A CHANGE IN THE GUT MICROBIOTA IS A FACTOR IN THE DEVELOPMENT OF GOUT IN HYPERURICEMIA

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Gout is a metabolic disease, the prevalence of which is growing worldwide and reaches 1-6% in developed countries (Shalnova S.A., 2014). Gout is characterized by chronic inflammation mediated by the presence of urate crystals (Nasonov E.L., 2016), the targets of which are not only the joints, but also the kidneys (Eliseev M.S., 2018) and the cardiovascular system (Singh J.A., 2014). The probability of detecting urate crystals in the gastrointestinal tract is very high, up to the formation of tofuses (Nasonova V.A., 2004). It was demonstrated (Chu Y, 2021) that the intestinal metagenome in gout was most similar in taxonomic structure, including analysis of 40 bacterial species, to that in ankylosing spondylitis (AS) and microbial functions to that in rheumatoid arthritis (RA) and AS. These data indicate that dysbiosis in gout is probably more consistent with dysbiosis in autoimmune diseases than in metabolic diseases. This suggests that the intestinal microbiota may have a general effect on immune processes.

The gut microbiota has the key importance for metabolism and immune regulation, and an imbalance in the composition of microorganisms can contribute to the development of various diseases. Current data on the role of the intestinal microbiota in the occurrence of chronic hyperuricemia (HU) and gout are presented, which is associated with the influence of the microbiota on the synthesis of purine-metabolizing enzymes and proinflammatory cytokines. It has been shown that the gut microbiota plays an important role in the pathophysiology of gout and can serve as a new therapy's target . Currently, the microbial index of gout is considered a potential method of early diagnosis of the disease, possibly already at the preclinical stage. The gut microbiota can be a starting point in the study of the pathogenesis of HU and gout. This makes it necessary to assess the pathogenetic relationship between individual-specific microorganisms, the microbiota as a whole, and the development of disorders of uric acid metabolism (UA), contributing to the emergence of HU and its transformation into gout. It is assumed that this approach will provide a more complete understanding of the participation of the intestinal microbiota in the synthesis of UA and its extrarenal excretion, as

well as about bacteria and bacterial enzymes that can be used as a probiotic coadjuvant for the treatment and prevention of gout.

The intestinal tract plays an important role in urate metabolism, including in gout, due to the characteristic features of the microbiota in such patients (Guo Z, 2016). When comparing patients with gout and healthy individuals, as well as those with asymptomatic HU, it was found that the intestinal environment enriched with UA forms differences in the composition of the microbiota associated with its excess (Kim HW, 2022). It can be assumed that HU affects the intestinal environment, causing changes in the qualitative and quantitative composition of the microbiota, which, in turn, can affect urate metabolism (Wang J, 2022).

Recent studies have shown that microbial diversity in the intestines of patients with gout is sharply reduced (Chu Y, 2021, Guo Z, 2016, Shao T, 2017). At the same time, the proposed model for the diagnosis of gout, based on characteristic metagenomic differences in the intestinal microbiota, demonstrated better sensitivity than the assessment of the level of serum UA (Guo Z, 2016). A comprehensive metagenomic study of the microbial signature revealed greater similarity of the gut microbiome in gout and autoimmune diseases (AS, RA) than in metabolic diseases (obesity, type 2 diabetes mellitus) (Chu Y, 2021), although gout itself is known to be associated with a high frequency of metabolic disorders. At the same time, the mechanisms underlying the relationship between purine metabolism, clinical manifestations of gout, and the intestinal microbiome are complex and have not yet been studied in detail.

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