

## MICROBIOME

## Shaping the gut microbiome

Human genetic variation influences the abundances of specific members of the gut microbiota, suggests a new study published in *Cell*.

High-throughput sequencing analyses have previously revealed substantial inter-individual microbiome variation at the same anatomical sites, although related individuals seem to have more similar microbiotas. Until now, this observation had been attributed to environmental factors such as diet, lifestyle and exposures.

To discern whether any members of the gut microbiota are heritable, the researchers compared microbiotas across >1,000 faecal samples obtained from 977 individuals, including 171 monozygotic (that is, identical) and 245 dizygotic (that is, fraternal) twin pairs. Indeed, Ley and colleagues found that certain components of the microbiota were more similar between twin pairs

than between unrelated individuals. Importantly, monozygotic twins had more highly correlated microbiotas than dizygotic twins, suggesting that some members of the microbiota are heritable.

Heritability of microbiota was estimated using the twin-based ACE model, which partitions the total variance into genetic effects (A), common environment (C), and unique environment (E). The investigators identified a number of microbial species that were heritable, including the most highly heritable taxon Christensenellaceae, a family within the bacterial phylum Firmicutes. This family, and the heritable microorganisms that co-occur with it — including the archaeal family Methanobacteriaceae, the bacterial family Dehalobacteriaceae and several unclassified species within the Firmicutes and Tenericutes phyla

— were enriched in lean versus obese individuals. Notably, transplantation of human faecal samples containing *Christensenella minuta* into germ-free mice induced a leaner phenotype than transplants lacking this species or those containing a heat-killed version of it.

Taken together, these findings lend support to the notion of a host genetic effect on the microbiome that can affect health. The next step will be to identify the genes that drive the heritability of different microbial taxa and to elucidate the mechanisms by which Christensenellaceae impacts host phenotype.

Linda Koch, Chief Editor,  
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