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Nurture trumps nature in study of oral bacteria in human twins

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A new long-term study of human twins by University of Colorado Boulder researchers indicates the makeup of the population of bacteria bathing in their saliva is driven more by environmental factors than heritability.

The study compares saliva samples from identical and fraternal twins to see how much "bacterial communities" in saliva vary from mouth to mouth at different points in time, said study leader and CU-Boulder Professor Kenneth Krauter. The twin studies show that the environment, rather than a person's genetic background, is more important in determining the types of microbes that live in the mouth.

For the new study, doctoral student Simone Stahringer sequenced the microbial DNA present in the saliva samples of twins. She and the research team then determined the microbes' identities through comparison with a microbe sequence database. Saliva samples were gathered from twins over the course of a decade beginning in adolescence to see how salivary microbes change with time.

After determining the oral "microbiomes" of identical twins, who share the same environment and genes, and the microbiomes of fraternal twins who share only half their genes, the researchers found the salivary microbes of the identical twins were not significantly more similar to each other than to those of fraternal twins. "We concluded the human genome does not significantly affect which bacteria are living in a person's mouth," said Krauter of CU-Boulder's molecular, cellular and developmental biology department. "It appears to be more of an environmental effect."

Krauter said while the twin data from the oral microbiome study indicates that genetics plays a more minor role, it's possible the genes still affect the oral microbiome in more subtle ways—an effect he plans to further explore.

A paper on the subject was published online Oct. 12 in the journal Genome Research. Other co-authors included doctoral student William Walters of MCD Biology, Jose Clemente and Rob Knight of the chemistry and biochemistry department, Robin Corley and John Hewitt of the Institute for Behavioral Genetics and Dan Knights, a former doctoral student in the computer science department.

The researchers also found that the salivary microbiome changed the most during early adolescence, between the ages of 12 and 17. This discovery suggests that hormones or lifestyle changes at this age might be important, according to the team.

Stahringer said that when several pairs of identical twins moved out of their homes and, for example, went off to college, the oral microbes they carried changed, which is consistent with the idea that the environment contributes to the types of microbes in the saliva. "We were intrigued to see that the microbiota of twin pairs became less similar once they moved apart from each other," Stahringer said.

Krauter said there appears to be a core community of oral bacteria that is present in nearly all humans studied. "Though there are definitely differences among different people, there is a relatively high degree of sharing similar microbial species in all human mouths," he said.

The authors say the new study has established a framework for future studies of the factors that influence oral microbial communities. "With broad knowledge of the organisms we expect to find in mouths, we can now better understand how oral hygiene and environmental exposure to substances like alcohol, methamphetamines and even foods we eat affect the balance of microbes," said Krauter.

The saliva samples used in the new study came from the university's Longitudinal Twin Study and Colorado Adoption Project, which have involved hundreds of identical and fraternal twin pairs. Researchers also are analyzing additional frozen saliva samples collected during their studies for another project assessing possible relationships of oral bacteria to drug addiction, he said.

CU has a strong research focus on the human microbiome. In a 2011 study led by the Washington University School of Medicine and involving CU-Boulder, researchers found the diversity and abundance of gut microbes in animals varied depending on whether they were carnivores, omnivores or vegetarians. Knight is a member of a national research team funded by the Bill & Melinda Gates Foundation to look at the gut microbes of normal and malnourished infants and children around the world in search of novel microbial therapeutics.

In 2012, some 200 researchers from the NIH-funded Human Microbiome Project, including eight CU-Boulder researchers, mapped the microbial makeup of healthy humans for the first time. The study involved nearly 250 healthy U.S. volunteers and targeted 15 to 18 individual sites on the body harboring microbial communities.

Other recent studies involving CU researchers included one that found the delivery methods of babies have a big effect on their individual microbiomes, and second that showed women have a greater diversity of hand bacteria than men. Another showed personal bacterial communities living on the fingers and palms of individual computer users can be matched up with bacterial signatures on the computers and computer mice they recently used, a potential new tool for forensic scientists in the future.

According to scientists, about 100 trillion microorganisms inhabit surfaces and cavities of our bodies, which amounts to roughly 10 microbes per human cell.

More information: Stahringer SS, Clemente JC, Corley RP, Hewitt J, Knights D, Walters WA, Knight R, Krauter KS. Nurture trumps nature in a longitudinal survey of salivary bacterial communities in twins from early adolescence to early adulthood. *Genome Res* doi: 10.1101/gr.140608.112

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