

TAXONOMICAL AND FUNCTIONAL CHARACTERIZATION OF THE INTESTINAL MICROBIOTA ASSOCIATED TO OBESITY

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Background and Aims:

The intestinal microbiota has been pointed out as a key factor in obesity, since it contributes to metabolic and immunological homeostasis in the host. The dysbiosis of the gut microbiota linked to obesity has been related to a higher Firmicutes to Bacteroidetes ratio, a lower gene richness and an alteration of the metabolic functions of the gut microbiota [1, 2, 3]. The main objective of this work was to outline the significance of the compositional and/or functional changes in the obese-associated intestinal microbiota.

Methods:

The taxonomic composition of the fecal microbiota of obese (Ob) and normal weight (Np) individuals was determined by high-throughput sequencing analysis using the Illumina Seq platform. Amplification of the 16S rRNA gene was carried out using as primers sequences directed towards the V3-V4 regions of the gene. Functional characterization was determined by measuring short chain fatty acids (SCFAs) by High Performance Liquid Chromatography (HPLC) and the ammonium concentration spectrophotometrically.

Results:

Data analysis did not show significant differences between Ob and Np individuals in the dominant phyla Bacteroidetes (13%), Firmicutes (76%), Actinobacteria (10%) and Proteobacteria (1.8%). Nevertheless, the proportion of Verrumicrobia was significantly higher in normal weight individuals (Np). At genus level, Collinsella, Alistipes, Clostridium, Clostridium XIVa, Romboutsia and Oscillibacter, among others, showed significant differences between both groups of individuals. Bacterial diversity according to the Chao1 index was significantly higher in Np individuals. Regarding the functional characterization, the fecal samples of Ob individuals showed the highest concentrations of acetic and butyric acids.

Conclusion:

In spite of the great interindividual variability, the microbiota of obese individuals is characterized by a higher or lesser proportion of certain microbial groups and a higher formation of SCFAs in relation to the microbiota of normal weight individuals.

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References: 1) Turnbaugh PJ, Hamady H, Yatsunenkov T, et al. A core gut microbiome in obese and lean twins. *Nature*. 2009; 457: 480-4. 2) Le Chatelier E, Nielsen T, Qin J, et al. Richness of human gut microbiome correlates with metabolic markers. *Nature*. 2013; 500: 541-6. 3) Shen W, Gaskins HR, McIntosh MK. Influence of dietary fat on intestinal microbes, inflammation, barrier function and metabolic outcomes. *J Nutr Biochem*. 2014; 25: 270-80.