

Researchers alter mouse gut microbiomes by feeding good bacteria their preferred fibers

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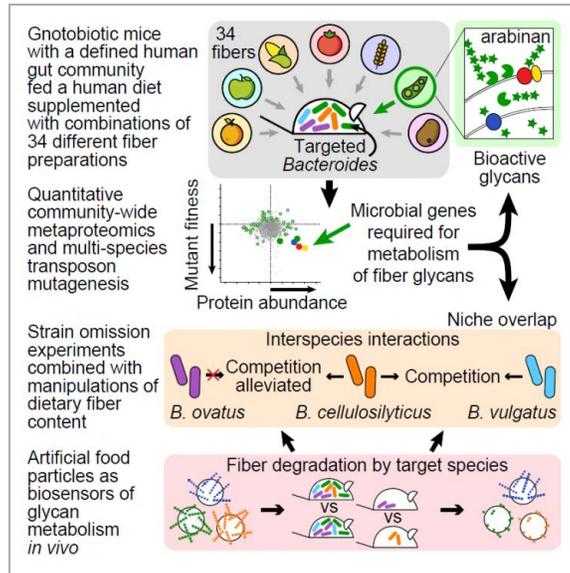


IMAGE: THIS GRAPHICAL ABSTRACT DEPICTS AN IN VIVO APPROACH EXPLAINS THE MECHANISM BY WHICH GUT MICROBES METABOLIZE DIETARY FIBERS AND PAVES A PATH TOWARDS THE DEVELOPMENT OF MICROBIOTA-DIRECTED FOODS THAT PROVIDE... [view more >](#)

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Humans choose food based on the way it looks, smells, and tastes. But the microbes in our guts use a different classification system--one that is based on the molecular components that make up different fibers. In a study published September 19 in the journal *Cell*, investigators found particular components of dietary fiber that encourage growth and metabolic action of beneficial microbes in the mouse gut.

The research aims to develop ways to identify compounds that can enhance the representation of health-promoting members of the gut microbial community. The goal is to identify sustainable, affordable dietary fiber sources for incorporation into next-generation, more nutritious food products.

"Fiber is understood to be beneficial. But fiber is actually a very complicated mixture of many different components," says senior author Jeffrey Gordon, a microbiologist at the Washington University School of Medicine in St. Louis. "Moreover, fibers from different plant sources that are processed in different ways during food manufacturing have different constituents. Unfortunately, we lack detailed knowledge of these differences and their biological significance. We do know that modern Western diets have low levels of fiber; this lack of fiber has been linked to loss of important members of the gut community and deleterious health effects."

The researchers started by testing 34 food-grade fiber preparations, many purified from byproducts of food manufacturing such as peels from fruits and vegetables that are thrown out during production of processed foods and drinks. They used mice initially raised under sterile conditions and then colonized with human gut microbes. The animals were fed a high-fat, low-fiber diet representative of diets typically consumed in the United States, with or without different types of supplemental fibers. The goal was to identify those fibers that were best at boosting the levels of key fiber-degrading bacterial species and promoting the expression of beneficial metabolic enzymes in the microbiome.

Since the mice had been colonized with a defined collection of human gut bacteria with sequenced genomes, the researchers knew all the genes that were present in their model human gut microbial community. This allowed them to perform a comprehensive, high-resolution proteomics study of all bacterial proteins whose expression changed in response to the different fiber types they tested. Combining these results with genetic screens, they were able to identify particular fiber sources, their bioactive molecular components, and the bacterial genes that increased for different *Bacteroides* species when they encountered different fibers. They focused on *Bacteroides* because members of this group of bacterial species contain genes responsible for metabolizing dietary fiber that are not present in the human genome.

For the second phase of the study, the investigators wanted to determine how different members of the microbial community interact with each other as they dine on dietary fiber. First author Michael Patnode, a postdoctoral fellow in Gordon's lab, developed fluorescently labeled artificial food particles with different types of bound carbohydrates from different fibers. Collections of these nutrient-containing particles were fed to mice colonized with defined microbial communities containing different combinations of *Bacteroides* species.

"We were excited to see how these 'biosensors' could be used to assess the processing of particular fiber components by particular bacterial species," Patnode says. By feeding these particles to mice that either carried or did not carry a dominant fiber-consuming species, the authors found that subordinate species were waiting in line to step up and consume the fiber.

"We had suspected there might be competition going on among the different strains and that some would be stronger competitors than others," Patnode says. Proteomics analyses and genetic screens confirmed that there was a hierarchy of fiber consumption among the species present in this model bacterial community.

Gordon explains that "it's important to understand how the presence of a particular organism affects the dining behavior of other organisms--in this case, with regard to different fibers. If we are going to develop microbiota-directed foods aimed at providing benefits to human health, it's important to find ways to determine which food staples will be the best source of nutrients and how the microbiota will respond."

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This work was supported by the National Institutes of Health, Mondelez International, and the U.S. Department of Energy. Gordon is a co-founder of Matatu, Inc., a company characterizing the role of diet-by-microbiota interactions in animal health. Elements of this report are the subject of patent applications that are currently being submitted.

Cell, Patnode et al.: "Interspecies competition impacts targeted manipulation of human gut bacteria by fiber-derived glycans" [https://www.cell.com/cell/fulltext/S0092-8674\(19\)30899-2](https://www.cell.com/cell/fulltext/S0092-8674(19)30899-2)

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