

# Map of Human Bacterial Diversity Shows Wide Interpersonal Differences

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Personalized bacterial communities located across the human body have wide implications for overall health, according to University of Colorado at Boulder study. Credit: Photo courtesy PDPhoto.org

(PhysOrg.com) -- A University of Colorado at Boulder team has developed the first atlas of bacterial diversity across the human body, charting wide variations in microbe populations that live in different regions of the human body and which aid us in physiological functions that contribute to our health.

The study showed humans carry "personalized" communities of bacteria around that vary widely from our foreheads and feet to our noses and navels, said CU-Boulder's Rob Knight, senior author on the paper published in the Nov. 6 issue of [Science Express](#). The researchers found

unexpectedly wide variability in bacterial communities from person to person in the study, which included nine healthy volunteers and which targeted 27 specific sites on the body.

"This is the most complete view we have yet of the microbial side of ourselves, one that our group and others will be adding to over the coming years," said Knight an assistant professor in CU-Boulder's chemistry and biochemistry department. "The goal is to find out what is normal for a healthy person, which will provide a baseline for further studies to look at people with diseased states. One of the biggest surprises was how much variation there was from person to person in a healthy group of subjects."

Co-authors on the Science Express study, the online version of Science magazine, included CU-Boulder's Elizabeth Costello, Christian Lauber, Micah Hamady and Noah Fierer, as well as Jeffrey Gordon from the Washington University School of Medicine in St. Louis.

There are an estimated 100 trillion microbes residing on and within each human being that are thought to collectively endow us with the essential traits we rely on for a variety of functions, including the proper development of our immune systems, efficient digestion of key foods and resistance to invasion by lurking microbial pathogens.

The CU-Boulder team looked high and low, analyzing microbial communities in places such as hair on the head, ear canals, nostrils, mouth, lower intestine, and 18 different skin sites ranging from foreheads and armpits, forearms, palms, index fingers, navels, the back of the knees and the soles of the feet. The team used the latest generation of massively parallel DNA sequencers and new computational tools developed at CU-Boulder.

The study subjects were sampled four times each over a three-month

period, typically after showering an hour or two earlier. Microbial DNA was then isolated directly from swabs used for sampling each body site, eliminating the standard culturing step. Specific bacterial RNA genes present in the DNA were then amplified using a technique known as PCR and the genes were then sequenced with high-capacity DNA sequencers, said Knight.

The specific bacterial RNA genes amplified from each sample, which were obtained from each body site of each individual, were "tagged" during the PCR step with a sample-specific DNA barcode developed by Knight's group. This allowed the team to pool hundreds of samples together prior to a single sequencing "run," reducing the cost and increasing the speed of the work.

Specific skin sites, as well as hair, nostril and ear canal sites, had the highest levels of variability within individuals over time and were roughly on a par with the human lower intestine, according to the study. The highest diversity skin sites were the forearms, palm, index finger, back of the knee and sole of the foot. The armpits and soles of the feet showed some similarities, perhaps because they are from dark and moist environments, said Fierer.

The mouth cavity showed the least variation in diversity both within individuals and between people, according to the study. The team also found the skin "head group" -- which included forehead, external nose, external ear and hair -- was dominated by one type of bacteria, while sites on the trunk and legs were dominated by a different group.

"We have an immense number of questions to answer," said Fierer, an assistant professor in CU-Boulder's ecology and evolutionary biology department who was a co-author on the study. "Why do healthy people have such different microbial communities? Do we each have distinct microbial signatures at birth, or do they evolve as we age? And how

much do they matter? We just don't know yet."

Costello, the first author on the paper who recently accepted a postdoctoral position at Stanford University, likened the analysis of human bacterial communities to charting the growth of newborns. "Just as babies are tracked for weight and height as they grow to see where they fall in relation to normal ranges, we'd like to be able to find out if there are normal ranges of microbial communities for humans that could be tracked over time."

In an intriguing microbial community "transplant" experiment, the team disinfected the forearms and foreheads of some test subjects, then "inoculated" both sites with [bacterial communities](#) harvested from the tongue. The tongue bacteria persisted longer on the forearms than foreheads, suggesting some bacterial populations more strongly prefer sebaceous, or oily sites.

"As some others have speculated, it may be that drier areas of the skin like forearms make generally more hospitable landing pads for bacteria," Costello said. The team did not find any significant difference in how easily a person's forehead or forearm could be colonized by his or her own "transplanted" microbes as opposed to those of other people.

"These patterns suggest that the search for microbial factors associated with disease, although difficult to ascertain due to the high intrinsic levels of variability among healthy individuals, may be achieved using broad profiling techniques such as those employed here," the authors wrote in Science Express.

Previous microbial studies of healthy individuals have generally focused on individual body habitats including the lower intestine, skin and mouth. The new study builds on a 2008 CU study on hand bacteria indicating that while more than 4,200 species of bacteria resided on 102

human hands, only about five species were shared by all 51 participants. The 2008 study also showed women had a greater diversity of bacteria on their palms than men.

Knight, also a faculty member in CU-Boulder's computer science department and who is a member of the university's Colorado Initiative in Molecular Biotechnology, said understanding the variation in human [microbial communities](#) holds promise for future clinical research.

"If we can better understand this variation, we may be able to begin searching for genetic biomarkers for disease," he said. The CU-Boulder researchers said it might someday be possible to identify sites on the [human body](#) that would be amenable to microbial community transplants with either natural or engineered microbial systems that would be beneficial to the health of the host.

Source: University of Colorado at Boulder ([news](#) : [web](#))

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