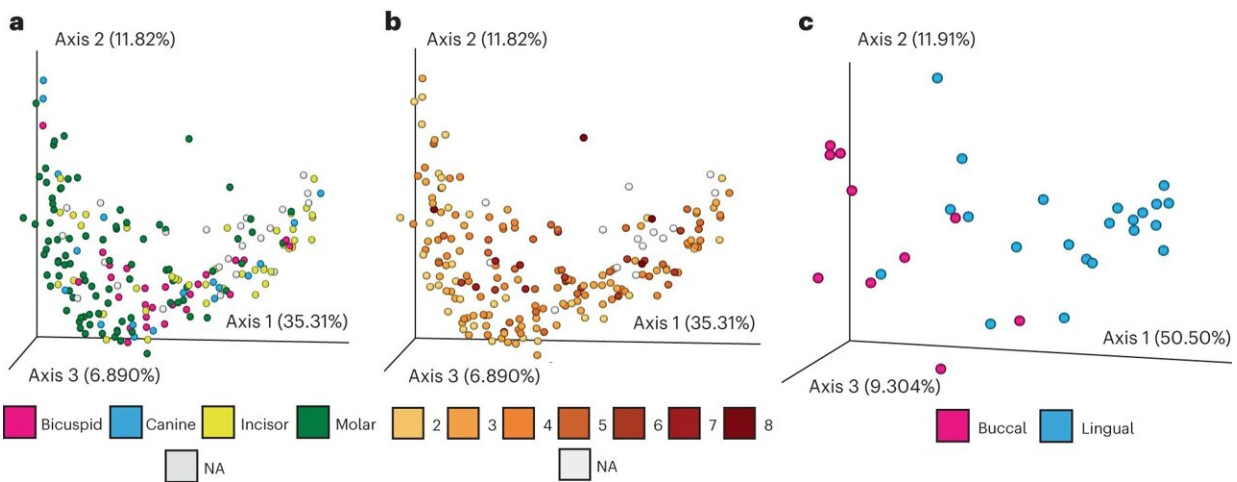


Study of ancient British oral microbiomes reveals shift following Black Death

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Oral geography and microbial compositions. **a–c**, The contributions of oral geography on bacterial and archaeal taxonomic compositions are shown by performing PCoA of Bray–Curtis distances for all teeth. The oral microbiota composition of each calculus sample is colored according to the tooth that was sampled (**a**), the approximated size of the dental calculus sample obtained for DNA extraction as described in Supplementary Information (**b**) or the surface of the tooth that was sampled, shown for molar teeth only (**c**). When information regarding oral geography was unavailable, samples are labeled as not applicable or ‘NA’. Credit: *Nature Microbiology* (2023). DOI: 10.1038/s41564-023-01527-3

The Second Plague Pandemic of the mid-14th century, also known as the Black Death, killed 30–60% of the European population and profoundly changed the course of European history. New research led by Penn State

and the University of Adelaide suggests that this plague, potentially through resulting changes in diet and hygiene, may also be associated with a shift in the composition of the human oral microbiome toward one that contributes to chronic diseases in modern-day humans.

"Modern microbiomes are linked to a wide range of [chronic diseases](#), including obesity, [cardiovascular disease](#), and poor mental health," said Laura Weyrich, associate professor of anthropology at Penn State.

"Uncovering the origins of these microbial communities may help in understanding and managing these diseases."

According to Weyrich, dietary changes are believed to have influenced oral [microbiome](#) evolution through time; however, few studies have directly examined the history of human oral microbiomes in a single population.

Weyrich noted that some studies have used the microbiomes of living Indigenous people who practice traditional subsistence lifestyles as a proxy for the microbiomes of pre-industrialized peoples. Yet, this strategy is faulty, she said, because modern-day non-industrialized populations may not have microbes that accurately reflect those that existed in the ancestors of industrialized peoples.

Additionally, she said, "This research places unnecessary responsibilities and obligations on Indigenous communities to participate in microbiome research, where the benefits of these studies may not directly serve Indigenous peoples."

A more accurate and ethically responsible method is to directly examine the oral microbiomes preserved within calcified dental plaque, known as calculus, from the ancestors of Industrialized people with the permission and collaboration of decedent populations and stakeholders. In the largest study to date of ancient dental calculus, Weyrich and her

colleagues collected material from the teeth of 235 individuals who were buried across 27 archaeological sites in England and Scotland from about 2,200 B.C. to A.D. 1853.

The findings were [published](#) in *Nature Microbiology*.

The researchers processed the samples in an ultra-sterile, ancient DNA laboratory to minimize contamination. They identified 954 microbial species and determined that they fell within two distinct communities of bacteria—one dominated by the genus *Streptococcus*—which is common in the oral microbiomes of modern Industrialized peoples—and the other by the genus *Methanobrevibacter*—which is now largely considered extinct in healthy Industrialized people.

Exploring the origins of these two communities, the team found that almost 11% of the total variation in microbiome species composition could be explained by temporal changes, including the arrival of the Second Plague Pandemic. But how could the Second Plague Pandemic contribute to changes in the oral microbiome?

"We know that survivors of the Second Plague Pandemic earned [higher incomes](#) and could afford higher-calorie foods," said Weyrich. "It's possible that the pandemic triggered changes in people's diets that, in turn, influenced the composition of their oral microbiomes."

The team used a novel approach to investigate whether a change in diet could have influenced the emergence of the *Streptococcus* group and the extinction of the *Methanobrevibacter* group. They assembled a list of functional differences among the bacteria in the two groups that could be linked to diet; for example, functions linked to high or low-dietary fiber digestion, carbohydrate metabolism, and lactose—a sugar in milk—metabolism.

The researchers found that the bacteria in the Streptococcus-dominated group had more functional traits that are significantly linked with low-fiber, high-carbohydrate diets, as well as dairy consumption—all of which characterize modern-day diets. By contrast, the Methanobrevibacter-dominated group was missing traits associated with dairy and sugar consumption, which characterized the diets of some ancient humans.

The team further determined that the Streptococcus group was associated with the presence of periodontal disease, which is characterized by infections and inflammation of the gums and bones around the teeth. When this disease progresses, bacteria can enter the bloodstream through the gum tissue and potentially cause respiratory disease, rheumatoid arthritis, coronary artery disease, and blood sugar issues in diabetes. The Methanobrevibacter group, on the other hand, was associated with the presence of skeletal pathologies.

"Our research suggests that modern-day oral microbiomes may reflect past changes in diet, resulting from the Second Plague Pandemic," said Weyrich. "Importantly, this work helps to inform our understanding of modern-day chronic, noncommunicable diseases."

More information: Gancz, A.S. et al, Ancient dental calculus reveals oral microbiome shifts associated with lifestyle and disease in Great Britain, *Nature Microbiology* (2023). DOI: [10.1038/s41564-023-01527-3](https://doi.org/10.1038/s41564-023-01527-3). www.nature.com/articles/s41564-023-01527-3

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