



FEATURE | INFECTIOUS DISEASES

 INFORMING PRACTICE

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Characteristics of the Gut Microbiome

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Four new studies provide a deeper understanding of the normal human gut microbiome.

Recognition of the role of the microbiome in overall health has been one of the most important changes in our understanding of normal physiology. As efforts increase to modify the microbiome to promote better health, full understanding of the normal gut microbiome is essential. Four new studies provide perspectives on this issue.

Falony and collaborators collected fecal samples from 1106 Flemish individuals in a confined region of Belgium and 1135 individuals from the Netherlands. The researchers performed microbiome phylogenetic profiling for both groups and compared with U.S. and U.K. data sets to create a total population of 3948 well-characterized microbiome profiles in Western, developed countries. A core microbiota shared in 95% of samples was identifiable that included 17 genera and had a median core abundance of 72%. Comparisons with fecal samples from New Guinea, Peru, and Tanzania lowered the core human microbiome to 14 genera. Comparison of the microbiome profiles of the Flemish individuals with questionnaire and health data identified 69 variables that correlated with microbiome variation; the most influential variable was medications.

Zhernakova and collaborators performed an analysis of the gut microbiome of 1179 Dutch individuals and assessed correlations between microbiome variations and 207 intrinsic and extrinsic host factors. They found that 18.7% of the variation in the microbiome composition was attributable to these factors. The levels of fecal chromogranin A, a protein secreted by enteroendocrine cells, were associated with the presence of 61 microbial species that contributed to approximately 53% of the microbiome abundance. Use of certain medications (antibiotics, proton-pump inhibitors, metformin, statins, and laxatives) notably affected the gut microbiome, as did dietary factors.

Noting that helminths were likely part of the normal human gut microbiome in the past, Ramanan and associates assessed the impact of parasitic worms on the gut microbiome in a mouse model. They found that presence of the worms induced resistance to colonization with inflammatory *Bacteroides* species and increased Clostridiales species. These changes in microbiome composition were associated with enhanced type 2 immunity. The authors also found that individuals living in a helminth-endemic area had a significant increase in *Bacteriodales* species and decrease in Clostridiales species after a deworming treatment.

Li and colleagues analyzed the gut microbiome of 10 individuals with metabolic syndrome who received fecal microbiota transplantation during a trial. In an analysis of single-nucleotide variants in the stool metagenomes, some donor species persisted through the 3-month observation period of the study, although the colonization success of the donor species varied markedly. Coexistence of donor and recipient species was extensive, and strain replacement varied considerably and did not correlate with clinical outcome measures.

COMMENT

These four studies provide a more in-depth understanding of the human gut microbiota in the Western world, including microbiota changes linked to the elimination of helminths in Western countries. The findings on how fecal microbiota transplantation affects gut microbiome composition will aid our understanding of the efficacy of this therapeutic modality on different disease states.

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