

Metagenomics Features of The Gut Microbiota in Metabolic Syndrome

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Abstract : The aim. To study the quantitative and qualitative colon bacteria ratio from patients with metabolic syndrome. Materials and methods. Fecal samples from patients of 2 groups were identified and analyzed: the first group was formed by patients with metabolic syndrome, the second one - by healthy individuals. The metagenomics method was used with the analysis of 16S rRNA gene sequences. The libraries of the variable sites (V3 and V4) gene 16S RNA were analyzed using the MiSeq device (Illumina). To prepare the libraries was used the standard recommended by Illumina, a method based on two rounds of PCR. Results. At the phylum level in the microbiota of patients with metabolic syndrome compared to healthy individuals, the proportion of Tenericutes was reduced, the proportion of Actinobacteria was increased. At the genus level, in the group with metabolic syndrome, relative to the second group was increased the proportion of Lachnospira. Conclusion. Changes in the colon bacteria ratio in the gut microbiota of patients with metabolic syndrome were found both at the type and the genus level. In the metabolic syndrome group, there is a decrease in the proportion of bacteria that do not have a cell wall. To confirm the revealed microbiota features in patients with metabolic syndrome, further study with a larger number of samples is required.

Keywords : gut microbiota, metabolic syndrome, metagenomics, tenericutes

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