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**Gut Microbiota Diversity in Malaysians: A Pilot Study**

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**ABSTRACT**

Our gut harbors a complex bioecology of over 100 trillion bacteria known as the gut microbiota, outnumbering human eukaryotic cells. The gut microbiota is associated with biochemical functions in metabolism, nutrient regulation and immune system modulation. Previous studies proposed variation of human gut microbiota between populations, and suggested the importance of investigating gut microbiota associated with geographical and lifestyle differences. To date, there is still no data about gut microbiota composition from the Malaysian population. In this study, we characterized the mucosa-associated gut microbiota in 15 Malaysians who had normal colonoscopy results. We performed 16S rRNA metataxonomic sequencing on gut mucosal tissue using the Illumina MiSeq platform using 16S rRNA primers targeting the V3/V4 regions, and conducted microbial function prediction analysis using PICRUSt. We found our study subjects to harbour bacteria mostly of the Firmicutes (35.1%) phylum, followed by Bacteroidetes (23.2%) and Fusobacteria (10.7%). At the genus level, we observed that Bacteroides (15.7%), Fusobacterium (10.7%) and Faecalibacterium (9.1%) were the most abundant gut bacteria in healthy Malaysians. Membrane transport and carbohydrate metabolism, processes important in cellular signaling pathways and biochemical energy harvest processes were overrepresented in these bacterial communities. Distinct patterns in bacteria genus assemblages and differences in functional genes between individuals were also noted; these could be potentially tailored as individual microbiota signatures. Our findings showed that the healthy gut microbiota among Malaysians is indeed considerably different from other populations, with a higher presentation of Bacteroides, Fusobacterium and Faecalibacterium species.