Blood Microbiome in Different Metabolic Types of Obesity

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Abstract : Background. Obese patients have unequal risks of metabolic disorders. It is accepted to distinguish between metabolically healthy obesity (MHO) and metabolically unhealthy obesity (MUHO). MUHO patients have a high risk of metabolic disorders, insulin resistance, and diabetes mellitus. Among the other things, the gut microbiota also contributes to the development of metabolic disorders in obesity. Obesity is accompanied by significant changes in the gut microbial community. In turn, bacterial translocation from the intestine is the basis for the blood microbiome formation. The aim was to study the features of the blood microbiome in patients with various metabolic types of obesity. Patients, materials, methods. The study included 116 healthy donors and 101 obese patients. Depending on the metabolic type of obesity, the obese patients were divided into subgroups with MHO (n=36) and MUHO (n=53). Quantitative and qualitative assessment of the blood microbiome was based on metagenomic analysis. Blood samples were used to isolate DNA and perform sequencing of the variable v3-v4 region of the 16S rRNA gene. Alpha diversity indices (Simpson index, Shannon index, Chao1 index, phylogenetic diversity, the number of observed operational taxonomic units) were calculated. Moreover, we compared taxa (phyla, classes, orders, and families) in terms of isolation frequency and the taxon share in the total bacterial DNA pool between different patient groups. Results. In patients with MHO, the characteristics of the alpha-diversity of the blood microbiome were like those of healthy donors. However, MUHO was associated with an increase in all diversity indices. The main phyla of the blood microbiome were Bacteroidetes, Firmicutes, Proteobacteria, and Actinobacteria. Cyanobacteria, TM7, Thermi, Verrucomicrobia, Chloroflexi, Acidobacteria, Planctomycetes, Gemmatimonadetes, and Tenericutes were found to be less significant phyla of the blood microbiome. Phyla Acidobacteria, TM7, and Verrucomicrobia were more often isolated in blood samples of patients with MUHO compared with healthy donors. Obese patients had a decrease in some taxonomic ranks (Bacilli, Caulobacteraceae, Barnesiellaceae, Rikenellaceae, Williamsiaceae). These changes appear to be related to the increased diversity of the blood microbiome observed in obesity. An increase of Lachnospiraceae, Succinivibrionaceae, Prevotellaceae, and S24-7 was noted for MUHO patients, which, apparently, is explained by a magnification in intestinal permeability. Conclusion. Blood microbiome differs in obese patients and healthy donors at class, order, and family levels. Moreover, the nature of the changes is determined by the metabolic type of obesity. MUHO linked to increased diversity of the blood microbiome. This appears to be due to increased microbial translocation from the intestine and non-intestinal sources.

Keywords : blood microbiome, blood bacterial DNA, obesity, metabolically healthy obesity, metabolically unhealthy obesity

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