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How do microbiome composition variations in rRNA sequencing correlate with disease severity in juvenile rheumatoid arthritis patients?

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Abstract

Juvenile rheumatoid arthritis (JRA), also termed juvenile idiopathic arthritis (JIA), is a chronic autoimmune condition in children characterized by joint inflammation and varied disease severity. Emerging evidence shows that microbiome dysbiosis, particularly alterations in gut and oral microbial communities detected by rRNA sequencing, may be linked to disease activity in JIA. However, existing studies present heterogeneous findings, use different sample types (fecal, oral plaque), and apply varied disease severity measures (e.g., JADAS-71, ACR criteria). Notably, no prior systematic review has comprehensively synthesized how microbiome composition variations correlate specifically with disease severity in JRA patients.

Before start

Data Sources: Relevant databases will be searched systematically, and studies will be screened according to explicitly stated inclusion criteria.

Methods

1 Population: Pediatric patients diagnosed with juvenile rheumatoid arthritis/juvenile idiopathic arthritis.

2 Exposure: Microbiome composition analyzed through rRNA sequencing techniques (e.g., 16S rRNA gene sequencing).

3 Outcome: Disease severity assessed by validated clinical criteria including, but not limited to, JADAS-71, ACR provisional criteria for inactive disease, Physician Global Assessment (PhGA), Parent Global Assessment (PGA), erythrocyte sedimentation rate (ESR), C-reactive protein (CRP), and other inflammatory markers.

4 Study Types: Observational studies (cross-sectional, cohort, case-control) investigating associations between microbiome variations and disease severity in JRA/JIA patients. Systematic reviews and meta-analyses relevant to the topic may also be included.

5 Data Sources: Relevant databases will be searched systematically, and studies will be screened according to explicitly stated inclusion criteria.

Data Extraction and Synthesis

6 Data on study design, participant characteristics, microbiome sample type and sequencing method, measures of disease severity, and reported associations between microbiome variations and disease severity will be extracted. Due to heterogeneity in methods and outcomes, a narrative synthesis will be performed, with summary tables presenting microbial taxa associated with active versus inactive disease states.

Rationale

7 Current research highlights patterns of gut and oral microbiome dysbiosis in JRA, with some taxa linked to disease activity phases. However, there is limited consensus on the direct correlation between microbiome composition and disease severity scores, and no comprehensive review focusing on this correlation exists, especially including multi-site microbiome data (fecal, oral). This systematic review aims to address this gap, providing clarity on the role of microbiome alterations in JRA disease progression.