；土壤呼吸；生态系统功能关系；随机性生态过程

Microbial biogeographic pattern in the southeastern Tibetan Plateau is linked to soil respiration

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Abstract

The Hengduan Mountains located at the southeastern Tibetan Plateau is a globally significant hotspot for biodiversity. The vast range of elevational gradients in this area provides diverse ecosystem types and biodiversity. Despite its importance, the biodiversity-ecosystem functioning (BEF) relationship of soil microorganisms, as the primary drivers of soil carbon processes, lacks investigations in this region. In this study, we sampled along an elevational gradient with 853-4,420 m a.s.l, examining the spatial patterns of bacterial and fungal diversity in the soil and further analyzing their relationship with soil respiration (Rs). Our findings reveal a robust positive correlation between β-diversity of bacteria and fungi and Rs, mediated by homogenous dispersal and dispersal limitation. By complementing common practices to examine BEF with α-diversity, we demonstrate that a focus on β-diversity offers novel insights into the BEF relationship and ecosystem modeling.

Keywords: Southeastern Tibetan Plateau; Microbial diversity; Soil respiration; Biodiversity-ecosystem functioning; Stochastic ecological processes

不同秸秆还田方式对旱地红壤细菌群落、有机碳矿化及玉米产量的影响

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摘要

为探讨长期不同秸秆还田方式对旱地红壤细菌群落、有机碳矿化及玉米产量的影响，基于中国科学院鹰潭红壤生态实验站设置的不同秸秆还田方式长期定位试验（9 a），选取不施肥（CK）、单施化肥（N）、化肥+秸秆（NS）、化肥+秸秆猪粪配施（NSM）和化肥+生物质炭（NB）这 5 个处理，通过高通量测序技术研究旱地红壤细菌多样性和群落结构差异，揭示了细菌群落对土壤有机碳矿化和玉米产量的影响机制。结果表明：①不同秸秆还田处理下，红壤化学性质发生显著变化，其中 NSM 处理对旱地红壤肥力的综合提升效果最好，并显著提高了玉米产量。②相比于 CK 和 N 处理，秸秆还田处理均提高了细菌多样性。主成分分析发现，秸秆还田处理改变了土壤细菌群落结构。③秸秆还田处理提高了土壤有机碳矿化能力，NSM 处理的土壤有机碳矿化速率和累积矿化量最高。④相关性分析表明土壤 AN/AP 比值显著改变了细菌群落结构，结构方程模型结果表明，土壤 AN/AP 比可能通过影响土壤细菌多样性和群落结构，间接提高了土壤有机碳矿化能力和玉米产量。本研究结果为协同提升旱地红壤生物多样性和耕地地力水平，保障健康红壤生态系统和粮食安全提供了科学依据。

关键词：秸秆还田；旱地红壤；细菌群落；有机碳矿化；玉米产量

Effects of Different Types of Straw Returning on the Bacterial Community, Organic Carbon Mineralization and Maize Yield in Upland Red Soil

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Abstract

To investigate the effects of straw returning on the bacterial community, organic carbon mineralization and maize yield in an upland red soil, a long-term field experiment (established in 2011) with different types of straw returning in corn mono-cropping system was performed at the National Agro-Ecosystem Observation and Research Station in Yingtan. The diversity and structure of the soil bacterial community were evaluated under five treatments (CK, no fertilizer; N, chemical fertilizer; NS, chemical fertilizer with straw; NSM, chemical fertilizer with straw and manure; NB, chemical fertilizer with biochar) using high-throughput sequencing technology. The effect of bacterial community was revealed on maize yield and soil organic carbon (SOC) mineralization. The results showed that fertilization treatments significantly changed chemical properties of red soil, such that the NSM treatment had the highest level of soil fertility and the maximal maize yield. The straw returning treatments (NS, NSM and NB) significantly increased the bacterial diversity compared to CK and N treatments. The principal component analysis (PCA) indicated that the straw returning treatments significantly affected the bacterial community structure. Straw returning significantly improved SOC mineralization capacity, with the maximal SOC accumulation and mineralization rate under the NSM treatment. Correlation analysis indicated that the structure of soil bacterial community was greatly influenced by AN/AP ratio. Structural equation modeling suggested that AN/AP ratio may indirectly improve SOC mineralization capacity and maize yield by shaping the bacterial diversity and community structure. Our results provide the basis for synergistically improving the microbial diversity and soil fertility, and protecting the health of red soil ecosystem and food security.

Keywords: Straw returning; Dryland red soil; Bacterial community; Organic carbon mineralization; Maize yield

Compositional stability of free-living and particle-attached bacterial community in a subtropical reservoir over 3 years under salinity fluctuation

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Abstract

Changes in salinity pose a dramatic influence on the ecological services and functions of freshwater ecosystem as its strong effect on microbial communities. Bacterioplankton, which can be generally classified into free-living (FL) and particle-attached (PA) bacterial communities according to the relationship with particulate matter, are main components of freshwater ecosystem and play key roles in maintaining material cycling and ecological stability. Numerous studies have explored the spatio-temporal dynamic, geographical distribution patterns, community assembly mechanism and metabolic potentials of FL and PA bacterial communities. However, knowledge of the stability of FL and PA bacterial communities under salinity fluctuations scenario is very limited. Here, we systematically explored the stability of FL and PA bacterial communities based on a high-frequency time series from a shallow urban reservoir (Xinglinwan Reservoir) in subtropical China over 3 consecutive years. Our results indicated that (1) salinity was the strongest environmental factor affecting the aquatic bacterial community compositions. Meanwhile, salinity increasing led to a significant increase of the compositional stability of FL and PA bacterial communities, though a significant decrease of their diversity; (2) the compositional stability of PA bacterial communities was significantly higher than that of FL bacterial communities at high-salinity levels and low-salinity fluctuation scenario, while less at low-salinity levels and high-salinity fluctuation scenario; (3) internal factors such as bacterial genome size and interaction strength of rare taxa, and external factors such as precipitation collectively contributed to different compositional stability patterns of FL and PA bacterial communities at different salinity scenario. Our study provides theoretical basis and fundamental datasets for maintaining the ecological management, restoration and protection of urban reservoirs.

Keywords: Eutrophic reservoir; Free-living bacteria; Particle-attached bacteria; Rare taxa; Genome; Interaction; Precipitation

Available nitrogen source contributes to shaping methane-consuming microbial communities in lake sediments

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Abstract

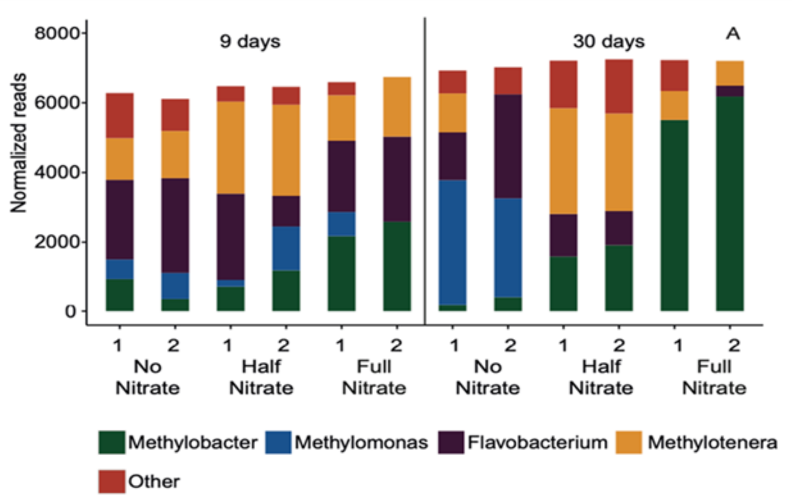
In this study, we addressed the role that available nitrogen plays in determining the composition of methane-consuming communities in a well-studied model system. We applied a multi-phase approach combining microcosm enrichments and synthetic model communities with high throughput sequencing.

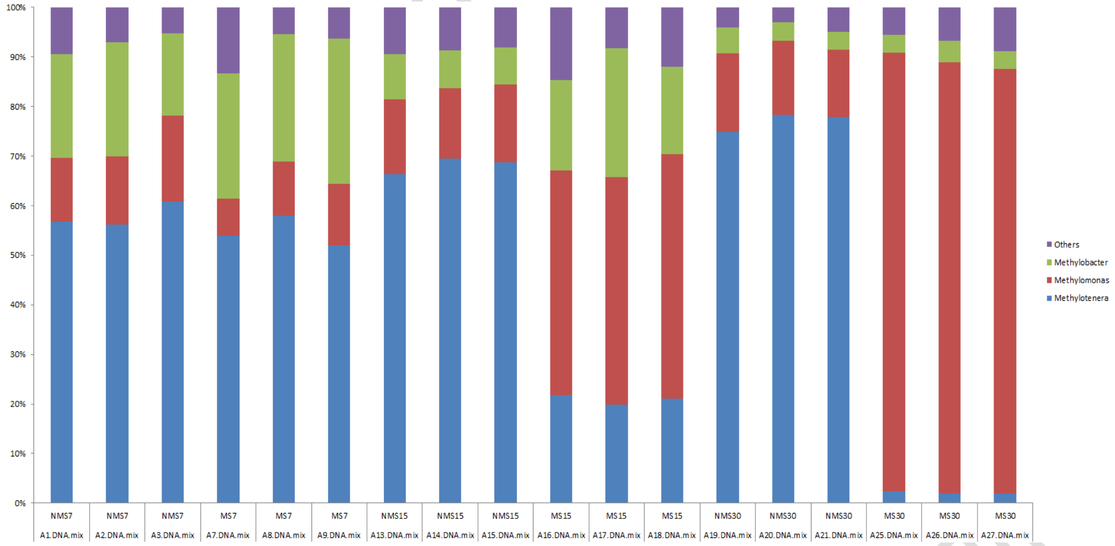
We first subjected sediment samples from Lake Washington to a 30-day incubation under conditions mimicking limited oxygen availability observed in the natural environment. Various growth media were utilized, including full and half nitrate mineral salt medium (NMS) as well as nitrogen source-free mineral salt medium (MS). Analysis of the 16S rRNA gene via Illumina sequencing on the 9th and 30th day revealed that *Methylomonas* strains exhibited increased competitiveness when atmospheric N_2 served as the sole available nitrogen source, consistent with our previous findings. However, the addition of half nitrate significantly inhibited the growth of a *Methylomonas* strain, resulting in a dominance of *Methylobacter* and *Methylotenera* species. This effect was even stronger in the presence of higher nitrate concentrations (1g KNO_3/L) in the medium.

Subsequently, we conducted a follow-up experiment using synthetic communities of three bacterial strains, incubated with NMS and MS for a 30-day period. Analysis of the 16S rRNA gene on the 7th, 15th, and 30th day showed that *Methylomonas* remained the dominant bacteria in the absence of nitrate. However, in the presence of nitrate as an available nitrogen source, *Methylomonas* did not dominate the community. Instead, associations between *Methylomonas* and *Methylotenera* were formed under nitrate addition.

Our findings suggest the presence of a cross-feeding mechanism between bacterial

communities, whereby the genus *Methylobacter* serves as a host for the survival of the non-methanotrophic genus *Methylotenera* under nitrate supplementation. These results provide valuable insights into the complex interactions and dynamics of methane-consuming communities in response to nitrogen availability.





展报

Evaluation and redesign of the primers for detecting nitrogen cycling genes in the environment

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Abstract

A better understanding of how nitrogen (N) cycling genes are involved in ecological processes is one of the crucial areas of microbial ecological research. Currently, most molecular biological techniques investigating N cycling genes in the environment heavily rely on the accuracy of the PCR primers, however, their specificity and coverage have not been comprehensively evaluated. Here, we collected a sequence database, NcycFunGen, for 22 marker genes involving in N cycling, which included 604,964 paired nucleotide and protein sequences with their taxonomic information. Then, a total of 608 published primers were fully evaluated through NcycFunGen, as well as against full-length sequences collected from KEGG. The results showed that the majority of primer pairs cover less than 30% sequences of target genes, and that 22.55% were not applicable for high-throughput amplicon sequencing (<100 bp or >550 bp). In general, this *in-silico* evaluation demonstrated that although many primers have been adopted in published studies, some of them should be validated and updated as needed according to updated gene database. Therefore, new degenerate primer pairs for *ureC* targeting urease, bacterial and archaeal *amoA* targeting ammonium monooxygenase, and *nifH* targeting nitrogenase were designed through NcycFunGen. These new primer pairs showed higher coverage and amplification efficiency, as well as amplicon lengths that were applicable for high-throughput amplicon sequencing. Then, in experiment, the updated *ureC* gene primer pair ureC607F/ureC898R has been applied to a urea amendment site by using both by droplet digital PCR and high-throughput amplicon sequencing, and their results displayed the better characteristics and broader usable taxonomic range than commonly used published *ureC* gene primer pairs. In conclusion, primer evaluation and redesign are highly recommended to improve the accuracy of primers targeting N cycling genes, which could facilitate amplicon-based N cycling studies in various environments.

Keywords: Nitrogen cycle; Database; Primer evaluation; Primer design

红树和半红树根际微生物多样性的产生和维持

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摘要

本文以海南岛三个地点的红树和半红树根际、非根际微生物群落结构的研究为例，从多样性差异、多样性的影响因子、群落结构的影响因子和群落生态过程入手，阐述了红树林生态系统中红树和半红树根际微生物的分布模式、物种共存、土壤环境因子与微生物群落之间的关系。发现红树和半红树根际土壤相对于其非根际土壤分别显著富集到不同微生物，红树显著富集到 Bacteroidota、Calditrichota、Campilobacterota、Deculfobacterita、Chloroflexi、Fusobacteriota、Latescibacterota、MBNT15、Nitrospirota 等门类；半红树显著富集到 Cyanobacteria、Planctomycetota、Verrucomicrobiota 等门类。红树和半红树相对于其非根际土壤均具有更高的 α 多样性，且根际微生物 α 多样性与土壤含水量显著正相关。含水量较高的红树根际土壤微生物具有更高的 α 多样性。红树和半红树相对于其非根际土壤均具有更低的 β 多样性，且红树根际微生物的 β 多样性更低，红树比半红树根际微生物具有更强的系统发育聚集性。水和盐是驱动红树和半红树根际微生物群落组成差异的主导环境因子。红树根际微生物相对于半红树具有更复杂、更紧密的网络结构，连通度和紧密中心度显著高于半红树根际微生物，表明红树根际微生物群落物种互作的聚集性和连接性更好。本研究促进对红树林生态系统微生物群落的了解和管理，以更好地应对气候变化、海平面上升对红树林生态系统的威胁。

关键词：红树；微生物生态；共现性网络

“稻虾共作”农业模式的长期过度利用导致稻田土壤细菌群落多样性和功能的降低

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摘要

近年来，“稻虾共作”模式因其经济效益高，在许多国家和地区尤其是在我国得到了迅速发展。然而，由于这种模式的过度利用而造成的稻田土壤微生物潜在的生态问题却鲜有人报道。经研究发现，与水稻单作相比，长期过度利用的“稻虾共作”模式会降低稻田土壤微生物丰富度和多样性。尤其表现在参与氮素分解利用的微生物丰度降低，参与碳素分解利用的微生物丰度增加，这直接导致了氮循环功能的减少和碳循环功能的增加。如，在水稻整个生长期内，共作模式土壤中芽孢杆菌属，硝化螺旋菌属和芽单胞菌属等的特异性敏感 OTU 丰度显著高于单作，而类诺卡氏菌属显著低于单作。同时，两种稻作模式，在水稻生长的不同阶段群落的形成均受各生育期特异性敏感变化的 OTU 驱动，由生育期敏感 OTU 构成的网络模块对于土壤养分的调控方面均具有正向协同效应。因此，发现生育期特异性敏感的 OTU 的物种分类、丰度和功能是制定“稻虾共作”模式土壤微生物生态管理策略的基础，对研究不同稻作模式土壤微生物群落构成和土壤健康具有重要意义。

关键词：稻虾共作；土壤养分；高通量测序；水稻生育期；微生物多样性

极酸性矿山排水（pH<3）中影响微生物群落的关键因素

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摘要

含硫矿物氧化溶解过程中会产生酸性矿山排水（Acid Mine Drainage, AMD）。AMD环境具有富硫、高金属浓度以及低有机质等特点，微生物多样性远少于其他环境，且酸性矿山排水中的微生物及其铁、硫元素代谢一直备受关注。AMD 作为地球上人为极端环境之一，具有相对简单的群落结构和地球化学特征，为研究微生物的适应进化以及微生物塑造环境的能力提供了模式系统，也提供了研究与其生态类似的远古微生物群落（距今约 25 亿年前“大氧化”事件）的可能。同时由于 AMD 会导致严重的环境污染问题，因此研究 AMD 具有实际治理指导意义。近些年来，不依赖于培养的微生物群落分析方法如 16S rRNA 基因克隆文库、扩增子测序、宏基因组测序以及宏转录组测序技术等已广泛用于酸性矿山排水的研究，使人们对其中的微生物多样性、群落结构和功能以及微生物与环境的相互作用有了更全面的认识。本研究从四个不同矿物类型的矿区收集极端酸性的 AMD 样品，测量了 AMD 的理化因子特征，并对其微生物群落进行了比较和分析。研究结果表明四个矿区的 $SO4^{2-}$、金属离子和温度具有显著差异；来源于铜矿区的 AMD 微生物多样性显著低于多金属矿区 AMD 群落。CCA 分析表明 Mg 和 $SO4^{2-}$ 是决定矿区微生物结构的主要因素。*Leptospirillum*，*Ferroplasma* 和 *Acidithiobacillus* 在不同矿物类型矿区的 AMD 中占主导地位，但显示出不同的分布模式。与铜矿区产生的 AMD 相比，多金属矿区 AMD 中发现了更多样化的微生物群落以及功能冗余，多金属矿区 AMD 环境中可能存在多种代谢底物以及多种代谢耦合。功能预测表明，微生物驱动着 AMD 环境中铁、硫、氮和碳代谢，并且这些代谢过程与环境中 Mg，$SO4^{2-}$、Fe^{2+}、 Ca 和温度显著相关。综上所述，本研究表明矿区的矿物类型不同可能导致 AMD 中微生物群落不同，且环境中 Mg^{2+}和 $SO4^{2-}$浓度是影响 AMD 微生物多样性、群落组成和代谢的主要因素。

关键词：酸性矿山排水；矿物类型；微生物多样性；微生物共现性；元素循环潜能

Minimizing extracellular DNA improves the precision of microbial community dynamic analysis in response to thermal hydrolysis

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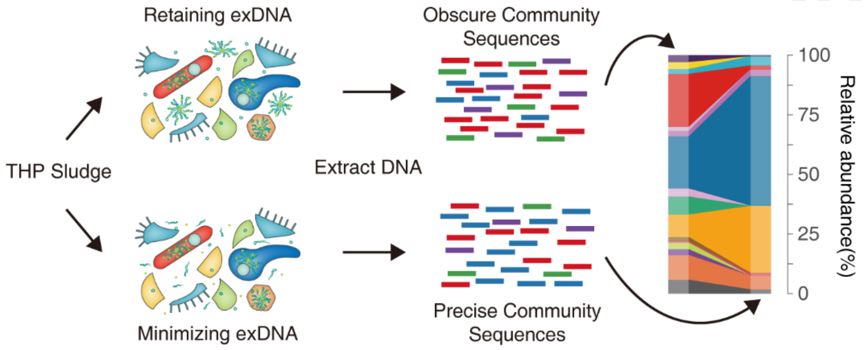
Abstract

Extracellular DNA (exDNA) can induce bias when evaluating the microbiota in wastewater treatment systems, particularly when cell lysis caused by thermal hydrolysis pretreatment (THP) releasing abundant DNA. However, the influence of such exDNA is still unknown. Accordingly, this study applied a pretreatment strategy for DNA extraction with proteinase K and DNase I to minimize the influence of exDNA when evaluating the sludge microbiota. Lactobacillus and Peptostreptococcus were confirmed as the main THP-resistant microorganisms. Gram-positive bacteria were more resistant to THP, implying that the presence of a cell wall could promote THP resistance in bacteria. Moreover, the ability to form spores did not affect the resistance of bacteria to THP. These findings showed that resistant microbiota could be effectively evaluated by excluding exDNA, which can provide important insights into the understanding of microbiota dynamic and the effects of pretreatment on the precision of microbiota analysis in sludge.



Keywords: Waste-activated sludge; Thermal hydrolysis; Extracellular DNA; Microbial community

根部内生菌通过调节植物-真菌界面的氮流量差异调节植物对 NO_3^- 和 NH_4^+ 营养的响应

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摘要

在土壤中，植物-真菌互作通常受到硝酸盐 (NO_3^-)/铵盐(NH_4^+)分布不均的影响，然而氮素形式影响植物-真菌互作的机制仍然有限。我们用根部内生真菌枫香拟茎点霉（*Phomopsis liquidambaris*）接种拟南芥，并评估了 NO_3^-或 NH_4^+营养下 *Ph. liquidambaris* 对植物生长的影响。结果表明，在 NO_3^-营养下，*Ph. liquidambaris* 接种提高幼苗生物量；在 NH_4^+营养下，真菌接种出乎意料地降低了幼苗生物量。在高 NH_4^+条件下，真菌定殖的根部显示出增加的 NH_4^+积累和 NH_4^+外排，叶部表现出增强的氧化应激和细胞死亡，类似于由 NH_4^+水平升高而引起的铵盐胁迫的响应。值得注意的是，*Ph. liquidambaris* 在植物-真菌界面降低了 NO_3^-但增加了 NH_4^+水平，其中真菌菌丝在与根部互作的过程中保留 NO_3^-但排出了 NH_4^+。一株亚硝酸还原酶缺陷菌株，排出 NO_3^-但吸收 NH_4^+，降低了拟南芥感知的 NH_4^+水平，并在高 NH_4^+营养下促进了植物生长和氮代谢。转录组学分析表明，*Ph. liquidambaris* 改变了植物感知微生物以及响应无机氮形式相关的基因表达。总而言之，我们的结果表明，植物-真菌界面处真菌调节的 NO_3^-/NH_4^+动态影响了植物对 NO_3^-和 NH_4^+营养的响应。该研究强调了根部内生菌在植物适应土壤氮营养中的重要功能。

关键词：氮素形式；根部内生真菌；氮流量；植物响应

石油扰动对土壤中微生物组成及其功能影响效应研究

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摘要

石油在生产、加工、储存和运输造成的土壤污染问题，对土壤生态功能造成严重危害。原位微生物经长期驯化，能够形成以石油为碳源的生理代谢功能，促进石油污染修复。然而受石油扰动后，原位微生物组成及其代谢功能相关问题的研究仍然较少。本研究收集了中国油库土壤样品，通过宏基因对原位微生物组成及其功能进行研究。研究结果表明，在种水平上，优势细菌为 *Pseudomonase_sp._LAM-KW06, Actinobactreia_bacterium, Acidobacteria_bacterium*，优势古菌为 *Candidatus_Bathyarchaeaeota, Thaumarchaeota, Euryachaeota*，优势真菌为 *Trichonephila_clavipes, Capra_hircus, Lupinus_albus*。通过共线网络分析表明，核心物种为 *Acidobacteria_bacterium, Actinobacteria_johnsonni, Actinobacteria_bacterium*。将收集的样品以南北纬度差异为分组，对物种生态位宽度进行计算，结果表明南方油库中物种的平均生态位宽度比北方物种高，说明南方油库土壤中生态位宽，物种的特化程度小，更倾向于泛化种，具有较强的竞争能力；而北方油库土壤中生态位相对较窄，在资源竞争中处于劣势。零模型和中性群落模型对微生物种水平进行拟合，结果表明物种组装模式以确定性过程为主导，说明环境中存在较强的生态过滤器，原位微生物受石油扰动产生适应能力。在物种代谢水平上，根据 KEGG 数据库对基因序列进行比对，碳循环的基因主要为多环芳烃降解基因，并与 *Proteobacteria, Dormibacteraeota, Candidatus_Bathyarchaeaeota* 显著相关；此外，大量的产甲烷基因有所表达，进一步证明油库土壤中原位微生物对石油降解具有丰富的代谢潜力。该研究揭示了受石油扰动土壤中微生物物种组成及其发挥的生态功能，为中国油库管理和石油污染修复提供参考依据和科学指导。

关键词：石油污染；微生物；生态模型；功能基因

Keystone taxa and community assembly process of different mangrove rhizosphere microbial communities

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Abstract

Mangroves form intimate relationships with the diverse root microbes, these microbes are important for mangrove growth and health. In order to understand how root microbiota of mangroves vary throughout different growth stages under field conditions, we sequenced the 16S rRNA gene of rhizosphere sediments of three mangrove species at two locations of Guangxi Province and Guangdong Province. Our results showed that the microbial alpha diversity and richness were positively correlated with total carbon content, both mangrove species and geographical location influenced the patterns of root microbiota shift that occurred during plant growth. Biomarker taxa with growth stages were identified by random forest model, most of those biomarker taxa were belong to *Deltaproteobacteria* and *Alphaproteobacteria*, and their relative abundance showed strongly correlation with total carbon and nitrogen contents. Although several environmental variables had significant influence on the microbial communities, the root microbiota was strongly driven by stochastic processes for each mangrove species.

Keywords: Microbial community; Mangroves; Biodiversity; Community assembly

Phylogenetic conservation of microbial responses to nitrogen fertilization and elevated ozone

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Abstract

Nitrogen (N) fertilization stimulates crop growth whereas elevated tropospheric ozone inhibits it, showing the antagonistic effect. However, whether and how N fertilization and elevated ozone interact to influence microbial community in agricultural soils remain unclear. To this end, we investigated bacterial and fungal communities in maize fields subjected to different levels of N fertilization (+60, +120, and +240 kg N ha^{-1}yr^{-1}) and elevated ozone (+ 60 ppb ozone). After a whole growing season treatment, we found that there was no interactive effect between N fertilization and elevated ozone on both bacterial and fungal communities, consistent with a lack of N fertilization and elevated ozone interaction on plant and soil geochemical properties. Nevertheless, amplicon sequence variants (ASVs) affiliated with Gammaproteobacteria, Deltaproteobacteria, Actinobacteria, Bacteroidetes and Planctomycetes responded ($P < 0.05$) consistently to N fertilization, but Alphaproteobacteria,

Gammaproteobacteria, Actinobacteria, Bacteroidetes, Chloroflexi, Elusimicrobia, Ascomycota and Glomeromycota responded ($P < 0.05$) consistently to elevated ozone, suggesting that microbial response patterns were phylogenetically conserved. Ozone-responsive microbes were even more phylogenetically conserved than N fertilization-responsive ones, as indicated by a larger mean genetic depth (average distance of the node to its descending tips), suggesting that elevated ozone had a stronger homogeneous selection (selected by similar environment) on microorganisms. Among the phylogenetically conserved phyla, the ozone-responsive bacterial phyla were generally correlated with plant biomass and soil NO_3^-, while the fungal phyla were correlated with plant biomass and soil dissolved organic carbon. Our results indicated that elevated ozone changed bacteria and fungi towards a more phylogenetic conserved community by altering soil fertilities, which provided important benchmarks for crop management strategies, such as regulations of soil microbial community by addition of microorganisms decreased by elevated ozone.

