

## MICROBIOME

## Your microbiome is what you eat

“  
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”

The old adage ‘you are what you eat’ could be extended to our gut microbiomes. Our diet shapes our gut microbiome by modulating the abundance of specific species and their individual or collective functions. Diet-induced changes in the gut microbiome could have important implications for host health as alterations in microbial functions affect host physiology and disease. Now, three recent studies highlight how the gut microbiome responds to dietary change, with potential consequences for host–microbiota interactions.

Zaramela, Martino and Alisson-Silva et al. investigated how the gut microbiome responds to a diet that is rich in *N*-glycolylneuraminic acid (Neu5Gc), a red-meat-derived sialic acid not found in humans that promotes inflammation and which may be associated with cancer. Neu5Gc is incorporated into host glycans, but whether bacterial sialidases facilitate the release of Neu5Gc from meat was unknown. Moreover, bacterial sialidases are thought to exhibit a preference for *N*-acetylneuraminic acid

(Neu5Ac) over Neu5Gc. The authors compared the gut microbiome of mice lacking *Cmah* (an enzyme that synthesises Neu5Gc)

that were fed a sialic acid-free diet, a Neu5Gc-rich diet or a Neu5Ac-rich diet. A Neu5Gc-rich diet induced changes in the microbiome, with Bacteroidales and Clostridiales members increasing the most. The authors then identified sialidases in mouse and human microbiomes with a previously unobserved preference for Neu5Gc and confirmed that mouse and human bacterial sialidases release Neu5Gc from red meat, thus potentially reducing inflammation.

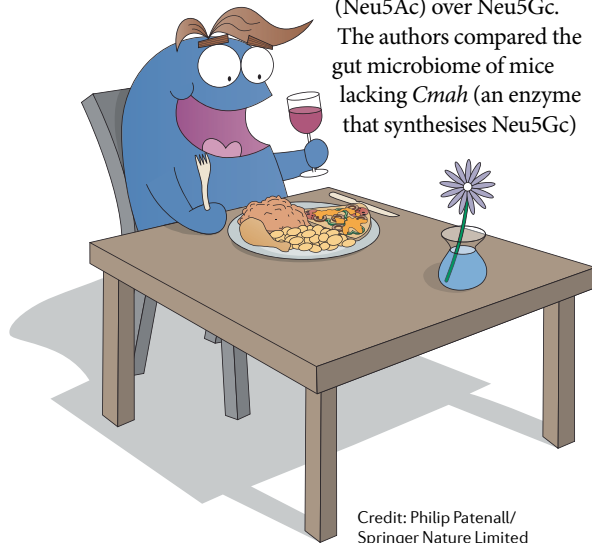
Ivey et al. investigated how the consumption of flavonoids affects the composition of the human gut microbiome. Flavonoids are a group of polyphenolic plant metabolites that are thought to provide health benefits when they are regularly consumed, such as improving blood pressure. The gut microbiota is known to influence the activity and bioavailability of flavonoids in the host, but how habitual flavonoid intake shapes the microbiome was unknown. The authors performed an ecosystem-based analysis of microbiome, nutritional and questionnaire data from >240 healthy adult men to assess whether consuming specific flavonoid subclasses drives patterns of microbial community assembly. The six flavonoid subclasses tested were associated with specific microbial community patterns. For example, *Eggerthella lenta* was associated with the consumption of flavonol and flavanone, and the abundance of *Adlercreutzia equolifaciens* was indicative of levels of flavonol and flavanol monomer consumption. By contrast, *Flavonifractor plautii* was inversely associated with the intake of a specific subclass. Consuming flavonoid-rich foods explained a large proportion of total community variance. Indeed, drinking tea once a week was associated with a substantial

change in the prevalence of 20 species comprising a subclass-specific microbial community.

Carmody et al. found that cooking shapes the gut microbiome. Cooking affects the physicochemical properties of foods, but whether cooking impacts the gut microbiome was unknown. The authors fed conventional mice meat-based or plant-based diets served cooked or raw and surveyed the gut microbiome. Whereas mice fed cooked or raw meat had a similar microbiome, a plant-based diet served raw altered gut microbial structure and function compared to the same diet served cooked. The microbiome of raw-fed mice showed higher expression of genes for metabolism of starch, sugar and xenobiotics, and starch digestibility was found to drive many of the cooking-related changes in the gut microbiome. Changes in the microbiome associated with cooking modulated host energy status and were also found in humans.

These studies highlight that the gut microbiome is plastic and responds to our diet. The knowledge gained from understanding the underlying mechanisms could lead to microbiome-informed personalized nutrition approaches that promote health.

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**ORIGINAL ARTICLES** Zaramela, L. S. et al. Gut bacteria responding to dietary change encode sialidases that exhibit preference for red meat-associated carbohydrates. *Nat. Microbiol.* <https://doi.org/10.1038/s41564-019-0564-9> (2019) | Ivey, K. L. et al. Role of dietary flavonoid compounds in driving patterns of microbial community assembly. *mBio* <https://doi.org/10.1128/mBio.01205-19> (2019) | Carmody, R. N. et al. Cooking shapes the structure and function of the gut microbiome. *Nat. Microbiol.* <https://doi.org/10.1038/s41564-019-0569-4> (2019)

**RELATED ARTICLE** Kolodziejczyk, A. A., Zheng, D. & Elinav, E. Diet–microbiota interactions and personalized nutrition. *Nat. Rev. Microbiol.* <https://doi.org/10.1038/s41579-019-0256-8> (2019)