

## New gut microbiome atlas builds most accurate profile of global gut health to date

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A new and freely available <u>Human Gut Microbiome Atlas</u> could help researchers and health care professionals around the world better understand how microorganisms in the gut impact disease, leading to more effective treatment.

The study, <u>published</u> in *Genome Research*, is an <u>international</u>



collaboration led by King's College London that identifies gut bacteria appearing in individuals with 23 separate diseases across 19 countries. Carried out in collaboration with MetaGenoPolis and the Science for Life Laboratory, the global study is the largest to date.

By tagging clusters of microbiome features to specific diseases, the authors believe this data could help diagnose and provide individual pathways for treatment for illnesses such as colorectal cancer and Crohn's Disease.

The human gut microbiome is the individual profile of bacteria and other microorganisms that live in the gut that helps perform key bodily functions, such as digestion. Recently, it has been shown to have a strong relationship with the development of a wide variety of diseases, including type two diabetes, depression and Alzheimer's <u>disease</u>.

Until now the information that exists on microbiomes has been fragmented. While data exists on the genetic makeup of individual microbes in the gut, these are siloed dependent on specific diseases. This prevents large-scale <u>comparative studies</u> and doctors from tailoring treatments to work with the microbiome of their patients.

Dr. Saeed Shoaie, Senior Lecturer in Systems & Synthetic Biology at King's College London and corresponding author said, "The human microbiome has been an increasingly promising field of study, but the lack of access to high-quality harmonized data has been a stumbling block for future impactful research. That's why we created the Human Gut Microbiome Atlas.

"The discovery of microbiome patterns common across disease will allow researchers to answer what constitutes a healthy or unhealthy gut microbiome. This will allow health care professionals to identify and diagnose diseases with greater clarity and implement effective



treatments that target areas of the microbiome, like dietary modifications or even microbiome transplants."

The team carried out a systematic survey of genetic data from more than 6,000 <a href="https://human.gut.microbiome">human.gut.microbiome</a> samples across North America, Europe and South and East Asia. Using machine learning models, they then classified which gut bacteria appeared most frequently in healthy individuals and those with specific diseases, tagging specific functions to specific bacteria.

By presenting a freely available data set to health professionals working in affected communities, the resource will empower better health care decision making at a community level.

In the future, the team hope to expand their work to produce oral and skin microbiome atlases to treat illnesses like eczema and psoriasis, as well as tracing antimicrobial resistance (AMR) in the gut.

AMR is projected to kill more than 10 million people a year by 2050. By tracing which <u>gut bacteria</u> are becoming resistant to antibiotics within global populations and environments, the group hope to improve and assess the efficacy of efforts to treat disease and combat AMR.

Dr. Frederick Clasen, Research Associate at King's College London and co-author of the study, said "The threat of AMR requires novel and innovative solutions, and using the microbiome holds great potential for improved diagnosis, surveillance, and treatments. We believe that the human microbiome atlas is an important step to unlocking the power of microbiome for this purpose."

**More information:** Sunjae Lee et al, Global compositional and functional states of the human gut microbiome in health and disease, *Genome Research* (2024). DOI: 10.1101/gr.278637.123



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