紫金铜矿堆浸系统菌群结构分析及功能菌种分离鉴定

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摘要

生物冶金是一种利用矿物与微生物相互作用从矿石或浓缩液中回收贵金属的技术，以其低能耗、环境友好等优势而广受关注。堆浸法是生物冶金中一种常见的工艺，它通过堆积矿石并向矿石堆中喷洒喷淋液进行矿物的浸出，在处理低品位、难溶黄铜矿中具有极大的应用潜力。微生物堆浸是多种微生物参与的工艺过程，矿堆中的不同微生物共同作用，通过调节碳、氮、铁、硫元素及环境电位的平衡，加速矿物溶解，实现金属的高效浸出。因此，对堆浸系统中的微生物及其功能、微生物间的相互作用及其与浸矿环境的关系进行解析，进一步分离获得浸矿体系微生物，可为通过人工构建微生物组，提高微生物堆浸的效率提供理论基础及微生物资源。

福建省上杭县紫金山矿区是我国特大型低品位铜矿区，率先采用生物堆浸技术实现了铜的高效浸出。本研究通过 16S rRNA 高通量测序技术研究了紫金铜矿堆浸系统中不同矿堆、不同高度矿堆样本及各矿堆浸矿排水样本中的微生物群落结构，解析了矿堆内部微生物的组成及其代谢活动、矿堆内部菌群和环境因子的关系及微生物间的共现性网络。研究发现，矿堆中丰度最高且主要差异菌群均为硫氧化菌如 *Acidithiobacillus* 和 *Sulfobacillus*，而浸矿排水中主要为钩端螺旋菌和极端嗜酸的古菌，在浸矿排水中还发现了一类可以耐受极酸、高铁硫及高重金属浓度的古菌新类群。经 Tax4Fun2 基因预测分析发现，生物堆浸系统中的能量代谢以硫代谢、甲烷代谢、碳固定等自养方式为主，此外还存在一系列抗酸和抗重金属离子的环境适应基因。与环境因子关联分析表明，pH 是与浸矿系统中群落组成最相关的环境因子。相关性分析发现，随着深度的增加，酸硫杆菌属是矿堆中最重要的功能菌群，它通过降低 pH、促进硫溶出等方式加速了矿石的氧化进程。在矿堆的微生物共现网络中，酸硫杆菌属与多种异养菌具有强烈的相互作用

关系，而在浸矿排水样品中铁原体科与多种自养菌具有较强的相互作用关系。

数据分析发现酸性矿水环境中仍有大量的菌种资源有待挖掘，为了获得浸矿系统中的功能菌群，设计了多种培养体系，分离获得了铁氧化、硫氧化及异养菌株共 77 株，分别属于变形菌门、厚壁菌门、放线菌门、酸杆菌门和硝化螺旋菌门的 21 个属，其中有 39 个潜在新种，目前已全部保藏于中国普通微生物菌种保藏管理中心 CGMCC。为了进一步了解该环境中微生物的作用和特点，对 *Conexibacter* 属的 2 个潜在新种进行了多相分类学鉴定，对其形态特征、系统发育、生理生化、化学组分和基因组特征进行了一系列研究，命名为新种 *Conexibacter tetrathiotrophus* S30A1T 和 *Conexibacter acidophilus* DBS9H8T。

综上所述，本研究通过高通量测序技术系统地研究了铜矿堆浸系统中微生物的演替及环境适应机制，并通过培养组学的方法挖掘了浸矿系统中的微生物资源、分析鉴定了其生理生化特性、分类地位及生态功能。研究结果可为提高生物冶金效率提供理论指导和菌种资源。

土壤反硝化功能菌多样性与功能分异的环境调控

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摘要

反硝化作用是在缺氧条件下将硝酸盐氮和亚硝酸盐氮逐步还原成 NO、N_2O 和 N_2 的过程。反硝化作用广泛存在于土壤中，能够保持生态系统的氮平衡，对于保持土壤肥力、调控温室气体排放等具有重要意义。同时，土壤反硝化作用也是温室气体 N_2O 排放的主要来源。据估计平均每年的土壤反硝化作用对全球 N_2O 排放的贡献达 56%-70%。前期研究发现，我国重要的农田土壤中，黑土和潮土土壤的反硝化功能和 N_2O 排放效率具有明显差异。本研究针对黑土和潮土反硝化功能差异的微生物机制进行研究，通过设置不同培养条件，从黑土和潮土中分离筛选得到 893 株菌株，并利用高通量方法鉴定两种土壤的细菌分离株，共得到黑土中 3 门 22 属 306 菌株，潮土中 3 门 33 属 336 菌株。结合反硝化功能基因扩增和反硝化功能验证，筛选得到反硝化功能菌，包括黑土中 14 属 43 株和潮土中 20 属 41 株。通过对优势的功能菌株进行生理生态学分析，从菌株水平揭示土壤优势反硝化菌的反硝化机制以及环境条件的变化对其产生的影响，从而为减少温室气体排放和土壤氮损失的微生物机制提供实验依据，为今后开展广泛和深入的研究提供一定的实验和理论基础，这对于减轻环境污染和促进农业可持续发展有着重大的意义。

关键词：反硝化作用；黑土；潮土；N_2O 排放；反硝化功能菌

利用宏基因组技术揭示污泥体系吲哚信号分子机制

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摘要

近年来，吲哚被认为是一种新型信号分子，能够调节微生物的毒性、耐药性、生物膜的形成及群感效应等生理生化行为。但在复杂群落中，吲哚信号分子的调控作用及调控机制尚且没有被研究过过。本研究中运行了 3 组序批式活性污泥反应器，分别投加 0 mg/L，50 mg/L，150 mg/L 吲哚信号分子，考察了不同浓度吲哚信号分子对于活性污泥中微生物群落的调控作用。三组反应器对 COD 和氨氮均有较好的处理能力，投加吲哚的两组反应器也在首个运行周期中便可以将吲哚完全去除。利用显微镜对污泥中的原生动物进行观察，发现随着吲哚浓度的升高，反应器中原生动物种类逐渐下降。毒性指标检测结果显示，吲哚的投加使得活性污泥中乳酸脱氢酶活性，谷胱甘肽含量和活性氧自由基浓度显著下降。此外，利用宏基因组测序手段考察了吲哚对活性污泥群落的影响。从宏基因组数据中提取 16s DNA，Lefse 分析表明，吲哚的添加使得 *Nitrospiraceae*，*Nannocystaceae*，*Rubinisphaeraceae* 等菌属丰度显著下降。而高浓度的吲哚的添加使得 *Ignavibacteriaceae*，*Anaerolineaceae*，*Comamonadaceae*，*Caulobacteraceae* 等菌属丰度的显著增加。对宏基因组中抗性基因的丰度进行提取与分析。结果表明，高浓度吲哚添加后的群落抗性基因总丰度显著增加，主要增加的抗性基因种类为 Aminoglycoside，Sulfonamide，Multidrug，Tetracycline 等。而低浓度吲哚的添加使得群落抗性基因的变化并不显著，这说明了控制在合理浓度中使用吲哚并不会使得群落抗性基因的富集。本研究为吲哚信号的实际应用提供了理论基础。

关键词：吲哚；信号分子；活性污泥；抗性基因

城市污水处理厂升级对受纳河流浮游微生物群落的影响

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摘要

采用常规生物处理工艺的城市污水处理厂排水中含有一定浓度的营养物质和微量污染物，在受纳水体的长时间积累会导致其生态系统的生物多样性减少与功能失调。据此，一些国家（如中国与瑞士）已经着手对污水处理厂常规工艺进行升级，以改善受纳水体的水质及保护水生生物的多样性与功能。由此衍生的一个关键科学问题是“污水处理厂升级是如何影响受纳水体生物群落与功能的？”。由于河流生态系统非常复杂，很难对全部生物群落进行分析，故选择相对简单且同时对环境变化非常敏感的微生物群落，来探讨污水处理厂升级导致的受纳水体的微生态效应。

以北京 2 条污水处理厂纳污河流作为研究对象，进行了 5 年的实地调查采样及实验室分析。其中通惠河在采样期间正在进行污水处理厂的升级改造，而清河已完成升级改造。结合污染物分析、16S rRNA 高通量测序及宏基因组测序，探讨了污水处理厂升级改造对受纳河流水质和微生物群落结构与功能（氮循环）的影响。研究结果表明，污水处理厂升级后，受纳河流中的总氮浓度显著降低，由 20~30mg/L 下降至 10mg/L，总氮浓度的降低反映在总有机氮的明显减少和硝氮的略微下降上。TN 的减少显著影响受纳河流微生物群落组成，同时导致群落间的相互作用更为紧密。16S rRNA 和宏基因组测序结果表明，污水处理厂的升级降低了受纳河流中硝化细菌的丰度，但增加了反硝化和硝酸盐异化还原细菌的丰度。此外，硝酸盐异化还原细菌与反硝化细菌的比值在污水处理厂升级后显著上升，参与 $NH4^{+}$-N 生成的细菌相对丰度明显增加，氮转化细菌的这种变化可能是为水生态系统提供足够的生物利用氮从而保证浮游生物的生长。

关键词：污水处理厂；受纳河流微生物群落；氮循环；生态效应

The succession of prokaryotic community attached on biodegradable plastic mulches during the degradation in soil

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Abstract

Despite the applications of non-degradable plastics or biodegradable plastic mulches (BDMs) in agriculture have been largely increased, the colonization and succession of the attached microbial community on BDMs during their degradation process remain poorly characterized. Here, we have buried four types of commonly used BDMs [polylactic acid (PLA), polybutylene adipate terephthalate (PBAT), PLA15%PBAT and PLA85%PBAT] and a classic polyethylene (PE) mulch in soil for 5 months. The results showed both plastic components and time significantly shaped the β-diversities of microbiota on the plastic mulches ($P<0.001$). The microbial compositions and structures in BDMs were significantly different with PE mulch, while by excluding PE mulch, the microbiota were varied more with months than their components within four BDMs. The Burkholderiales and Pseudonocardiales orders were predominant in most BDMs across different time points, the genus Ramlibacter was revealed as the common biomarker to both PLA and PBAT by a Random Forests model and all biomarkers of them belonged to the dominant order Burkholderiales. Besides, the degradation-related and pathogen-related functional taxa were enriched in all mulches among forty functional groups, while surprisingly, potential pathogens were even more on BDMs than PE mulches. In addition, for the community assembly in all mulches, the drift and dispersal processes played more important roles than the selections, and particularly the contribution of stochastic drift would increase along the degradation process on BDMs while the selection decreased that was totally opposite on PE mulch. Overall, our results demonstrated some degradation species and pathogens were specially enriched on BDMs, though stochastic process also had important impacts on the community assembly on these agriculture mulches. It suggested that as similar as conventional plastic mulch, the large usage of BDMs could be some potential hazards to crop and our health.

Keywords: Biodegradable plastic mulches; Prokaryotes; Plastisphere; Biodegradation; Soil

富营养化港湾温度变化对原核微生物群落的影响特征研究

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摘要

海水温升对微生物群落演替有显著影响，是近年微生态研究的热点，其中温升影响下的微生物群落组装过程和互作机制是近年微生态研究的热点，但在港湾富营养化背景下的温升效应仍缺乏深入研究。原核微生物是海洋微生物群落的重要组成部分，且在海洋微生态系统中发挥着重要作用。基于此，本研究在富营养化港湾——三门湾开展年度微生物群落调查，研究温升背景下原核微生物群落组成、组装机制及互作特征，揭示富营养化条件下原核微生物群落对温升的响应。结果表明，随着温度升高，原核微生物群落 α-多样性显著降低；温度是原核微生物群落组成和结构变异的主要驱动因素。各主要类群对温度响应有显著差异，如高温偏向型以拟杆菌为主，低温偏向型以变形菌为主，温度不敏感型主要是疣菌群。研究发现，原核微生物群落的组装机制受到温度变化的影响。互作网络结果显示，高温组各个节点之间的互作关系较低温组更为紧密。本研究表明，在富营养化港湾，温度仍然是微生物群落演替的主要驱动因素，且对解析港湾富营养化背景复合温升效应下生态系统的响应特征具有重要意义。

关键词: 温升；富营养化；互作网络；原核微生物群落跨年度变化；三门湾

水生植物内生细菌多样性及其固氮功能研究

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摘要

内生菌广泛存在于植物组织中，具有丰富的物种多样性，成为植物内生态系统中的重要组成部分。植物内生菌可能具有促进植物生长、增强植物抗逆等功能。水生植物对湿地生态功能起到关键作用，其内生菌多样性及其功能的研究报道较少。本研究采用高通量测序技术对常见的 12 种水生植物（包括挺水植物、浮叶植物、沉水植物生活型）内生细菌多样性进行了分析，结果表明不同水生植物内生菌多样性存在差异。水葱具有最高的多样性指数，荇菜最低。水生植物内生细菌群落中主要为变形菌门（Proteobacteria）、拟杆菌门（Bacteroidete）、厚壁菌门（Firmicute）和放线菌门（Actinobacteria）。挺水植物（除水葱外）内生菌群落物种相似，假单胞菌属（*Pseudomonas*）、寡养单胞菌（*Stenotrophomonas*）、Ochrobactrum 和假苍白杆菌属（*Pseudochrobactrum*）为共有的优势菌属，研究表明 *Stenotrophomonas* 可能存在固氮和促进植物生长的能力，而沉水植物和浮叶植物主要优势菌属为肠杆菌属（*Enterobacter*）。各水生植物内生菌的差异与生活型存在一定的关系，但也并非完全对应，内生菌群落组成和多样性差异的内在机制尚不清楚。进一步采用固氮酶基因（*nif*H）检测发现香蒲、菖蒲、芦苇、水葱、灯心草和菱的内生菌群落具有固氮菌，qPCR 定量拷贝数为 2.34×10^2 copies·g^{-1}-4.54×10^7 copies·g^{-1}，水葱、香蒲和菖蒲具有较高的 *nif*H 拷贝数。内生菌 *nif*H 基因的高通量测序结果表明各植物固氮内生菌多样性存在较大差异，香蒲和菖蒲固氮内生菌多样性较高，灯心草最低。各植物主要固氮内生菌组成和相对丰度存在较大差异。固氮菌 *Rhodopseudomonas* 和 *Sinorhizobium* 在菱中具有较高的相对丰度，*Geobacter* 和 *Desulfovibrio* 是芦苇和菖蒲内生菌的优势固氮菌。固氮内生菌主要归属于 Cluster I和 Cluster III。通过无氮培养发现只有菖蒲和菱存活，且菖蒲生物量显著增长，进一步通过 ^{15}N 同位素示踪直接测定法显示菖蒲和菱根内具有明显的固氮作用。本研究揭示了不同水生植物内生菌群落多样性与结构以及固氮内生菌组成均存在显著差异，并证实了水生植物内生菌固氮的作用，为进一步深入研究内生菌及其宿主的相互关系建立了基础。

堆肥过程中基质碳氮比诱导的抗生素抗性基因变异及去除机制

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摘要

为了更加清晰的了解堆肥过程中由初始底物引起的抗生素抗性基因去除的潜在机制，我们研究了芦苇秸秆和牛粪在不同碳氮比堆肥过程中理化性质、细菌群落组成、真菌群落组成、ARGs 相对丰度和移动遗传基因(MGEs)相对丰度的动态变化。结果显示，细菌群落的演替主要表现为厚壁菌门(Firmicutes)和放线菌门(Actinobacteria)的动态平衡，而真菌群落的演替主要体现在子囊菌门（Ascomycota）始终为主要真菌。堆肥过程中，细菌和真菌之间主要通过负向做用进行互做。在堆肥之后，LL 堆垛（C/N≈26）对 ARGs 的去除效率高于 HL 堆堆垛（C/N≈35），而 MGEs 在 HL 堆垛中完全降解，却在 LL 堆垛中富集 2.3%。ARGs 相对丰度的大幅下降可能是由于潜在宿主细菌属 *Advenella*、*Tepidimicrobium*、*Proteiniphilum*、*Acinetobacter*、*Pseudomonas*、*Flavobacteria* 和 *Arcbacter* 大量的减少。偏最小二乘路径模型(PLS-PM)显示，细菌群落的演替比 MGEs 在 ARGs 去除中发挥更重要的作用，而真菌群落通过见解影响细菌群落来改变 ARGs 的格局。堆肥处理对直接因子和间接因子均有影响。本研究揭示了真菌群落对 ARGs 的影响，并强调了不同碳氮比的堆肥处理对 ARGs 去除机制的作用。

Variations in antibiotic resistance genes and removal mechanisms induced by C/N ratio of substrate during composting

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Abstract

For a comprehensive insight into the potential mechanism of the removal of antibiotic resistance genes (ARGs) removal induced by initial substrates during composting, we tracked the dynamics of physicochemical properties, bacterial community composition, fungal community composition, the relative abundance of ARGs and mobile genetic genes (MGEs) during reed straw and cow manure composting with different carbon to nitrogen ratio. The results showed that the successive bacterial communities were mainly characterized by the dynamic balance between Firmicutes and Actinobacteria, while the fungal communities were composed of Ascomycota. During composting, the interactions between bacteria and fungi were mainly negative. After composting, the removal efficiency of ARGs in compost treatment with C/N ≈ 26 (LL) was higher than that in compost treatment with C/N ≈ 35 (HL), while MGEs were completely degraded in HL and enriched by 2.3% in LL. The large reduction in the relative abundance of ARGs was possibly due to a decrease in the potential host bacterial genera, such as Advenella, Tepidimicrobium, Proteiniphilum, Acinetobacter, Pseudomonas, Flavobacteria and Arcbacter. Partial least-squares path modeling (PLS-PM) revealed that the succession of bacterial communities played a more important role than MGEs in ARGs removal, while indirect factors of the fungal communities altered the profile of ARGs by affecting the bacterial communities. Both direct and indirect factors were affected by composting treatments. This study provides insights into the role of fungal communities in affecting ARGs and highlights the role of different composting treatments with different carbon to nitrogen ration on the underlying mechanism of ARGs removal.

Keywords: Antibiotic resistance genes (ARGs); Mobile genes elements (MGEs); Bacterial communities; Fungal communities; Carbon to nitrogen ratio; ARGs removal mechanism

两株三氯乙烯同化降解菌及其应用

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摘要

随着化工领域的快速进步，氯代烃溶剂如三氯乙烯（TCE）由于其稳定的化学性质和低廉的价格被大量制造出来并且广泛地应用到工业、农业和军事之中。然而 TCE 可经呼吸道和皮肤吸收进入人体并具有较大的毒性，因此有必要挖掘氯代烯烃生物降解资源，开发高效的污染修复方法。目前的生物修复方法聚焦于厌氧条件下的还原性脱氯过程，高氯代烯烃在厌氧脱氯微生物的作用下被逐级还原脱氯为低氯代烯烃（二氯乙烯、氯乙烯），在某些微生物的作用下还可以继续还原，完全脱氯生成无害化的乙烯。随着还原脱氯的进行，脱氯速率会减慢，其中氯乙烯脱氯为乙烯的过程非常缓慢，是此过程中关键的限速步骤。而大多数厌氧脱氯微生物无法完全还原脱氯导致毒性更强的中间产物积累、且伴随修复效率低和周期长等问题。能够充分还原脱氯的微生物种类稀少并且对于生长环境的严苛要求，具有局限性和成本高等问题。

本研究前期通过对高浓度 TCE 和苯污染的土壤进行采样和长期的富集后，从中分离出两株从未报道过脱氯功能的三氯乙烯同化降解菌 *Cytobacillus oceanisediminis* SH48 和 *Lysinibacillus fusiformis* SH13，二者都可以在好氧条件下同化三氯乙烯，从而实现对其的降解。两株菌株生长对环境条件要求低，能够在不添加额外生长基质的条件下以三氯乙烯为自身生长所需的唯一碳源与能源，有效降解氯代烃污染物，释放无机游离氯离子且无毒性中间产物积累，该菌株或由其制备的微生物菌剂可用于氯代烃污染的工业污染场地的土壤或地下水的生物修复，具有重要应用前景。

研究成果将有助于环境微生物资源的开发和新的降解基因的挖掘，拓宽污染场地原位修复的可利用资源。

关键词：三氯乙烯；脱氯；同化菌；绿色

Continental and temporal scale biodiversity of mudflat intertidal viromes in China

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Abstract

Viruses constitute the most diverse and abundant living entities in the Earth's biosphere. However, our understanding of this tiniest life form in complex ecosystems remains limited. Here, we recovered 20,102 viral operational taxonomic units from 96 intertidal sediment metagenomes spanning twelve coastal regions from the southmost to northmost in China to examine the diversity, functional potential, and ecological mechanisms of intertidal viromes at the continental scale. In addition, we also performed the continuous sampling of intertidal sediments over the 1-year period in Qingdao of China to investigate the temporal patterns of viruses. Our results demonstrated high viral taxonomic diversity and functional potential in intertidal zones, carrying important functional traits that can be potentially transferred to microbial hosts and mediate biogeochemical cycles including carbon, nitrogen, and sulphur. The concordant biogeographic patterns (distance-decay relationship) and temporal turnovers (time-decay relationship) were observed for viruses and their host microbes. Viral communities were generally habitat specific that low overlaps were observed among intertidal samples or different habitats. The virus-host interactions of the whole community were relatively stable with time. Overall, these findings expanded our understanding of intertidal viromes within an ecological framework, providing novel insights into the virus-host coevolutionary arms race.

Keywords: Intertidal viromes; Auxiliary Metabolic genes; Biogeographic patterns; Temporal turnovers; Virus-host interaction

Distinct ecological mechanisms drive the spatial scaling of abundant and rare microbial taxa in a coastal sediment

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Abstract

Microbes are ubiquitous in the Earth's biosphere, executing essential ecosystem functions and maintaining ecosystem stability. Unraveling the ecological mechanisms that drive the patterns of microbial communities across space and time is an essential issue in microbial biogeography. This study links microbial spatial scaling with ecological mechanisms and aiming to provide novel mechanistic insights into the biogeographic patterns followed by different types of microbes.

The Beibu Gulf region in the northwest of the South China Sea was selected as our study area, which is a semi-enclosed, typical subtropical Marine bay. A total of 29 sediment samples were collected across Beibu Gulf. Two typical spatial scaling models, including the diversity-area relationship (DAR) and the distance-decay relationship (DDR), were investigated using high-throughput sequencing techniques. To overpass the ambiguous definition of abundant and area taxa in microbial ecology, the α- and β-diversity indices were extended to Hill number. The contribution of abundant and rare microbial taxa on DAR and DDR was verified by increasing the diversity order *q*, i.e. decreasing the weight on rare microbial taxa. Null model analysis, which quantifies the contribution of different ecological processes to the construction of microbial communities, was used to explore the relationship between local community assembly mechanisms and spatial scale patterns of microorganisms.

As a result, both environmental heterogeneity and community assembly mechanism were responsible for the differences in microbial spatial scale patterns. Strong spatial scaling patterns were observed for the whole community and rare subcommunities. In contrast, only weak patterns were observed for abundant subcommunities. The strong contribution of rare taxa to microbial spatial scaling was further confirmed by extending the spatial scale diversity indices (DAR and DDR) to Hill numbers. Furthermore, strong ecological drift and dispersal limitation underlay the strong spatial scaling patterns of rare subcommunities, whereas a high degree of homogeneous selection weakens the spatial scaling of abundant subcommunities. Such differed contribution of homogeneous selection and dispersal limitation exhibited by abundant and rare subcommunities was also verified by a deep sequencing experiment. The results demonstrated that rare taxa were responsible for the spatial scaling patterns of sediment microbial communities in the Beibu Gulf. Different ecological mechanisms mediated the different biogeographic patterns of abundant and rare taxa. This study provided novel insight into the spatial scaling followed by different types of microorganisms.

Keyword: Microbial communities; Microbial biogeography; Diversity-area relationship; Distance-decay relationship; Environmental heterogeneity; Local community assembly

Origin, selection and succession of coastal intertidal zone-derived bacterial communities associated with the degradation of various lignocellulose substrates

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Abstract

Terrestrial microbial consortia were reported to play fundamental roles in the global carbon cycle and renewable energy production through the breakdown of complex organic carbon. However, we have a poor understanding of how biotic/abiotic factors combine to influence consortia assembly and lignocellulose degradation in aquatic ecosystems. In this study, we used 96 in situ lignocellulose enriched, coastal intertidal zone-derived bacterial consortia as the initial inoculating consortia and developed 384 cultured consortia under different lignocellulose substrates (aspen, pine, rice straw and purified Norway spruce lignin) with gradients of salinity and temperature. As coastal consortia, salinity was the strongest driver for assembly, followed by Norway spruce lignin, temperature and aspen. Moreover, a conceptual model was proposed to demonstrate different succession dynamics between consortia under herbaceous and woody lignocelluloses. The succession of consortium under Norway spruce lignin is greatly related with abiotic factors, while its substrate degradation is mostly correlated with biotic factors. A discrepant pattern was observed in the consortium under rice straw. Finally, we developed four groups of versatile, yet specific consortia. Our study not only reveals coastal intertidal wetlands are important natural resources to enrich lignocellulolytic degrading consortia, but also provides insights into the succession and ecological function of coastal consortium.

Keywords: Lignocellulose degradation; Bacterial consortium; Consortium succession; Coastal intertidal zone; Enrichment

Distinct ecological processes mediate domain-level differentiation in microbial spatial scaling in intertidal zone

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Abstract

Spatial scaling of biodiversity, such as taxa-area relationship (TAR) and distance-decay relationship (DDR), are typical ecological patterns followed by both microbes and macrobes in natural ecosystems. Previous studies focusing on microbes mainly aimed to address whether and how different types of microbial taxa differ in spatial scaling patterns, leaving the underlying mechanisms largely untouched. In this study, the spatial scaling of different microbial domains and their associated ecological processes in an intertidal zone were comparatively investigated. Significant spatial scaling of biodiversity could be observed across all microbial domains, including archaea, bacteria, fungi, and protists. Among them, archaea and fungi were found with much stronger DDR slopes than bacteria and protists. For both TAR and DDR, rare subcommunities were mainly responsible for the observed spatial scaling patterns, except for the DDR of protists and bacteria. This was also evidenced by extending the TAR and DDR diversity metrics to Hill numbers. Further statistical analyses demonstrated that different microbial domains were influenced by different environmental factors and harbored distinct local community assembly processes. Of these, drift was mainly responsible for the compositional variations of bacteria and protists. Archaea were shaped by strong homogeneous selection, whereas fungi were more affected by dispersal limitation. Such differing ecological processes resulted in domain-level differentiation of microbial spatial scaling. This study links ecological processes with microbial spatial scaling, and provides novel mechanistic insights into the diversity patterns of microbes belonging to different trophic levels.

Keywords: Spatial scaling; Microbial domains; Taxa-area relationship; Distance-decay relationship; Local community assembly; Environmental heterogeneity

LCdb 数据库揭示地球生态系统中木质素降解微生物群落的分布、基因组潜力和组装

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摘要

木质素作为地球上丰富的有机碳，在全球碳循环中发挥着至关重要的作用。然而，我们对全球木质素降解微生物群落的了解仍然难以捉摸。一个很大的障碍是缺乏全面准确的木质素降解功能基因数据库。在这里，我们首先开发了一个精选的功能基因数据库(LCdb)，用于木质素降解微生物群落的宏基因组分析。通过 LCdb，我们清晰地描述了全球生物地理学中木质素降解微生物群落。陆地微生物群落表现出最高的多样性，但相关性最低，表现出明显的功能冗余特性。相反，在水生群落中观察到了较低的多样性，但对较低多样性的反应是强烈的相关性，在分类学和功能性状水平上都表现出明显的生态位分化。具体而言，dypB 和 dypA 在地球生态系统中广泛存在，表明它们在木质素解聚中发挥着重要作用。河口群落和海洋群落分别以漆酶和超氧化物歧化酶为特征。值得注意的是，古菌在木质素降解中的作用在海洋生态系统中得到了揭示。环境因素对功能性状的影响很大，但对分类群的影响较弱。零模型分析进一步验证了功能性状的组成是确定性的，而分类组成是高度随机的，表明环境选择的是功能基因而不是分类群。我们的研究不仅为通过宏基因组测序研究木质素降解微生物群落提供了一个有用的工具，而且促进了对全球木质素降解菌群落的生态作用和特征的理解。

关键词：木质素；数据库；功能基因；全球

中国滩涂潮间带空间尺度上古菌群落结构与功能的差异研究

李焱

摘要

尽管古菌在生态学和进化方面扮演着重要角色，然而关于滩涂古菌的研究尚属有限，对其生态群落和功能在空间尺度上的变化，了解仍存不足。本研究采用微观多样性和宏观多样性以及水平基因转移（HGT）等研究方法，揭示了滩涂生态系统中古菌群落组成的空间变化特征，特别是在中纬度地区，古菌群落结构发生显著变化。在功能方面，我们发现古菌的生物学功能在空间尺度上呈现稳定趋势。古菌在滩涂系统中承担的生态功能受到环境因子（如总氮含量、水分等）的显著影响。此外，我们观察到滩涂古菌内部的水平基因转移频繁发生，这对于维持古菌群落的生态功能稳定起到了重要作用。本研究的发现强调了滩涂古菌生态学的重要性，并为进一步研究提供了基础。对滩涂古菌生态群落和功能的空间尺度上的变化加深理解，有助于更好地把握滩涂生态系统的动态特征，并为保护和管理滩涂生态系统提供科学依据。

Rhizophagus irregularis 联合生物炭对盐碱胁迫柳枝稷生长、抗氧化酶活性及光合特性的影响

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摘要

土壤盐碱化是严重影响植物生长最主要的非生物胁迫因素之一。为进一步揭示在丛枝菌根真菌和生物炭处理下，柳枝稷对盐碱胁迫的响应。本试验研究了在盐碱胁迫下根内根孢囊霉（*Rhizophagus irregularis*，Ri）联合生物炭（BC）对柳枝稷生物量、抗氧化酶、叶绿素、光合作用的影响。结果表明：盐碱胁迫下(1) Ri、BC 和 Ri+BC 处理植株地上和地下生物量均显著高于 CK 处理（$p<0.05$）；(2) Ri 和 BC 单独或联合应用均显著增加植物叶片相对叶绿素含量、抗氧化酶活性，提高了叶片蒸腾速率、气孔导度、电子转移速率、净光合速率和光合强度，保护了 PSII；(3) Ri+BC 处理组植株蒸腾速率、气孔导度、净光合速率、PSII 效率、表光电子传递速率和光化学猝灭系数均达到最大值，增幅在 38%~54%之间；(4) 通过对不同处理光响应和 CO_2 响应曲线的拟合，发现 Ri+BC 处理组柳枝稷光饱和点和光补偿点分别达到 1786.2μmol/m^2/s、12.5μmol/m^2/s，最大羧化速率和最大电子传递速率分别达到 48.4 μmol CO_2/m^2/s 、153.6 μmole$^-$/m^2/s。在盐碱胁迫下，Ri+BC 处理表现出较强的光适应能力和较高的 CO_2 同化效率。我们的研究结果表明，Ri 联合生物炭能通过提高叶片抗氧化酶活性和光合特性来增强植物对盐碱胁迫的耐受性，促进植物生长。Ri 联合 BC 改良技术也为盐碱地的高效开发与利用提供新的思路。

关键词：根内根孢囊霉；生物炭；盐碱胁迫；叶片抗氧化酶；叶绿素荧光

Effects of *Rhizophagus irregularis* combined with biochar on the growth, antioxidant enzyme activity and photosynthetic properties of switchgrass (*Panicum virgatum*) under saline-alkali stress

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Abstract

Soil salinization is one of the most important abiotic stress factors that seriously affect plant growth. To further reveal the response of switchgrass (*Panicum virgatum*) to salinity-alkali stress under treatment with mycorrhizal fungi and biochar. this experiment investigated the effects of *Rhizophagus irregularis* (Ri) combined with Biochar (BC) on switchgrass biomass, antioxidant enzymes, chlorophyll and photosynthesis under salinity-alkali stress. The results showed that : under salinity-alkali stress (1) Ri, BC, and Ri +BC treatment plants had significantly higher shoot and root biomass than CK treatment ($p<0.05$); (2) Ri and BC, alone or in combination, significantly increased the relative chlorophyll content and antioxidant enzyme activities of plant leaves, increased leaf transpiration rate, stomatal conductance, electron transfer rate, net photosynthetic rate and photosynthetic intensity, and protected PSII;

(3) Plant transpiration rate, stomatal conductance, net photosynthetic rate, PSII efficiency, surface photoelectron transfer rate and photochemical burst coefficient all reached maximum values in the Ri+BC treatment, with increases ranging from 38% to 54%; (4) By fitting the light response and CO_2 response curves of different treatments, it was found that the light saturation point and light compensation point of switchgrass in Ri+BC treatment reached 1786.2 μmol/m^2/s and 12.5 μmol/m^2/s, respectively, and the maximum carboxylation rate and maximum electron transfer rate reached 48.4 μmol CO_2/m^2/s and 153.6 μmol e$^-$/m^2/s, respectively. Under salinity-alkali stress, the Ri+BC treatment exhibited stronger light acclimation and higher CO_2 assimilation efficiency. Our results show that Ri combined with BC can enhance plant tolerance to salinity-alkali stress and promote plant growth by increasing leaf antioxidant enzyme activity and photosynthetic properties. Ri combined with BC improvement technology also provides new ideas for efficient development and utilization of salinity-alkali lands.

