

Looking for clues to healthy aging in Malaysia - correlation among gut microbiota composition, intestinal permeability and cognitive frailty parameters in older adults

Nurul Izzati Ahmad Fadzuli¹, Kalavathy Ramasamy^{1,2}, Siong Meng Lim¹, Maw Pin Tan², Hui Min Khor², Ai Huey Tan², Abu Bakar Abdul Majeed^{3*}

¹Collaborative Drug Discovery Research (CDDR) Group, Faculty of Pharmacy, University Teknologi MARA (UiTM) Cawangan Selangor, Kampus Puncak Alam, 42300 Bandar Puncak Alam, Selangor Darul Ehsan, Malaysia

²Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia

³Brain Degeneration and Therapeutics Group, Faculty of Pharmacy, University Teknologi MARA (UiTM) Cawangan Selangor, Kampus Puncak Alam, 42300 Bandar Puncak Alam, Selangor Darul Ehsan, Malaysia

*Corresponding author: abubakar@uitm.edu.my

According to the World Health Organization, healthy aging is “the process of developing and maintaining the functional ability that enables wellbeing in older age.” Maintaining mental capacity goes along way in ensuring a useful and fruitful aging. Cognitive frailty (CF) is a geriatric syndrome characterised by physical frailty and cognitive impairment but without a clinical diagnosis of dementia. In spite of being a significant public health concern, the understanding of CF remains to be fully elucidated. Nevertheless, the aetiology of CF is believed to be multifactorial. In fact, there is now a large body of evidence which indicates the importance of gut microbiota homeostasis in healthy ageing. This raises the need to understand CF from the perspective of gut dysbiosis (imbalanced gut microbiota), which leads to increased intestinal permeability and intestinal inflammation. As such, this study aims at uncovering the correlations among CF parameters, gut microbiota and intestinal permeability in older adults. To this end, older adults above 60 years of age were recruited. A total of 137 stool samples were collected, homogenised and extracted for DNA. PCR was performed to amplify DNA prior to preparation of DNA library. This was then followed by 16S rRNA gene sequencing on amplicon V3-V4 hypervariable sections using Novaseq6000 Illumina. The stool samples were also subjected to ELISA for detection of intestinal barrier markers. The outcomes were analysed for correlation with CF parameters. In terms of microbiota composition, *Proteobacteria* phylum was found to be strongly and negatively correlated with functional reach ($r=-0.76$), hand grip strength ($r=-0.71$), Visual Cognitive Assessment Test (VCAT) score ($r=-0.84$) and Montreal Cognitive Assessment (MoCA) score ($r=-0.71$) but strongly and positively correlated with Timed Up and Go (TUG) ($r=0.74$) and UCLA Three-Item Loneliness Scale ($r=0.70$). *Firmicutes* phylum, on the other hand, was found to be strongly and positively correlated with functional reach ($r=0.71$) and VCAT score ($r=0.71$). In terms of intestinal barrier markers, there was a weak and negative correlation ($r=-0.22$) between alpha-1-antitrypsin (AAT) and hand grip strength. Altogether, the present findings have unveiled important insights into the understanding of the relationship among CF, gut microbiota and intestinal barrier in older adults. Hence, modulating the gut microbiota may have consequences on the neurological functions of older adults.

AUTHORS' DECLARATION

The authors confirm that our presentation does not contain any material which has been accepted for presentation or published before and that to the best of our knowledge and belief, it contains no materials previously published or written by another person, except where due

reference is made. We also grant the organiser permission to copy the presentation in part or in whole, subject to the usual acknowledgements.