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Original Investigation | Neurology

The Hidden Players: Gut Microbiota and Its Impact on Multiple Sclerosis
Study type: Systematic review

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Key Points

Question:
How does gut microbiota influence the progression of Multiple Sclerosis (MS)?

Findings:
Dysbiosis & MS Pathology:
MS patients show **reduced gut microbial diversity**, leading to **inflammation and neurodegeneration**. **harmful bacteria (Akkermansia, Blautia)** are increased, while **anti-inflammatory bacteria (Bifidobacterium, Roseburia, Faecalibacterium, Prevotella)** are reduced.
Short-Chain Fatty Acids (SCFAs):
Low SCFA levels **worsen inflammation**, affecting **T-cell activation and blood-brain barrier integrity**, contributing to MS progression.

Meaning:
Gut microbiota **plays a crucial role in MS development** by influencing immune responses and neuroinflammation.
Modulating gut bacteria could be a promising **therapeutic approach** for MS.

Abstract

Importance:
Multiple Sclerosis (MS), a chronic autoimmune and neurodegenerative disorder, is characterized by demyelination of the central nervous system (CNS), including the spinal cord, leading to motor, sensory, and cognitive impairments. MS affects women approximately three times more than men. The latest studies have highlighted the link between gut microbiota and MS. The gut bacteria influence the immune system and neuroinflammation; hence, an imbalance in the gut microbiota, or dysbiosis, can exacerbate MS pathology.

Objective:
To evaluate current findings on the relationship between the gut microbiome and MS.

Evidence Review
A systematic search of PubMed, ScienceDirect, and Google Scholar databases were conducted. The inclusion criteria involved systematic reviews published between 2015 and 2024 using key terms, gut microbiota, multiple sclerosis, and short-chain fatty acids.

Findings:
The review included 12 studies involving 570 MS cases and 478 controls. 80% of the studies analyzed both alpha and beta diversity and reported reduced microbial diversity in both MS patients, exacerbating MS via inflammation. Prevalent harmful bacteria in dysbiosis, such as Akkermansia and Blautia, promote inflammation, whereas beneficial bacteria like Bifidobacterium, Roseburia, Faecalibacterium, and Prevotella, known for producing anti-inflammatory short-chain fatty acids (SCFAs), are diminished. A decrease in SCFA-producing bacteria causes low butyrate levels, and worsening inflammation in MS. SCFAs is known to cause neuroinflammation by inflaming T cells and crossing the blood-brain barrier (BBB).

Conclusion and Relevance
Dysbiosis is observed in MS patients and may impact the disorder's progression. SCFA-producing bacteria are altered in MS patients, contributing to chronic inflammation, a hallmark of the disease. More research is needed, focusing on the specific bacteria involved in MS and identifying ways to modulate the microbiota, which could lead to novel approaches for the diagnosis and treatment of MS.

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