Keywords: Rhizophagus irregularis; Biochar; Salinity-alkali stress; Leaf antioxidant enzymes; Chlorophyll fluorescence; Light response curve

巨型厌氧氨氧化颗粒的群落组装机制：厌氧氨氧化菌及其共生菌之间的互作关系

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摘要

厌氧氨氧化菌倾向于在工程系统中形成较大尺寸的颗粒，但人们对此类厌氧氨氧化聚集体（> 1.0 mm）中群落组装和物种共存之间的联系知之甚少。本文分别从大规模的畜禽养殖污水处理厂（即 SwAmx）和实验室规模的上流式厌氧氨氧化反应器（即 LuAmx）中随机采集各 100 个颗粒污泥样品，以探索它们目前尚不清楚的微生物多样性和生态特征。基于 16S rRNA 基因扩增子序列研究发现，在 SwAmx 中观察到主坐标和颗粒直径之间的相关性较弱。根据 Lenenthal 等人对变异系数（CV）的定义，本研究发现 CV 数值存在波动性，且 SwAmx 中的功能菌群分布在中等 CV 数值范围内（即 $50\% < \mathrm{CV} < 100\%$），表明特定物种没有明显的异质性和同质性。进一步零模型分析发现，随机过程（如扩散限制）主导了两个反应器中的群落组装。特别是在 SwAmx 反应器中，确定性过程（如同质选择）是负责脱氮的功能组（如厌氧氨氧化菌、氨氧化菌和反硝化菌）的主要驱动力。此外，我们通过共生子网络揭示了 SwAmx 和 LuAmx 反应器中厌氧氨氧化菌与其共生物种之间存在显著的负相关性。尽管这项研究揭示了两个反应器中厌氧氨氧化巨型颗粒的组装机制，但它受到废水处理厂类型和样本的时间及数量的限制。未来应从更广泛的反应器中收集更大的样本集，结合更全面的组学分析技术（如宏转录组学、宏蛋白质组学和代谢组学）来破译操作参数和共生物种之间的相关性。总的来说，这项工作证明了微生物群落组装和功能特征的互作关系，可用于促进工程厌氧氨氧化系统中微生物群落的管理。

关键词：厌氧氨氧化菌；巨大颗粒；群落组装；共生物种

一株西瓜枯萎病生防菌的抑菌效果及其鉴定

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摘要

为了筛选西瓜枯萎病生防菌株并探究其抑菌效果，以齐齐哈尔市园艺研究所棚室内西瓜根际土为材料，利用平板对峙法筛选到一株高效抑制西瓜枯萎病菌的拮抗菌株 J4，其具有产淀粉酶、葡聚糖酶、蛋白酶以及铁载体的能力，其衰亡期无菌发酵液对 Fusarium oxysporum f. sp. niveum (Fon)菌落生长抑制率为 71.87%。利用 2’,7’-二氯二氢荧光素二乙酸酯 (DCFH-DA) 荧光探针检测发现，菌株 J4 诱导 Fon 菌丝细胞活性氧 (ROS) 的积累；菌株 J4 无菌发酵液 (CFS)引起 Fon 菌丝超氧化物歧化酶 (SOD)、过氧化氢酶 (CAT)、过氧化物酶 (POD) 和谷胱甘肽还原酶 (GR) 活性及可溶性蛋白、MDA 含量的显著升高。经 16S rDNA 序列检测其被鉴定为 Bacillus siamensis。盆栽试验结果表明，菌株 J4 对西瓜枯萎病具有明显的生防效果，防治效果为 72.6%。综上所述，菌株 Bacillus siamensis J4 对西瓜枯萎病菌具有较强的抑制作用，对西瓜枯萎病有明显的防治作用，在西瓜枯萎病生物防治中具有广泛的应用前景。

关键词：生防菌；西瓜专化型尖孢镰刀菌；活性氧；抗氧化酶；无菌发酵液

谷氨酸母液生物转化浆液发酵条件优化及促生效果

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摘要

谷氨酸母液生物转化浆液来源于谷氨酸母液，含有丰富的蛋白质、氨基酸、蔗糖和有机酸等有机物。高浓度的营养物质让大部分微生物生长困难，酵母因其对环境适应性强，生长繁殖速度快的特点，在这种浆液中有较高的生态竞争力，同时酵母也常常作为微生物肥料的发酵菌株，在农业上广泛应用。本研究以菌体干重产量为指标，筛选库德里阿兹威氏毕赤酵母作为发酵菌株；基于单因素实验，确定酵母发酵的主要影响因素为葡萄糖添加量、摇瓶装液量和培养时间；采用响应面法，确定最优发酵条件为 9%的葡萄糖添加量，187 mL/250 mL 的摇瓶装液量，培养时间 98 h。在上述条件下测得菌体干重产量为 0.551%，与响应面分析模型预测值 0.548%接近。发酵液浸种提高水稻、玉米和小麦种子的发芽率，促进根的生长。综上所述，以浆液作为发酵底物，不仅能够生产酵母菌体蛋白，同时能够促进禾本科作物生长。为后期谷氨酸母液生物转化提供理论基础和技术指导。

关键词：谷氨酸母液生物转化浆液；库德里阿兹威氏毕赤酵母；发酵条件优化；种子萌发

玉米根际促生菌 *Enterobacter huaxiensis* LN01 的促生效应研究及其基因组解析

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摘要

玉米是我国重要的粮食作物。近年来，为了提高玉米产量，化肥的大量施用已严重危害到了土壤健康。植物根际促生菌 (PGPR) 可以促进植物的生长和改善健康，利用 PGPR 来提高作物产量是实现可持续农业的一个关键目标。因此，本研究通过筛选培养基，从玉米根际土壤中分离 PGPR，并测定其溶磷、解钾、固氮、吲哚乙酸 (IAA) 合成能力；结合盆栽实验，验证其对玉米的生长促生作用。最后，通过全基因组学测序，挖掘菌株促生相关基因。经 16S rDNA 和全基因组测序，菌株 LN01 被鉴定为 *Enterobacter huaxiensis*。菌株 LN01 具有溶磷、解钾、固氮以及 IAA 分泌能力，其相关数值分别为 58.33 mg/L、15.6 mg/L、 15.14 mg/L 和 42.2 mg/L。菌株 LN01 对植物地上部生物量和地下部交叉数、节点数及根长有显著促进作用。此外，LN01 菌株的全基因组分析表明， LN01 基因组包含一条 5379004 bp 的染色体和六个质粒，平均全基因组 GC 含量为 55.1%。该基因组预计包含 5004 个编码序列(CDSs)。能够在 NR、Swiss-Prot、COGs、KEGGs、GO 和 Pfam 数据库注释到的 CDs 数量分别为 4973、4219、4085、3285、2793 和 4400。LN01 的基因组包括 87 个 tRNA 和 25 个 rRNA，溶磷 (*pstABCS*、*phoABEOR*、*phnACDEFGHIJKLP* 和 *ugpABCE*)，解钾 (*kdpABC*、*kefBCFG*、*trkAH* 和 *kup*)，生物固氮 (*nirBCD*、*nasA*、*glnA*、*gltBD* 和 *nrtABC*)，IAA 合成 (*trpABSCFRGD*) 和铁获取 (*fhuBCDEF*、*afuABC*、*efeOBU* 和 *fepCDG*) 的基因。通过 antiSMASH 分析，菌株 LN01 具有四种次级代谢物生物基因簇，包括非核糖体肽合成酶、萜烯、硫肽和芳基多烯。综上所述，菌株 LN01 具有一定的促生功能且全基因组分析数据进一步阐明了其生长促进机制，为研制微生物肥料提供了技术支持，并展现了菌株 LN01 作为农用生物肥料的优秀种质资源的巨大潜力。

关键词：玉米；根际促生菌；全基因组；植物促生效果

土壤增温和新近光合产物输入途径对杉木幼林土壤微生物多样性和群落组成的影响

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摘要

温度升高和碳的可利用性对土壤微生物群落的影响可能会对生物多样性和未来气候产生重要影响。我们在亚热带的杉木幼林进行了 7 年的原位土壤增温（+4℃），并通过尼龙网隔离法设置不同新近光合产物输入梯度（无隔离、隔离根系和隔离菌丝）。结果发现，当土壤温度升高 4℃，微生物多样性，尤其是细菌的多样性显著下降。增温也使细菌和真菌的物种组成从富营养型向寡营养型转变。如放线菌门、厚壁菌门、毛霉门相对丰度增加，变形菌门、担子菌门相对丰度降低。新近光合产物输入梯度对细菌和真菌多样性无显著影响，但改变了其物种组成。与隔根和隔离菌丝相比，无隔离中寡营养型物种相对丰度较低。另外，增温降低了细菌群落共生网络的复杂性和稳定性，同时加剧了物种之间的竞争。我们的研究结果表明长期土壤温度升高已经导致微生物群落发生重组，尤其是新近光合产物输入最多的无隔离处理，这为进一步探讨微生物群落在生态系统中发挥的生态功能提供了理论指导。

关键词：土壤微生物；新近光合产物；亚热带森林；杉木幼林；土壤增温

生防菌淡紫紫孢菌对聚己二酸对苯二甲酸丁二醇酯(PBAT)的生物降解

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摘要

从土壤中分离得到一株淡紫紫孢菌 YGTC2302，测定其对烟粉虱的生防功能以及对聚己二酸对苯二甲酸丁二醇酯(PBAT)的降解能力。淡紫紫孢菌 YGTC2302 基因组全长 37396383bp，编码基因 10187 个，菌株在 PBAT 培养基上形成水解圈，并且可以分泌蛋白酶和脂肪酶。YGTC2302 在土壤环境中处理的 PBAT 膜,30d 降解 12.5%，表面逐渐失去光泽出现孔洞，亲水性增加，PBAT 膜在降解的过程中发生了酯键断裂和羟基生成的现象。

基于特征序列探究人类病原菌在环境中的存在特点

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摘要

在评估环境中的人类病原体造成的风险时，当前研究大多数集中于单一类群或特定的环境背景，缺乏在整个人类环境中的全面评估。为了在整体上了解人类病原体的分布规律，本研究应用了一种先前已发表的基于 k-mer 的方法，全面收集人类致病菌的基因组，并生成了 239 种原核人类病原体的特征序列。接下来，利用公共数据库中的环境鸟枪宏基因组学数据集探究不同的介质、不同人类活动强度的环境类型中病原体的分布特点，结果表明，空气中具有最高的病原菌 α 多样性，不同介质具有不同的优势物种和显著不同的病原菌群落组成，*Cutibacterium acnes*，*Ralstonia picketti* 分别是空气和沉积物中最占优势的病原菌，而水体、土壤中相对丰度最高的物种均为 *Acinetobacter lwoffii*。在人类活动影响较大的区域，病原菌的组成与自然区域不同，丰度与多样性会显著提高。总之，本研究提供了一套便捷地从宏基因组数据集中全面识别并定量所有人类病原菌的方法流程，为全面评估环境中的人类病原体风险提供了思路。

关键词：微生物生态学；健康风险；人类病原体

深度共熔溶剂分离木质素和季铵化木质素回收纤维素酶

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摘要

本研究利用采用氯化胆碱和乳酸形成的低共熔试剂（DES）分离木质素，并将其通过化学改性合成具有 pH 响应的木质素季铵盐（DESL-Nx）用于回收纤维素酶。

木质素提取效果最好的条件是 120℃、24 h。此时木质素纯度为 97.86±2.7%，产率为 79.93±2.3%。以 3-氯-2-羟丙基三甲基氯化铵（CHPTAC）为铵化剂，对用 DES 提取的木质素（DESL）进行铵基化，制得不同季铵化程度的木质素季铵盐。其中 DESL-N15 在 pH 值 3.8，浓度为 2 g/L 时，沉淀率为 93.68±2.8%，回收纤维素酶滤纸酶活为 72.67±1.9%。在循环回收纤维素酶过程中补加纤维素酶，可以稳定地维持酶解效率。利用 DESL-N15 的 pH 响应性循环回收纤维素酶可以节约酶的使用量，并逐步提高酶解效率。

关键词：低共熔溶剂；木质素；季铵化改性；pH 响应；回收纤维素酶

Lignin separation by deep eutectic solvent and quaternization lignin for cellulase recovery

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Abstract

In this study, a deep eutectic solvent (DES) based on choline chloride and lactic acid was used to separate lignin and chemically modified it to synthesize pH-responsive lignin quaternary ammonium salt (DESL-Nx) for cellulose recovery enzymes. The best conditions for lignin extraction were 120 °C for 24 h. At this time, the purity of lignin was 97.86±2.7%, and the yield was 79.93±2.3%.3-chloro-2-hydroxypropyltrimethylammonium chloride (CHPTAC) was used as the ammonium agent to aminate the DES-extracted lignin (DESL) to obtain lignin quaternary ammonium salt with different degrees of quaternization. Among them, when the pH value of DESL-N15 was 3.8 and the concentration was 2 g/L, the precipitation rate was 93.68±2.8%, and the enzyme activity of recovered cellulase filter paper was 72.67±1.9%. Supplementing cellulase in the process of recycling cellulase can stably maintain the enzymatic hydrolysis efficiency. Using the pH-responsive recycling of DESL-N15 to recycle cellulase can save enzyme usage and gradually improve the enzymatic hydrolysis efficiency.

Keywords: Deep eutectic solvent; Lignin; Quaternary modification; pH response; Cellulase Recovery

基于拉曼光谱与人工智能算法的病原菌分级分类识别

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摘要

病原微生物如细菌、病毒、真菌等广泛存在于环境中，严重威胁全球公共卫生安全。发展病原微生物快速检测技术，对于减少病原菌扩散传播，防控传染性疾病，维护生物安全具有重要意义。拉曼光谱作为一种无需培养、无损、快速地细菌鉴定方法近年来得到广泛关注，它可以提供细菌的全景式表型指纹图谱信息用于细菌鉴定，结合机器学习算法可以进一步提取拉曼谱图中的细微差异。但是由于拉曼光谱是一种表型方法，许多参数会影响光谱信号，如微生物的生长阶段、表型异质性等，然而，关于这些参数对拉曼-机器学习识别结果的影响，目前仍缺乏系统性地比较和研究。为此，本研究采集 14 种病原菌与非病原菌拉曼谱图建立数据库，通过线性判别分析、随机森林、支持向量机以及基于注意力机制的神经网络分别进行分类识别，建立革兰氏阴性/阳性、抗性、菌株、生长阶段四级分类模型，探究各级分类是否会对识别结果造成影响以及不同算法识别准确率的高低。此外，对每一级进行分类识别并通过 PCA-LDA 聚类向量分析对细菌发生改变的主要生物标记峰进行分析。结果表明：（1）不同分类下细菌的生长阶段会对拉曼结合机器学习识别工作产生影响，每一级分类模型识别准确率分别为 91.5%、98.31%、66%、100%；（2）细菌种类以及生长状态增多时，传统机器学习算法识别准确率会有所下降，深度学习更能够适应多种分类细菌的识别；（3）引起差异的主要拉曼贡献峰分配成分为蛋白质。本研究为拉曼光谱结合机器学习快速识别病原菌技术的实际应用提供了理论和技术支撑。

关键词：拉曼光谱；机器学习；病原菌；生长阶段

Classification and identification of pathogenic bacteria based on Raman spectroscopy and artificial intelligence algorithm

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Abstract

Pathogenic microorganisms such as bacteria, viruses, and fungi exist widely in the environment, posing a serious threat to global public health security. The development of rapid detection technology of pathogenic microorganisms is of great significance for reducing the spread of pathogenic bacteria, preventing and controlling infectious diseases, and maintaining biosafety. Raman spectroscopy, as a non-destructive and rapid method for bacterial identification without culture, has attracted wide attention in recent years. It can provide panoramic phenotypic fingerprint information of bacteria for bacterial identification, and combine with machine learning algorithms to further extract subtle differences in Raman spectroscopy. However, since Raman spectroscopy is a phenotypic method, many parameters will affect the spectral signal, such as the growth stage of microorganisms, phenotypic heterogeneity, etc. However, there is still a lack of systematic comparison and research on the impact of these parameters on the recognition results of Raman combined with machine learning. To this end, this study collected 14 kinds of pathogenic and non-pathogenic bacteria to establish a database, through linear discriminant analysis, random forest, support vector machine, and attentional neural network classification recognition, respectively, to establish Gram-negative/positive, resistance, strain, growth stage four-level classification model. Explore whether different classification levels will affect the recognition results and the recognition accuracy of different algorithms. In addition, each level was classified and identified, and the main biomarker peaks of bacterial changes were analyzed by PCA-LDA cluster vector analysis. The results showed that: (1) the growth stage of bacteria under different classifications had an impact on the recognition work of Raman combined machine learning, and the recognition accuracy of each classification model was 91.5%, 98.31%, 66% and 100%, respectively; (2) when the bacterial species and growth state increase, the recognition accuracy of traditional machine learning algorithms will decrease, and deep learning can better adapt to the recognition of various types of bacteria; (3) the main component of Raman contribution peak was protein. This study provides theoretical and technical support for the practical application of Raman spectroscopy combined with machine learning to rapidly identify pathogens.

Keywords: Raman spectroscopy; Machine learning; Pathogenic bacteria; Growth stage

镉污染稻田功能微生物原位修复技术的研究

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摘要

微生物驱动土壤重金属的活化移除是最具有前景的耕地重金属污染修复技术之一，而微生物处理后土壤含镉处理液的净化回收是实现微生物原位修复技术的关键环节。本研究将定向筛选的复配功能菌群运用于镉污染稻田原位修复试验，结果表明：功能菌群对土壤总镉和有效镉的活化移除效率可达到13.8-48.3%；微生物群落分析表明：土壤中*Metallibacterium*、*Acidithiobacillus* 和 *Alicyclobacillus* 的相对丰度在处理过程中逐渐升高，土壤微生物群落结构显著改变，其主要受到外源输入的营养元素以及微生物处理前后引起的土壤有效镉、总镉含量和pH值变化的影响；进一步分析发现处理液中存在大量的Cd、N、P和K营养元素及微生物资源，具有较高的回收利用价值；利用活性炭（C）、腐殖酸（H）和单分子纳米材料（S）净化含镉处理液，发现处理液中共存阳离子及溶液pH对Cd的吸附效率有显著影响，对Cd的吸附作用主要发生在Fe和Al之后；最后将净化的处理液应用于微生物培养和土壤修复，发现净化后的处理液可直接用于微生物培养而无需额外添加营养成分，且对土壤修复效率比原始微生物菌剂更高。由此可见，微生物活化移除修复技术可以有效降低土壤总镉和有效镉含量，通过进一步探索微生物处理液的净化回用工艺，促进了水资源、营养元素及微生物资源循环利用，降低了修复成本，推进了镉污染稻田绿色、高效、快速修复技术的实现。

关键词：微生物；镉污染；生物修复；生态学

厌氧乙烷氧化驱动的硝酸盐还原：微生物富集和宏基因组分析

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摘要

湿地和海洋生态系统产生了大量的天然气，这些气体的大部分在被排放到大气中之前会被微生物原位消耗。乙烷是天然气中仅次于甲烷的第二大组分，由于其对环境的潜在影响，乙烷引起了人们的关注。然而，关于厌氧条件下乙烷氧化的研究通常与硫酸盐还原相关。在这项研究中，我们尝试使用乙烷作为唯一的电子供体来支持硝酸盐的还原。通过长期微生物富集和反应器运行，硝酸盐被还原，并且反应器中没有亚硝酸盐的积累，最高的硝酸盐还原速率为 15.7 mg NO_3^--N·L^{-1}·d^{-1}。16S rRNA 高通量测序结果显示，属于变形菌门的微生物在反应器运行的所有阶段中的相对丰度占据绝对优势。宏基因组数据分析表明鉴定到了编码完整的反硝化、异化硝酸盐还原为氨（DNRA）和甲烷氧化途径的基因。根据基因组数据构建了可能的乙烷和硝酸盐代谢途径的基因草图。乙烷被推测通过甲烷单加氧酶氧化，最终被氧化为二氧化碳。乙烷氧化产生的电子可能通过细胞色素传递，以支持反硝化过程。未来的研究可以集中在寻找可能的氧气来源和解释该系统中潜在的碳-氮-硫循环机制等方面。

关键词：厌氧乙烷氧化；反硝化；甲烷单加氧酶；DNRA

外源菌 Rhodococcus qingshengii 对石油烃污染土壤的强化修复及新生群落功能模块的解析

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摘要

石油烃作为人类最重要的资源，在全世界范围内广泛使用，大量的石油在自然和人为的因素作用下进入土壤，带来了严重的石油土壤污染问题。石油污染物会影响土壤理化性质、干扰植物的正常生长、破坏群落结构等，是不容忽视的环境问题。微生物修复中的生物强化是最有效的修复方法之一，具有针对性强、污染物去除率快等特点，但其可行性和对土壤群落内部影响还有待进一步研究。本研究将石油烃外源降解菌 Rhodococcus qingshengii 接种于石油烃污染的土壤，研究其生物强化过程和土壤微生物群的重组。结果表明，菌种接种了 42 天后，对 0#柴油的降解率最高的分组达到了 86.37%，高通量测序结果表明，接种菌种在土壤微生物群落中存活良好，并保持了较高的丰度。外源菌种显著影响了土壤微生物群落结构和演替过程，并形成了与接种菌相关的功能菌群。

关键词：微生物群落；石油烃降解；共现网络；功能菌群

Exogenous bacteria Rhodococcus qingshengii enhanced remediation of soil contaminated with petroleum hydrocarbons analysis of the functional modules of the newborn community

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Abstract

Petroleum hydrocarbons, as the most important resource for human beings, are widely used worldwide. A large amount of oil enters the soil under the influence of natural and human factors, leading to serious soil pollution caused by petroleum. Petroleum pollutants can affect soil physical and chemical properties, interfere with the normal growth of plants, and damage community structures, which are environmental issues that cannot be ignored. Bioaugmentation in microbial remediation is one of the most effective remediation methods, which has the characteristics of strong pertinence and fast pollutant removal rate. However, its feasibility and internal impact on soil communities need further research. In this study, Rhodococcus qingshengii, an exogenous petroleum hydrocarbon degrading bacterium, was inoculated into petroleum hydrocarbon contaminated soil to study its Bioaugmentation process and the recombination of soil microbial community. The results showed that after 42 days of inoculation, the group with the highest degradation rate of 0 # diesel reached 86.37%. High throughput sequencing results showed that the inoculated strains survived well in the soil microbial community and maintained a high abundance. Exogenous bacterial species significantly affect the structure and succession process of soil microbial communities, and form functional microbial communities related to inoculation bacteria.

Keywords: Microbial community; Petroleum hydrocarbon degradation; Co-occurrence network; Functional microbial community

Temperature-mediated microbial carbon utilization in China's Lakes

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Abstract

Microbes play an important role in aquatic carbon cycling but we have a limited understanding of their functional responses to changes in temperature across large geographic areas. Here, we explored how microbial communities utilized different carbon substrates and the underlying ecological mechanisms along a space-for-time substitution temperature gradient of future climate change. The gradient included 47 lakes from five major lake regions in China spanning a difference of nearly 15 °C in mean annual temperatures (MAT). Our results indicated that lakes from warmer regions generally had lower values of variables related to carbon concentrations and greater carbon utilization than those from colder regions. The greater utilization of carbon substrates under higher temperatures could be attributed to changes in bacterial community composition, with a greater abundance of Cyanobacteria and Actinobacteriota and less Proteobacteria in warmer lake regions. We also found that the core species in microbial networks changed with increasing temperature, from *Hydrogenophaga* and Rhodobacteraceae, which inhibited the utilization of amino acids and carbohydrates, to the *CL500-29-marine-group*, which promoted the utilization of all almost carbon substrates. Overall, our findings suggest that temperature can mediate aquatic carbon utilization by changing the interactions between bacteria and individual carbon substrates, and the discovery of core species that affect carbon utilization provides insight into potential carbon sequestration within inland water bodies under future climate warming.

Keywords: Bipartite networks; Lakes; Microbial carbon utilization; Molecular ecological networks; Temperature

A potential strategy for microbial conversion of pig manure wastewater into microbial fertilizer

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Abstract

The pig industry generates copious amounts of pig manure wastewater(PMW)from its production process, and the excessive accumulation of this PMW poses a challenge to the environment. Conventional treatment processes for pig manure are often time-consuming, inefficient, and add an extra burden to the industry. This study aims to develop a novel technique for converting PMW into liquid microbial fertilizer. This study includes the following three parts of the experimental process: (1)Optimised pretreatment of PMW by oxidation using hydrogen peroxide(H_2O_2). Upon completion of the pretreatment, the PMW was treated with screened ammonia-nitrogen degrading bacteria(N7, N8, and H6) and DMC microflora to achieve deodorization and nitrogen retention. (2)The screened PGPG microflora can be used to ferment the PMW that has been biologically deodorized and autoclaved to produce microbial fertilizers. (3)The functions of microbial fertilizers were tested through experiments conducted on rice cultivation. The results demonstrated that the utilization of both ammonia-nitrogen degrading bacteria and DMC microflora resulted in a significant reduction of over 80% of gas emissions from PMW. The use of DMC microflora is more effective in reducing gas emissions and optimizing the liquid environment than using a single bacteria treatment. Additionally, DMC microflora has the added benefit of removing odorous volatile organic compounds (p-methyl phenol). The PMW microbial fertilizers containing PGPR microflora exhibit high levels of nutrient concentration, biomass, and maturity. It is satisfying that the relevant parameters of fertilizers also meet the Chinese standards for microbial liquid fertilizers. Finally, microbial fertilizers enhance the physicochemical environment of soil and increase the abundance of plant growth-friendly microbial communities such as *Rhizobiaceae* and *Bacillaceae*, resulting in the promotion of rice growth.

Keywords: Pig manure wastewater; Microbial fertilizer; Biological deodorization; Microflora; Plant growth promotion

一株中度嗜盐不动杆菌对原油的生物降解研究

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摘要

由于缺乏耐盐、耐碱的原油降解菌，盐碱环境下原油(或石油)污染的生物修复具有挑战性。新分离到的一株能够降解原油的不动杆菌 D2 具有中等的盐碱度。生理特征表明，D2 菌株在 pH=9 和 NaCl 浓度为 2% w/v 时的原油降解最适条件。此外，D2 可以耐受 pH 11 和 NaCl 浓度为 8% w/v 的环境。动力学分析表明，D2 对原油(0.2%和 0.5% w/v)的生物降解符合一级动力学模型，k 常数为 0.089 ~ 0.111 d?1，石油降解半衰期为 6.24-7.79 d。气相色谱分析结果表明，菌株 D2 能降解大部分饱和烃，对短链烷烃的去除效率更高。菌株 D2 还能去除芳香烃，平均效率为 33.4%。综上所述，一株中度亲盐性不动杆菌是一种适合于石油污染盐碱地和油田采出水生物修复的候选菌株。

关键词：不动杆菌；原油降解；耐盐碱；石油污染修复

一株抗西瓜枯萎病菌的筛选、鉴定及抑菌物质分析

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摘要

为了筛选西瓜枯萎病拮抗菌株并探究其抑菌效果，以齐齐哈尔市园艺研究所棚室内西瓜根际土为材料，利用平板对峙法筛选到一株优良的拮抗 *Fusarium oxysporum* f. sp. *niveum* (Fon) 的菌株 J4，盆栽试验证明其对西瓜枯萎病的防治效果为 72.6%。经全基因组学鉴定为 *Bacillus methylotrophicus* J4，该菌株可产生蛋白酶、淀粉酶、葡聚糖酶、纤维素酶并有分泌铁载体的能力，其衰亡期无菌上清液 (CFS)对 Fon 菌落生长抑制率为 71.87%。通过扫描电子显微镜(SEM) 和共聚焦激光扫描显微镜(CLSM) 观察，结果表明，J4 的 CFS 使 Fon 孢子表面凹陷，破坏其细胞膜的完整性，造成细胞死亡；利用 2’,7’-二氯二氢荧光素二乙酸酯 (DCFH-DA) 荧光探针检测发现，菌株 J4 诱导 Fon 菌丝体 ROS 的积累；J4 CFS 引起 Fon 菌丝超氧化物歧化酶 (SOD)、过氧化氢酶 (CAT)、过氧化物酶 (POD) 、谷胱甘肽还原酶 (GR) 活性及可溶性蛋白和 MDA 含量的显著升高。该菌株基因组中含有 13 个抑菌功能的次级代谢产物合成基因簇 Surfactin、Fengycin、Iturin、Bacillibactin、Bacilysin、Bbacillaene 和 Butirosin 等)，经 LC-MS 非靶代谢组学及超高液相色谱系统和高分辨率质谱 (UHPLC-ESI-MS/MS)分析，明确 J4 菌株 CFS 中含有 3 种多肽化合物 (Iturin A、Fengycin 和 Surfactin)，利用平板涂布法证明了 3 种脂肽具有抑制 Fon 菌丝生长的能力，推测菌株 J4 上清液中的抑菌功能物质是 Iturin A、Fengycin 和 Surfactin。综上所述，菌株 J4 对西瓜枯萎病有较强的防效，在西瓜枯萎病生物防治中具有广泛的应用前景。

关键词：拮抗菌株；西瓜枯萎病；生物防治；氧化损伤；次级代谢产物

利用木糖高效产氢菌株的筛选及其对秸秆水解液抑制物耐受性能研究

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摘要

木糖是秸秆水解液中含量仅次于葡萄糖的可发酵碳源，但是目前大部分产氢微生物只能利用水解液中的葡萄糖，鲜有微生物可以利用木糖进行高效产氢。本研究筛选出一株可以利用木糖进行高效产氢发酵的菌株，并研究了该菌株对于秸秆水解液抑制物的耐受性。结果表明：以木糖作为唯一碳源，通过筛选分离，获得一株高效利用木糖发酵产氢的兼性厌氧菌株，经鉴定该菌株为 *Enterobacter cloacae*。该菌株利用木糖的氢气转化率为 0.95 mol H_2/mol-木糖，产氢能力在已报导的兼性厌氧产氢菌中居于前列。菌株以木糖作为唯一碳源时，对典型的秸秆水解液中的抑制物的耐受能性为：乙酸>5-羟甲基糠醛>香豆酸>紫丁香醛>香草醛>糠醛。利用葡萄糖和木糖的混合糖作为碳源时，在抑制物 5-羟甲基糠醛或香豆酸存在的条件下，混合糖体系累计产氢量相对于单一木糖或者单一葡萄糖体系均有下降，相对于单一碳源，在混合糖体系中抑制物对于菌株产氢量影响更明显。三维荧光光谱分析显示该菌株释放的溶解性有机物在IV、V 区域的荧光强度显著减弱，说明抑制物对菌株的抑制作用主要体现在对其生物量的抑制。进一步对产氢代谢的关键酶的基因表达水平进行分析，分析结果显示秸秆水解液抑制物的存在抑制了产氢代谢过程中的木糖异构酶和氢化酶基因的转录。以上研究表明，*E.cloacae* LK112 在是一株可以高效利用多种碳源的产氢菌株，在以秸秆为底物进行生物制氢的过程中具有一定潜力。

关键词： 生物制氢；木糖；秸秆；水解液抑制物

Screening of xylose efficient hydrogen-producing strain and their tolerance to straw hydrolysate inhibitors

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Abstract

Xylose is a fermentable carbon source whose content in straw hydrolysate is only less than glucose. However, most hydrogen-producing microorganisms can only use glucose in hydrolysate, and few microorganisms can use xylose to produce hydrogen efficiently. In this study, a strain that can use xylose for high efficiency hydrogen-producing fermentation was screened and its tolerance to the inhibitor of straw hydrolysate was studied. The results showed as follows: using xylose as the sole carbon source, a facultive anaerobic strain was obtained and identified as *Enterobacter cloacae*. The hydrogen conversion rate of xylose was 0.95 mol H_2/mol -xylose, and the hydrogen production capacity of this strain was higher than that of facultative anaerobic hydrogen producing bacteria reported. When xylose was used as the only carbon source, the inhibition ability of the strain to the typical straw hydrolysate was : acetic acid > 5-hydroxymethylfurfural > coumaric acid > lilac aldehyde > vanillin > furfural. When the mixed sugar of glucose and xylose was used as carbon source, the cumulative hydrogen production of the mixed sugar system decreased compared with that of a single xylose or a single glucose system in the presence of the inhibitor 5-hydroxymethylfurfural or coumaric acid. Compared with a single carbon source, the inhibitor had a more obvious effect on the hydrogen production of the strain in the mixed sugar system. 3-D Excitationemission matrix (EEM) analysis showed that the fluorescence intensity of dissolved organic matter released by the strain was significantly weakened in the IV and V regions, indicating that the inhibitory effect of the inhibitor on the strain was mainly reflected in the inhibition of its biomass. The gene expression levels of key enzymes in hydrogen production metabolism were further analyzed. The results showed that the presence of straw hydrolysate inhibitors inhibited the transcription of xylose isomerase and hydrogenase genes in the process of hydrogen production metabolism. The above studies indicate that *E.cloacae* LK112 is a hydrogen producing strain that can efficiently utilize multiple carbon sources, and has certain potential in the process of biological hydrogen production using straw as substrate.

