Diet-Associated Variability in the Elderly Gut Microbiome

Dorrain Low,[1] Kai Xuan Tee,[1] Oliver Meldrum,[1] Giuseppe D'Agostino,[1] Hye Jin Kim,[1] Alicia Kang,[1] Rikky Purbojati,[1] Lakshmi Chandrasekaran,[1] Daniela Drautz-Moses,[2] Yifan Yang,[2] Bobby Cheon,[3] Aimee Elizabeth,[1] Lai Guan Fong,[1] Yulan Wang,[1] Parasuraman Padmanabhan,[1] Stephan Schuster,[1] Sven Pettersson,[4] John Chambers,[5] and Balazs Gulyas[6]

[1]Nanyang Technological University; [2]National Institute of Education and Nanyang Technological University; [3]Nanyang Technological University and Singapore Institute for Clinical Sciences; [4]Nanyang Technological University and National Neuroscience Institute; [5]Nanyang Technological University and Imperial College London; and [6]Nanyang Technological University and Karolinska Institutet

Objectives: The gut microbiome adapts to diet variations, which contribute to interindividual variability in human host metabolism and environmental factors. Microbe-diet studies have largely focused on specific diets (e.g., high-fat Western, Mediterranean-style) in American and European populations, with limited studies on compositionally-different diets in Asian populations. This study aimed to understand how diet composition modulates the gut microbiome in a Singapore multi-ethnic population.

Methods: We performed metagenomic sequencing of faecal samples from 118 healthy individuals (66 ± 5 years old), and estimated their food and nutrient intakes from 3-day food records (IRB-2018–01-011). Multivariate associations between microbial composition (species) and functional potentials (pathways, enzymes) with diet variables were analysed using linear mixed models with Benjamin-Hochberg correction, and adjusted for age, sex, BMI, physical activity, energy intake and medications. Permutational multivariate analysis of variance, based on Bray-Curtis dissimilarity metric, was applied to quantify variance within the microbiome that is explained by diet variables.

Results: We found gut microbes (5 phyla, >100 species) significantly associated with one of four observed dietary patterns ($P < 0.05$), various food groups and nutrients (q < 0.1). The microbiome was driven by intake and diversity of plant-based foods. *Parabacteroides* and *Blautia* species, and microbial metabolism of energy, carbohydrate and glycan were associated with increased intakes of white rice and noodles. *Prevotella* species were associated with increased intakes of legumes, wholegrains and plant protein. *Lachnospira, Clostridium and Fournierella* species, and microbial lipid metabolism were associated with energy-dense diet. Lastly, *Firmicutes, Eubacterium, Ruminococcus* and *Roseburia* species as well as microbial regulation of amino acid metabolism were associated with high-fibre diet.

Conclusions: This study provides new insights into gut microbial variations by distinct Asian dietary composition, supporting the feasibility of intervening habitual diets to reshape the gut microbiome for better health.