

FEATURES OF THE COLON MICROBIOME IN PATIENTS WITH OBESITY WITH DIFFERENT PHENOTYPES

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Microbiome is a set of bacteria, fungi, viruses inside a person and on the surface of their skin. It is distributed unevenly in our body, its localization distinguishes the microbiome of the skin, mouth, intestines, etc. At present, the concept of heterogeneity in obesity is being developed, because not all obese patients are prone to the development of metabolic dysfunction. The urgency of the work lies in the need to understand and determine the dependence of obesity development on the colon microbiome composition.

The aim of the study is the features of the microbiome of the colon by metagenomic analysis in patients with different phenotypes of obesity and in healthy people.

Materials and methods. Bacteriological research by the method of metagenomic analysis was carried out on the basis of the department of microbiology of DMU. 150 people (50 men and 100 women, mean age 35.1 ± 4 years) were combined into clinical groups: healthy people with normal body weight ($n=70$); obese patients ($n=80$), including metabolically healthy ($n=35$) and metabolically unhealthy ($n=45$). High-quality and quantitative assessment of the intestinal microbiome was performed by metagenomic analysis. Total DNA was isolated from fecal samples and sequencing of the variable region of the variable v3-v4 region of the 16S rRNA gene was performed.

Results and discussion. There were statistically significant ($p < 0.05$) differences in quantitative and qualitative indicators of the studied microorganisms of the colon in healthy people without obesity and in patients with different phenotypes of obesity. In healthy patients, the quantitative characteristics are slightly increased for *Bacteroidetes* and decreased for *Firmicutes* compared to patients with metabolically healthy obesity. In patients with metabolically healthy obesity, in the microbiome of the colon there is an increase in the number of *Firmicutes* and a decrease in *Bacteroidetes* compared with those in metabolically unhealthy obesity. In healthy patients, the quantitative characteristics are slightly increased for *Bacteroidetes* and decreased - for *Firmicutes* compared to patients with metabolically healthy obesity.

Conclusions. In obese patients, increased amounts of *Proteobacteria*, *Bacteroidetes* and decreased amounts of *Actinobacteria*, *Firmicutes*. Healthy adults and obese patients in the intestinal microbiome in 100% of cases register 4 phylotypes of microbiomes (*Actinobacteria*, *Bacteroidetes*, *Firmicutes*, *Proteobacteria*). The data obtained in patients with different phenotypes of obesity indicate a change in the microbiome of the colon.