Keywords: Biohydrogen; Xylose; Straw; Hydrolysate inhibitor

Highly active microorganisms degrading Polystyrene microplastics sorted by Single-cell Raman-D_2O

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Abstract

Plastic production, accumulation, and contamination is continuously and severely increasing due to rapid urbanization and industrialization, low recycling rates, and non-degradable nature. Researches on the insects and their gut microbiome in degrading plastics highlighted the great rewarding prospect of plastics biodegradation and harmless disposal. However, mining of functional microbes from nature employed a traditional “culture first, screen second” paradigm that resulted in inefficient, time-consuming and labor-intensive investment of consumables on growing non-target and even irrelevant microbes restricted to specific environmental conditions. Herein, Single-cell Raman-D_2O coupled with targeted metagenomics was applied to screen and sort out the highly active microbes degrading polystyrene from the gut microbiome of *Tenebrio molitor* larva. Physical and chemical characterization methods including scanning electron microscope (SEM), contact angle test, gel permeation chromatography (GPC), HPLC-MS analysis, etc., were employed to determine changes in the structure and verify the degradation of plastics. This method can serve as a valuable and generally applicable approach for in situ plastics-degrading microbial assessment and mining from complex natural conditions, greatly promoted searching for efficient degradation strains or synthesizing functional microorganisms to reduce plastic contamination.

Keywords: Polystyrene; Plastics biodegradation; Single-cell Raman-D_2O; *Tenebrio molitor* Larvae; Gut microbiome

低温好氧颗粒污泥信号分子调控机制及强化策略研究

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摘要

好氧颗粒污泥目前在低温条件下难以启动，运行不稳定，导致其在北方污水设施中较难运行实现。本课题旨在考察恒温启动变温运行过程中好氧颗粒污泥的理化性质、污染物处理效能、 EPS 含量组成成分、信号分子 EPS 成分的变化规律，并将其与颗粒污泥系统中的微生物群落组成的变化规律相结合，得出好氧颗粒污泥形成及运行的微生物学机制。

通过在 10℃和 25℃启动再变温运行两个反应器，考察好氧颗粒污泥的形成特征，结果表明在第 120 d 时，粒径分别达到 390.589μm 和 892.282μm，温度冲击时，污泥浓度、沉降性能均会出现下降的趋势；LB-EPS 浓度变化不大而 TB-EPS 则均出现先降低后升高的趋势；c-di-GMP 浓度在形成颗粒后下降稳定在 110mg/g VSS；高通量测序技术考察微生物群落结构变化，Proteobacteria 在 R2 中均高于 R1 中的各个阶段，最高达到 72.37%，在形成颗粒时稳定在 30.8%-52.78%之间，Actinobacteriota 具备着分泌 c-di-GMP 的能力，在颗粒形成前期，其浓度大量升高，从 1.2%升高至 6.2%，当颗粒形成后，丰度下降。

小麦种内抗赤霉病菌株的筛选及全基因组测序分析

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摘要

内生菌在植物组织中普遍存在，产生的代谢物可以直接抑制病原菌的生长，甚至促进寄主植物的生长发育。在农业生产中发掘和利用具有生防潜力的微生物资源是减少植物病害和保障国家粮食安全的重要举措。在小麦种内筛选出具有拮抗禾谷镰刀菌的生防菌株，解析优势生防菌株 JB7 的基因组信息，研究其抑菌机制。通过平板对峙和抑制孢子萌发法对小麦种内的优势生防菌株进行分离和筛选。利用二代测序 Illumina Hiseq 与三代测序 PacBio 结合的方式，对生防菌 JB7 进行全基因组测序，并对其进行基因注释和代谢系统分析。从小麦籽粒中共筛选出 40 株的内生菌中有 23 株拮抗禾谷镰刀菌的内生菌，其中菌株 JB7 的平板抑菌率达 55.72%，并且可以产生降解纤维素、葡聚糖、蛋白酶活性。鉴定结果表明菌株 JB7 为甲基营养型芽孢杆菌，基因组全长 3,929,792 bp，其 GC 含量为 46.5%，编码基因 3747 个。甲基营养型芽孢杆菌 JB7 具有通过定殖（生物膜形成）、拮抗（产生抗生素）和诱导抗性（产生诱导系统抗性物质）机制从而控制植物疾病的能力甲基营养型芽孢杆菌 JB7 拮抗禾谷镰刀菌方面有明显效果。此外，还发现菌株 JB7 基因组中含有一系列促进植物生长、触发植物免疫和产生抗生素的基因。

酵母废水发酵产菌体蛋白的初步探究

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摘要

酵母废水是一种高浓度的有机废水，是国际公认治理难度较高的工业废水之一，排放的废水中存在未被完全利用的有机质，例如糖分、维生素、酵母蛋白质、胶体物质等大量营养元素物质且含量达到 70%左右，都是宝贵的资源，利用微生物处理废水成为了一个新的角度,本实验旨在以酵母废水作为廉价培养基，将实验前期筛出的 X-1 菌株（费比恩塞伯林德纳氏酵母）对其在酵母废水液体培养基中进行发酵，以活菌数为评价指标，通过单因素结合响应曲面法、正交实验对其进行条件优化，研究以酵母废水为廉价培养基液体发酵菌体蛋白前期实验探究，实验结果表明：酵母废水稀释 10 倍，葡萄糖添加量 1.7%，胰蛋白胨添加量 1%，磷酸二氢钾添加量 0.05%，接种量 5%，培养时间 72 小时，发酵液 pH 值 6.0，在此发酵条件测得的活菌数最高为2.1×10^{8}CFU/mL。

关键词：酵母废水；费比恩塞伯林德纳氏酵母；条件优化；活菌数

ddPCR surpasses classical qPCR technology on quantitating bacteria and fungi in environments

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Abstract

In recent years, quantitative real-time PCR (qPCR) has been widely used in measuring bacterial and fungal quantities in various ecosystems, as well as relevant Fungi to Bacteria ratio (F:B ratio). Nowadays, droplet digital PCR (ddPCR) started to be applied in the same area, but no study has systematically compared qPCR and ddPCR on quantitating both bacteria and fungi in environmental samples. Here, we designed the probe-primers combinations targeting 16S rRNA gene and Internal Transcribed Spacer (ITS) for bacterial and fungal detections respectively, and tested both SYBR Green and TaqMan approaches in qPCR and ddPCR methods for the mock community and real environmental samples. In mock community, comparing to qPCR approaches, the quantification results of ddPCR were significant closer to preset values ($P < 0.05$) and had smaller coefficients of variations ($P < 0.05$). In environmental samples, ddPCR stably quantified ITS and 16S rRNA gene concentrations in all four habitats without abnormal overestimation or underestimation, and the F:B ratio obtained by ddPCR was consistent with PLFA. Our results indicated that ddPCR had better precision, repeatability, sensitivity and stability in bacterial and fungal quantitation than qPCR, and was more appropriate for F:B ratio evaluation in soil samples. Therefore, ddPCR technology is promising for microbial quantification in environmental monitoring and evaluation.

Keywords: Droplet digital PCR; Quantitative real-time PCR; Microbial quantification; Fungi to bacteria ratio; Environmental microbiology

The large-scale spatial patterns of ecological networks between phytoplankton and zooplankton in coastal marine ecosystems

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Abstract

Although autotrophic phytoplankton and heterotrophic zooplankton both play important roles in the food web of marine ecosystem, their comprehensive interactions and spatial patterns at continental scale remain poorly studied. Here, we collected 251 seawater samples along 13,000 km of Chinese coastline, and microscopically investigated the latitudinal gradients of planktonic diversities. In total, 307 phytoplanktonic and 311 zooplanktonic species were visually identified. Using the newly developed Inter-Domain Ecological Network (IDEN) approach, the phytoplankton-zooplankton interaction networks were constructed. We found that the phytoplankton-zooplankton network structure was varied across three regions, more complex and numerous connections along the southern coast than in the north. In addition, some particular associations between zooplanktonic and phytoplanktonic groups were found to be localized in specific regions. For example, autotrophic Chaetoceros lorenzianus was only associated with heterotrophic copepods in the nouthern regions. Furthermore, and the seawater temperature and salinity were the major driving force for shaping planktonic interaction networks. These results provide a deeper understanding of planktonic biogeography and phytoplankton-zooplankton interaction patterns.

Keywords: Biogeography; Bipartite network; Large scale; Plankton; Phytoplankton-zooplankton interaction; Topological property

Functional diversity of *Siganus canaliculatus* intestinal microbiome under different dietary interventions

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Abstract

The constant increase of aquaculture production and wealthy seafood consumption has forced the industry to explore alternative and more sustainable raw aquafeed materials, and macroalgae as a sustainable aquafeed ingredient have been used to replace marine feedstuffs in many farmed fish. However, how do intestinal microbiome of fish respond to the macroalgae carbohydrates in the diet and their digestion mechanism are unclear. As an excellent natural marine source of nutritional lipids for humans, *Siganus canaliculatus* is one of the most important consumers of macroalgae and favorite eating *Gracilaria lemaneiformis*. Here, we applied shotgun metagenomics to explore the responds of intestinal microbiome to different dietary fiber ratio and sources, and found that the α-diversity of the intestinal microbiome of *S. canaliculatus* fed with the high fiber diet increased significantly ($P < 0.05$), and the relative abundance of genes involved in carbohydrate degradation and SCFAs production was significantly ($P < 0.05$) increased under the high fiber dietary pattern. Functional annotations by CAZymes showed significant ($P< 0.05$) separations among three dietary patterns. Additionally, we reconstructed 88 high-quality MAGs, and genes related to fiber and algal degradation were abundant in the high fiber dietary pattern, indicating that those MAGs could play an important role in the digestion of *G. lemaneiformis*. The results indicated that different fiber levels affected carbohydrate metabolism and SCFAs production of *S.canaliculatus* intestine microbiomes, which may contribute to improvements on nutrition and energy metabolism of the host. This ecological and mechanistic understanding of the fish microbiome could increase the available food resources and environmentally friendly aquaculture.

Keywords: *Siganus canaliculatus*; *Gracilaria lemaneiformis*; Intestinal microbiome; Dietary pattern; Fiber; Metagenomics

Construction of the potential E2 degradation pathway based on the enriched bacteria community from mangrove sediment

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Abstract

Estradiol (E2) is the most potent of natural estrogens. As it flows through the marine, E2 would be disturbing the balance of an ecosystem and endanger public health. Mangrove is an important coastal wetland with abundant microbial diversity and activities, which can effectively remove various organic pollutants. However, bacterial communities response to E2 and their co-metabolism in the process of degradation are limited. This study aimed to utilize co-metabolism as a means to degrade E2 by mangroves-derived bacterial communities. There are six stable bacterial communities from the six mangroves along the Southern Sea of China, which was successfully established through successive co-acclimation of indigenous microorganisms. All microcosms are capable of efficiently degrading E2 after 15 days. The results showed that Alpha- and Gammaproteobacteria became abundant at the late domesticating phase with the dominant families of Rhizobiaceae, Methylophagaceae, Rhodanobacteraceae, Chitinophagaceae and the unclassified bacteria affiliated into Gammaproteobacteria. One hundred and twelve metagenome-assembled genomes (MAGs) were primarily consisted of Alpha- and Gammaproteobacteria. In addition, genomes of uncultivated bacteria Armatimonadetes and Chlamydiae were first reported to involve in degradation of E2. Based on analysis of typical MAGs, which contained genes encoding for dehydrogenase (OecA or 17β-HSD) and oxygenases (OecB, OecC or CYP450), which are key enzymes for E2 degradation. Metagenomic analysis revealed mangroves-derived bacterial communities were able to degrade E2, and then entered the 9,17-Dioxo-1,2,3,4,10,19-

hexanorandrostan-5-oic acid (HIP) metabolic pathway or enter the amino acid metabolic pathway. The predicted biodegradation pathways involved in syntrophic associations of an E2-degrading consortium were reconstructed. The results in this study provide new insights into the microbial E2 degradation in mangrove sediments.

Keywords: Mangrove; Estrogen; Microbial ecological metabolic network; Community succession; Biodegradation

Keystone taxa and community assembly process of different mangrove rhizosphere microbial communities

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Abstract

Mangroves form intimate relationships with the diverse root microbes, these microbes are important for mangrove growth and health. In order to understand how root microbiota of mangroves vary throughout different growth stages under field conditions, we sequenced the 16S rRNA gene of rhizosphere sediments of three mangrove species at two locations of Guangxi Province and Guangdong Province. Our results showed that the microbial alpha diversity and richness were positively correlated with total carbon content, both mangrove species and geographical location influenced the patterns of root microbiota shift that occurred during plant growth. Biomarker taxa with growth stages were identified by random forest model, most of those biomarker taxa were belong to *Deltaproteobacteria* and *Alphaproteobacteria*, and their relative abundance showed strongly correlation with total carbon and nitrogen contents. Although several environmental variables had significant influence on the microbial communities, the root microbiota was strongly driven by stochastic processes for each mangrove species.

Keywords: Microbial community; Mangroves; Biodiversity; Community assembly

Temporal changes in global soil respiration since 1987

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Abstract

As the second-largest terrestrial carbon (C) flux, soil respiration (R_S) has been stimulated by climate warming. However, the magnitude and dynamics of such stimulations of soil respiration are highly uncertain at the global scale, undermining our confidence in future climate projections. Here, we present an analysis of global R_S observations from 1987–2016. R_S increased ($P < 0.001$) at a rate of 27.66 g C m^{-2} yr^{-2} (equivalent to 0.161 Pg C yr^{-2}) in 1987–1999 globally but became unchanged in 2000–2016, which were related to complex temporal variations of temperature anomalies and soil C stocks. However, global heterotrophic respiration (R_h) derived from microbial decomposition of soil C increased in 1987–2016 ($P < 0.001$), suggesting accumulated soil C losses. Given the warmest years on records after 2015, our modeling analysis shows a possible resuscitation of global R_S rise. This study of naturally occurring shifts in R_S over recent decades has provided invaluable insights for designing more effective policies addressing future climate challenges.

Keywords: Soil respiration; Climate change; Soil organic carbon

Response of rhizosphere microbial communities of mangrove plant and *Spartina alterniflora* to tidal elevation gradients

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Abstract

Mangrove ecosystems are ecologically important in cycling of carbon, nitrogen, sulfur and phosphorus at the interfaces of sea and land, when they are facing serious threats from *Spartina alterniflora* invasion and global climate change nowadays. In this study, we selected mangrove wetlands at the Yunxiao National Mangrove Reserve, planted *Kandelia obovata* and *Spartina alterniflora*, and analyzed their rhizosphere microbial communities under the progress of sea-level-rise (0-250 cm) simulated by setting 'Marsh Organ'. After one-year incubation, the plant growth results showed that *S. alterniflora* adapted to a narrower range of sea level (0-150 cm) than *K. obovata* (0-200cm), and the contents of nitrate and phosphate in the rhizosphere soil significantly positively correlated with water levels, while the sulfate content significantly negatively correlated with water levels. High-throughput real-time quantitative PCR further profiled the metabolic flow of C, N, P and S cycling driven by rhizosphere microbial communities. The results indicated that rhizosphere microbes could be active in nitrogen mineralization, phosphonate uptake, poly-pi dissolving and sulfur reduction at the low and middle tides when prefer to drive the processes of denitrification and phosphonate dissolution with weaken activity of sulfur oxidation-reduction, suggesting the functional response of the rhizosphere microbial communities to the increased sea level. 16S rRNA gene high-throughput sequencing further showed 58-62% of genera responded to water levels variation, including *Bacillus*, *Paenisporosarcina*, *Woeseia*, and *Longispora*, which are known to play a role in sulfur reduction, nitrogen fixation, and phosphate dissolution. We also found significantly different genera between *K. obovata* and *S. alterniflora,* such as *Psychrobacter*, *Desulfatiglans* and *Desulfobulbus*, which are known to be largely involved in sulfur reduction, indicating that *K. obovata* and *S. alterniflora* rhizosphere microbial communities may function differently for sulfur cycling. This study provides insights into potential ecological effects of sea-level-rise and *S. alterniflora* invasion on sedimental microbial communities.

Key words: Tidal gradients; Mangrove ecosystems; *Spartina alterniflora*; C/N/P/S element cycling; Rhizosphere

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Environmental heterogeneity determines the response patterns of microbially mediated N-reduction processes to sulfamethoxazole in river sediments

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Abstract

The widespread occurrence of antibiotics in aquatic ecosystems leads to potential ecological risks to organisms, in turn affecting microbially mediated processes. Here, we investigated the response of dominant N-reduction processes to the frequently detected antibiotic sulfamethoxazole (SMX) along the Chaobai River with regional environmental heterogeneity, including denitrification, anaerobic ammonium oxidation (anammox), dissimilatory nitrate reduction to ammonium (DNRA), and nitrous oxide (N_2O) release. We found two divergent SMX response patterns for denitrification in contrasting scenarios of geochemical properties. In the context of low nitrate and carbon, SMX weakened denitrification with a slightly stimulation first. Whereas SMX directly inhibited denitrification when nitrate and carbon were sufficient. High SMX concentration suppressed anammox (26–72%) and DNRA activities (48–84%) via restraining the activities of anammox and DNRA bacteria. Notably, SMX increased the contribution of denitrification to N-reduction at the expense of DNRA to N-reduction, leading to a shift in nitrogen conversion towards denitrification. Additionally, SMX stimulated N_2O emission (up to 91%) due to superior restraint on process of N_2O reduction to N_2 and an incline for N-reduction towards denitrification, thereby exacerbating greenhouse effect. Our results advance the understanding of how nitrogen cycling is affected by SMX in aquatic ecosystems with environmental heterogeneity.

Keywords: Denitrification; Anammox; DNRA; Functional genes; Microbial community

Xenobiotics response and antibiotic production of a novel Rhodospirillales strain, *Candidatus* Pearlrium lutea, gen, nov., sp. nov

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Abstract

Members of Rhodospirillales affiliated with a group of photosynthetic anoxygenic bacteria can use light to grow and are abundant in estuarine sediments, but few studies have been reported to illustrate their metabolic potential. We report here the first genomic and functional analysis of a novel Rhodospirillales species isolated from estuarine sediments. Total nine sequenced genomes were classified into three clone frames. This bacterium, like a few Rhodospirillales, has a higher GC content (~68.21%) indicative of a steady translation level. Phylogenetic analysis places this Rhodospirillales within a new genus we define as "*Candidatus* Pearlrium". Using the Earth Microbiome Project and SRA databases, we also demonstrate that members of "*Ca*. Pearlrium" are found globally in places with rich organic matters. Genomic analysis showed that "*Ca*. P. lutea" took part in degrading xenobiotics, such as polycyclic aromatic hydrocarbons. "*Ca*. P. lutea" had the capability to produce nitrogen through denitrification. Additionally, "*Ca*. P. lutea" possesses the NtrY-NtrX and GlnL-GlnG two-component system to sense and respond to extracellular nitrogen. "*Ca*. P. lutea" had five identified secondary metabolite regions. Among them, a multiple secondary metabolite synthesis gene cluster (transAT-PKS, NRPS, PKS-like, T3PKS, terpene) was predicted, which might be used to yield a novel antibiotic like macrobrevin. According to the prediction of software interproscan, P-loop containing nucleoside triphosphate hydrolase associated with the biosynthesis of some secondary metabolites was dominant in "*Ca*. P. lutea" genomes. Kinds of glycoside hydrolases (GH13, GH23, etc) and glycosyl transferases (GT2, GT4, etc) were also detected. Given these data, along with functional genes expression under several organic matters, we speculate that “*Ca*. P. lutea” can be one of the most important sources of natural antibiotics.

Keywords: *Candidatus* Pearlrium lutea; Rhodospirillales; Xenobiotics degradation; Multiple gene clusters

Spatial distribution patterns across multiple microbial taxonomic groups

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Abstract

In most terrestrial ecosystems, the spatial distribution of soil bacterial communities presents a distance-decay relationship (DDR), even in the vertical dimension. However, whether this pattern is universal among all soil microbial taxonomic groups, and how body size influences this distribution, remains elusive. In this study, we obtained a total of 140 samples from two adjacent ecosystems, nontidal and tidal soils, in the Yellow River Delta (YRD), and measured the distance-decay relationship between topsoil and subsoil for bacteria, archaea, fungi and protists (rhizaria). Our results showed that the entire community generally fitted the DDR patterns ($P < 0.001$), this was also true at the kingdom level ($P < 0.001$, with the exception of the fungal community), and for most individual phyla (47/75) in both ecosystems and with soil depth. Additionally, these results presented a general trend that the community turnover rate of nontidal soils was higher than tidal soils ($P < 0.05$), and that the rate of topsoil was also higher than that of subsoil ($P < 0.05$). Also, microbial spatial turnover rates displayed a negative relationship with body sizes in nontidal topsoil ($R^2 = 0.29$, $P = 0.009$), suggesting that the smaller the body size of microorganisms, the stronger the spatial limitation was in this environment. However, in tidal soils, the body size effect was negligible, probably owing to the water's fluidity. Moreover, community assembly was judged to be deterministic (normalized stochasticity ratio, NST < 50%), and heterogeneous selection was the dominant assembly process in the different environments. Variation partitioning analysis showed that geographic distance was much more influential than environmental factors in shaping community composition. Specifically, the soil salinity in these ecosystems was the major environmental factor in selecting the distributions of microbial communities. Overall, this study revealed that microbial community compositions at different taxonomic levels followed a relatively consistent DDR distribution pattern, and their community assembly was determined by heterogeneous selection, which was primarily contributed by spatial distribution and salinity in this coastal area.

Keywords: Dispersal limitation; Environmental selection; Taxonomic levels; Body size; Salinity

Metagenomics insights into the performance and methanogenesis metabolic mechanism under gradient domestication of human feces high-solids anaerobic digestion

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Abstract

High-solids anaerobic digestion (HSAD) could treat higher volume waste with same digester size, and lower energy requirements than liquid anaerobic digestion. Nevertheless, rich protein waste mono-HSAD would more likely result in ammonia inhibition. Herein, long-term semi-continuous human feces (HF) AD was conducted under mesophilic, with granular sludge as inoculum, and by gradually increasing total solid (TS) loadings for achieving HF HSAD successful domestication. The methane production dynamic parameters, microbial communities, and methanogenesis metabolism pathways were analyzed for comprehending the mechanism of in the process of domestication HF HSAD. The results showed that TS and VS methane production rate of TS 11% were the highest. TS 16% was the highest tolerated concentration. With the increasing of TS from 13% to 17%, high concentrations HF would suppress the growth of predominant methanogens (*Methanothrix soehngenii*, *Methanothrix* sp., and *Methanothrix harundinacea*), and facilitate acidogenic bacteria (*Defluviitoga tunisiensis*, *Methanoculleus bourgensis*, and *Tepidanaerobacter acetatoxydans*) rapidly proliferated. In this study, granular sludge as inoculum could efficiently remove pathogens (*E. Coli*, 99.80% at TS 11% and *Salmonella*, 88.98% at TS 12%) under mesophilic AD. Whether TS was lower than 12% or higher than TS 13%, the expression of methanogenesis key enzymes-encoding genes (mcr, frh, and fwd) would be inhibited with the TS loadings gradually increasing. The types of methanogenesis of different TS loadings would change with the TS loading change.

The above studies provide important data and theoretical support for HF HSAD under semi-continuous mesophilic, and provide effective disposal method of in rural areas HF environmental safety issues.

Keywords: Metagenomics; Human feces; Anaerobic digestion; Granular sludge; Metabolism pathways

Mechanisms of niche-neutrality balancing can drive the assembling of microbial community

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Abstract

One hotspot of present community ecology is to uncover the mechanisms of community succession. In this study, niche-neutrality dynamic balancing and co-occurrence network analysis, were integrated to investigate the dispersal dynamics of microbial communities in a freshwater river continuum in subtropical China. Results showed that in the clean upstream river, stochastic processes could increase species diversities, and organize communities into relatively loosely linked and stable networks with higher modularity and more modules. However, when conditions became degraded under heavy pollution, the influence of neutrality diminished, and niche-based selection imposed more constraints on communities and guided the assembling processes in certain directions: depleting species richness, strengthening interspecies connections and breaking boundaries of modules. Consequently, communities became more sensitive to fluctuations so as to deal with the harsh conditions efficiently. Another interesting finding was that, both as keystone taxa of communities, module hubs were mostly neutrally distributed generalists with high abundances, and were beneficial to many related operational taxonomic units. In contrast, connectors were less abundant and their distributions were more subjected to the environments. Therefore, connectors were probably responsible for the information transmission between microbial communities and environments, as well as between different modules, and thus could restrict the dispersal of microbes and guide the direction of community assembly.

Keywords: Co-occurrence network analysis; Freshwater microbial community; Key taxa; Neutrality; Niche

Season and Age of Neighborhood Gardens Shape Phyllosphere Microbiota Associated with Respiratory Diseases

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Introduction

Neighborhood gardens are the primary source of human microbial exposure. Phyllosphere microbes are intimately connected to the surrounding environment and can have a strong influence on human respiratory health.However, the effects of environ-mental factors (e.g., season, land-use and garden age) on the respiratory diseases (RDs) associated microbiota in phyllosphere in the neighborhood gardens remain poorly characterized. Here we investigated phyllosphere microbial communities (PMCs) in 72 neighborhood gardens in (i) two seasons (warm and cold), (ii) two garden age categories (old and young), and (iii) different locations (urban and rural) in Shanghai. The objectives of this study are to explore 1) how significant is the seasonal variation in PMCs, especially the RDs-associated microbiota, and 2) whether these microbes respond to the urban-rural gradient in neighborhood gardens with varying ages.

Adding metabolic complementarity evidence into co-occurrence network analysis with metagenome-scale metabolic modeling

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Abstract

The microbial communities are complex interconnected ecological communities that cross-feed, communicate, and coevolve, but hard to be directly observed. The co-occurrence patterns and metabolic models are two commonly used approaches to infer microbial interactions. However, the synthetical applications of both approaches were rarely brought up to resolve complicated microbial interactions in ecosystems. Here, we used both methods on microbial communities based on the Metagenome-Assembled Genomes (MAGs) from a temperature-gradient hot spring habitat. We found that both networks could reflect that the microbial community pattern tends to become denser, but the species compositions of networks can be very different since they were constructed using different interacting evidence. Substances such as amino acids and cofactors were identified as essential evidence of metabolic exchange in the hot spring microbe community. We also observed the phenomenon of genome streamlining and how microbes adapt to it. This study provides an integrated method and pipeline to improve the understanding of the co-occurrence network and significant evidence of metabolic complementarity for it.

Keywords: Co-occurrence network; Metabolic complementarity; Metagenome-scale metabolic modeling; Microbial interactions

Symbiotic Interactions of Dominant Grasses and Rhizosphere Bacteria in the Tibetan Plateau

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Abstract

Beneficial interactions between grass and rhizosphere microorganisms are pivotal for grass fitness. Nevertheless, the molecular mechanisms underlying the symbiosis between grass and rhizosphere microorganisms in the natural habitat of the Tibetan Platea remain elusive. Here, we investigated the symbiotic relationship between the dominant grass and rhizosphere bacteria community in the QTP region by sequencing the 16S rRNA genes. Our results demonstrated that the dominant grasses of *Poa L.* and *Stipa L.* engage in multiple selections of rhizosphere bacteria, choosing to symbiotically interact with bacteria that are most beneficial to their healthy growth. Moreover, *Poa L.* is more capable of forming symbiotic relationships with rhizosphere bacterial communities, particularly with *Solirubrobacteraeeae, Micromonosporaceae,* and *67-14*, establishing strong symbiotic associations. Additionally, we found *Poa L.* has higher rRNA operon copy numbers, indicating that *Poa L.* are more dynamically active with greater resource competitiveness in the natural bible. In summary, the present study enhances our understanding of symbiotic mechanisms between grasses and the rhizosphere bacterial communities in natural habits in the QTP region, where the symbiosis between grass and beneficial rhizosphere microorganisms thus improves grasses production performance.

Keywords: Dominant grass; Rhizosphere; Symbiotic Interactions; The Tibetan Platea region

In situ reductive dehalogenation of groundwater driven by innovative organic carbon source materials: Insights into the organohalide-respiratory electron transport chain

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Abstract

The research into the biostimulation of reductive dehalogenation has already made significant progress. However, few studies have attempted to determine whether additional carbon source materials match the metabolic mechanism of functional microorganisms, particularly from the perspective of electron transfer chain. In the present study, the effectiveness of bioreactive carbon source materials coupled with metabolic mode of *Shewanella oneidensis* MR-1 (MR-1) was comprehensively evaluated in the reductive dechlorination using natural polymer materials as feedstock. The results showed that humic acid (HA) can promote the reductive dechlorination of chlorinated ethenes (CEs) by increasing the content of propionic acid in volatile fatty acids (VFAs) with slowly generate electrons. The addition of nanoscale zero-valent iron (nZVI) overcome the hydrolysis limiting-rate step of macromolecular substances and improved the meanwhile VFAs production. Transcriptome analysis revealed that the key functional enzymes genes of extracellular electron transfer (EET) transmission, carbohydrate uptake and fatty acid biosynthesis, was significantly enriched under the action of carbon source materials, confirmed that the metabolic mode of MR-1 can be directionally regulated by electron donors. Moreover, the high expression of malate synthase genes resulting in significant differences in tetrachloroethylene (PCE) and trichloroethylene (TCE) degradation efficiencies. Electron transfer capacity (ETC) revealed that the HA rich in quinones functional groups plays an important role to accelerated the transfer of electrons by having strong electronic acceptance. This innovative discovery can be used to facilitate a predictive understanding of halide-bioremediation at contaminated sites.

