

Twin study finds that gut microbiomes run in families

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Does host genotype shape the microbiome? This visual abstract shows the findings of Goodrich et al. present a gut microbiome analysis of 1,126 twin pairs, which extends the association between host genetics and select bacterial taxa. Lactase nonpersistence was linked to higher levels of Bifidobacteria. Other gene/microbe links relate to diet and barrier defense. Credit: Goodrich et al./*Cell Host & Microbe* 2016

A genome-wide association analysis of over 1,000 twins in the UK supports that some parts of our microbiomes are inherited and shaped—not through a spread of microbes from parent to child, but through our genes. The results, revealing new examples of heritable bacterial species—including those related to diet preference, metabolism, and immune defense—appear May 11 in *Cell Host & Microbe*'s special issue on the "Genetics and Epigenetics of Host-Microbe Interactions."

"We set out to find out about human [genes](#) that are implicated in the regulation of the gut microbiome, and we found some that are," says senior author Ruth Ley, an Associate Professor in the Department of Microbiology at Cornell University and the study's senior author. One connection they were able to make was between the LCT gene, which is involved in making the enzyme that helps the body digest dairy, and a type of microorganism called Bifidobacterium, which is commonly used in probiotics. They also found links between specific gut bacteria blood pressure and self/non-self recognition.

"Based on our research, we identified more than a dozen [microbes](#) with known links to health that are heritable," says Ley, also director of the Department of Microbiome Science at the Max Planck Institute for Developmental Biology in Tübingen, Germany. "These microorganisms are environmentally acquired, but the genome also plays a part—by

determining which microorganisms are more dominant than others."

The investigators analyzed the gut microbiomes of 1,126 pairs of [twins](#) who were part of the TwinsUK Study. This multiyear research effort, which includes a total of 12,000 twins, is looking at a number of diseases and conditions. By including data from both identical and fraternal twins who were raised together, the study seeks to account for both environmental and genetic contributions.

The twins in the current study had already had their genomes analyzed, and 1.3 million small genetic variations (also known as single-nucleotide polymorphisms or SNPs) were known for each participant. The investigators used the genome-wide association approach to look for connections between genetic variations between twin pairs and certain bacterial types that were present and stable in the study subjects.

"The overall numbers in this study were still small for genome-wide association analysis, but they help validate some of the findings we've seen in smaller studies," Ley says. The analysis confirmed earlier findings that several other types of bacteria are also heritable, but specific genes connected to those differences were not found. "This type of study opens up many questions but doesn't give us a lot of answers yet," Ley says. "It gives us lots of ideas to study."

More information: *Cell Host & Microbe*, Goodrich et al.: "Genetic Determinants of the Gut Microbiome in UK Twins" [www.cell.com/cell-host-microbe ... 1931-3128\(16\)30153-6](http://www.cell.com/cell-host-microbe ... 1931-3128(16)30153-6) , DOI: [10.1016/j.chom.2016.04.017](https://doi.org/10.1016/j.chom.2016.04.017)

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