

Alteration of gut microbiota composition in obese adults; a possible link between obesity and fatty liver disease.

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Background: Worldwide epidemic of obesity increase the risk of nonalcoholic fatty liver disease as a common complication of obesity. Evidences have been shown the intestinal microbial changes in obesity. Gut dysbiosis, leaky gut and increased bacterial translocation into the liver via the gut–liver axis probably play crucial roles in hepatic fat deposition in obese patients. In the present study, we aimed to compare gut microbiota composition in obese and normal-weight Iranian adults.

Methods: This case-control study was conducted on 30 healthy normal-weight subjects and 27 obese adults aged between 20 to 45 years. Exclusion criteria were pregnancy and lactation, smoking, having cardiovascular disease, kidney and liver disorders, inflammatory bowel diseases, diabetes and cancer, history of digestive tract surgery, history of antibiotic therapy, acute and chronic diarrhea over the last month. Gut microbiota composition was assessed using 16S rRNA amplicon sequencing on Illumina MiSeq platform at Nucleomics core, KU Leuven. Concentration of faecal short chain fatty acids (SCFAs) were measured using gas chromatography. Comparison of microbiota-related variables between two groups was done with Wilcoxon rank-sum test and Benjamini–Hochberg false discovery rate adjustment was used for multiple testing corrections.

Results: The participants' mean age in the obese and control groups was 42 and 34 years, respectively ($P = 0.01$). No significant differences have been shown in gut microbial diversity and total microbiota composition between obese and normal-weight adults. The relative abundances of *Lactobacillus* and *Streptococcus* were higher in obese adults and *Akkermansia*, *Bacteroides*, *Alistipes*, *Parabacteroides*, *Barnesiella*, *Flavonifractor*, *Victivallis* and *Odoribacter* were more abundant in normal-weight adults ($P < 0.05$). Faecal butyrate concentration was higher in normal-weight group, while acetate and propionate had non-significant increase in obese group.

Conclusion: We have observed that some genera with different abundances between two groups were specific for Iranian population, indicating the necessity of microbiota examination in different countries. Moreover, high abundance of *Parabacteroides*, *Flavonifractor*, *Alistipes*, *Odoribacter* has been reported in patients with nonalcoholic fatty liver disease, suggesting microbiota-dependent relationships between obesity and fatty liver.

Keywords: Gut microbiota, obesity, dysbiosis, fatty liver disease