

Comparison of the gut microbial community between obese and lean people in Chinese male and female populations

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The gut microbiota was recently shown as a mediator of obesity. The diversity of gut microbes is determined by a variety of factors, such as diet, gene, age, gender etc. Gender is one of the most important factors, however, the gender-related gut microbes in obese Chinese population remains unclear. We analyzed 16S rRNA sequence of the gut microbiota in male and female Chinese people from lean to obese. We observed that at the phylum level, *Firmicutes*, *Bacteroidetes*, *Proteobacteria*, and *Actinobacteria* were dominant from underweight to obese state. In male individuals, Phylum *Fusobacteria*, classes *Fusobacteriia*, *Gammaproteobacteria*, orders *Bifidobacteriales*, *Pasteurellales*, *Enterobacteriales*, *Fusobacteriales*, families *Enterobacteriaceae*, *Fusobacteriaceae*, *Pasteurellaceae*, *Clostridiaceae*, and genera *Fusobacterium*, *Haemophilus*, SMB53 increased significantly in obese people compared to lean people. In female individuals, Families *Paraprevotellaceae*, *Prevotellaceae*, genera *Prevotella* increased significantly in obese people compared to lean people. The change of diversity (alphadiversity, Inv.Simpson, Shannon, and Simpson) indexes were also different between male and female, they increased gradually from underweight to obese in male, except Simpson to health, but decreased from underweight to overweight in female, though increased in obese. Our findings demonstrate the patterns and the differences of gut microbe between male and female individuals from underweight to obese in Chinese population, which may help us to better understand the relationship among gender, obesity and gut microbes.

Biography

Meirong Zhang is currently the Assistant Professor Huazhong University of Science Technology, China.

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