Abstract IDDF2021-ABS-0140 Figure 1

Kruskal-Wallis test. Differentially abundant bacterial phyla, family and species were identified by calculating Log2Fold-Change of taxa in the unbalanced BCs compared to Neutral.

Results There were 135 Neutral, 59 QD, 24 PD and 12 DH subjects. 16 participants exhibited two or more unbalanced BCs. PD exhibited significantly lower alpha diversity (Shannon, Simpson) than Neutral ($p<0.05$). Fusobacteria (phylum) was elevated in PD ($p<0.01$). At the species level, Streptococcus gallolyticus was significantly higher in all three unbalanced BCs relative to Neutral. Fusobacterium mortiferum and Sutterella wadsworthensis were higher in PD than Neutral. Faecalitalea spp. was higher in DH than Neutral (IDDF2021-ABS-0140 Figure 1. Log2FoldChange of differentially abundant bacteria in QD, PD and DH as compared to Neutral).

Conclusions Varying TCM BCs exhibit unique microbiota signatures. Participants with unbalanced BCs are associated with greater dysbiosis compared to participants with Neutral BC. The lower alpha diversity in PD is consistent with that in obese and metabolic syndrome patients (Stanislawski et al. 2019; Oh et al. 2021). Streptococcus gallolyticus, a species associated with gastrointestinal malignancy (Chand et al. 2016), was significantly higher in all three unbalanced BCs and thus may serve as a potential biomarker for identifying patients with unbalanced BCs.

IDDF2021-ABS-0150 | **INFLUENCE OF ETHNICITY ON THE GUT MICROBIOTA OF SINGAPOREAN AND MALAYSIAN COMMUNITIES**

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Background Singapore and Malaysia are neighbouring countries with similar ethnic make-up: Chinese, Indian, and Malays. However, Singapore is a high-income economy while Malaysia is a middle-income economy. Such a difference has resulted in some levels of dichotomy in diet and lifestyles. In this study, we sought to investigate the gut-ethnic variation across the two neighbouring countries with varying levels of economic development.

Methods A total of 439 relatively healthy Malaysian (n=190) and Singaporean (n=249) adults (>18) were included, comprising Chinese (n=240), Indian (n=74), Malay (n=40), and the indigenous Jakun community (n=85). The sequences were processed with DADA2 and annotated using the SILVA database.

Results Country of origin explained the most variation in the gut microbiota (PERMANOVA, Pseudo-F=80.798, R^2=0.156, p=0.001; IDDF2021-ABS-0150 Figure 1. Ordination). Importantly, ethnicity was still significantly
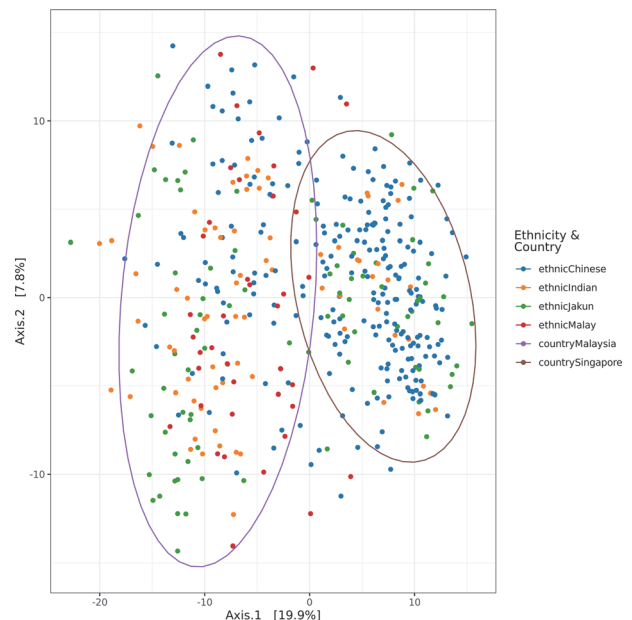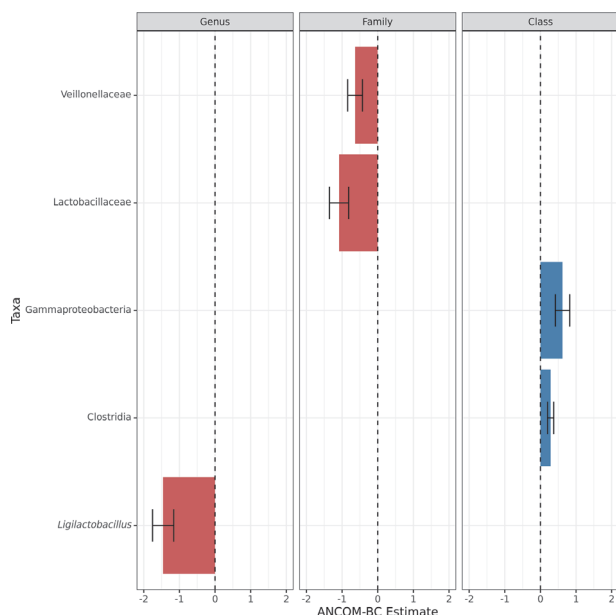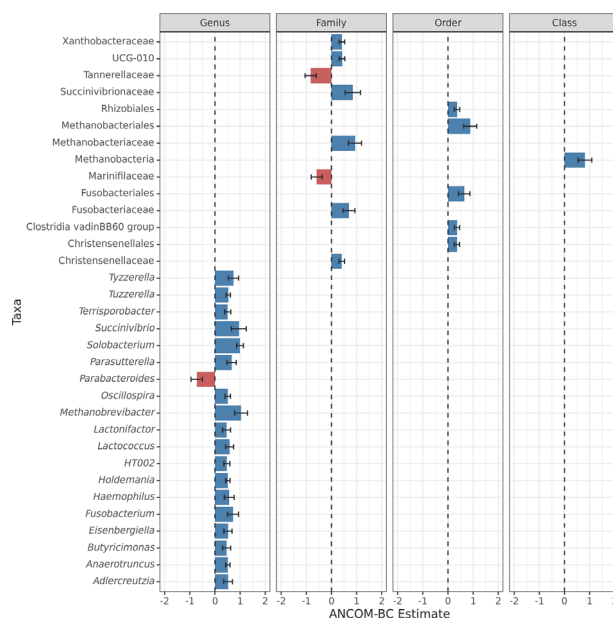