Keywords: Natural polymer materials; Chlorinated ethenes; *Shewanella oneidensis* MR-1; Reductive dichlorination; Electron transfer chain

PCycDB: a comprehensive and accurate database for fast analysis of phosphorus cycling genes and microorganisms

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Abstract

Phosphorus (P) is one of the most essential macronutrients on the planet, and microorganisms play a key role in P cycling in all living things and ecosystems. However, mechanistic understanding of key P cycling genes (PCGs) and microorganisms (PCMs) as well as their ecological functions remains elusive even with the rapid advancement of metagenome sequencing technologies. One of major reasons is a lack of comprehensive and accurately annotated functional gene databases. In this study, we constructed a well-curated P cycling database (PCycDB) with 117 gene families and 10 P metabolic processes, achieving an annotation accuracy of 99.76% for simulated gene dataset and a positive predictive value of 95.70%. The developed PCycDB was used to analyze P cycling microbial communities from seven habitats (deep-sea, eutrophic lake, mariculture, mangrove, surface ocean, permafrost and wastewater treatment plant), showing the heterogenous distribution of PCGs and PCMs. The results demonstrate that PCycDB is a useful tool for our understanding of microbially-driven global biogeochemical P cycling and possible mechanisms in the environment with high coverage, high accuracy, and rapid analysis of metagenome sequencing data.

Keywords: Phosphorus; Metagenome sequencing data analysis; Phosphorus cycling gene/microorganisms; Phosphate solubilizing microorganism

采用生物正交非典型氨基酸标记法(BONCAT)分离并表征厌氧氨氧化(anammox)菌群中翻译活性组分

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摘要

解析活性和非活性群体对于理解微生物如何在其本土环境中发挥作用至关重要。在这项研究中，我们提出了一种快速、灵敏和低成本的方法，联合生物正交非典型氨基酸标记（BONCAT）、荧光激活细胞分选（FACS）和 16S rRNA 基因测序方法，分离和表征厌氧氨氧化（anammox）菌团中翻译活性和非活性组分。该法最快可在培养 8 h 后即检测出具有翻译活性的 anammox 细菌。整体而言，BONCAT 获得的翻译活性菌群的相对丰度与基于 RNA 方法的结果显示出良好的相关性，但两种方法的活性菌群群落结构具有显著差异。这两种方法的结合将有助于更加深入了解微生物群落中的活性组分和功能。基于 BONCAT 方法，我们首次发现 anammox 菌团中约 70%的细胞具有翻译活性，且活性组分与非活性组分的群落结构显著不同。翻译活性组分与非活性组分之间相对丰度的变化表明，在 anammox 菌团中存在着群体性和特定分类群的翻译活性异质性。令人惊讶的是，即使处在合适的生态位，超过 1/4 的 anammox 细菌仍不具有翻译活性，这可能是由密度依赖的资源变得有限时种内竞争激烈所致。总之，我们采用 BONCAT 方法提供了对 anammox 菌群生态生理学的新见解，并为将该方法扩展到其他活性污泥处理系统奠定了基础。

关键词：厌氧氨氧化；BONCAT-FACS；翻译活性和非活性；16S rRNA 基因测序；翻译活性异质性

Contrasting vertical distribution between prokaryotes and fungi in different water masses on Ninety-East Ridge, Southern Indian Ocean

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Abstract

The microbial diversity of the Indian Ocean has been extensively investigated, but little is known about the community composition of microbes in the Southern Indian Ocean. In the present study, we divided 60 water column samples on Ninety-East Ridge (NER) into five water masses according to the temperature–salinity curves. We presented, for the first time, a full description of the microbial biodiversity on NER through high-throughput amplicon sequencing approach, including bacteria, archaea, and fungi. We found that bacteria exhibited higher richness and diversity than archaea and fungi across the water masses on NER. More importantly, each water mass on NER featured distinct prokaryotic microbial communities, as indicated by the results of non-metric multidimensional scaling. In contrast, fungi were eurybathic across the water masses. Redundancy analysis results demonstrated that environmental factors might play a pivotal role in the formation and stability of prokaryotic communities in each water mass, especially that of archaea. In addition, indicator species suggested by linear discriminant analysis effect size might be used as fingerprints to recognize corresponding water masses on NER. These results provide new insights into the vertical distribution, structure, and diversity of microorganisms on NER from the perspective of water mass.

Keywords: Ninety-East Ridge; Temperature–salinity curve; Microbial vertical distribution; Water mass; Microbial diversity

人工湿地对昼夜交替及根系泌氧的响应：性能和微生物机制

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摘要

人工湿地作为一种基于自然的污水处理系统，与自然环境保持着物质和能量的持续交换。根际是根系周围的动态区域，是研究植物与根际微生物相互作用的关键界面。光照条件可驱动植物生长和微生物代谢活性发生节律性变化，调控植物和微生物之间的相互作用，进而影响人工湿地的污染物处理效能。因此，探究植物和微生物相互作用对光照的响应机制将有助于加深根际在污染物去除中的作用的认识。本研究探究了昼夜交替对人工湿地根际微生物群落的影响。结果表明，在人工湿地稳定运行时，其内部环境存在动态交替机制，本研究显示的核心微生物群落、微生物代谢活性和污染物去除的节律性变化验证了这一机制。结果表明，微生物对污染物的去除(如总氮)在白天条件下比在夜间条件下高 1.31 倍。随着昼夜节律进化的根际核心微生物类群(如 *Chloroflexus* 和 *Beijerinckia*)主要与碳、氮、磷和能量代谢有关，夜间平均相对丰度较低。尽管白天也观察到较高的微生物代谢活性，但夜间条件下与碳和氮代谢功能相关的基因水平较高。结构方程模型 (SEM) 分析进一步表明，环境因素在驱动微生物去除污染物过程中具有显著影响，微生物群落在夜间对污染物去除的促进作用大于白天。此外，植物与微生物之间复杂的相互作用构成了人工湿地去除污染物的基础。植物通过光合作用向根际分泌氧气，根系泌氧(ROL)对功能微生物的活性和丰度起着关键作用。然而，垂直空间尺度下 ROL 对微生物群落生态位分化的影响却鲜有研究。本研究结果表明，ROL 随深度降低，促进了根际微生态系统的氧化还原。上层高水平的 ROL 可支持好氧菌(*Haliangium*)的供氧，促进 COD(60%)和 NH_4^+-N(50%)的去除，而下层反硝化菌(如 *Hydrogenophaga* 和 *Ralstonia*)和甲烷氧化菌(*Methanobaterium*)的富集可促进反硝化作用。功能预测结果进一步证实，在根际氧浓度梯度的作用下，根际中催化硝化和反硝化过程的基因丰度分别在上层和底层显著增强。这将有助于进一步揭示根际效应，提高对人工湿地污染物去除机制的认识。综上所述，本研究可为人工湿地中植物与微生物的相互作用提供见解，并为人工湿地的设计和运行提供科学的指导。

关键词：人工湿地；昼夜交替；根系泌氧；污染物去除；微生物群落

Constructed wetlands treating synthetic wastewater in response to day-night alterations and radial oxygen loss: Performance and mechanisms

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Abstract

Constructed wetlands (CWs), as nature-based wastewater treatment systems, continuously maintain exchanges of material and energy with the natural environment. The rhizosphere, a dynamic zone surrounding plant roots, served as a key interface for studying plants-microbial interactions. Light condition can drive rhythmic changes in plant growth and microbial metabolic activity and regulate the interactions between plants and microorganisms, thereby affecting the pollutant treatment performance of CWs. Therefore, research on mechanisms of plant-microbe interactions in response to light condition will deepen the understanding of the role of rhizosphere in pollutants' removal of CWs. Herein, we investigated the effects of day-night alterations on the rhizosphere microbial community in CWs. The results revealed that a dynamic alternate mechanism existed in the inner environment when the CWs were in steady operation, which was validated by rhythmic changes in the core microbial community, microbial metabolism activity, and pollutant removal shown in this study. The results showed that pollutant removal (e.g., total nitrogen) due to microbial processes was 1.31 times higher under daytime conditions than under nighttime conditions. Core microbial taxa of the rhizosphere that evolved with circadian rhythm (e.g., *Chloroflexus* and *Beijerinckia*) were mostly associated with carbon, nitrogen, phosphorus, and energy metabolism, with lower average relative abundance identified at night. Although higher activity of microbial metabolism was also observed in the daytime, nighttime conditions demonstrated higher gene levels that were related to carbon and nitrogen metabolic functions. Structural equation model (SEM) analysis further suggested that environmental factors exerted a significant influence in driving microbial processes for pollutant removal and that the microbial community played a greater role in promoting pollutant removal under nighttime conditions than under daytime conditions. Besides, complex interactions between plants and microorganisms form the basis of CWs for pollutant removal. Plants can secret oxygen produced by photosynthesis to the rhizosphere, radial oxygen loss (ROL) plays a key role in the activity and abundance of functional microorganisms. However, little has been done to explore how ROL would influence the niche differentiation of microbial communities at different vertical spatial scales. We demonstrate that ROL decreases with depth, promoting an oxidation-reduction rhizosphere microecosystem in CWs. The high level of ROL in the upper layer could support the oxygen supply for aerobic bacteria (*Haliangium*), facilitating the COD (60%) and NH_4^+-N (50%) removal, whereas the enrichment of denitrifiers (e.g., *Hydrogenophag*a and *Ralstonia*) and methanotrophs (*Methanobaterium*) in the lower layer could stimulate denitrification. The function prediction results further certified that the abundance of genes catalyzing nitrifying and denitrification processes were significantly enhanced in the upper and bottom layers, respectively, which was attributed to the oxygen concentration gradient in the rhizosphere. This study contributes to further unraveling the rhizosphere effect and enables an improved understanding of the decontamination mechanisms of CWs. In summary, this study analyze the response mechanisms of plant-microbial interactions, which provide valuable insights into plant-microbial interactions and scientific information for the design and operation of CWs.

Keywords: Constructed wetlands; Day-night alterations; Radial oxygen loss; Pollutant removal; Microbial community

滨海城市水环境抗生素抗性基因的赋存特征及其形成机制

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摘要

抗生素抗性基因（Antibiotic resistance genes, ARGs）的环境污染及其潜在健康风险近年来受到广泛关注，被认为是一类生物新污染物。城市景观水体是居民亲水活动的主要场所之一，其生态环境安全对于保障城市人群健康具有重要意义，然而有关城市景观水体 ARGs 的赋存水平、分布特征及其形成机制尚不清楚，且较缺乏对城市水循环不同关键节点的协同研究。我们采用 16S rRNA 基因扩增子测序、高通量定量 PCR、多元统计与生态零模型等技术，系统研究了滨海城市厦门水源地水库、污水处理厂和景观水体中 ARGs 的分布格局及其形成机制，主要发现：1）厦门水源地水库、景观水体和污水厂进出水分布有 237 种 ARG 亚型，ARGs 的分布具有明显的生境异质性。移动遗传元件（Mobile genetic elements, MGEs）介导的随机过程是市政污水和小型景观水体 ARGs 传播扩散的主要生态学机制，导致污水、小型景观水体成为 ARGs 的分布热区。多生境对比分析发现，新德里金属-β-内酰胺酶 1（*blaNDM-1*）是污水的特征 ARGs 之一，说明 *blaNDM-1* 可能在厦门人群中广泛传播，其健康风险亟待评估；2）城市景观泻湖的水体 ARGs 有着明显的季节动态变化，夏冬季 ARGs 的种类与丰度显著高于春秋季，且随机过程对夏冬季 ARG 群落的构建具有较强影响。微生物源示踪分析表明，污水漏排、溢流导致人类粪便污染筼筜湖水体，致使水体中粪便菌和 MGEs 含量上升，进而间接通过随机过程促进 ARGs 传播。网络分析发现，转座子 *tnpA*-07 是介导筼筜湖湖水体 ARGs 水平基因转移的关键 MGEs 元件；3）城市泻湖沉积物 ARGs 的种类和丰度分别是对照（西藏）湖泊的 11 倍和 53 倍，说明城市化进程对 ARGs 的传播有着促进效应。网络分析表明，厌氧微生物类群是沉积物 ARGs 的潜在宿主。结构方程模型分析表明，沉积物理化因子与重金属通过作用于生物因子（MGEs、微生物群落等）分别对沉积物 ARG 赋存水平施加正向和负向效应，说明移动遗传元件介导的水平基因转移与微生物群落介导的垂直基因转移分别是影响沉积物 ARG 丰度和群落组成的主要机制。这些发现为深入认识城市水环境 ARGs 传播扩散的生态机理及城市水环境安全保障措施的制定提供了重要科学依据。

关键词：抗生素抗性基因；移动遗传元件；微生物群落；城市水环境；高通量定量 PCR

藻菌共生体介导的抗生素抗性基因去除机制研究

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摘要

磺胺类抗生素抗性基因（ARGs）中的亚类 *sul1* 是大多数富营养化水体中的优势基因。本文主要探究了普通小球藻（*Chlorella vulgaris*）和地衣芽孢杆菌（*Bacillus licheniformis*）形成的藻菌共生体系对携带 *sul1* 的外源 ARGs 质粒的去除性能与机制。研究结果表明，藻菌共生体系对 *sul1* 的去除率达到了 97.2%。在藻菌正常生长的前提下，藻菌胞内碳代谢、氮代谢、氨酰 t-RNA 生物合成、糖蛋白分布等过程的提升与加强对 *sul1* 的去除具有显著正向影响（$P<0.05$）。qPCR 检测结果表明，藻菌共生体系中 *sul1* 的绝对丰度几乎为 0 gene copies/mL，显著低于单藻或单菌体系（1×10^6gene copies/mL）。藻菌共生体系对外源 *sul1* 的复制具有显著的抑制作用，携带 *sul1* 的 ARGs 质粒被藻菌吸附于表面后，通过跨膜运输进入胞内并聚集于易染色质区域，该区域可有效阻断 *sul1* 的转录与复制。藻菌共生体是一种非常具有前景的水体生态修复技术，有望为水环境中 ARGs 及其他新型污染物的去除提供重要参考作用。

关键词：抗生素抗性基因；藻菌共生体；普通小球藻；地衣芽孢杆菌

r-K 选择理论：微生物生态策略框架下的土壤生态学问题

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摘要

r-K 选择理论是 19 世界 70 年代提出的一个生态学概念，最初用于描述植物和动物的生长和生殖特征，通常 r-策略者在养分丰富条件下，具有较快的生长速率，但生命周期短能耗高；而 K-策略者耐受养分较低的条件，生长缓慢，生命周期长。90 年代初，微生物生态学家将这一概念借用到微生物生态研究中，基于微生物生长、底物偏好和养分利用将微生物生态策略分为 r-策略和 K-策略。在水生微生物群落中，通常用“富营养-寡营养”概念来代表“r-K”策略。但 r-K 策略是否适用于土壤微生物群落尚不明确，例如，这个概念是否能描述大部分土壤微生物的生态策略，哪些土壤微生物可以被纳入这个理论框架中，r-K 选择理论能否解释大部分的土壤生态学过程。本文综述了土壤微生物潜在的 r-和 K-策略的生理生化和遗传学特征，并尝试利用 r-K 选择理论阐释土壤生态学过程。r-策略微生物通常具有较高的生长速率，细胞较小，移动性强；碳利用效率低，细胞碳氮比和碳磷比低；对外界干扰抵抗力差，但竞争力强，生境较宽泛；对养分输入响应迅速，偏好利用易降解碳组分。而 K-策略微生物则具有相反的生理生化特征。r-策略微生物基因组 GC 含量变异较大；核糖体拷贝数高；编码鞭毛蛋白和趋化因子的基因丰富；跨膜转运蛋白 ATP-依赖型转运子为主；编码易降解碳（例如纤维素）基因丰富，而编码难降解碳（例如木质素）基因丰度较低。微生物 r-K 策略可用于解释微生物地理分布（例如海拔梯度格局）、微生物对养分输入的响应（例如氮输入和秸秆还田）、以及气候变化相关的微生物学过程（例如与有机碳矿化温度敏感性和激发效应）等土壤学和生态学问题。

关键词：r-K 选择理论；土壤微生物宏基因组学；微生物地理分布；全球变化微生物学

晋北矿区生态修复进程中土壤微生物群落特征

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摘要

对山西高原矿区生态修复进程中的不同复垦措施和复垦年限土壤细菌、古菌和真菌群落的演替方面的研究工作进行总结。对山西省孝义市露天矿区复垦区四种植被的四种施肥方式的土壤呼吸、酶活性和微生物群落的研究发现，植被覆盖度会影响土壤水热动态，覆盖度高的样地土壤呼吸与温度拟合系数高，而覆盖度低的样地土壤呼吸与水分拟合系数高；土壤细菌、古菌和真菌的丰度在不同植被恢复间差异显著，植被修复类型比施肥对矿区复垦生态影响效应更为显著。

对安太堡矿区 41 个样地的植被进行了调查，并通过高通量测序研究了土壤微生物群落演替特征，结果表明，植被和土壤理化特征对三域微生物多样指数的影响并不一致，细菌和古菌主要是植被因子影响，而真菌主要是受土壤理化因子的影响，三域微生物中受植被和土壤因子协同影响最大的为真菌，次之为细菌；CCA 分析发现，影响细菌群落组成最主要的因子为植被均匀度指数，复垦年限是影响土壤古菌和总群落组成的最为显著的因子，而土壤氮含量是影响真菌群落组成最为显著的因子。

对安太堡矿区不同恢复年限的油松林作土壤理化特征、酶活性、土壤细菌、古菌和真菌的丰度和群落组成进行分析发现，在矿区复垦进程中随复垦年限的增加，土壤营养成分、微生物丰度和多样性以及酶活性显著增加，土壤酶活性与微生物丰度之间的相关性显著，而与微生物多样性间的相关性较弱。随着复垦年限的延长，子囊菌门的菌群在减少，而担子菌门的菌群在增加。土壤 pH 在微生物代谢群落结构和细菌群落结构的演替中发挥着显著的作用，而土壤有机碳是真菌群落演替的主要驱动因子；矿区土壤综合质量肥力指标随着复垦年限显著增加，为 logistics 增加趋势，土壤肥力约在复垦年限 20 年后可达到未干扰地的水平。

关键词：矿区生态修复；微生物多样性；碳代谢；酶活性；复垦措施

The soil loading weights for DNA extraction significantly affect the examination of microbial diversity but not abundance

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Abstract

As the cornerstone of most soil microbial diversity and abundance research, soil DNA extraction is inherently influenced by the loading weights of soils. However, the effects of soil loading weights for DNA extraction on microbial community analysis remain poorly understood. In this study, soils were collected from desert, meadow, forest, and cropland ecosystems to examine the effects of soil loading weights (i.e., 0.010, 0.025, 0.250, 0.500, and 1.000 g) on microbial community analysis. Soil microbial abundance and diversity were analyzed through real-time PCR and NovaSeq high-throughput sequencing, respectively. The results showed that soil loading weights for DNA extraction did not significantly affect microbial abundance determination. In contrast, microbial richness, community composition and functional prediction significantly varied with different soil loading weights for DNA extraction. Microbial richness obtained from 0.010 and 0.025 g of soils was significantly lower than that obtained from 0.250-1.000 g of soils. In addition, microbial community composition significantly differed among the technical replicates using 0.010 or 0.025 g of soil for DNA extraction. However, when the soil loading weights for DNA extraction exceeded 0.500 g, the microbial community composition and predicted functional profiles were no longer affected by soil loading weights, and the variations among technical replicates significantly decreased. Collectively, these findings suggest that the analysis of soil microbial diversity rather than abundance is substantially affected by the soil loading weights for DNA extraction, and more than 0.500 g of soil is recommended for DNA extraction to ensure the reliability of soil microbial research.

Keywords: Soil microorganisms; Microbial diversity; Microbial abundance; Soil DNA extraction; Soil loading weights

SNP-based mapping reveals recombination of microbial population across in-depth mangrove sediments

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摘要

红树林湿地作为蓝碳系统的重要组成部分，具有生产率高、有机质丰富、元素循环快等特点。红树林沉积物微生物作为元素循环的重要驱动者而备受研究人员关注，但前期研究主要关注于微生物群落组成，而对种群内基因的多样性研究较少。为了阐明红树林沉积物中微生物种群的单核苷酸多样性（single nucleotide polymorphism，SNP）及其与环境选择的关系，本研究采集了珠海淇澳岛红树林自然保护区中本地红树种秋茄的沉积物样品（5 个 1m 沉积物柱，分 10 层）并对其进行了宏基因组测序。通过采用基因拼装技术，我们最终获得了 490 个完整度大于 50%且污染率小于 10%的 Metagenome Assembled Genomes（MAGs）。这些 MAGs 分布于 234 个不同的分类物种，其中有 18 个高分布频率的种群为 Proteobacteria、Desulfobacterota 和 Chloroflexota。选择这些种群中高质量（完整度大于 80%）的 MAGs 作为 Reference Genomes（RGs）进行不同样点的核苷酸多样性及其与环境因子的关联分析，我们发现 5 个高分布频率的种群平均单核苷酸多样性与深度有着显著的相关性（$p < 0.05$）。这些被鉴定出的 SNP 广泛分布于代谢、蛋白质家族、信号转导过程等相关基因中，各个 RGs 不同功能基因与不同的环境因子均有着显著的相关性（$p < 0.05$），这说明单个物种内出现的突变和同源重组经过环境选择形成了遗传变异。该研究结果对于阐明红树林沉积物的微生物功能多样性的形成和维持机制有着重要的意义。

关键词：宏基因组；单核苷酸多样性；环境因子；功能基因

微生物流式细胞术在微生物生态学研究中的应用：以揭示无外源微生物输入连续流反应器的群落聚合过程为例

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摘要

在完全封闭的微环境当中（例如反应器），微生物群落结构的演变不受外来物种输入所左右。在此基础上稳定的外部环境会逐步筛选最具生存优势的适应性物种，促使微生物群落结构变化并最终与之平衡。基于上述原理人们会期望通过对环境的控制约束驯化微生物以获得预期的群落结构与功能。然而，越来越多的证据表明同样的环境条件约束确实会导致相似的群落功能响应，但群落结构的差异化却很难避免。即便是在同样接种并严格控制培养条件的平行反应器中这种不确定性同样可以被观测到。为了揭示这一现象背后的生态机制，我们从单细胞水平上对五个平行运行的连续流反应器进行了约100 个代时的研究，并通过生态学分析手段量化了群落结构的变化。尝试通过人为施加的中等程度温度扰动（30-40 摄氏度的阶梯变化）作为潜在群落调控手段，对群落结构的差异化过程加以控制。研究结果：1.低斜率对数正态型秩序丰度曲线（lognormal rank-ordered abundance curves）表明中性随机组装过程相比于确定性物种筛选过程在群落组装中更为重要，即微生物种间差异对群落聚合的影响较小，亚群落的生态漂变以及群落间 β-多样性增加，都支持这一结论；2.我们也同样观察到了生态位分化的现象，例如最初适应期间和温度干扰后更加陡峭的几何型秩序丰度曲线（geometric rank-ordered abundance curves）以及微生物/环境参数之间显著增强的互作关系。

关键词：微生物生态学；微生物流式细胞术；单细胞检测；群落聚合原理

Damming impact on biogeographic patterns and ecological processes of planktonic bacterial and eukaryotic communities in the upper Yangtze River

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Abstract

Planktonic bacterial and eukaryotic communities play important roles in biogeochemical cycles, but their biogeographic patterns and community assembly processes in large rivers impacted by dams remain unclear. The purpose of this research was to investigate the large-scale genetic diversity and biogeography patterns within large cascade dams and to reveal the key drivers (damming and near-shore anthropogenic activities) in shaping planktonic bacterial and eukaryotic communities. At present, there have been over 15 large dams along the main stem of the upper Yangtze, including the Three Gorges Dam, the Xiluodu Dam, Xiangjiaba Dam, the Baihetan Dam and the Wudongde Dam. In this study, 16S rRNA and 18S rRNA gene high-throughput sequencing approaches were used to investigate bacterial and eukaryotic communities from 24 sampling sites in the upper Yangtze River during the flood season (August) and dry season (March). The upper Yangtze River in our study were divided into dam-affected zones and river zones on the basis of the influence of the dams. In all, 48 samples in the dry and flood seasons were collected from the upper Yangtze River. A total of 2,940 and 869 OTUs for planktonic bacteria and eukaryotes were obtained by high-throughput sequencing respectively. There was a significant and negative relationship between the geographical distance and the Bray-Curtis similarity of the bacterial and eukaryotic communities in both the dry and flood seasons ($p < 0.01$), which indicated that the microbial taxa exhibited a robust distance-decay pattern, suggesting that geographical distance was important in structuring the microbial community and determining the spatial dissimilarity in the river network. Moreover, the α-diversity index decreased significantly from the upstream to the downstream. Principal coordinate analysis of the eukaryotic plankton taxa yielded a distinct biogeographical distribution pattern between different seasons and locations. The results showed that there were significant differences in bacterial and eukaryotic communities between two zones and that dams significantly reduced the α-diversity of bacterial communities. The co-occurrence network analysis indicated that the network in the river zone was denser than that in the dam-affected zone and that the relationships among species of bacterial were more complex than those in eukaryotic network. Compared with the planktonic eukaryotic community network, the planktonic bacterial community network had more keystone species. There were significantly more keystone OTUs in the river zone than in the dam-affected zone, and their abundance also showed a similar trend. Dispersal limitation and ecological drift were the main processes influencing planktonic bacterial and eukaryotic communities in the dam-affected zone, respectively, whereas the role of deterministic processes increased in the river zone. Anthropogenic activities and hydraulic conditions affected suspended sediment and controlled microbial diversity in the river zone. These results suggest that dams impact planktonic bacteria more strongly than planktonic eukaryotes, indicating that distribution patterns and processes of bacterial and eukaryotic communities in large rivers are significantly different. In addition, our findings show that planktonic bacterial and eukaryotic community across the upper Yangtze River exhibit an ecological succession along the river continuum, and this is primarily driven by the combination of environmental, spatial and hydrological variables in the river-reservoir system.

Keywords: Bacteria; Eukaryotes; Biogeography patterns; Keystone species; Ecological process; Large cascade dams

小幅盐度变化改变了城市水库微型真核浮游生物的群落构建和共存网络

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摘要

微型浮游生物是水库生态系统的重要组成部分，具有极高的多样性，在元素循环和生态系统稳定性维持中发挥关键作用。在气候变化和人为活动等多重压力下，内陆淡水水体盐碱化现象日益增加，淡水水生生物生长、发育甚至繁殖已受到不同程度的不利影响。因此，保护淡水生物多样性已成为全球面临的挑战之一。当前，需要更全面深入地了解水库微型浮游生物群落多样性如何适应环境因素的干扰。本研究通过调查中国亚热带城市水库（杏林湾水库），使用高通量测序技术和生态统计方法，在连续 13 个月高分辨率时间序列中研究了微型真核浮游生物多样性、群落构建和网络稳定性对小幅盐度变化的响应。结果发现，与其他因素相比，盐度与微型真核浮游生物群落结构的相关性更为显著。水体盐度的小幅增加显著改变了水库微型真核浮游生物群落组成，并导致生物多样性显著降低。此外，盐度通过调控确定性和随机性生态过程之间的平衡塑造了群落构建，且随着盐度的上升，确定性过程越来越重要。更重要的是，核心浮游生物子网络在低盐度水平较为稳定，而卫星浮游生物子网络在中/高盐度水平具有较高的稳定性。我们的研究结果为城市内陆水体浮游生物生态学以及盐度变化对微生物群落构建的影响提供了新见解。

关键词：亚热带水库；浮游生物；群落构建；网络稳定性

不同微生物过程和控制因子影响农业和城市河流温室气体 N_2O 排放水平

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摘要

农业和城市河流是人为间接 N_2O 排放的热点区域，然而人们对其相关的微生物过程认识不足。本研究测定了太湖农业和城市河流的 N_2O 排放速率，并测定了水体和底泥中 N_2O 产生和消耗相关的微生物过程。结果表明，农业河流水体溶解 N_2O 浓度和排放速率均显著高于城市河流。应用 7 中以风速为基础的扩散系数 *k* 值模型评估表明，由于低估了城市河流的 N_2O 排放系数（EF_{5r}），IPCC 方法显著低估了城市河流 N_2O 排放量。逐步多重回归表明风速和 NO_3^-浓度分别是影响农业和城市河流的关键因子。*nirK* 型反硝化细菌在城市河流水体产生 N_2O，而 nirS 性反硝化细菌在农业河流底泥消耗 N_2O。藻类释放有机物促进水体反硝化细菌 *Flavobacterium*，而底泥中硫还原细菌通过种间电子传递促进反硝化细菌 *Dechloromonas*。我们的结果表明农业和城市河流水体和底泥差异化的微生物和微生物过程决定了 N_2O 排放水平。

关键词：N_2O；土地利用；评估模型；微生物过程；共发生网络

厌氧产甲烷条件下菲生物降解的代谢途径探究

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摘要

Polycyclic aromatic hydrocarbons (PAHs) are ubiquitous environmental contaminants that can be aerobically biodegraded. However, strategies for anaerobic biodegradation of PAHs are needed because of the persistence of PAHs in anoxic environments. In this study, we obtained a highly enriched anaerobic, PAHs-degrading co-culture DYM1, from petroleum-polluted soil collected from Shandong province in China. About 93 % of phenanthrene (104.5 μM) has been removed under methanogenic conditions after incubation with co-culture DYM1 for 4 d, and produced 33.68 μmol CH4. DYM1 significantly degraded other PAHs in 4 days without supplementary terminal electron acceptors, including naphthalene, anthracene, fluorine, fluoranthene, pyrene, benz[a]anthracene and benzo[a]pyrene. Co-culture DYM1 is consists of two microorganisms (a degrading bacterium Paracoccus sp. strain PheM1 and an aceticlastic methanogen Methanosaeta concilii.) that utilize different carbon sources in a syntrophic metabolic process of phenanthrene. The biotransformation processes of phenanthrene degradation under methanogenic conditions were explored by metabolite and enzyme analyses. Carboxylation, which is catalysed by UbiD-like carboxylase, was first found to be the initial steps of the methanogenic phenanthrene-degrading pathway based upon the detection of 2-phenanthroic acid and 4-phenanthrene acid. Reduction and hydration of the benzene rings were followed by the initial reaction. Hydrated phenanthroic acid metabolites were newly detected and characterized in anaerobic conditions. Anaerobic degradation of phenanthrene without terminal electron acceptor addition sheds light on a poorly understood and environmentally relevant biological process. A better understanding of the biological processes that can remediate PAH-contaminated anoxic environments is necessary to develop effective bioremediation strategies for these widespread pollutants.

