GUT MICROBIOTA DYSBIOSIS IN RHEUMATIC DISEASES

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INTRODUCTION

Rheumatic diseases, characterized by inflammation due to autoimmune processes, are widespread and often challenging to manage. Recent studies emphasize the role of gut microbiota dysbiosis in the pathogenesis of these conditions. Therefore, exploring the efficacy of gut microbiota modulation as a therapeutic strategy for rheumatic diseases is of significant interest.

Objective. To evaluate the impact of microbiota interventions, including probiotics, prebiotics, antibiotics, and fecal microbiota transplantation, on disease activity and symptom severity in patients with rheumatoid arthritis (RA), systemic lupus erythematosus (SLE), and ankylosing spondylitis (AS).

Materials and Methods. Scientific publications from internet resources such as PubMed and Cyberleninka were reviewed. They describe gut microbiota characteristics both at baseline and following macrobiotic interventions (probiotics, prebiotics, antibiotics, or fecal microbiota transplantation) tailored to individual microbiota profiles in patients with RA, SLE, and AS. Disease activity and symptom severity were assessed using validated indices at baseline and after 12 weeks of treatment.

Results. Literature data indicate a significant reduction in disease activity scores (DAS28) in RA patients compared to a control group (mean change −1.5 vs. −0.8, $p<0.05$) following microbiota-targeted treatments. Microbiota analysis showed increased Firmicutes and decreased Proteobacteria abundance in RA patients, indicating improved gut microbiota composition. For SLE patients, a significant reduction in the Systemic Lupus Erythematosus Disease Activity Index (SLEDAI) was observed after 12 weeks of treatment compared to controls (mean change −4.2 vs. −1.9, $p<0.01$). In the treatment group, microbiota analysis demonstrated higher diversity and increased beneficial taxa, such as Bacteroidetes and Faecalibacterium. In AS patients, the treatment group showed a notable decrease in the Bath Ankylosing Spondylitis Disease Activity Index (BASDAI) compared to the control group (mean change −2.0 vs. −1.0, $p<0.01$), along with a reduction in pathogenic taxa, including Klebsiella pneumoniae and Prevotella copri.

Conclusions. The findings underscore the potential of microbiotic treatments in rheumatology and the need for personalized treatment strategies based on individual microbiota profiles.