

# Study suggests the bacterial ecology that lives on humans has changed in the last 100 years

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A University of Oklahoma-led study has demonstrated that ancient DNA can be used to understand ancient human microbiomes. The microbiomes from ancient people have broad reaching implications for understanding recent changes to human health, such as what good bacteria might have been lost as a result of our current abundant use of antibiotics and aseptic practices.

Cecil M. Lewis Jr., professor of anthropology in the OU College of Arts and Sciences and director of the OU Molecular Anthropology Laboratory, and Raul Tito, OU Research Associate, led the research study that analyzed microbiome data from ancient human [fecal samples](#) collected from three different [archaeological sites](#) in the Americas, each dating to over 1000 years ago. In addition, the team provided a new analysis of published data from two samples that reflect rare and extraordinary preservation: Otzi the Iceman and a soldier frozen for 93 years on a glacier.

"The results support the hypothesis that ancient [human gut](#) microbiomes are more similar to those of non-human primates and rural non-western communities than to those of people living a modern lifestyle in the United States," says Lewis. "From these data, the team concluded that the last 100 years has been a time of major change to the human gut microbiome in cosmopolitan areas."

"[Dietary changes](#), as well as the widespread adoption of various aseptic and antibiotic practices have largely benefited modern humans, but

many studies suggest there has been a cost, such as a recent increase in autoimmune related risks and other health states," states Lewis.

"We wish to reveal how this co-[evolutionary relationship](#) between humans and bacteria has changed, while providing the foundation for interventions to reconstruct what has been lost. One way to do this is to study remote communities and non-human primates. An alternative path is to look at ancient samples and see what they tell us," Lewis says.

"An argument can be made that remote traditional communities are not truly removed from modern human ecologies. They may receive milk or other food sources from the government, which could alter the microbial ecology of the community. Our evolutionary cousins, non-human primates are important to consider. However, the human-chimp common ancestor was over six million years ago, which is a lot of time for microbiomes to evolve distinct, human signatures."

Retrieving ancient human microbiome data is complementary to these studies. However, studying ancient microbiomes is not without problems. Assuming DNA preserves, there is also a problem with contamination and modification of ancient samples, both from the soil deposition, and from other sources, including the laboratory itself.

"In addition to laboratory controls in our study, we use an exciting new quantitative approach called source tracking developed by Dan Knights from Rob Knight's Laboratory at the University of Colorado in Boulder, which can estimate how much of the ancient microbiome data is consistent with the human gut, rather than other sources, such as soil," explains Lewis.

"We discovered that certain samples have excellent gut microbiome signatures, opening the door for deeper analyses of the ancient human gut, including a better understanding of the ancient humans themselves,

such as learning more about their disease burdens, but also learning more about what has changed in our gut today."

**More information:** The paper, "Insights from Characterizing Extinct Human Gut Microbiomes," will be published in the journal *PLOS ONE*.

Provided by University of Oklahoma

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