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SCLEROSIS**
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How Eating Meat Affects MS via Gut Microbiome, Immune Cells Detailed



by *Lindsey Shapiro, PhD* | February 2, 2022

relationship between meat consumption and how it affects gut bacteria, immune cell profiles, and metabolism was identified in people with **relapsing-remitting multiple sclerosis** (RRMS) participating in a small study.

Specifically, a diet rich in meat was associated with a decrease in *Bacteriodes thetaiotaomicron*, a common gut bacteria that works to digest carbohydrates; higher levels of pro-inflammatory T-helper 17 (TH17) immune cells; and a greater abundance of blood metabolites linked to meat metabolism.

“We found a number of gut bacteria associated with MS and severity of disability of MS patients. We also found increased autoimmune markers and signature metabolites in MS,” Yanjiao Zhou, MD, PhD, assistant professor at the University of Connecticut (UConn) and a co-principal study investigator, said in a **press release**.

“But what is really interesting is how these systems connect with each other, and how diet is involved in these connections,” Zhou said.

The study, “**Alterations of the host-gut microbiome interactions in multiple sclerosis**,” was published in *eBioMedicine*.

The causes of **multiple sclerosis** (MS) are not fully understood, but the disease is thought to

arise from a combination of genetic and environmental factors.

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December 15, 2021

by *BNS Staff*

Expert Voices: Diet and Nutrition for People With Multiple Sclerosis

Recently, the gut microbiome — the collection of microorganisms within the gut — has been **implicated** in MS development through its effects on the immune system. This raises the possibility that **diet**, through its impact on the gut microbiome, could be involved in MS immune dysfunction.

To shed light on this potential relationship, a team led by researchers at UConn Health and Washington University School of Medicine monitored 24 untreated adult RRMS patients and 25 healthy people, a control group, for six months while all remained on their typical diet. Microbiome composition, immune cell profiles, metabolism, and food intake were analyzed.

Participants were predominantly female, with a mean age of 38.9 for healthy controls and 40.2 for patients. None of the MS patients

or patients. None of these patients experienced a relapse during the study period. Measurements were taken at the study's start (baseline) and again six months later.

Overall, diet was not different between the MS and control groups at baseline. Results also showed no overall significant differences in microbiome composition between these groups at the study's start.

“These findings are consistent with prior studies that showed only modest gut microbiome difference between MS patients and healthy controls,” the researchers wrote.

They next looked at whether individual gut bacteria differed between patients and controls.

A decreased abundance of multiple species of bacteria was identified in MS patients. Some species — namely, *Bifidobacterium longum*, *Clostridium leptum*, and *Faecalibacterium prausnitzii* — are known to be involved in immunomodulation.

A lesser abundance of other bacteria classified under the genera *Faecalibacteria*, *Prevotella*, *Lachnospiraceae*, and *Anaerostipes* was also evident in MS patients. Some of these bacteria are already linked to the suppression of demyelination — damage to the protective coating on nerve cells — which is the

predominant feature of MS, the researchers noted.

These bacteria do this through the production of butyrate, a short-chain fatty acid (SCFA).

Notably, butyrate showed a trend toward decreased levels in the stool of MS patients in this study. **Previous studies** also reported low SCFA levels in MS patients.

“In summary, decreased relative abundances of bacteria with immunomodulatory properties seem to characterize gut microbiome changes in MS patients vs. controls,” the researchers wrote.

Patients’ degree of MS disability, as measured by the expanded disability status scale (EDSS), also appears to be associated with gut microbiome composition.

Specifically, higher levels of four bacteria — *Collinsella aerofaciens*, *Coprococcus comes*, *Phascolarctobacterium succinatutens*, and *Sutterella wadsworthensis* — were evident in patients with higher EDSS scores, meaning greater disability. “These findings suggest that specific gut microbes may be associated with the degree of disability in MS patients,” the researchers wrote.

Notably, *Sutterella* and *Collinsella* are reported to associate with other inflammatory conditions.

An analysis of the microbiome in relation to

immune cell profiles in the blood of MS patients revealed overall higher levels of several types of immune cells, including subsets of B-cells, T-cells, and TH17 cells.

This finding suggests “an overactive peripheral pro-inflammatory response in untreated MS patients,” the researchers wrote.

The scientists also looked at metabolites, the products of metabolism. Differences in the abundance of 118 metabolites between patients and controls were observed, including an increase in S-adenosyl-L-methionine (SAM), which is known to be involved in meat metabolism.

Methionine, which is involved in SAM synthesis and Th17 cell activation, was also enriched in MS patients, suggesting a link between immune function and metabolism. Indeed, statistical analyses revealed a significant correlation between immune and metabolic profiles in the patient group.

A closer look at the data revealed a connection between meat consumption and lower levels of *B. thetaiotaomicron*, the gut bacteria involved in carbohydrate (fiber) digestion from vegetables.

Greater meat consumption was also linked to an increase in circulating TH17 cells and SAM levels

increase in circulating Th17 cells and SAM levels.

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Altogether, the results suggest “a potential correlation network linking meat servings with decreased gut microbe *B. thetaiotaomicron*, increased Th17 cell and greater abundance of meat-associated blood metabolites,” the team wrote. “However, our analyses do not indicate the directionality of regulation between each,” and it remains unclear which of these factors might cause changes to the rest.

The researchers hope to conduct a larger study, allowing them to capture changes at different stages of disease severity.

They also emphasized that their analysis of multiple different systems, called multi-omics, allowed them to find previously unidentified relationships, and its use could help identify treatment approaches.

“This is the first study using an integrated approach to analyze the interplay between diet, gut microbiome, the immune system and

gut microbiome, the immune system and metabolism and their contribution to disease pathogenesis and progression in people with MS,” said Laura Piccio, MD, PhD, an associate professor then at Washington University and the study’s other co-principal investigator.

It opens a new modality to address future scientific questions by not looking at one individual factor, but at their complex interactions. This approach can lead to the identification of relevant networks that could be manipulated for disease prevention or therapeutic intervention,” Piccio added.

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About the Author



Lindsey Shapiro, PhD Lindsey earned her PhD in neuroscience from Emory University in Atlanta, where she studied novel therapeutic strategies for treatment-resistant forms of epilepsy. She was awarded a fellowship from the American Epilepsy Society in 2019 for this research. Lindsey also previously worked as a postdoctoral researcher, studying the role of

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Tags

diet, gut bacteria, gut microbiome, inflammation,
metabolism, SCFA, Th-17 cells

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