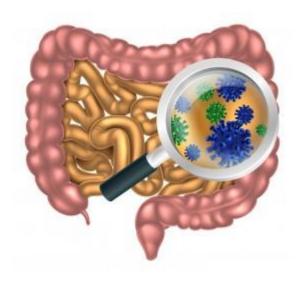




## New study confirms differences in gut bacteria in people with MS

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The human gastrointestinal tract is home to thousands of different kinds of bacteria, which are collectively known as the "gut microbiome" or microbiota. These bacteria are important in the digestion of food, the absorption of nutrients, and the production of vitamins and other beneficial substances.

Evidence has been accumulating that the gut microbiome also affects the host's immune system, and disruptions to the balance of gut bacteria has been implicated in some inflammatory and autoimmune diseases, such as rheumatoid arthritis and type 1 diabetes. There is also emerging evidence that gut bacteria may play a role in the development of MS.

What causes the inflammatory processes leading to MS is poorly understood, but it is likely to be due to a mixture of both genetic and environmental factors, and gut bacteria may be one such environmental factor. In the latest issue of *Nature Communications*, researchers from the Harvard Medical School have published some compelling data further linking the gut microbiome to MS.

The <u>study</u> used next-generation DNA sequencing technologies to sequence microbial DNA to identify the bacteria in fecal samples from over 100 people (60 with MS and 43 without MS). They then used that data to map differences in the gut bacteria between the two groups of people.

Broad changes in the types of bacteria were observed in the group of people with MS and more precise analysis revealed further changes within each category of bacteria. Interestingly some of the bacteria shown to be more abundant in people with MS have already been shown to modulate the human immune system and be involved in other autoimmune diseases. Importantly, the researchers showed that these differences remained significant even when they controlled for other factors that might affect gut bacteria such as diet, age, gender and body mass index.

These results confirm a slightly smaller <u>study</u> published a couple of days earlier from the Mayo Clinic, which also showed specific changes in the type of gut bacteria colonising the gastrointestinal tract of people with MS. In that study the scientists also identified differences in the diversity or richness of gut bacteria between patients in the active phase of the disease and the remitting phases of the disease. They showed that remitting patients and healthy controls both showed greater microbial diversity than patients with active disease.

The Harvard researchers also conducted additional studies of the activity of different types of immune cells in the people with MS compared to the healthy control group. They showed that changes in the abundance of some bacteria types were linked with changes in the activity of the immune system. This further implicates these specific gut bacteria in modulating the immune system in a way that may make people more susceptible to developing MS.





In addition, the Harvard research team divided the people with MS in the study into two groups, those who had taken disease-modifying agents such as interferon beta and glatiramer acetate in the last six months prior to the tests and those who were not on treatments. The people with MS on treatment were shown to have a microbiome more similar to the healthy volunteers. The authors of the study commented that "it is conceivable that treatment may act to normalise a proinflammatory microbiota.", but further work is needed to confirm whether this is the case. The Mayo study reported that the diversity of microbial life doesn't appear to be affected by treatment but didn't investigate this area extensively, nor did they comment on the effect of treatment on the broad types of bacteria.

Taken together the results of these studies show that alterations in the human gut microbiome, and associated changes in the immune system can correlate with MS and MS treatments. However, as these studies only looked at people with established MS, it can only show a correlation with disease, but it cannot yet be determined whether the bacteria drive the immunological changes leading to MS or whether immunological changes in MS drive the change in bacteria. Regardless this is an important observation, and potentially will mean that bacteria may be used to predict MS, and manipulating the gut bacteria may be a future therapeutic target in the fight against MS.

This is an exciting area of research with much more work to be done, and similar studies are being carried out by other groups internationally.