

Tracing microbes between individuals towards personalized oral health care

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The human body is home to a complex ecosystem of microbes increasingly recognized as having a critical role in both health and disease. Viruses can attack and change the composition of bacterial communities, yet little is known about how this might influence human health. In a study published online today in *Genome Research*, scientists have performed the first metagenomic analysis of a bacterial immune system in humans over time, finding that the defenses of the oral microbiome are unique and traceable, information that could help personalize oral health care in the future.

With recent advances in sequencing technologies, researchers are now sampling the [genetic diversity](#) of entire microbial and viral communities at once, including those residing within us. Recent studies have investigated viral communities of the respiratory and digestive tracts, suggesting that viruses might influence the microbial ecosystem and health of the human host. Less is known about how viruses affect the oral microbiome, which could have significant implications for diseases of the [oral cavity](#).

A strategy for monitoring the interaction between [bacterial communities](#) and viruses is to sequence specific [bacterial DNA](#) elements that confer acquired immunity against viral attack, called clustered regularly interspaced short palindromic repeats (CRISPRs). Bacteria integrate foreign DNA from encountered pathogens into "spacers" between the repeats, using the spacers to later recognize and respond to the attacker.

In this study, a team of scientists has for the first time analyzed the evolution of the CRISPR bacterial immune system over time in the human body, specifically investigating the oral microbiome. "We knew that bacteria developed specific resistance to viruses," said David Pride of the University of California, San Diego and lead author of the report, "but before this study, we had no idea of the extent to which certain oral bacteria in humans have utilized these resistance mechanisms against viruses."

Pride and colleagues obtained saliva samples from four healthy subjects over the course of 17 months, sequencing CRISPR elements from multiple streptococcal bacteria, the predominant oral community members in many people. The team's analysis of CRISPR repeat and spacer sequences revealed that although there is a set of CRISPRs maintained within each subject over time, ranging from 7% to 22%, there was a remarkable amount of change observed even in short periods.

"Each time we sampled our human subjects, approximately one-third of the immune repertoire in the bacterial community was new," Pride explained, "which suggests that the development of resistance to viruses is occurring at least on a daily basis, if not more frequently."

Pride added that because the bacterial immune repertoire was traceable within the individuals over time, they should be able to track the system within each person and also track bacteria passed between subjects.

"Because these immune features can be used to track bacteria and their respective viruses in humans," Pride said, "it may open the door to more personalized [oral health](#) care, where lineages of microbes are traced as a part of routine health care for individuals."

More information: Pride DT, Sun CL, Salzman J, Rao N, Loomer P,

Armitage GC, Banfield JF, Relman DA. Analysis of streptococcal CRISPRs from human saliva reveals substantial sequence diversity within and between subjects over time. *Genome Res*
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