

Distinct compositional profiles of gut microbiota over hepatic steatosis severities in non-diabetic obese women.

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Dysfunction of the gut microbiota has been implicated in the development of hepatic steatosis, which is generally a symptom at the early stage of metabolic fatty liver disease (MAFLD), known as non-alcoholic fatty liver disease (NAFLD). Elucidating gut microbial signatures associated with MAFLD has been urged to treat dysbiosis and to alleviate steatosis severities. Here, we analyzed 57 whole metagenomics sequencing (WGS) samples of non-diabetic obese women with biopsy-proven hepatic steatosis in Spain and Italy. We separated those samples into ‘absent and slight’ and ‘moderate or severe’ group, less than 33% and more than 33% steatosis, respectively. We found that microbial diversities were significantly reduced in the group with more steatosis. In addition, the beta diversity between two groups was significantly discriminant at the species taxonomy rank. We selected 113, 137 and 641 significantly differentially abundant taxa across all taxonomic ranks between the two groups, through Wilcoxon rank-based method, Lefse, and ANCOM-BC, respectively. Finally, 6 microbial taxa that were discovered across all the methods were then filtered, which consist of order – Christensenellales, Monoglobales\_A, Opitutales, Victivallales, Family – QALW01, and Genus – UMGS1338. We statistically confirmed that the abundance of those 6 taxa were significantly enriched in the group showing more severe steatosis. Our study implicates there are significant associations between hepatic steatosis and gut microbial compositions, which might be utilized to further clinical applications. Nevertheless, our study might be suffered from the confounders such as country, BMI, and age, which makes the test results unreliable. Thus, the future study need to be conducted in careful consideration of any confounders that researchers can handle to elicit more reliable and applicable conclusions.