关键词：多环芳烃；厌氧降解；产甲烷；代谢途径

解析厌氧氨氧化的乙烷抑制

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摘要

厌氧氨氧化和硝化是两种常见的微生物氨氧化过程，对微生物氮循环至关重要。众所周知，短链烷烃(C_2-C_8)可以与氨单加氧酶相互作用而抑制硝化过程，然而短链烷烃是否会影响厌氧氨氧化过程还是一个悬而未决的问题。本研究证实了乙烷对厌氧氨氧化过程的显著抑制作用并揭示了其抑制机理。乙烷对厌氧氨氧化过程的急性抑制是一种浓度依赖并可逆的效应，0.86 mM 乙烷可导致 50%的厌氧氨氧化活性抑制(IC_{50})，而 1.72 mM 乙烷几乎完全抑制厌氧氨氧化活性。在经过 30 天的 0.09 mM 乙烷暴露后，厌氧氨氧化菌的氨氧化速率和亚硝酸盐还原速率分别从 202 和 267 mg N L^{-1} d^{-1} 迅速地降至 1 和 1 mg N L^{-1} d^{-1}，同时厌氧氨氧化菌丰度从 61.9%降至 9.5%。在乙烷暴露条件下，研究发现厌氧氨氧化菌胞内氨氮浓度显著降低，且转录组分析表明厌氧氨氧化菌涉及氨转运的基因表达显著上调。因此，乙烷可通过抑制氨的摄取从而抑制厌氧氨氧化过程。正如乙烷是多种厌氧环境中仅次于甲烷的第二丰富的烷烃，乙烷可能对由厌氧氨氧化驱动的氮循环产生重要影响，应在未来进一步研究。

关键词：厌氧氨氧化；乙烷暴露；急性抑制；慢性抑制；氨转运

珠江河口沉积物中氮循环功能基因的空间分布格局

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摘要

微生物（细菌和古细等）是全球生物地球化学循环的主要驱动力。阐明微生物生物地理分布及其驱动过程对于预测环境变化将如何影响生物地球化学循环非常重要。以往微生物生物地理学的研究常常聚焦在物种的层面。然而，越来越多的研究表明微生物群落的功能特性通常与其物种组成是解耦的，并且与物种相比，功能结构与环境变化和生态系统功能的相关性更高。因此直接研究微生物功能基因的生物地理分布就十分必要。氮循环是地球上最重要的生物地球化学过程之一。自然界中，氮可以以多种价态（-3 到 +5）存在，不同价态之间的转换主要是由微生物功能基因驱动的。目前我们对微生物氮循环功能基因的生物地理分布还缺乏足够的了解，这阻碍了对氮循环的系统性理解。在这里，我们使用珠江口沉积物作为研究系统，利用宏基因组学技术研究了所有关键氮循环基因的多样性和丰度的空间分布格局。我们发现参与反硝化和硝酸盐异化还原为铵途径的功能基因比参与其他过程（即固氮、硝化、同化亚硝酸盐还原）的基因具有更高的多样性和丰度。某些氮循环基因的多样性和丰度的空间分布在一定程度上是解耦的。具体而言，*narG*、*napA*、*nirK*、*nrfA* 的多样性在靠近河流出口处更高，而 *narG*、*napA*、*norB* 的丰度在珠江口下游更高。这些基因的空间变化主要受水深、C/N 和 NH_4^+ 的驱动。此外，参与相同通路（如反硝化作用）的氮循环基因对环境变化的响应不一致，并且参与不同氮循环步骤的主要类群也不相同，这一定程度上解释了为什么单个功能基因的丰度往往不是特定氮循环过程速率的可靠代理。总的来说，我们的研究表明，研究微生物功能基因的生物地理学可以从生物地理学的角度扩展我们对氮循环的认知。因此，我们建议本研究提出的问题也应该在其它生态系统中被回答。并且随着来自不同生境的宏基因组数据的不断积累，我们最终可以绘制一幅氮循环功能基因的全球分布图，而这幅图将为我们从生物地理学的角度理解全球氮循环提供重要的基础信息。

关键词：功能生物地理学；氮循环功能基因；多样性；河口

Evaluation and redesign of the primers for detecting nitrogen cycling genes in the environment

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Abstract

A better understanding of how nitrogen (N) cycling genes are involved in ecological processes is one of the crucial areas of microbial ecological research. Currently, most molecular biological techniques investigating N cycling genes in the environment heavily rely on the accuracy of the PCR primers, however, their specificity and coverage have not been comprehensively evaluated. Here, we collected a sequence database, NcycFunGen, for 22 marker genes involving in N cycling, which included 604,964 paired nucleotide and protein sequences with their taxonomic information. Then, a total of 608 published primers were fully evaluated through NcycFunGen, as well as against full-length sequences collected from KEGG.

The results showed that the majority of primer pairs cover less than 30% sequences of target genes, and that 22.55% were not applicable for high-throughput amplicon sequencing (<100 bp or >550 bp). In general, this in-silico evaluation demonstrated that although many primers have been adopted in published studies, some of them should be validated and updated as needed according to updated gene database. Therefore, new degenerate primer pairs for ureC targeting urease, bacterial and archaeal amoA targeting ammonium monooxygenase, and nifH targeting nitrogenase were designed through NcycFunGen. These new primer pairs showed higher coverage and amplification efficiency, as well as amplicon lengths that were applicable for high-throughput amplicon sequencing. Then, in experiment, the updated ureC gene primer pair ureC607F/ureC898R has been applied to a urea amendment site by using both by droplet digital PCR and high-throughput amplicon sequencing, and their results displayed the better characteristics and broader usable taxonomic range than commonly used published ureC gene primer pairs. In conclusion, primer evaluation and redesign are highly recommended to improve the accuracy of primers targeting N cycling genes, which could facilitate amplicon-based N cycling studies in various environments.

Keywords: Nitrogen cycle; Database; Primer evaluation; Primer design

两种典型农田土壤中反硝化细菌菌群对土壤 N_2O 排放的影响机制

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摘要

农田过量施氮引起的氧化亚氮排放引起了人们的广泛关注。微生物组如何调节土壤中 N_2O 的机制尚不清楚。本研究通过对中国广泛分布的两种农田土壤——黑土和潮土进行不同碳氮条件下的微宇宙培养试验，比较其 N_2O 排放及相关反硝化细菌和基因。结果表明，在所研究的三种不同施肥条件下，黑土中 N_2O 的动态积累量均显著高于潮土。尽管潮土中反硝化基因数量显著增加，但 N_2O 产生基因(*narG*、*nirS*、*nirK*)与 N_2O 还原基因(*nosZ*)的比例在黑土和潮土中无显著差异。但两种土壤的反硝化细菌群落存在明显差异。特别是通过对黑土优势反硝化菌 *Rhodanobacter* 的分离菌株的检测，发现其反硝化基因的缺失和无 N_2O 还原能力，是黑土中 N_2O 积累量较高的主要原因。而潮土中富集的 *Castellaniella* 属细菌的分离菌株是具有较高反硝化效率的完全反硝化菌，这种反硝化菌可能是潮土中形成的 N_2O 能够快速被还原为氮气的主要原因。两种土壤中反硝化菌种类和表型的差异导致了 N_2O 的产生和还原效率的差异，进而造成两种土壤 N_2O 排放量的差异。通过将 *Castellaniella* 属细菌接种到黑土中，减少了 92%以上的 N_2O 排放。本研究揭示了土壤环境塑造的微生物菌群对两种重要农业土壤 N_2O 排放模式的影响，并证明了利用微生物菌剂减少农田土壤 N_2O 排放量的策略可行性。

关键词：农田土壤；反硝化；反硝化基因；细菌群落；N_2O

植物发育时期驱动玉米微生物组的生态角色分化

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摘要

植物各个部位都生活着多样的微生物群落，对宿主植物的养分吸收、病害抵御和环境胁迫适应等方面具有重要影响，但目前对于植物发育时期如何影响作物微生物组的群落构建、生态功能以及微生物互作网络仍然缺乏系统的认识。本研究考察了玉米不同发育时期下土壤及植物部位（包括根和叶的表面和内部）的细菌和真菌群落演替动态及其互作网络模式，并以田间放置的塑料植物作为背景对照，评估了大气环境对叶际微生物群落的影响，并通过宏基因组测序进一步探究了叶际微生物组的潜在生态功能。结果表明，植物不同发育时期对作物微生物组的多样性、群落组成、确定性/随机性群落构建以及互作网络模式具有较强影响，且对叶表微生物组的影响最为强烈。溯源分析表明大气环境是叶表微生物群落的重要来源，叶表微生物组同时受到植物生长发育和季节相关的环境因子（如温度和降水）的共同影响。网络分析和随机森林模型分析进一步表明，作物苗期的细菌群落在微生物共现网络和作物产量预测中更为重要，随着植物生长，真菌的作用越来越重要。宏基因组分析结果表明，苗期的玉米叶表微生物组具有更高的功能多样性和更高丰度的养分供应相关的基因，而后期则富集了更多与氮同化和碳降解相关的基因。此外，属于放线菌门、伯克氏菌科以及根瘤菌科的潜在有益细菌在植物发育早期显著富集，而腐生真菌在后期显著富集。以上结果表明，植物生长发育时期对其微生物组的组成和功能具有较强的调控作用，细菌和真菌群落分别在不同时期发挥主要生态角色。这些发现可以为未来作物微生物组精准调控、微生物菌剂开发以及农业可持续生产提供重要参考。

关键词：作物微生物组；时间动态；群落构建；微生物互作网络；宏基因组

产甲烷古菌变身食甲烷生长的生理生态学研究

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摘要

厌氧生物圈的产甲烷古菌与甲烷氧化古菌是大气甲烷最主要的“源”与“汇”，二者的产甲烷与食甲烷功能在调控全球甲烷收支平衡与减缓温室效应方面扮演着重要角色。目前，虽然对产甲烷古菌生长代谢机理的认识已较为深入，但甲烷氧化古菌由于生长缓慢、无纯菌分离，严重阻碍了利用生物化学、遗传学等手段对于食甲烷生长代谢机理的研究。本研究首次发现了与甲烷氧化古菌亲缘关系较近的两株从海底沉积物中分离的模式产甲烷古菌 *Methanosarcina acetivorans* 与 *Methanococcoides orientis* 具有以甲烷作为唯一碳源和能源的食甲烷生长代谢功能，该功能需要耦合胞外三价铁或腐植酸的还原，甲烷最终被不完全氧化为乙酸与/或甲酸等产物。本研究通过测定食甲烷生长过程中所积累的生物量、甲烷氧化量、三价铁还原量、乙酸与/或甲酸的生成量，精准计算了 *M. acetivorans* 与 *M. orientis* 所进行甲烷转化的化学计量数与热力学自由能，并基于 *M. acetivorans* 与 *M. orientis* 完备的基因组注释信息，合理推断了截止目前最详细的甲烷厌氧氧化代谢途径，进一步证实了长期存在的科学假设，即甲烷厌氧氧化是通过逆转产甲烷代谢途径实现的。本研究不仅建立了研究食甲烷生长代谢分子机制的理想平台，而且对于进一步认识由产甲烷古菌与甲烷氧化古菌所介导的影响地球气候的甲烷循环过程具有重要科学价值。

关键词：产甲烷古菌；甲烷厌氧氧化；甲烷循环；温室气体；厌氧生态系统

Ecophysiology of methanotrophic growth moonlighted by methanogenic archaea

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Abstract

Methanogenic and methanotrophic archaea in anaerobic biosphere are the main "source" and "sink" of the atmospheric methane. The methanogenic and methanotrophic functions play important roles in regulating global methane budget and mitigating the greenhouse effect. Currently, although the growth and metabolic mechanism of methanogenic archaea has been understood very well, slow growth of methanotrophic archaea and lack of isolation of pure strain have hindered the rigorous mechanistic study of methanotrophic growth via biochemical and genetic approach. This study, for the first time, reports that *Methanosarcina acetivorans* and *Methanococcoides orientis*, which were isolated from marine sediments and phylogenetically-related to methanotrophic archaea, are able to undergo methanotrophic growth with methane as the sole carbon and energy source, driven by extracellular reduction of Fe(III) or humic acids. Methane is partially oxidized to acetate and/or formate as end products. This study calculated the stoichiometry and thermodynamic free energy of methane conversion by measuring the amounts of biomass accumulation, methane oxidation, Fe(III) reduction, acetate and/or formate production. This study also reasonably proposed the most detailed metabolic pathway for anaerobic methane oxidation to date based on sufficient genome annotations of *M. acetivorans* and *M. orientis*, validating the long-term scientific hypothesis that anaerobic methane oxidation is achieved by reversing methanogenesis. This study not only offers an unprecedented platform for further study molecular mechanism of methanotrophic growth, but also contributes to understanding the methane cycling that impacts global warming governed by methanogenic and methanotrophic archaea.

Keywords: Methanogenic archaea; Anaerobic methane oxidation; Methane cycling; Greenhouse gas; Anaerobic ecosystems

象山港真核微生物群落季节性演替机制研究

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摘要

微生物群落组装过程和互作网络是微生物生态学的焦点问题，该问题的揭示有利于阐明和预测不同季节微生物群落的动态演替。真核微生物是海洋中的重要类群，但真核微生物群落季节性组装过程，特别是针对单个物种群落，如重要寄生类群共甲藻的研究仍极为有限。基于此，我们在富营养化港湾—象山港进行月度采样，研究象山港表层海水中真核微生物总群落和共甲藻的季节性演替、组装过程和共现模式。结果表明，真核微生物群落在四季中主要由甲藻、绿藻、硅藻等组成，春夏季节主要的物种是绿藻，秋冬季节主要是甲藻；共甲藻是甲藻中丰度最高的类群，其在夏秋季节的丰度较高，共甲藻的 GroupI和II占据主导地位，GroupIV仅在秋季出现。真核微生物群落组装过程由同质选择和漂移共同主导，但扩散限制作用在秋冬季节显著增强；共甲藻群落组装在四季均由漂移过程主导。网络分析发现，真核微生物群落的互作在冬季的连接紧密，春季松散；共甲藻在冬季主要与甲藻互作，春季与绿藻互作最紧密，夏季共甲藻与硅藻的互作比例升高，其在秋季与甲藻、绿藻、硅藻的互作趋于均衡，冬春季节的宿主选择明显多于夏秋季节。此外，我们发现真核微生物群落之间的互作随着同质选择作用的增强而减少。综上，本研究阐明了富营养化港湾中真核微生物群落的季节演替模式及塑造因素，为预测海洋生态系统在不同环境下的动态发挥重要作用。

关键词: 群落组装；互作网络；真核微生物群落季节演替；共甲藻；象山港

硝酸盐异化还原限制了海水养殖水体中氮的去除

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摘要

氮素污染已成为养殖系统的主要环境问题。海水养殖中约有 50～80% 的总氮被纳入水体或沉积物中，造成养殖环境恶化，产生的污染超过了生态系统的自净能力，从而引起了人们的广泛关注。本研究通过评估中国广东省沿海渔业养殖中沉积物和水体微生物群落和功能差异，揭示不同鱼类养殖中水体中总氮含量较高的微生物学机制。结果显示，在三种鱼类养殖（鱼类、虾类、鱼虾混养）方式中沉积物间隙水和水体中总氮含量主要是硝态氮积累，水体中硝态氮含量均值是沉积物的 2.41 倍，鱼类养殖模式水体中硝态氮含量高于虾类和鱼虾混养模式。NMDS 结果显示沉积物和水体的细菌群落结构组成差异明显，同时养殖模式改变了沉积物细菌群落结构组成。通过评估六种参与氮循环的细菌菌群相对丰度（属水平），发现水体中参与氨化、异化氮还原和同化氮还原细菌的相对丰度不仅高于沉积物，同时高于反硝化细菌菌群相对丰度，这表明水体硝态氮主要通过氨化或氮还原途径，而不是通过反硝化生产氮气排放，功能预测结果同样支持该观点。鱼虾混养可以有效降低鱼类养殖水体硝态氮含量，原因可能是鱼虾混养沉积物具有较少硝化细菌相对丰度和较弱的硝化潜力，从而缓解了沉积物中氮素以硝酸盐形式释放到水体。本研究在海水养殖氮素污染治理中提供了重要的微生物理论依据。

关键词：海水养殖；氮素污染；细菌群落；反硝化；异化和同化氮还原

Comammox *Nitrospira* contribute most to nitrification in a coastal aquaculture system

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Abstract

Nitrification that converts ammonium to nitrate via nitrite is important in aquaculture as it drives nitrogen removal processes including denitrification and anaerobic ammonium oxidation (anammox). Understanding how aquaculture affects nitrifiers especially newly discovered Comammox (complete ammonia-oxidizers) is important for sustainable aquaculture, as aquaculture is a nitrogen-rich system and the impact of aquaculture on surrounding environments is a serious environmental concern. In this study, we compared how environmental factors could change with the addition of fish feed, and explored how nitrifying communities responded by analysis of diversity and composition of key functional genes of Comammox *amoA*, AOA *amoA*, AOB *amoA* and *Nitrospira nxrB*. We found that the addition of fish feed altered environmental conditions dramatically with an increase of nitrogen related parameters (NH_4^+, NO_2^-, NO_3^-, TIN, TON and TN), and a decrease of carbon, sulfur and phosphate related parameters (POC, DOC, TOC, TC, TS, ES, AVS, TP, TOP and PO_4^{3-}). These changes subsequently impacted the diversity, community structure and potential interactions of nitrifying communities. Specifically, large fish pond sediments had (1) lower abundance of Comammox *amoA* ($1.37^7 \pm 2.06^6$ v.s. $2.18^7 \pm 2.34^6$ copies/g wet sediment), (2) lower within-beta-diversity of nitrifying communities (with highly similar nitrifiers in large fish ponds), and (3) lower complexity of community networks compared to small fish ponds. Random forest analysis suggested that the richness and abundance of Comammox *Nitrospira* contribute most to nitrification in aquaculture systems ($P < 0.05$). These results advance our understanding about how aquaculture alters nitrifying communities, highlight the important of Comammox *Nitrospira* to nitrogen removal.

Keywords: Aquaculture; Comammox; Nitrifying community; Diversity; Network

CeO_2 纳米颗粒通过改变细菌交流和质粒转移调控抗生素抗性基因的传播

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摘要

抗生素抗性基因（antibiotic resistance genes，ARGs）在农业生态系统中的传播和扩散，对全球公共卫生安全和食品安全构成重大威胁。近年来，纳米材料对环境中 ARGs 归趋的潜在影响引起了国内外的广泛关注。CeO_2 纳米颗粒（Nanoparticles，NPs）因在 1-50 mg/L 浓度范围内具有提高农作物产量和抗性的功能而在纳米农业中被广泛应用。本项研究探讨了不同浓度 CeO_2 NPs 对大肠杆菌之间 ARGs 接合转移的影响。我们的结果表明，在相对较高的 CeO_2 NPs 浓度（25 和 50 mg/L）下，RP4 质粒的接合转移频率增强了 118-123%。然而，低浓度的 CeO_2 NPs（1 和 5 mg/L）却显著抑制大肠杆菌间的接合转移。低浓度 CeO_2 NPs 对接合转移的抑制机制主要是由于：(1) CeO_2 NPs 降低了大肠杆菌胞内 ROS 的含量；(2) CeO_2 NPs 通过抑制大肠杆菌胞外聚合物质中多糖的合成而减弱了细胞间的粘性；(3) CeO_2 NPs 干扰了大肠杆菌 ATP 的合成途径导致质粒接合转移相关基因的表达量下降。我们的发现强调了 NPs 对 ARGs 传播的影响具有浓度依赖性，为在使用纳米农业技术的同时选择适当的 NPs 浓度以减少 ARG 的传播提供了证据。

关键词：纳米颗粒；抗生素抗性基因；水平基因转移；细菌交流；质粒转移

Microbiota dynamics and community assembly patterns in the world's largest water diversion canal

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Abstract

Large water diversion projects are important constructions for reallocation of human-essential water resources. Deciphering microbiota dynamics and assembly mechanisms underlying canal water ecosystem services especially during long-distance diversion is a prerequisite for water quality monitoring, biohazard warning and sustainable management. Using a 1432-km canal of the South-to-North Water Diversion Projects as a model system, we answer three central questions: how bacterial and micro-eukaryotic communities spatiotemporally develop, how much ecological stochasticity contributes to microbiota assembly, and which immigrating populations better survive and navigate across the canal. We applied quantitative ribosomal RNA gene sequence analyses to investigate canal water microbial communities sampled over a year, as well as null model- and neutral model-based approaches to disentangle the microbiota assembly processes. Our results showed clear microbiota dynamics in community composition driven by seasonality more than geographic location, and seasonally dependent influence of environmental parameters. Overall, bacterial community was largely shaped by deterministic processes, whereas stochasticity dominated micro-eukaryotic community assembly. We defined a local growth factor (LGF) and demonstrated its innovative use to quantitatively infer microbial proliferation, unraveling taxonomically dependent population response to local environmental selection across canal sections. Using LGF as a quantitative indicator of immigrating capacities, we also found that most micro-eukaryotic populations (82%) from the source water sustained growth in the canal and better acclimated to the hydrodynamical water environment than bacteria (67%). Taxa inferred to largely propagate include *Limnohabitans* sp. and *Cryptophyceae*, potentially contributing to water auto-purification. Combined, our work poses first and unique insights into the microbiota assembly patterns and dynamics in the world's largest water diversion canal, providing important ecological knowledge for long-term sustainable water quality maintenance in such a giant engineered system.

Keywords: Bacterial community; Micro-eukaryote; Stochastic assembly; Deterministic assembly; Population growth

Diversity and function of rhizosphere and endosphere microbiome of *Ginkgo biloba*

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Abstract

The description of the living fossil *Ginkgo biloba L.*, performing a well-developed root system, and their interaction with kinds of microbes in the environment, calls into question the metabolic potential and niches differentiation of microbes in *G. biloba* root. Here, we totally collected sixty-three samples of soil and root tissues from the given soil depths. Random forest (RF) model and FEAST prediction to detect bacterial taxa that accurately distinguish *G. biloba* root and rhizosphere samples. Different compartments had unique core microbial taxa with *Micromonosporaceae* and *Nectriaceae* shared among them. Functional analysis showed that genes about aerobic nitrite oxidation and nitrification were found more abundant in rhizosphere soils than root endosphere compartments, especially for rhizosphere soils with the depth of 50cm. Additionally, these compartments differ in aromatic compound degradation and aerobic chemoheterotrophy. What could not be ignored was that Nitrososphaerales bins belonging to the new phylum Thermoproteota constituted multiple novel species and took part in nitrogen metabolisms in rhizosphere soils. Functional expression and content of flavonoids and lactones were also measured in order to illustrating the metabolic potential of related medicinally secondary metabolites in *G. biloba* root. Our findings suggest that deep soil microbial communities have large contribution to energy metabolisms in *G. biloba* root than surface soil microbial communities. These plant-associated microbial communities and their relevance for the synthesis of medicinal ingredients in *G. biloba* root, is influenced by niches differentiation.

Keywords: *Ginkgo biloba* root; Metabolic expression; Nitrososphaerales; Flavonoids; Lactones

宏基因组学揭示了农田和森林土壤中抗生素抗性组的差异

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摘要

揭示农田和森林土壤抗生素抗性组差异，对于评估两种生态系统相互转换的生态效应是至关重要的，但相关研究仍鲜有开展。本研究在区域尺度以配对的方式采集了中国西南地区 30 个地点的农田和森林土壤，基于宏基因组、扩增子测序和 qPCR 等方法探究了农田和森林土壤微生物及抗生素抗性组的差异。研究发现，森林土壤的微生物多度显著高于农田，微生物群落组成也表现出显著的差异。在农田和森林土壤中均检测到以万古霉素、多药和杆菌肽抗性基因为主的多种抗生素抗性基因，且在两种生态系统中存在显著的差异。森林土壤中总 ARGs 拷贝数显著高于农田土壤，但丰富度却显著低于农田土壤。农田土壤的抗生素抗性基因与重金属抗性基因及病原微生物的共现性均显著高于森林土壤。因此，农田土壤的重金属污染更有可能导致抗生素抗性基因富集，且农田土壤的抗生素抗性基因更容易导致耐药病原菌的出现。此外，本研究还发现森林生态系统的抗生素抗性基因与可移动遗传元件的相关性更强，这表明森林土壤抗生素抗性基因的横向转移能力更强。以上研究结果表明，农田和森林土壤的抗生素抗性组差异显著，研究结果为“退耕还林”等生态工程的环境效应评估提供了重要科学依据。

关键词：农田；森林；抗生素抗性组；宏基因组；土壤微生物

有机肥通过提升微生物群落复杂性和稳健性促进了粮食产量增加

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摘要

长期施用有机肥有利于改善土壤质量和提高粮食产量。土壤中微生物群落成员之间并不是孤立存在的，它们之间存在复杂的相互作用，在农田土壤中长期施用有机肥对微生物群落复杂性与粮食产量的影响还不明确，因此，采用中国科学院海伦农业生态实验站27年定位试验分析长期施用有机肥条件下土壤养分、细菌真菌群落组成、群落复杂性和稳健性与粮食产量的关系。与不施肥处理（F0）相比，化肥处理（F1）和化肥+有机肥处理（F2）玉米产量分别增加了89.2%和117.5%。土壤属性主成分分析表明，施肥显著改变了土壤环境，且土壤环境与粮食产量呈显著正相关（R2=0.558，P<0.0001）。不同施肥处理显著改变了土壤细菌和真菌群落组成（P = 0.001），形成了各自的指示性模块，而且各处理的敏感物种都集中在指示模块中。对每个施肥处理分别进行network分析，以节点数、边数量和关键物种数量衡量群落复杂程度。结果表明，F2处理细菌和真菌群落复杂程度最高，F0处理最低。对各个处理微生物群落稳健性和脆弱性进行检验，发现F2处理细菌和真菌稳健性最高，脆弱性最低，而F1处理增加了微生物群落不确定性。功能分析表明，F2处理中细菌群落包含更多种类的功能群，显著增加了真菌腐生类群，降低了致病类群相对丰度。最后通过随机森林回归模型检验各个属性对产量的影响，%lncMSE结果显示土壤环境、微生物群落组成和群落复杂性都对产量有显著的影响，但IncNodePurity结果中仅有微生物群落复杂性对产量有显著的影响。因此，有机肥通过提高微生物群落复杂性（相互作用）和稳健性（抗环境变化能力）来支撑更多的生态功能和更大程度的功能冗余，改善土壤生态系统的服务功能，同时也表明施用有机肥是生态友好的增加粮食产量的方式。

关键词：有机肥；微生物群落；复杂性；稳健性；产量

Organic fertilizers increase yield by improving microbial community complexity and robustness

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Abstract

Long-term application of organic fertilizers is beneficial for improving soil quality and crop yield. Microbial community members in soils do not exist in isolation and there are very complex interactions among them. However, the contribution of complexity of microbial community to crop yield under long-term fertilization is not clear. We evaluated changes in soil nutrients, microbial community properties, and the contribution of these changes to crop yield after 27 years of different fertilization treatments. Compared with no fertilizer (F0), the yield increased by 89.2% and 117.5% in mineral fertilizer treatment (F1) and mineral fertilizer + organic fertilizer treatment (F2), respectively. The PCA analysis of soil properties showed that fertilization significantly changed the soil environment, which was positively correlated with the yield (R^2=0.558， $P<0.0001$). The different fertilization treatments significantly changed soil bacterial and fungal community compositions and formed indicative modules, and the sensitive species of each treatment were concentrated in the indicator modules. The network analysis was performed for each treatment to measure the community complexity by the number of nodes, edges and keystone taxa. The results indicated that soil bacterial and fungal communities had the highest complexity in F2 and the lowest in F0. The examination of microbial community robustness and vulnerability across treatments showed that F2 had the highest robustness and the lowest vulnerability, while F1 treatment increased microbial community uncertainty. Functional analysis showed that the bacterial community in the F2 contained more kinds of functional groups, and organic fertilizer significantly increased the relative abundance of the saprophyte group and decreased pathogenic group. Finally, the Random Forest Regression Models examined the impacts of those properties on yield, %lncMSE results showed that soil environment, microbial community composition and community complexity all significantly affected the yield, but only microbial community complexity affected the yield in the IncNodePurity results. Our results provide evidence that organic fertilizer supports more ecological function groups and a greater degree of functional redundancy by increasing microbial community complexity (interactions) and robustness (resistance to environmental change), ultimately improving the soil ecosystem services, indicating that the application of organic fertilizer is a friendly way to increase yield.