Abstract IDDF2021-ABS-0150 Figure 1

associated with the gut microbiota even after adjusting for the country, age and sex (PERMANOVA, Pseudo-F=4.206, R^2=0.019, p=0.001). Several taxa were found to be differentially abundant across ethnicity (ANCOM-BC, q<0.05). Notably, Ligilactobacillus, a lactic acid bacteria, was elevated among Indians (IDDF2021-ABS-0150 Figure 2. Ancom.ci) and reduced among Malay (IDDF2021-ABS-0150 Figure 3. Ancom.cm) relative to Chinese, suggesting that differences in the dietary pattern were responsible for the observed gut variation. Jakun exhibited the most differentially abundant gut microbiota (IDDF2021-ABS-0150 Figure 4. Ancom), with an elevated abundance of 18, 6, 5, and 1 genera, families, order, and class, respectively. The higher diversity of the Jakun was likely a reflection of their more traditional
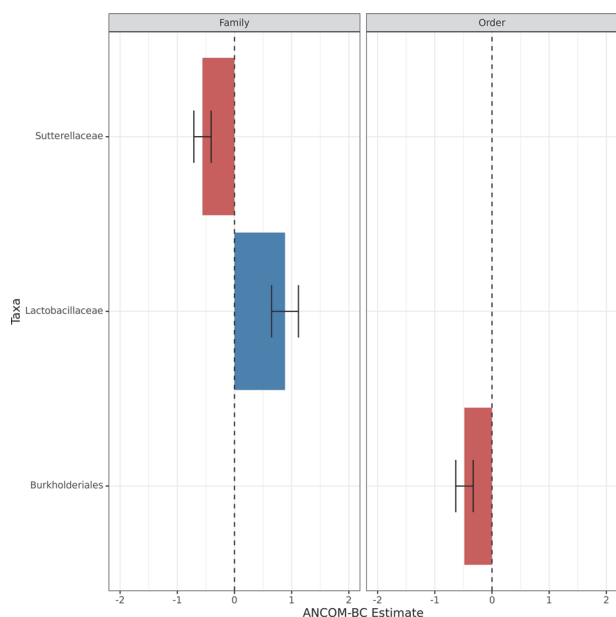
Abstract IDDF2021-ABS-0150 Figure 2

Abstract IDDF2021-ABS-0150 Figure 3

Abstract IDDF2021-ABS-0150 Figure 4

way of life, which has been associated with better gut diversity and health, compared to the Chinese, Indian and Malay of both countries, in particular, the higher abundance of Methanobacteria in Jakun has been inversely associated with irritable bowel syndrome.

Conclusions Gut-ethnic differences persist across geographical regions, which was likely due to similar lifestyle and cultural practices by individuals sharing similar ancestry. These signals provide potential biomarkers on the role of the gut microbiota in the aetiology of the unequal disease burdens affecting the different ethnic groups in this multicultural region.

GUT FEELINGS IN DEPRESSION: MICROBIOTA DYSBIOSIS IN RESPONSE TO ANTIDEPRESSANTS

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Background Antidepressants are a lifesaver for many people worldwide, regardless of their age or gender. Antidepressant therapy has been the choice for patients with depression, anxiety, and schizophrenia. The gut-brain axis (GBA) is a bidirectional pathway illustrating the communication between the brain and the gut microbiota and vice versa. Many studies have demonstrated the establishing of gut dysbiosis status in major depressive disorder. Meanwhile, the impact of antidepressant treatments on gut microbiota composition remains underexplored. Interestingly, several classes of antidepressants drugs, including monoamine oxidase inhibitors (MAOIs), selective serotonin reuptake inhibitors (SSRIs), N-methyl-d-aspartate