

# Microbiome

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## THE HUMAN MICROBIOME

The human body is home to trillions of microorganisms, including bacteria, viruses, fungi, and other assorted “bugs.” In a healthy adult, these microbiota outnumber human cells 10 to 1, and include thousands of distinct species that have co-evolved with humans and are thought to influence human health and disease. These species, their combined genomes, and the biological interactions they share with each other and their human hosts combine to make up the “human microbiome.”

Microbial communities are known to vary from site to site within an individual, and from person to person – especially across localities and cultures. However, research has shown that the microbiome stays relatively stable within an individual across his or her lifetime, and that, despite differences in microbial composition between individuals, the biological functions served by the microbiome remain consistent over time, and from person to person.

While most bugs in our microbiome are harmless, and even beneficial (e.g., breaking down nutrients and helping to regulate the immune system) changes or imbalances in the microbial ecosystem have been linked to various disease states. This has made the microbiome an area of focus for researchers in recent years as scientists try to understand the dynamics of the microbiome and its connection with human disease. A better understanding of these dynamics and the host-microbe relationship could lead to new diagnostic approaches, or to tailored therapies for those diseases in which the microbiome plays a role.

## MICROBIOME RESEARCH AT BROAD

Over the last seven years, the Broad Institute of MIT and Harvard has helped systematically uncover, catalog, and analyze the microbial inhabitants of the human microbiome. Research is now focused on using “multi-omics” techniques, including whole genome sequencing, as well as proteomic, metabolomic, and transcriptomic analyses, to better understand how microbiota are acting on and interacting with their human hosts in health, and during disease progression.

Broad was part of the Human Microbiome Project (HMP) Consortium, an NIH-funded collaboration between several genome sequencing centers dedicated to understanding the properties of the microbial communities living in the human body, and to analyzing their roles in human health and disease. Broad researchers are now involved in phase two of HMP, the Integrative Human Microbiome Project (iHMP), where they lead a multi-institutional effort to understand how the human gut microbiome changes over time in adults and children with Irritable Bowel Disease (IBD).

In addition to research on IBD, Broad scientists are building tools and methods to accelerate research on the microbiome, and are actively investigating the role of the microbiota in the development of various diseases and conditions such as cancer and urinary tract infections.

*The material above is collected from the following sources:*

- [NIH – Human Microbiome Project](#)
- [American Society for Microbiology](#)

*Last updated May 2015*



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