Keywords: Organic fertilizer; Microbial community; Complexity; Robustness; Yield

三江平原不同植被类型湿地土壤微生物碳源代谢多样性、丰度和酶活性特征

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摘要

湿地土壤微生物可参与土壤有机碳分解和固定，在调控湿地生态系统碳循环和维持碳汇功能方面发挥重要作用。为明确三江平原不同湿地植被类型下土壤碳循环相关微生物和酶活性特征，选取三江平原甜茅、薹草、小叶章、水稻、芦苇 5 种不同植被类型湿地，分析土壤微生物碳源代谢多样性、丰度和酶活性差异特征。结果表明，不同湿地植被类型下土壤微生物代谢活性（AWCD）均随培养时间的延长逐渐增大，在 48 h 内微生物利用碳源的能力较弱，48-168 h 期间微生物代谢活性快速增加，168 h 后步入平稳期。甜茅湿地表层（0-15 cm）土壤微生物代谢活性最高，AWCD 值达到 0.82。土壤微生物 Shannon 丰富度指数、Shannon-evenness 均匀度指数、Simpson 优势度指数和 McIntosh 多样性指数均表现为甜茅湿地最高，芦苇湿地最低。不同湿地植被类型下土壤微生物对碳源利用能力不同，甜茅、薹草和水稻湿地对氨基酸类和多聚物类碳源具有更高的利用能力，小叶章湿地更倾向于利用氨基酸类和有机酸类碳源，芦苇湿地对氨基酸类和胺类碳源的利用能力更高。薹草湿地表层土壤细菌、真菌和固碳菌丰度均显著高于其它湿地；小叶章湿地亚表层（15-30 cm）土壤固碳菌、固氮菌和反硝化细菌丰度显著高于其它湿地。薹草和小叶章湿地土壤 RubisCO 酶活性高于其它湿地，薹草湿地表层土壤 β-葡萄糖苷酶和酸性磷酸酶活性最高。除小叶章湿地外，其它湿地土壤表层酶活性均高于亚表层。不同植被类型湿地土壤微生物代谢活性和 Shannon 指数、Shannon-evenness 指数和 McIntosh 指数均与土壤微生物量碳含量呈显著正相关关系，土壤微生物 Shannon 指数、Shannon-evenness 指数、Simpson 指数与土壤 pH 值呈显著正相关关系，说明湿地植被类型和土壤活性碳含量是影响土壤微生物活性和多样性的重要因子，而且土壤微生物多样性与土壤 pH 密切相关。土壤氨氮和溶解有机碳对土壤微生物丰度和酶活性的解释率分别为 73.1%和 85.4%。本研究明确了不同湿地植被类型下土壤碳循

环相关微生物和酶活性差异及其影响因子，为探明湿地生态系统植被-土壤-微生物关联机制及“双碳”背景下湿地生态系统固碳减排提供重要的理论依据。

关键词：土壤微生物；湿地；植被类型；土壤酶；Biolog-ECO

微生物氮循环新过程——产氧反硝化及其潜在生态效应

朱宝利 [1]

摘要

氮素循环和相关微生物的研究已有一个多世纪的历史，但是我们对微生物氮循环的了解还不够全面，新的微生物氮转化过程被不断发现，其中就包括产氧反硝化。产氧反硝化最初在厌氧甲烷氧化细菌 Ca. Methylomirabilis oxyfera 中提出。和传统的反硝化过程不同，产氧反硝化过程中，一氧化氮（NO）在 NO 歧化酶（Nod, NO dismutase）催化下直接生成 N_2 和 O_2，而不经过 N_2O，因此被认为是“环境友好”型氮转化过程。蛋白序列分析发现，Nod 与 NO 还原酶（qNor）同源，但是在关键功能位点发生了标志性突变，与其催化 NO 歧化功能相吻合。大家最初认为，产氧反硝化过程仅存在于 M. oxyfera 类等特殊微生物中；然而，利用 nod 基因作为分子标志，我们发现环境中 nod 基因多样性很高并且分布广泛，在污水处理系统、受污染的地下水、湖泊和农田等环境中均有高丰度分布。系统发育分析表明，环境 nod 基因序列形成多个跨门类群，说明产氧反硝化微生物系统发育具有多源性，其代谢潜能也将非常多样。目前，除了知道产氧反硝化微生物参与甲烷代谢之外，在稳定同位素（^{13}C）标记的甲苯降解微宇宙培养中，我们发现 nod 基因也得到了标记，暗示产氧反硝化微生物可能也参与到芳香烃的降解。值得注意的是，我们研究还发现，水稻田中分布着多种产氧反硝化微生物，其丰度和土壤中传统反硝化细菌相当。但是，作为一个新的氮转化功能类群，产氧反硝化微生物在环境氮循环和氧化亚氮排放中的作用和贡献需要进一步的研究。

Understanding the heterogeneity of host-associated microbial communities

Lei Dai[1]

Abstract

The realization that microbial communities, associated with virtually all multicellular organisms, have tremendous impact on their hosts' health and development is considered one of the most important scientific discoveries in the last decade. In this seminar, I will introduce our recent efforts to characterize the heterogeneity of host-associated microbiome in three different aspects: 1) Dynamics. There is growing evidence that baseline composition may be an important contributor to the personalized response of gut microbiome. We developed computational approaches to study key factors underlying the heterogeneity in microbiome dynamics. 2) Space. The spatial heterogeneity of microbial communities has been observed across different habitats, ranging from human gastrointestinal tract to plant rhizosphere. We developed in situ spatial analysis of microbiome at single cell resolution, which is crucial for elucidating the principles governing the assembly of microbiome. 3) Strain. The within-species functional heterogeneity has been increasingly recognized as an important factor in shaping the ecology and evolution of microbiome. We developed bioinformatics tools to infer strain-level composition and functional profiles from metagenomics data. In summary, we have developed novel methods to study the dynamical response, spatial structure and strain-level diversity of microbial communities. These methods will open up new dimensions to understand the complexity of microbiome and facilitate the precise engineering of microbiome.

稻田土壤中的塑料际是微生物汞甲基化的热区

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摘要

微塑料(MPs)作为一种新兴污染物在农业生态系统中广泛积累，并对生物地球化学过程产生重要影响。然而，水稻土中 MPs 如何影响汞(Hg)向神经毒性甲基汞(MeHg)的转化仍然知之甚少。本研究以中国两种典型水稻土(即黄壤和红壤)为研究对象，研究了 MPs 对汞甲基化的影响及相关微生物群落。结果表明，在两种水稻土中，MPs 的添加均显著提高了 MeHg 的生成，这可能由于塑料际比周围大块土存在更高的汞甲基化潜能。汞甲基化微生物组成在塑料际和大块土中存在显著差异，黄壤中的 *Geobacterales* 和红壤中的 *Methanomicrobia* 在塑性际中占比高于大块土。此外，还发现非汞甲基化微生物和汞甲基化微生物在塑料际中的联系相比于大块土壤更为紧密。塑料际和大块土中截然不同的汞甲基化潜能可能归因于这些微生物的差异。这些结果表明塑料际是 MeHg 产生的独特生境，并为农业土壤中 MPs 积累的环境风险提供了新的认识。

关键词：微塑料；塑料际；甲基汞；汞甲基化微生物

地理上孤立的河流剖面中抗生素抗性特征及影响因素

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摘要

河流生态系统是抗生素耐药基因(Antibiotic resistance genes, ARGs)最重要的储存库之一，但 ARGs 在河流生态系统不同区域的发生情况及其对生物和非生物因素的响应并不清楚。在这项研究中，我们采用了宏基因组的方法来解读中国中东部河流生态系统不同环境中 ARG 类型和数量。采样点位于中国中东部不同的河流剖面上，它们在地理上是自然隔离的，这些采样点的人类活动方式和强度、气候、环境因子等方面可能会存在差异，而 ARGs 的赋存可能会受到这些差异的影响。

我们选择了中国中东部河流生态系统的 30 个不同河流剖面进行了样品采集，每个河流剖面上收集四个复合样品（四种介质），包括根际土（0-20cm，R）、表层岸边土壤（0-20cm，FB）、亚表层岸边土壤（40-60cm，SB）和沉积物（0-20cm，S）（图 1）。本研究观察到归属于 24 种 ARG 类型的 469 个 ARG 亚型，且具有多变的多样性（丰富度，44 至 206）和丰度（6.85 ×/Gb 至 105.68 ×/Gb），而其中多重耐药基因占主导。我们根据差异分析的结果，将同一介质样品（R/FB/SB/S）分为南北两个部分(秦岭淮河线为界)(SR, NR/SFB, NFB/SSB, NSB/SS, NS)，并对不同生境中 ARGs 的赋存现状、宿主关系、影响因素进行了分析。结果显示，四种介质中 ARGs 的数量和丰度在南部区域各样点中间趋势较为平稳，而在北方波动幅度较大。而南北区域均是沉积物具有相对较多的特有 ARGs。在对南方、北方的同一介质样品进行差异 ARGs 分析时发现，多重耐药基因在差异 ARGs 中占主导地位。而南北差异是由 ARGs 的出现频率不同和生境选择差异共同导致的。而分别对南方和北方不同介质进行差异 ARGs 分析时发现，南部存在差异的基因主要为四环素类耐药基因和 beta-内酰胺类耐药基因，北部的差异基因主要为多重耐药基因。而在南方和北方中不同介质差异均由差异 ARGs 的出现频率不同导致。我们从群体（整体相关性）、个体（contig 上的共现）水平分别对 ARGs 宿主进行了分析，结果发现多重耐药基因的宿主关系最为复杂。分析表明，用相关性识别 ARGs 宿主时会导致结果失真，而不能准确的反应样品本身 ARGs 的宿主关系。同时，使用相同的

方法对 ARGs、MGEs 和 VFs 的共现进行了分析，在个体水平上，三者之间没有出现共现关系，而对三者相关性进行分析时发现，在 SR、NR、NSB、NS 均存在有显著相关性存在。在研究非生物因素（海拔、经纬度、年均温、年降水量、人口密度、土地利用类型、土壤类型、理化指标等）对 ARGs 的影响时发现，除亚表层岸边土壤样品外，建筑用地的面积百分比与 ARGs 均呈显著正相关关系。

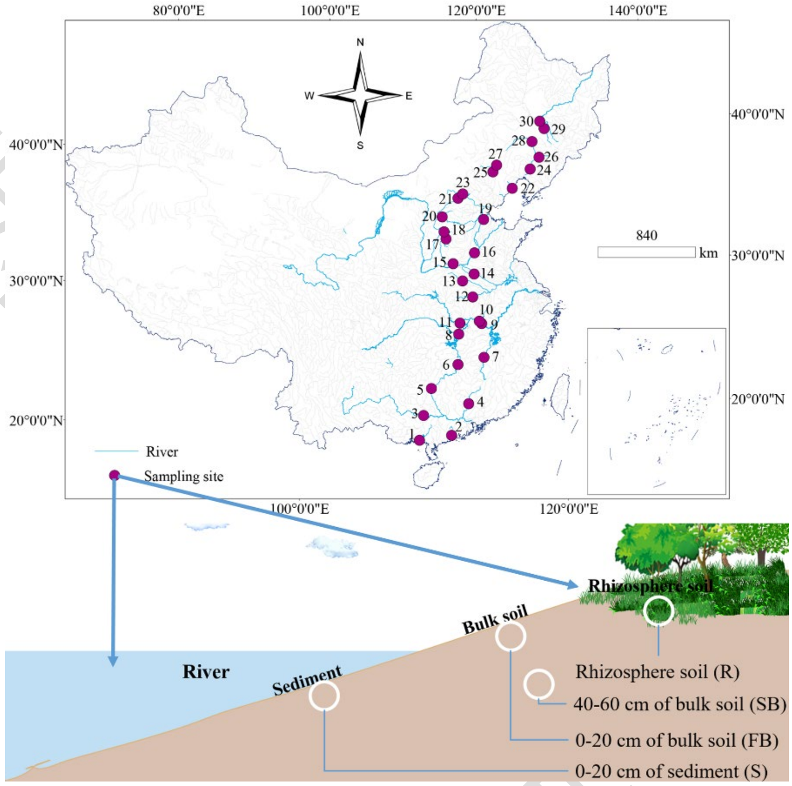

图 1 采样点分布和河流生态系统中的四种介质

关键词：抗生素耐药基因；河流；宏基因组；人类活动；生物因素

两种典型农田土壤中反硝化细菌菌群对土壤 N_2O 排放影响的微生物机制

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摘要

农田过量施氮引起的氧化亚氮排放引起了人们的广泛关注。微生物组如何调节土壤中 N_2O 的机制尚不清楚。本研究通过对中国广泛分布的两种农田土壤——黑土和潮土进行不同碳氮条件下的微宇宙培养试验，比较其 N_2O 排放及相关反硝化细菌和基因。结果表明，在所研究的三种不同施肥条件下，黑土中 N_2O 的动态积累量均显著高于潮土。尽管潮土中反硝化基因数量显著增加，但 N_2O 产生基因(*narG*、*nirS*、*nirK*)与 N_2O 还原基因(*nosZ*)的比例在黑土和潮土中无显著差异。但两种土壤的反硝化细菌群落存在明显差异。特别是通过对黑土优势反硝化菌 *Rhodanobacter* 的分离菌株的检测，发现其反硝化基因的缺失和无 N_2O 还原能力，是黑土中 N_2O 积累量较高的主要原因。而潮土中富集的 *Castellaniella* 属细菌的分离菌株是具有较高反硝化效率的完全反硝化菌，这种反硝化菌可能是潮土中形成的 N_2O 能够快速被还原为氮气的主要原因。两种土壤中反硝化菌种类和表型的差异导致了 N_2O 的产生和还原效率的差异，进而造成两种土壤 N_2O 排放量的差异。通过将 *Castellaniella* 属细菌接种到黑土中，减少了 92%以上的 N_2O 排放。本研究揭示了土壤环境塑造的微生物菌群对两种重要农业土壤 N_2O 排放模式的影响，并证明了利用微生物菌剂减少农田土壤 N_2O 排放量的策略可行性。

关键词：农田土壤；反硝化；反硝化基因；细菌群落；N_2O

新型微生物电化学短程反硝化耦合厌氧氨氧化工艺自养脱氮

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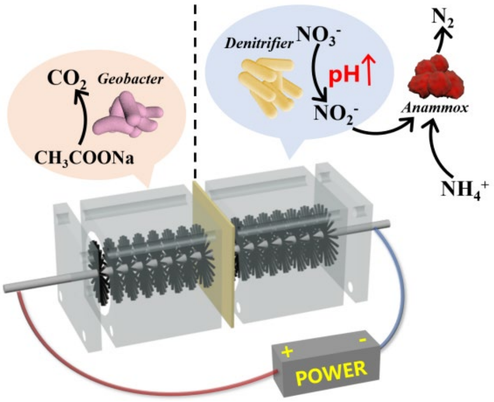
摘要

本研究提出了一种高效节能的废水处理新方法，该方法将生物电化学短程反硝化与厌氧氨氧化工艺相结合，可以同时去除废水中的硝酸盐和铵根。含硝酸盐废水直接进入生物电化学系统的阴极，不添加外部碳源。阴极发生短程反硝化，产生的亚硝酸盐与含 NH_4^+废水一起进入厌氧氨氧化反应器共同去除。微生物电化学系统以厌氧池污泥为阴极接种源，经过 48 天的驯化，反应器性能稳定，阴极的亚硝酸根转化率可稳定在 60 ± 9%。实验结果表明，阴极液 pH 和阴极电势对硝酸盐还原的最终产物有重要影响。阴极反硝化过程产生的自碱度（pH>8）会抑制亚硝酸根还原酶的活性，有利于亚硝酸根积累。此外，给电化学系统施加不同的外电压改变其阴极电势也会影响最终产物，结果表明阴极电势低于–0.542 ± 0.121 V vs Ag/AgCl 时，硝酸根还原以产生气态氮为主；当阴极电势高于–0.404 ± 0.095 V vs Ag/AgCl 时，阴极电势越低亚硝酸根积累越多。耦合厌氧氨氧化工艺后，总氮去除效率保持在 85%-89%，其中厌氧氨氧化对脱氮的贡献占 78%-81%。微生物群落分析表明，自养反硝化微生物 *Thiobacillus* 在阴极生物膜中占优，可能在阴极短程反硝化过程中发挥关键作用。qPCR 的结果表明周质的硝酸还原酶（napA）的表达远高于亚硝酸还原酶（nirK 和 nirS），导致了亚硝酸根的积累。该研究提出了一种新的自养脱氮技术，在低碳氮比脱氮方面有很高的应用前景。

关键词：自养脱氮；厌氧氨氧化；生物阴极；短程反硝化



Ammonia-oxidizing archaea overweight bacteria contributing to nitrification and plant productivity with straw returning

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Abstract

Straw returning has been proposed as an effective strategy for not only profoundly enhancing soil fertility, but also improving soil nitrogen (N) cycling and N utilization efficiency (NUE). Yet, how and to what extent the ammonia-oxidizing archaea (AOA) and bacteria (AOB) communities in response to the straw returning treatments in a red soil remains poorly understood. We conducted a 9-year field experiment to investigate the impacts of straw returning on the AOA and AOB communities, potential nitrification activity (PNA), plant productivity, and NUE in the plant rhizosphere soil. The field experiment included the five treatments: No fertilizer, CK; NPK fertilizer, N; NPK fertilizer with straw, NS; NPK fertilizer with straw and pig manure, NSM; NPK fertilizer with straw biochar, NB. Here, we observed that the straw returning treatments significantly enhanced the abundance and diversity (Shannon index and Chao1 richness) of AOA and AOB communities, and significantly modified the composition and co-occurrence network compared with the non-amended treatments (CK and N). Importantly, network analysis revealed that straw returning treatments triggered more competitive associations with potential keystone taxa in the AOA-AOB network. The AOA community was dominant in the acid soil, which contributed more pronouncedly to PNA than the AOB community. Structural equation modelling suggested that the competitive interaction with keystone taxa promoted the AOA and AOB diversity, and consequently accelerated PNA, plant productivity, and NUE under straw returning treatments. Overall, our findings provide insights into the functional roles of ammonia-oxidizer community in the straw-induced positive effect on nitrogen cycling dynamics.

Keywords: Ammonia-oxidizing archaea and bacteria; Keystone taxa; Plant productivity; Potential nitrification activity; N use efficiency, Straw returning

酵母菌处理废水中群体感应信号分子筛查及其对细胞形态的调控

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摘要

废水处理中酵母细胞在某情况下会转化为菌丝形态而导致沉降性降低，严重时影响系统运行的稳定性。本研究发现在丝化诱导培养基（YCBP）中添加培养热带假丝酵母（*Candida tropicalis*）后的 YPD 上清液或 YCBP 上清液，均可抑制菌丝形成，证明该菌株存在群体感应现象（QS）。通过顶空固相微萃取-气相色谱质谱联用在 YPD 上清液和小型 SBR 装置中检测出群体感应信号分子（QSMs）-反式-法尼醇和 2-苯乙醇；而在 YCBP 上清液中检测出 2-苯乙醇；同时均检测到了一种细胞丝化抑制物-2,4-二叔丁基苯酚。随后将检测出的化合物添加到 YCBP 中，查明了投加 QSMs 和丝化抑制物恢复细胞形态的最佳作用时间点。结果表明：丝化诱导条件下 0-3 h 内，添加反式-法尼醇、2-苯乙醇和 2,4-二叔丁基苯酚在一定程度上抑制了从酵母到菌丝的形态转变，其中 300 μM 反式-法尼醇对菌丝数和菌丝长度最大抑制率分别为 78.1±3.5%和 59.4±12.7%；100 μM 2,4-二叔丁基苯酚的抑制率分别达到了 98.5±2.3%和 86.8±5%。系统运行中添加 QSMs 或者菌丝抑制物有望抑制酵母细胞丝化从而建立高效稳定的酵母菌废水处理系统。

关键词：酵母菌；群体感应物质（QSMs）；丝化抑制物；细胞形态；调控

Quorum sensing molecules in yeast wastewater treatment and its regulation on yeast cell morphology

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Abstract

Yeast cells can transform from yeast form into mycelium form under some circumstances, resulting in a poor cell settleability, and seriously deteriorate the stability of system operation. In this study, it was found that the supernatant of yeast extract peptone dextrose medium (YPD) or yeast filamentation-inducted medium(YCBP) after cultivating *Candida tropicalis* could inhibit mycelial transformation in the YCBP, which proved that this strain can secret Quorum sensing molecules (QSMs). QSMs–(E,E)-Farnesol and 2-Phenylethanol were detected in YPD supernatant and lab-scale SBR reactor by Solid phase micro-extraction-gas chromatography mass spectrometry(SPME-GC-MS). 2-phenylethanol and 2,4-Di-tert-butylphenol, an inhibitor of cell filamentation was detected in the supernatant of YCBP. Finally, the detected compounds were added to YCBP, and the optimal supplement time of QSMs and filamentation inhibitor to restore cell morphology was investigated. The results showed that the addition of (E,E)-Farnesol,2-phenylethanol, and 2,4-Di-tert-butylphenol can inhibit the transformation from yeast form into mycelium form at 0-3 h, with the maximum inhibition rates of mycelium number and length of 78.1±3.5% and 59.4±12.7% for 300 μM (E,E)-Farnesol, respectively. For 100 μM 2,4-Di-tert-butylphenol, the highest inhibition rates of mycelium number and length were 98.5±2.3% and 86.8±5%. Supplements of QSMs or filamentation inhibitors to the system is expected to inhibit yeast filamentation and establish an efficient and stable yeast wastewater treatment system.

Keywords: Yeast; Quorum sensing molecules (QSMs); Filamentation inhibitor; Cell morphology; Regulate

荟萃分析揭示了用于诊断虾病发病率的通用肠道细菌特征

沙浩男

Abstract

Increasing evidence has emerged supporting a tight link between gut bacterial community and shrimp health. However, whether certain taxa are universally indicative of diverse shrimp diseases is unclear thus far. The emergence of high-throughput DNA sequencing technology has provided unprecedented insight into the microbial composition of diseased versus healthy shrimps. However, a single independent case study rarely yields a general conclusion predictive of the disease in shrimp. Here, we attempt to account for the divergences in gut microbiota between healthy and diseased shrimp using a meta-analysis. We found that the gut bacterial community of diseased shrimp was distinct from the healthy one, alpha diversity was consistently greater in the gut bacterial community of healthy shrimps. After ruling out the age-discriminatory and disease-specific orders, a random forest method identified 18 bacterial OTUs that categorized the health status of the shrimp with an accuracy > 95%.The bacterial network analyses that the microbiota of healthy shrimp gut harbored more diverse bacterial taxa with more competitive interactions, while the diseased microbiota showed opposite pattern. Microbial-mediated functions predicted by PICRUSt showed that the functional pathways involved in genetic information processing, energy metabolism, environmental information processing significantly decreased in diseased shrimp compared with those in healthy cohorts. These findings indicate that shrimp disease initiation can be accurately diagnosed using gut bacterial indicators.

Keywords: Meta-analysis; Gut microbiota community; Random forest; Shrimp disease

近海沉积物中微生物群落与微塑料

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摘要

新污染物的生态效应和环境影响是环境领域研究热点之一。微塑料被定义为直径小于 5 mm 的塑料微粒微，是目前广受关注的新污染物。自 2004 年 Thompson 首次提出微塑料的概念后，研究人员已在各种环境中检测到了微塑料的存在。近海地区位于陆海交界处，连接了人类陆地活动与海洋环境。近海沉积物既会作为汇，接受陆源排放的微塑料，同时又会作为源，将微塑料输送到远洋，在其中生存的各种生物也可能受到微塑料影响。但是微塑料是否对生态系统造成影响仍未知晓。微生物在全球分布极广，作为环境中主要的分解者，同时是生态系统生物量最大、多样性最高的生命形式，可以视为生态系统中的传感器。因此研究近海生态系统中微生物对微塑料的响应十分重要。

杭州湾地区历史悠久，受人类生活生产影响较大，选取杭州湾为研究对象。于 2018 年 4 月采集 10 个站点的上覆水和沉积物，标记为 HB1~HB10。对样品进行理化因子、微塑料和宏基因组数据分析。从水质指标来看，海湾整体呈现出富营养化趋势。主要污染因子为氮、磷、及有机污染；从河口到海湾，随着人类影响的减弱，水质条件逐渐变好。对沉积物中微塑料分析发现，样本微塑料含量平均值达到 101±64 个/g，主要集中在<10 μm 粒径大小。

通过对微生物群落宏基因组数据的质量控制和评估，拼接基因注释，构建非冗余基因集，比对数据库后获得群落物种和功能组成。共检出 45 个门，368 个属，其中细菌群落在整体群落中占据主导地位，在门水平上，以 Proteobacteria 为主，其次为 Actinobacteria 和 Firmicutes。其中 HB5 相较其他站点微生物组成差异较大，主要体现在 Firmicutes 占比高。在属水平上，除 HB5 外，各采样点间群落组成差异不大，HB5 主要在 Staphylococcus 差异与其他站点差距较大。整体来看，群落多样性与丰富度均较高。通过对微生物群落动力学分析，发现所有群落均共享相似动力学参数，为群落构建机制提供了非中性的解释。使用 R 语言、Past 4.0 等软件进行多元统计分析。发现杭州湾微生物群落受环境因素显著影响，其中水中的有机污染物石油类和多氯联苯显著影响了微

生物物种组成，水温显著影响了微生物功能组成，微塑料作为一种特殊的环境因子，对群落物种组成及功能结构未构成显著影响。

关键词：宏基因组；微塑料；杭州湾；沉积物

电控厌氧膜生物反应器设计与膜污染控制机制研究

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摘要

厌氧膜生物反应器（AnMBR）具有能耗低、应用范围广、可资源回收等优点，得到了国内外环境工程学者和工程师们的广泛关注和研究，但严重的膜污染限制了AnMBR 的推广和应用。本研究采用不锈钢导电微滤膜做阴极，用铁板/石墨做阳极，将电场、电絮凝与厌氧膜生物反应器（AnMBR）耦合，利用电场和电絮凝协同缓解膜污染、提升出水水质和产气效率。探究了电场（EF）联合电絮凝（EC）对微生物群落多样性以及甲烷代谢途径的影响，分析了电化学减缓 AnMBR 膜污染的作用机制，为电化学-厌氧膜生物反应器（eAnMBR）技术的工程应用提供科学基础。

研究发现在电絮凝厌氧膜生物反应器（阳极为铁电极，EC-AnMBR）中，电场联合絮凝不仅可以强化总磷的去除，还能够显著减缓膜污染、延长膜组件使用寿命。综合污染物去除效果和膜污染控制情况，确定 0.6 V 为最佳工作电压；相比常规 AnMBR，EC-AnMBR 对总磷的去除率提升了 19.2%，膜组件连续使用时间延长 85%。在 EC-AnMBR 中，在电极反应和电场联合作用下，微生物群落丰度和均匀度升高，有利于形成较稳定的微生物生态系统。电场刺激和铁离子的存在可加速沼气的生成，有利于以甲基营养途径为主的产甲烷菌的生长，丰富了产甲烷菌的丰度和代谢途径，为甲烷生产提供了相对稳定、完整的代谢系统。

eAnMBR 中采用导电不锈超滤膜可增大对污染物的静电排斥作用，同时作为阴极产生气体冲刷作用可限制污染物在膜表面的附着。电场联合絮凝缓解 EC-AnMBR 膜污染的主要机制是：铁离子絮凝和电场刺激降低了 EC-AnMBR 中 EPS 的含量，有效缓解了膜有机污染。EC-AnMBR、外加电场厌氧膜生物反应器（阳极为石墨电极，EF-AnMBR）和 AnMBR 中 EPS 浓度大小与跨膜压差衰减的结果相吻合，EPS 的浓度与 AnMBR 的膜污染情况呈正相关关系。电场的存在，加强了污染物间的静电排斥作用，从而降低粘度。电絮凝作用可增大污泥絮体粒径，迅速增长大于膜孔径而有效避免膜孔堵塞，缓解膜污染；外加电场增强了阴极膜组件与污染物间的静电排斥作用，同时可以引发有机物

分子极化，进而促进其沿电场方向发生同向凝聚也对污泥粒径增大有一定贡献，电场和絮凝协同作用下形成疏松多孔的滤饼层，显著减少 EC-AnMBR 不可逆膜污染。

关键词：导电膜；电絮凝；膜污染；厌氧微生物；甲烷代谢

石油扰动对土壤中微生物组成及其功能影响效应研究

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摘要

石油在生产、加工、储存和运输造成的土壤污染问题，对土壤生态功能造成严重危害。原位微生物经长期驯化，能够形成以石油为碳源的生理代谢功能，促进石油污染修复。然而受石油扰动后，原位微生物组成及其代谢功能相关问题的研究仍然较少。本研究收集了中国油库土壤样品，通过宏基因对原位微生物组成及其功能进行研究。研究结果表明，在种水平上，优势细菌为 *Pseudomonase_sp._LAM-KW06, Actinobactreia_bacterium, Acidobacteria_bacterium*，优势古菌为 *Candidatus_Bathyarchaeaeota, Thaumarchaeota, Euryachaeota*，优势真菌为 *Trichonephila_clavipes, Capra_hircus, Lupinus_albus*。通过共线网络分析表明，核心物种为 *Acidobacteria_bacterium, Actinobacteria_johnsonni, Actinobacteria_bacterium*。将收集的样品以南北纬度差异为分组，对物种生态位宽度进行计算，结果表明南方油库中物种的平均生态位宽度比北方物种高，说明南方油库土壤中生态位宽，物种的特化程度小，更倾向于泛化种，具有较强的竞争能力；而北方油库土壤中生态位相对较窄，在资源竞争中处于劣势。零模型和中性群落模型对微生物种水平进行拟合，结果表明物种组装模式以确定性过程为主导，说明环境中存在较强的生态过滤器，原位微生物受石油扰动产生适应能力。在物种代谢水平上，根据 KEGG 数据库对基因序列进行比对，碳循环的基因主要为多环芳烃降解基因，并与 *Proteobacteria, Dormibacteraeota, Candidatus_Bathyarchaeaeota* 显著相关；此外，大量的产甲烷基因有所表达，进一步证明油库土壤中原位微生物对石油降解具有丰富的代谢潜力。该研究揭示了受石油扰动土壤中微生物物种组成及其发挥的生态功能，为中国油库管理和石油污染修复提供参考依据和科学指导。

关键词：石油污染；微生物；生态模型；功能基因

合成反硝化微生物群落多样性和稳定性对热干扰的响应

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摘要

稳定的生态系统是维持可持续性发展的保障。而在当今全球气候变暖的趋势下，生物多样性不断丧失，影响生态系统的稳定性及生态功能。因此，研究微生物群落多样性与生态系统稳定性对全球变暖的响应对于维持生态系统服务功能具有重要意义。本研究通过合成微生物生态学理论和方法，利用反硝化菌 *Shewanella* 构建了具有多样性梯度为 1、2、4、8、12 的合成反硝化群落（SDMCs），并分析了热干扰对 SDMCs 功能（包括生物量、反硝化功能和群落组成）的影响、生物多样性和稳定性（抵抗力和恢复力）的关系，探究了生物多样性与稳定性的关系及其机制。研究结果表明，高物种丰富度群落的生物量比低物种丰富度群落更能抵抗热干扰并具有更强的恢复力，而合成反硝化群落的反硝化功能及群落组成的抵抗力和恢复力随多样性增加无显著变化（$p > 0.05$），这可能是物种丰富度高的合成群落具有高度功能冗余。本研究使用合成微生物群落的方法，揭示了微生物群落的多样性和稳定性的相关性，对生物多样性保护和生态系统可持续性发展具有重要意义。

关键词：生物多样性；稳定性；群落功能；反硝化；希瓦氏菌

益生菌对中华绒螯蟹(*Eriocheir sinensis*)肠道微生物群落的影响

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摘要

益生菌已经成为实施中华绒螯蟹(*Eriocheir sinensis*，CMCs）健康养殖的重要技术手段之一。然而，益生菌在中华绒螯蟹养殖生态系统中的应用效果仍不确定。肠道微生物群通常是水生动物健康的综合评价指标，但目前益生菌如何影响中华绒螯蟹肠道微生物群却鲜有报道。在我们的研究中，我们使用 16S rRNA 扩增子技术研究了在养殖过程中 CMC 肠道微生物群落响应益生菌的机制。出乎意料，我们研究显示益生菌在 CMC 的肠道中的定植效果较差。我们还发现，短期益生菌的应用对 CMC 的生长性能和肠道微生物群落的 α-多样性没有明显的影响，但它明显改变了肠道微生物群落的 β-多样性。值得注意的是，益生菌提高了 CMC 肠道微生物群中丁酸盐等的代谢力。共现网络表明，CMC 肠道的微生物群落表现出对外源益生菌添加的响应性，同时正相关性的增高表明益生菌加强提高肠道微生物群落细菌之间的合作。综上所述，我们的结果为益生菌在 CMC 肠道微生物生态系统中的作用提供了重要的见解。

关键词：中华绒螯蟹；益生菌；肠道微生物群落；代谢预测；共现网络

Response of Chinese mitten crab (*Eriocheir sinensis*) intestinal microbiota to commercial probiotic application

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Abstract

Probiotics have emerged as promising alternatives of antibiotics for maintaining the health of the Chinese mitten crab (CMC) *Eriocheir sinensis*. However, the efficacy of probiotic application in CMC culture ecosystems remains uncertain. Intestinal microbiota is often comprehensive indicators of aquatic animal health, but the effects of probiotics on CMC intestinal microbiota remain poorly understood. In this study, we used 16S rRNA gene amplicon sequencing to investigate the mechanisms underlying changes to the intestinal microbial community following probiotic application in CMC culture. Disappointingly, our data showed there was poor probiotic colonization in the intestines of pond-reared CMCs. We also found that the short-term application of probiotics had no significant impact on CMC growth performance or the alpha diversity of the microbial community, although it significantly changed the beta diversity. Remarkably, the probiotics promoted butanoate metabolism in the CMC intestinal microbiota. According to a co-occurrence network, the microbiome of the CMC intestine manifested rapid responses to probiotic application, and cooperation between intestinal microbial communities may have been enhanced. Taken together, our results provide important insights into the roles of probiotics in the CMC intestinal microbial ecosystem.

