MS changes the microbiome subtly but similarly, whether in US or Asia

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Disruption of Bacteroides-Prevotella correlative network in MS. a, b
Correlations shared between MS and controls. c Correlations that are unique in controls. d Correlations that are unique in MS. Credit: Genome Medicine (2024). DOI: 10.1186/s13073-024-01364-x

Many studies have shown multiple sclerosis (MS) is associated with
changes to the bacteria in a person's gut—but the changes reported were all over the map. Now, UConn researchers have analyzed the results of seven studies across the U.S. and Asia and found a subtle but consistent signal.

MS is a disease in which the immune system attacks the protective coating on nerves, causing numbness, vision problems, difficulty walking, and other nervous system problems as the disease progresses. MS affects about 1 million people in the U.S. and millions more elsewhere in the world.

It might not seem as though MS has anything to do with the bacteria in the digestive tract, but there is a strong connection between our immune system and our gut. That community of bacteria, also called the gut microbiome, helps us regulate immune response.

Many scientific studies have tried to determine if there is a gut—immune system connection for MS. The studies compare the gut microbiome composition of healthy people to that of MS patients. But each one has found a different list of bacteria associated with MS.

Yanjiao Zhou, a UConn School of Medicine microbiome scientist, decided to take several of these studies and look at the data from all of them together, a technique called a meta-analysis. Meta-analysis enhances statistical power, and can find signals that are lost in the noise of smaller studies.

Qingqi Lin, first author of the paper, a joint Ph.D. student in Dr. Zhou's lab and Dr. Yufeng Wu's lab in the Computer Science Engineering Department, took a deep dive into the data analysis. They describe their results in Genome Medicine.

Lin and Zhou found that each study had a unique microbiome profile.
After statistically controlling for study-associated variation, they did find a few consistent signals. Notably, there was a decrease in bacteria from the genus Faecalibacterium, and an increase in bacteria from the genus Actinomyces, in people with MS.

In addition, the normal relationship between bacteria from the genus Bacteroides and the genus Prevotella was missing in people with MS. People with MS had significantly less Prevotella overall than healthy people. While the role of Actinomyces in immune regulation is not well understood, a reduction of Faecalibacterium has been associated with different immune and metabolic diseases.

"For a long time, people have questioned whether there are true microbiome signatures in MS. Our findings support the idea of a microbiome signature," and find it even across continents, Zhou says.

"While we are happy that the microbiome differences between MS and healthy people are finally settled, it is important to study the functional microbiome biomarkers in MS next," to see if the differences can be useful in diagnosing and monitoring the course of the disease.


Provided by University of Connecticut
