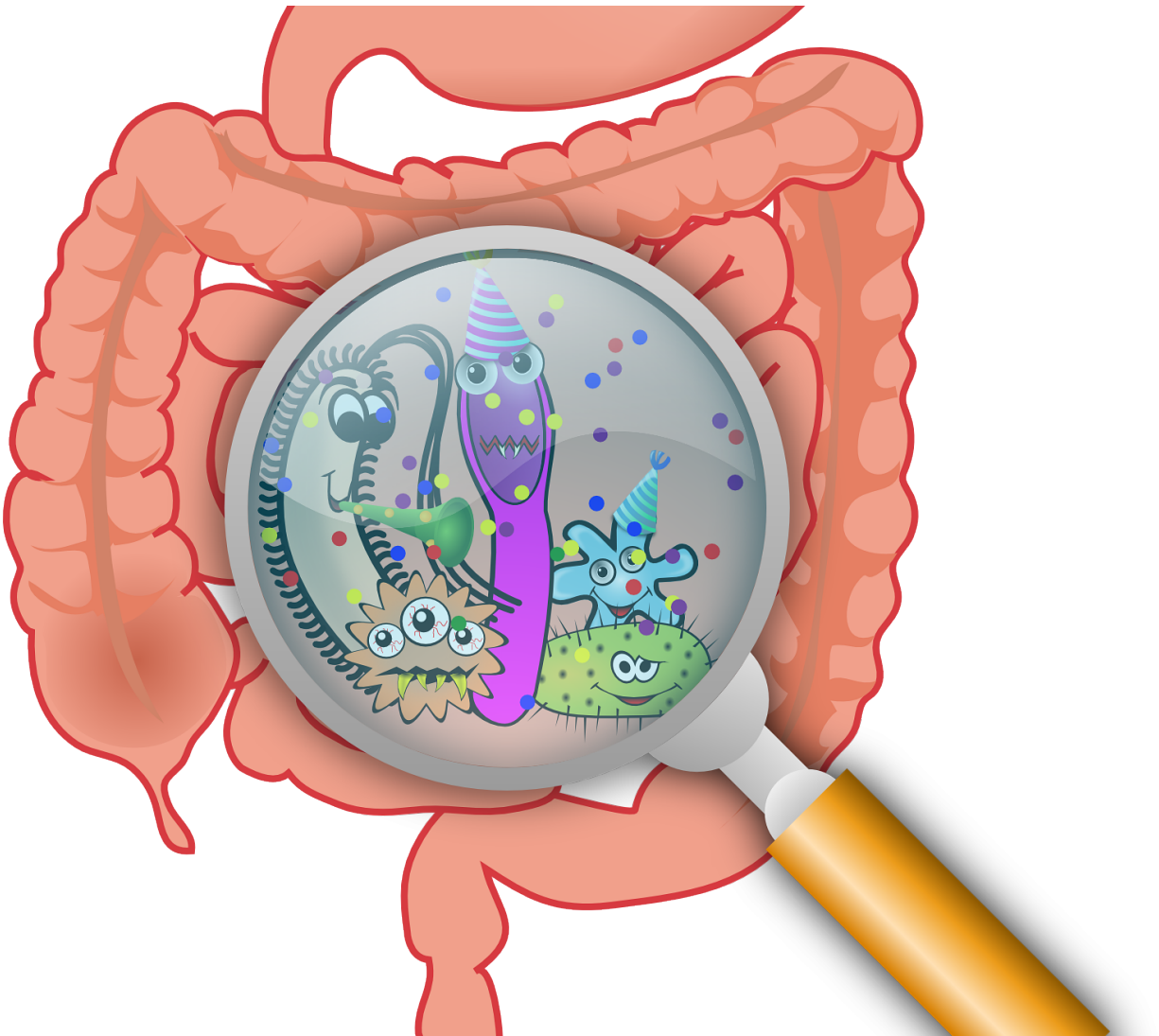


Thousands of new microbial communities identified in human body

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A new study of the human microbiome—the trillions of microbial organisms that live on and within our bodies—has analyzed thousands of new measurements of microbial communities from the gut, skin, mouth, and vaginal microbiome, yielding new insights into the role these microbes play in human health.

The study, from researchers at Harvard T.H. Chan School of Public Health, Broad Institute of MIT and Harvard, and University of Maryland School of Medicine, presents a three-fold expansion of data from the National Institutes of Health Human Microbiome Project, providing unprecedented depth and detail about human microbial diversity. The new information allows researchers to identify differences that are unique to an individual's [microbes](#)—just like some human genome variants are unique to each individual—and track them across the body and over time.

The study will be published online September 20, 2017 in *Nature*.

"This study has given us the most detailed information to date about exactly which microbes and molecular processes help to maintain health in the [human microbiome](#)," said Curtis Huttenhower, associate professor of computational biology and bioinformatics at Harvard Chan School, associate member of the Broad Institute, and senior author of the study.

This study is an expanded second phase of the Human Microbiome Project, originally launched in 2007 to identify and characterize human microbes, explore microbes' relationship to health and disease, and develop computational tools to analyze the microbes. The microbiome has been linked to everything from allergies to cancer.

The researchers analyzed 1,631 new samples from 265 individuals, from diverse body sites and at multiple points in time. The scientists used DNA sequencing tools that allowed them to precisely identify which

organisms are present in various body sites, as well as what they might be able to do. Examining microbes at multiple time points further allowed them to determine which parts of the community might change slowly, rapidly, or stay relatively stable over time.

The findings:

- Provide one of the largest profiles of non-bacterial members—viruses and fungi—of the microbiome across the body
- Identified microbes with specific strains within each body site
- Profile the biochemical activity that allows microbes to help maintain human health
- Identify how the microbes and their biochemistry change over time

Huttenhower said the new study also emphasizes how much scientists still don't know about the makeup and function of the human microbiome. Learning more about it will take time, he said.

"Just as sequencing one human genome, without information about variability or context, didn't immediately lead to extensive new drugs or therapies, so too will we need to look at the microbiome with an extremely fine lens, in many different contexts, so that we can understand and act on its specific, personalized changes in any individual disease or condition," said Jason Lloyd-Price, postdoctoral associate at the Broad Institute, postdoctoral fellow at Harvard Chan School, and lead author of the study.

He added that the study also provides a large data resource to the scientific community that will help drive future research, discoveries, and the development of new methods in studying the human [microbiome](#).

More information: Jason Lloyd-Price et al, Strains, functions and dynamics in the expanded Human Microbiome Project, *Nature* (2017).
[DOI: 10.1038/nature23889](https://doi.org/10.1038/nature23889)

Provided by Harvard T.H. Chan School of Public Health

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