Keywords: Chinese mitten crab (*Eriocheir sinensis*); Probiotics; Metagenomic prediction; Intestinal microbiota; Microbial network

不同工业污水处理系统活性污泥微生物群落多样性及构建机制

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摘要

污水处理系统（WWTPs）中的微生物对水净化至关重要，具有保护公众和环境健康的作用。污水处理系统中细菌群落的多样性和构建过程被认为对水处理性能有直接影响。然而，在工业废水处理系统（IWWTP）中，缺乏对活性污泥细菌群落构建的科学理解。基于 16S rRNA 基因序列，我们分析了位于中国东南部典型工业园区的两个工业污水厂（制药工业和染料工业）细菌群落多样性和构建机制。结果表明，制药和染料污水厂的细菌群落组成存在现在差异，这可能是由于受不同环境因素、操作条件和进水水质的影响。中性模型和零模型分析表明，两个工业污水厂活性污泥中的细菌群落受到随机过程（即扩散和漂移）的强烈驱动，细菌群落由随机过程塑造。同时，分子生态网络分析发现，细菌群落间相互作用以正相关为主，倾向于促进彼此生长。两个工业污水厂中细菌群落的生态网络拓扑特征和复杂性没有显著差异，表明不同工业污水处理系统中的细菌群落具有相似的物种相互作用。在共生网络中，变形菌和拟杆菌是潜在的关键类群，显示出它们作为“生态系统引擎”在群落中的巨大影响力。本研究增强了我们对工业废水处理系统活性污泥细菌群落构建的理论理解，并为从理论角度指导污水处理提供了重要的启示。

关键词：工业污水处理系统；活性污泥；细菌群落构建；生态网络

Microbial community diversity and assembly mechanism in activated sludge from two different industrial wastewater treatment plants system

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Abstract

Microorganisms in wastewater treatment plants (WWTPs) are essential for water purification to protect public and environmental health. The diversity and assembly of bacterial communities in wastewater treatment plants is thought to have a direct influence on system performance. However, scientific understanding of activated sludge bacterial community assembly is lacking in industrial wastewater treatment plants systems (IWWTPs). Here, we analysed the 16S rRNA gene sequences from two IWWTPs (Pharmaceutical and Dyestuff IWWTPs) located in a typical industrial park, southeastern China. The results showed that bacteria from pharmaceutical and dyestuff IWWTPs exhibited contrasting community compositions, which might be owing to influenced by different environmental factors and influent water quality. Neutral model and null model bacterial communities in activated sludge in the two IWWTPs were strongly driven by stochastic processes (i.e. dispersal and drift). Molecular ecological network analysis showed that bacteria tended to co-occur rather than co-exclude. The network topological characteristics and complexity didn’t show significant difference between bacterial communities in two IWWTPs, indicating that the bacterial communities in two IWWTPs have similar species interaction. In the co-occurrence networks, proteobacteria and bacteroidetes were the potential keystone taxa, showing their large influence in the community as “ecosystem engineers”. This study enhances our mechanistic understanding of the IWWTPs activated sludge bacterial communities and provide important implications for wastewater treatment processes.

Keywords: IWWTPs; Activated sludge; Bacterial community assembly; Ecological network

热带雨林刀耕火种弃耕地恢复过程中的土壤微生物群落结构和功能变化

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摘要

土壤微生物在生物地球化学循环中发挥着重要作用，研究地上植物的变化如何影响土壤微生物群落、多样性和功能及其响应机制，对指导森林生态系统管理和功能调控，以及应对全球变暖等重大全球性环境问题具有重要意义。利用高通量测序技术，研究了海南岛霸王岭热带低地雨林刀耕火种弃耕后形成的不同自然恢复阶段（15 年、30 年和 60 年）森林类型和老龄林的土壤微生物群落结构，并利用 FAPROTAX 和 FUNGuild 功能注释进行了功能变化特征分析。与老龄林相比，刀耕火种后弃耕地恢复初期土壤有机质等显著增加（$P<0.05$），并在 60 年恢复阶段逐渐接近老龄林。刀耕火种对土壤微生物多样性产生了不同程度的影响，土壤细菌多样性指数（香农指数和丰富度指数）和真菌丰富度指数显著降低（$P<0.05$），经过 60 年自然恢复的森林土壤细菌和真菌仍然没有完全达到老龄林水平。不同恢复阶段土壤微生物群落结构与老龄林存在显著差异（$P<0.01$）。Mantel 分析表明，土壤硝态氮、有效磷和全磷是影响土壤微生物群落的主要环境因子。功能分析表明，15 年恢复后次生林的大多数土壤细菌功能群的相对丰度低于老龄林，但在参与碳、氮循环的功能群中，次生林中的化能异养和固氮作用功能群的相对丰度高于老龄林；土壤真菌外生菌根相对丰度随着恢复时间增加逐渐降低，丛枝菌根的相对丰度随着恢复时间增加逐渐增高。土壤 pH、全氮、全钾、水解性氮、硝态氮与大多数土壤细菌功能群有显著相关性（$P<0.01$）；而大多数环境因子与外生菌根有显著正相关关系（$P<0.05$），与丛枝菌根和植物病原菌有显著负相关关系（$P<0.05$）。研究结果表明，刀耕火种对土壤微生物群落结构和多样性产生显著影响；经过 60 年的自然恢复过程，仍没有恢复到老龄林水平。

关键词：刀耕火种；群落演替；微生物多样性；环境因子；功能预测

Changes of Soil Microbial Community Structure and Function during Slash and Burn Abandoned Tillage Natural Restoration in Tropical Rainforest

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Abstract

Soil microorganisms play important roles in biogeochemical cycles. Studying how the change of aboveground plants affect soil microbial communities, diversity and functions and its response mechanisms, will be of great significance for guiding the management and functional regulation ecosystems and addressing major global environmental issues such as global warming. Using high-throughput sequencing technology, we studied the soil microbial community structure of forest types in different natural restoration stages (15-, 30-, 60-year-old) and old forests after slash and burn abandoned cultivation, and functional changes were analyzed by using FAPROTAX and FUNGuild functional annotation. Most soil nutrients in slash and burn abandoned tillage increased significantly in the early stage of restoration compared with the old forest (P <0.05), and gradually approached the aged forest in the recovery stage of 60 years. The effects of slash and burn on soil microorganisms were different, soil bacterial diversity index (Shannon index and richness index) and fungal richness index were significantly affected (P <0.05), soil bacterial and fungal diversity has not reached the level of the old growth forest completely after 60 years natural restoration. There were significant differences among soil microbial communities between different restoration stages and old growth (P <0.01). Mantel analysis showed that soil $NO_3^-{-}N$、Available phosphorus and Total Phosphorus were the main environmental factors affecting the soil microbial community. The functional analysis showed that the relative of most soil bacterial functional groups in the secondary forest was lower than that in the old forest, and the relative abundance of chemoheterotrophy、aerobic chemoheterotrophy and nitrogen fixation functional groups involved in carbon and nitrogen cycle in the secondary forest was higher than that in the old forest; the relative abundance of soil fungi ectomycorrhizal decreased with the restoration, while arbuscular mycorrhizal increased. with the progress of nature restoration, the function of soil fungi gradually approached the level of the old forest. Spearman correlation analysis showed that soil pH、total nitrogen、total potassium、$NO_3^-{-}N$ was significantly correlated with most of the soil bacterial functional groups($P<0.01$), most of the environmental factors were positively correlated with ectomycorrhizal($P<0.01$), were significant negative correlation with arbuscular mycorrhizal and plant pathogens($P<0.05$). The results showed that soil microbial community was significantly affected by slash and burn, It has not recovered to the level of old growth after 60 years of natural restoration.

Keywords: Slash and burn; Community succession; Microbial diversity; Environmental factors; Function prediction

EGCG 抑制福氏志贺菌作用机制研究

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摘要

福氏志贺菌是常见致病菌，它除了能直接导致食品污染外，还能够在各类加工设备及其表面形成生物膜，一旦形成成熟的生物膜，即使是经常清洗，但随着生物膜内细菌抵抗力增强，机械地冲洗甚至擦洗仍然无法彻底将其清除，导致细菌在加工设备表面继续繁殖进而更大范围的形成生物膜，最终引发各大的污染。表没食子儿茶素没食子酸酯(EGCG)是茶叶中的主要儿茶素。其抑菌作用引起广泛关注，但抑菌机制仍然不十分明确。本论文以福氏志贺菌为对象，对 EGCG 的抑制福氏志贺菌的机制进行进一步研究。主要研究结果如下:

(1) EGCG 对福氏志贺菌的抑菌性研究

EGCG 对福氏志贺菌游离菌的 MIC 是 400μg/mL，说明 EGCG 对福氏志贺菌有良好的抑菌效果。EGCG 对福氏志贺菌生长曲线的影响表明，不添加 EGCG 的菌悬液的 OD 值不断增长且在 12h 时其 OD 值大于其它实验组，说明 EGCG 可有效抑制福氏志贺菌的生长。

(2) EGCG 对福氏志贺菌生物膜的影响

50 μg/mL EGCG 即可抑制福氏志贺菌形成生物膜，当 EGCG 浓度达到 100μg/mL 时，对生物膜有较强抑制。由此可知 EGCG 对福氏志贺菌生物膜具有良好且稳定的抑制作用。EGCG 可能是通过抑制细菌生物膜主要成分多糖的合成，来抑制福氏志贺菌形成生物膜，随着 EGCG 浓度增加，抑制作用增强。EGCG 对福氏志贺菌生物膜形成的抑制作用可能是通过抑制 mdoH 基因及其产物蛋白 OpgH 蛋白的表达，从而抑制福氏志贺菌胞外多糖的合成，生物膜形成被抑制。

(3) EGCG 对福氏志贺菌抑菌机制

EGCG 对福氏志贺菌的抑菌机制可能是氧化应激的影响。用 EGCG 处理福氏志贺菌后，测定细菌胞内活性氧 （ROS）、过氧化氢（H2O2）和超氧化物歧化酶（SOD）含量的发生变化，即 EGCG 可能激活福氏志贺菌氧化应激反应，从而抑制细菌生长。

关键词：EGCG；福氏志贺菌；生物膜；抑菌机制

不同种植年限的重楼根系微生物群落演替规律

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摘要

重楼是一种多年生草本药用植物，通常需生长 8-10 年才可采收，其主要入药部位的根茎在种植前期年生长量极小，如何有效提高重楼生长速率对重楼产业尤为重要。因此，本研究以生长了 2 年、3 年和 4 年的重楼为研究对象，通过细菌 16S rRNA 基因扩增测序研究了重楼块茎根围土、根际土及重楼块茎内生微生物群落随着生长年限的变化规律。结果表明：随着种植年限增加，根围土壤 pH、有效钾和总钾含量显著降低，根内主要存在的薯蓣苷元和重楼皂苷 VII 含量也呈下降趋势。微生物群落结果表明：根围土和根际土壤中细菌 α 多样性显著高于根内生微生物，而不同组分的微生物群落结构也存在显著差异。与根围土相比，重楼根际和根内具有更少的 OTUs，但富集了大量固氮和解磷微生物，且三个部分的固氮和解磷微生物的相对丰度都随着种植年限的增加而增加。PICRUSTs 结果表明，根际土和根内生微生物群落中固氮酶和磷酸酶基因丰度显著高于根围土。同时，根围土和根际土微生物群落中的固氮酶和磷酸酶基因丰度随着种植年限增加显著增长，而在根内生微生物群落中没有明显趋势。分子网络分析表明，重楼根际土和根内生微生物的分子网络结构随种植年限增加变得更加复杂，而根围土没有显著变化。随着种植年限的增加，根围土中的群落组装有随机性主导转向确定性主导，而根际土和根内生群落则相反。以上研究结果表明随着种植年限增长，重楼根系会富集特定的功能微生物菌群，如固氮和解磷微生物，这可能对重楼生长发挥着重要作用，这为后续开发促进重楼生长和提高重楼入药品质的微生物菌剂奠定了基础，也为其他药用植物的相关研究提供参考。

关键词：重楼；固氮解磷；促生长；根系微生物

秸秆堆肥还田和根际合成菌群对土壤及玉米生长的影响

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摘要

农作物秸秆含有丰富的氮、磷和钾等营养元素，是一种重要的生物质资源。每年约40.0%的秸秆被燃烧，造成严重的资源浪费和空气污染问题。秸秆还田作为一种生态友好型处理方法被广泛应用，但在实践中发现秸秆还田干扰作物种植，滋生病原体或虫害，并使土壤和肥料中的养分固定化。研究发现堆肥过程中的高温和各种微生物介导的生化过程可消灭病原体并回收养分，但是目前关于秸秆堆肥还田的研究报道较少。本研究采用 0、2.5、5 和 7.5 t/hm^2 秸秆堆肥覆盖还田和翻埋还田，研究其对土壤理化性质、微生物群落结构和玉米生理指标的影响，进而探明最佳的还田方式以及玉米产量提升的关键因子；从秸秆堆肥还田样地玉米根际土中，筛选根际促生菌 (PGPR)。通过菌株间相互作用，将玉米根系定殖的 PGPR 构建合成菌群同时阐明合成菌群促生机制。主要研究结果如下：

秸秆堆肥还田对土壤化学性质没有影响，但显著改善土壤团粒结构，尤其是 7.5 t/hm^2 秸秆堆肥覆盖还田减少玉米花粒期土壤中> 2 mm 机械稳定性团聚体含量。同时，细菌群落结构比真菌群落结构对秸秆堆肥还田响应更显著。在秸秆堆肥翻埋还田和覆盖还田过程中，秸秆堆肥覆盖还田提升玉米产量，同时 7.5 t/hm^2 秸秆堆肥覆盖还田对玉米产量提升效果最好。最终，确定最佳的还田方式为覆盖还田，还田量采用 7.5 t/hm^2。在科水平上，2 个真菌 (Trichocomaceae 和 Didymellaceae) 和 5 个细菌 (Xanthomonadaceae、Rhizobiaceae、Micrococcaceae、Micromonosporaceae 和 Microbacteriaceae) 以及 >2 mm 机械稳定性团聚体与玉米产量提升显著相关。所有环境因子的共同作用可以解释玉米产量提升的 81.36%。其中，Xanthomonadaceae 科、Rhizobiaceae 科和 >2 mm 机械稳定性团聚体的贡献率大于其他环境因子的贡献率。

细菌群落结构作为玉米产量提升的关键因子。因此，采用筛选培养基，在秸秆堆肥覆盖还田样地玉米根际土中共筛选到 20 株不同种属的 PGPR。其中，一株属于

Rhizobiaceae 科，其余 19 株 PGPR 属于 Bacillaceae 科、Sphingomonadaceae 科、Moraxellaceae 科、Pseudomonadaceae 科和 Enterobacteriaceae 科。20 株 PGPR 菌株均具有分泌 IAA、赤霉素、解磷、解钾和固氮能力，并能显著促进植株生长。但是，已有的 PGPR 菌株中只有 *Pseudomonas hunanensis* SM15、*Enterobacter huaxiensis* SM16、*Klebsiella pneumoniae* SM17 和 *Klebsiella granulomatis* SM18 能够在玉米根系定殖。

构建一个由 *Priestia aryabhattai* SM03、*Acinetobacter guerrae* SM12、*Klebsiella pneumoniae* SM17 和 *Klebsiella granulomatis* SM18 组成的合成菌群。合成菌群对玉米根部细菌群落的影响高于玉米根际土壤微生物群落，同时合成菌群成员中 *Klebsiella* 属作为优势菌属在玉米根系上定殖，其相对丰度达到 30%。接种合成菌群第 3 天，微生物功能与细胞增殖相关，而第 30 天与土壤微生物营养物质转换和抗菌物质生产有关。植物激素信号途径作为与植物生长发育相关的关键通路，在玉米根系中富集。参与该通路的关键基因（*AUX/IAA*、*SAUR*、*ARR-B*、*ABF*、*ERF1*、*TCH4*、*JAZ* 和 *PR-1*）均上调表达。

综上所述，秸秆堆肥覆盖还田通过优化土壤团粒结构，改善抗病微生物群落结构，进而提高玉米产量。该研究为解决秸秆焚烧造成的环境污染问题和保障人们粮食安全具有重要科学意义和实际应用价值。

关键词：秸秆堆肥还田；根际促生菌；合成菌群；微生物群落功能；植物激素信号转导

Links among bacterial dormancy potential, community assembly, and species turnover under short-term temperature response

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Abstract

Dormant microbiome is regarded as a crucial role during community assembly acting on species turnover, which could largely influence microbial biogeographic pattern. However, the evidential chain of dormancy potential regulates species turnover through altering community assembly remains incomplete due to the limited knowledge of the dormancy categorization and difficulty of experimental verification. Here, we designed a soil translocation experiment to reveal the temperature response of microorganisms, and used 16S rRNA gene amplicon sequences to generalized bacterial characteristic with respect to species turnover and community assembly, then combining PICRUSt-estimated metagenomes to predict different strategy of dormancy potential. Our study found that species turnover significantly decreased 15.62% after translocation cooling process, but insignificantly increased 3.26% after translocation warming process. Dormancy potential in our study increased after translocation except toxin–antitoxin (TA) systems revealing a decreasing trend after cooling translocation. Thereinto, TA systems positively dominated species turnover by altering bacterial community assembly from variable selection to homogeneous selection in cooling translocation process, while sporulation positively dominated species turnover through enhancing dispersal limitation in warming translocation process. These results suggested that the short-term temperature response of dormancy potential regulates bacterial species turnover through altering community assembly. This study represents one of the first efforts to highlight the chain of evidence with links among bacterial dormancy potential, community assembly, and species turnover under short-term temperature response. Understanding the bacterial dormancy potential underlying species turnover and community assembly may help the prediction of total soil microbiome feedback to a changing climate.

Keywords: Dormancy potential; Species turnover; Community assembly; Soil translocation; Forest soil

Recovery trajectories and community resilience of biofilms in receiving rivers after wastewater treatment plant upgrade

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Abstract

Wastewater treatment plant (WWTP) upgrades can reduce both nutrient and micropollutant emissions into receiving rivers, thus modifying the composition and function of biological communities. However, how microbial communities vary and whether they can be restored to levels found in less-polluted rivers remains uncertain. Aquatic biofilms are sensitive to environmental change and respond rapidly to bottom-up pressure. Thus, we used 12 flumes configured in three experimental treatments to mimic the dynamic processes of biofilm microbial communities occurring in a wastewater-receiving river following WWTP upgrade, with rivers containing two levels of nutrients and micropollutants used as references. We compared the biofilm microbial biomass, carbon source utilization, and community composition among the three “blocks”. Results showed that the metabolic patterns of the carbon sources and composition of the biofilm bacterial communities in the flumes mimicking a receiving river with WWTP upgrade recovered over time to those mimicking a less-disturbed river. The restoration of potential carboxylic acid-consuming denitrifying bacteria (i.e., *Zoogloea*, *Comamonas*, *Dechloromonas*, and *Acinetobacter*) likely played a significant role in this process. Combining quantitative analysis of the denitrification genes *nirS* and *nosZ*, we confirmed that the denitrification function of the river biofilms recovered after WWTP upgrade, consistent with our previous field investigation.

Keywords: Wastewater treatment plant upgrade; Biofilms; Carboxylic acid-consuming bacteria; Recovery; Denitrification

Responses of sediment resistome, virulence factors and potential pathogens to decades of antibiotics pollution in a shrimp aquafarm

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Abstract

Aquaculture ecosystem has become a hotspot of antibiotics resistance genes (ARGs) dissemination, owing to the abuse of prophylactic antibiotics. However, it is still unclear how and to what extent ARGs respond to the increasing antibiotic pollution, a trend as expected and as has occurred. Herein, a significant sediment antibiotic pollution gradient was detected along the drainage ditch after decades of shrimp aquaculture. The increasing antibiotic pollution evidently induced the diversity and tailored the community structures of ARGs, mobile genetic elements (MGEs), virulence factors and pathogens. The profiles of ARGs and MGEs were directly correlated with sediment terramycin and sulphadimidine. By contrast, virulence factors were primarily affected by nutrient variables. The pathogens potentially host both diverse virulence factors and ARGs. More than half of the detected ARGs subtypes non-linearly responded to increasing antibiotic pollution, as supported by significant tipping points. However, we screened seven antibiotic concentration discriminatory ARGs that could be served independent variable for quantitatively diagnosing situ total antibiotic concentration. Co-occurrence analysis depicted that notorious aquaculture pathogens of *Vibrio harveyi* and *V. parahaemolyticus* potentially hosted ARGs that confer resistance to multiple antibiotics, while priority pathogens for humankind, i.e. *Helicobacter pylori* and *Staphylococcus aureus*, harbored redundant virulence factors. Collectively, the significant tipping points and antibiotic concentration-discriminatory ARGs may translate into warning index and diagnostic approach for antibiotic pollution. This study greatly adds our understanding on the interplay among ARGs, MGEs, pathogens, virulence factors and geochemical variables under the scenario of increasing antibiotic pollution.

Keywords: Increasing antibiotic pollution; Antibiotics resistance gene; Pathogens; Tipping points; Antibiotic concentration-discriminatory ARGs

A novel metagenomic assembly-free strategy for identifying the composition of ARG-carrying microbial community

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Abstract

Effective risk assessment and control for environmental antibiotic resistance require comprehensive information of not only the composition of antibiotic resistance genes (ARGs) but also the assembly characteristics of ARG-carriers. Owing to the advancements in sequencing technologies and bioinformatic methods, the strategies based on metagenome-assembled contigs and genomes have been developed and used for the identification of ARG-carriers in different habitats, whereas limited by complex computational processes. In this study, we created a new bioinformatic pipeline to screen ARG-carrying microbial community (ACMC) based on metagenomic short reads without assembly; then we applied both read- and assembly-based strategies to identify ARG-carriers from the metagenomic datasets of coastal sediments. The major results revealed by the new strategy were validated by both metagenomic assembly strategies, which phylogeny acted as primary determinant for the distribution and spread of ARGs in the coastal sediments and ARGs were mainly carried by Gammaproteobacteria and Firmicutes, especially enriched in several potential pathogens such as Staphylococcus aureus. Due to minimizing the information loss, the new strategy further discovered that stochastic processes were dominant in the assembly of total ACMC, but the primary ARG-carriers were still shaped by deterministic processes; and conditionally rare and abundant taxa (CRAT) of ACMC played an important role in carrying ARGs. In addition, compared with the analyses using assembled contigs and genomes, the analysis using ARGs-like reads reduced computation time by 79.8% to 93.7%, respectively. Our new pipeline successfully screens out ARG-carriers in the environment in a direct and fast way, which will be a great help for long-term surveillance of environmental resistome in the future.

Keywords: Antibiotic resistance genes (ARGs); ARGs-like reads; Host; Metagenomics; Coastal environment

Season and age of neighbourhood gardens shape phyllosphere microbiota associated with respiratory diseases

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Abstract

Neighborhood gardens are the primary source of human microbial exposure. Phyllosphere microbes are intimately connected to the surrounding environment and can have a strong influence on human respiratory health. However, the effects of environmental factors (e.g., season, land-use, and garden age) on the respiratory diseases (RDs) associated microbiota in phyllosphere in the neighborhood gardens remain poorly characterized. Here we investigated phyllosphere microbial communities (PMCs) in 72 neighborhood gardens in (i) two seasons (warm and cold), (ii) two garden age categories (old and young), and (iii) different locations (urban and rural) in Shanghai. Our results showed that the phyllosphere bacterial communities were less diverse in the cold season than warm season, with the exception of Gammaproteobacteria, which had the opposite pattern. Although the phyllosphere bacterial and fungal communities were driven by the surrounding land-use parameters, their compositions were similar between urban and rural areas. Interestingly, 95.9% of RDs-associated bacterial species (e.g., *Streptococcus anginosus*) and 61.6% of RDs-associated fungal species (e.g., *Alternaria alternata*) were enriched in the young gardens under the cold season, suggesting a high possibility of respiratory inflammation. Taken together, our findings indicate that PMCs are poor in diversity but rich in RDs-associated microbiota in newly constructed gardens, thereby likely increasing the prevalence of respiratory diseases, especially during the cold season. We highlight the importance of the garden age to promote urban microbial diversity and human respiratory health.

Keywords: Neighborhood gardens; Phyllosphere microbial communities; Seasonal variation; Garden age; Respiratory diseases

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Effect of Lactic acid bacteria by different concentrations of copper based on non-target metabolomic analysis

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Abstract

Copper (Cu) is an essential element for mammals, but excess intake can have detrimental health consequences. The potential impact of different Cu (II) concentrations on human health remains unclear. In this study, a strain of lactic acid bacteria (LAB), L23121, was selected as a prebiotic indicator strain to indirectly assess the effects of food-limited Cu (II) concentrations on the functions of intestinal microbes. We used non-target metabolomics, automatic growth curve detector, scanning electron microscopy (SEM), and Fourier Transform Infrared Spectroscopy (FTIR) to investigate the effects of Cu on L23121. The study revealed show that, at low Cu (II) concentrations, the Pentose phosphate pathway and Pyrimidine metabolism of the lactic acid bacteria were affected, resulting in a decrease in the content of beneficial secondary metabolites, and a significant decrease in the cell activity. As Cu (II) concentrations increase, the key amino acid and lipid metabolisms were affected, leading to the inhibition of growth and primary metabolites production by the bacteria. Under high concentration of Cu (II), the surface adhesion of the bacteria was distorted and covered with significantly large particles, and the functional groups of the cells were significantly shifted. As a probiotic, the abundance of lactic acid bacteria in the intestine is significantly reduced, which will inevitably seriously damage intestinal homeostasis. Thus, to protect human intestinal microbes' health, it is recommended to limit the concentration of Cu in food.

Keywords: Heavy metals; Lactic acid bacteria; Copper toxicity; Beneficial metabolites; Primary metabolites

基于 EGSB 反应器的果蔬废水可持续产甲烷研究

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摘要

果蔬废弃物（FVW）作为一类含水量（81%~92%）极高的有机质垃圾，需妥善处理，以避免环境污染及资源浪费。通过两条处理线分别对 FVW 的固体和液体组份进行更具有针对性的甲烷化似乎是提高工艺效率的一种新策略。本研究首先对 FVW 进行物理性的破碎挤压预处理，将收集到的液体组份-果蔬废水（FVWw）利用厌氧膨胀颗粒污泥床（EGSB）反应器进行厌氧生物处理，从而达到可持续的甲烷生产。经过 240 天的连续中温运行，验证了 EGSB 反应器用于 FVWw 厌氧生物处理的可持续产甲烷方法可行性。整个运行过程中将机负荷率（OLR）从 1 g COD L^{-1} d^{-1} 增加至 8 g COD $L^{-1}d^{-1}$，以探究反应器的运行性能。通过调节水力停留时间（HRT）和进水浓度实现了反应器酸化后的有效调控，确保了系统中甲烷生产的稳定性。结果发现该反应器在 OLR 为 5 g COD $L^{-1}d^{-1}$ 时获得了最大甲烷产率 0.301 L g^{-1}COD。并根据 EGSB 反应器污泥的产甲烷活性，估计其最大负荷能力约为 8 g COD L^{-1} d^{-1}。对体系中菌群结构进行了分析，发现 *Metanosaeta* 和 *Metanosarcinas* 的富集是保证果蔬废水持续产甲烷的关键，而 *Metanothrix* 和 *Metanosrevibater* 在高负荷条件下表现出竞争优势。研究结果支持在实践中从 FVWw 中高效回收生物能源。

关键词：厌氧生物处理；果蔬废水；甲烷生产；EGSB 反应器

Research on sustainable methane production from fruit and vegetable wastewater based on EGSB reactor

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Abstract

Fruit and vegetable waste (FVW), as a type of organic waste with extremely high water content (81%~92%), needs to be properly treated to avoid environmental pollution and resource waste. More targeted methanation of solid and liquid components of FVW via two treatment lines appears to be a new strategy to improve process efficiency. In this study, the physical crushing and extrusion pretreatment of FVW was first carried out, and the collected liquid component-fruit and vegetable wastewater (FVWw) was treated by anaerobic organism treatment in anaerobic expanded granular sludge bed (EGSB) reactor, so as to achieve sustainable methane production. After 240 days of continuous operation at medium temperature, the feasibility of sustainable methane-producing method in EGSB reactor for anaerobic biological treatment fed with FVWW was verified. Throughout the operation, the organic loading rate (OLR) was increased from 1 g COD L^{-1} d^{-1} to 8 g COD L^{-1} d^{-1} to explore the operational performance of the reactor. By adjusted the hydraulic retention time (HRT) and the influent concentration, the effective control of the reactor after acidification was realized, and the stability of methane production in the system was ensured. The results showed that the reactor achieved a maximum methane yield of 0.301 L g^{-1} COD at an OLR of 5 g COD L^{-1} d^{-1}. According to the methanogenic activity of sludge in EGSB reactor, the maximum load capacity was estimated to be about 8 g COD L^{-1} d^{-1}. Analysis of the microbial community structure in the system revealed that the enrichment of Metanosaeta and Metanosarcinas is the key to ensuring the sustained methane production of FVWw, while Metanothrix and Metanosrevibater exhibited competitive advantages under high load conditions. The research results support the efficient recovery of bioenergy from fruit and vegetable wastewater in practice.

Keywords: Anaerobic organism treatment; Fruit and vegetable wastewater; Methane production; EGSB reactor

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