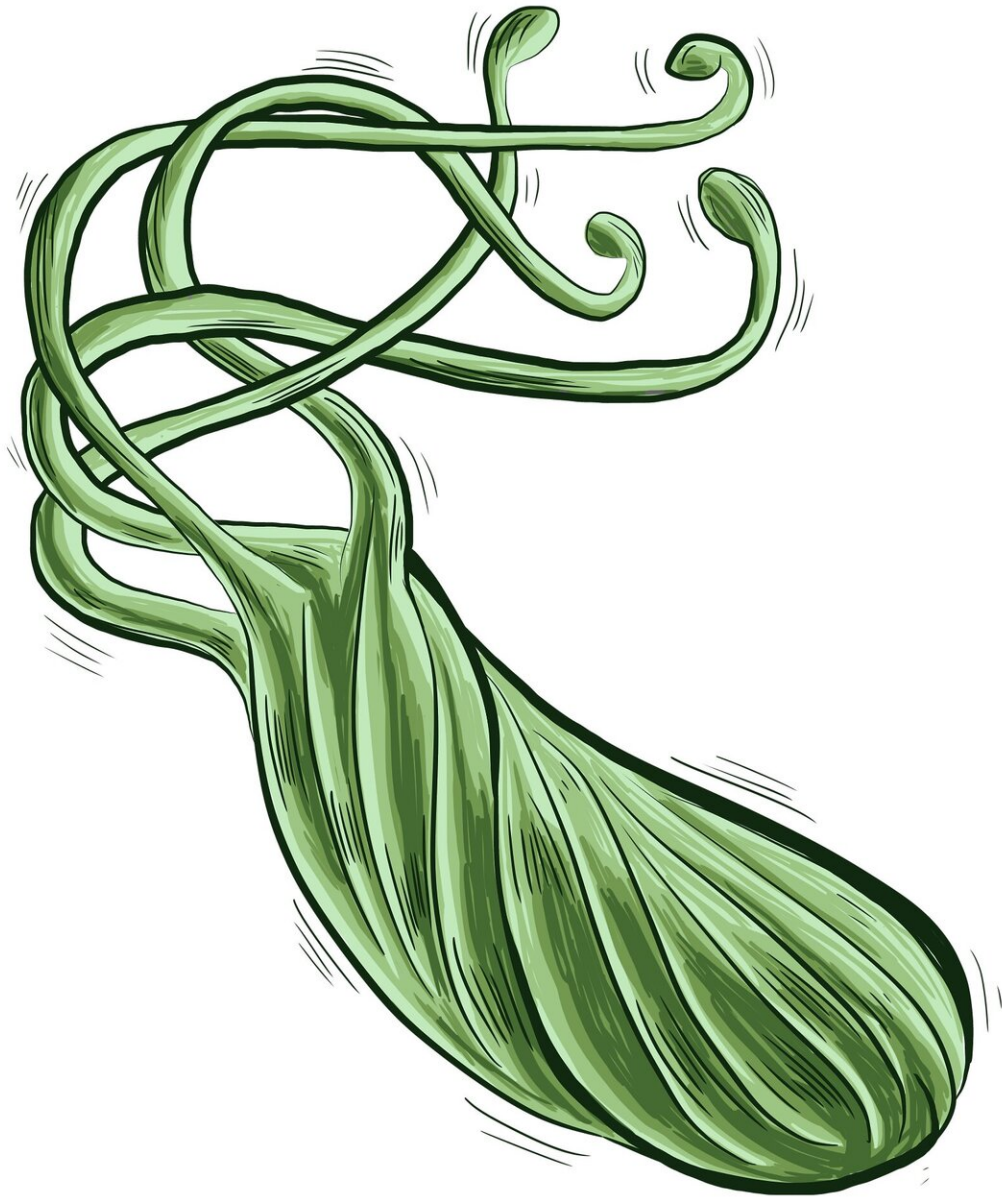


# Early migrations of Siberians to America tracked using bacterial population structures

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Early migrations of humans to the Americas from Siberia around 12,000 years ago have been traced using the bacteria they carried by an international team including scientists at the University of Warwick.

Using samples of a stomach bacteria called *Helicobacter pylori*, which has shared a tight co-evolutionary relationship with humans for at least the past 100,000 years, analyses using new statistical techniques provide evidence that humans colonised the Americas through a pre-Holocene migration of evolutionarily ancient northern Eurasians across the Bering land bridge.

The study entitled "*Helicobacter pylori*'s historical journey through Siberia and the Americas" is published this week (14 June) in the journal *Proceedings of the National Academy of Sciences (PNAS)* by a team of researchers led by Professor Yoshan Moodley at the University of Venda, South Africa.

The research used [genetic information](#) on *H. pylori* catalogued in EnteroBase at the University of Warwick to trace the evolutionary history of the bacteria. *H. pylori* is a stomach bacteria that infects approximately half of individuals worldwide, but scientists have found that its genetic sequence also varies with the region that it is identified in.

Previous analyses had identified three populations of *H. pylori* from individuals in Eurasia and the Americas, and current data demonstrates that *H. pylori* from Siberia define additional previously unknown subpopulations of those groupings. The data also indicated one of these [bacterial populations](#), which includes *H. pylori* from indigenous

Americans, was distributed over the breadth of Siberia, suggesting that this population may have travelled with humans to the Americas at some point.

However, classical statistical analyses of the sequences were partially inconsistent with each other. To reconstruct the most likely evolutionary history for *H. pylori* in Siberia, researchers compared the most likely evolutionary models and timings using a technique called approximate Bayesian computation (ABC). The results showed that a tiny population of *H. pylori* colonised the Americas in a single migration event approximately 12,000 years ago.

Professor Mark Achtman of Warwick Medical School at the University of Warwick, senior co-author on the paper, said: "This project began in the early 2000s, when nothing was known about the genetic diversity of *Helicobacter pylori* in central Asia. By 2007, hundreds of Siberian *H. pylori* strains had been cultivated and selected genes had been sequenced. But repeated attempts by multiple talented population geneticists failed to shed light on their evolutionary history.

"This study now uses the powerful approach of ABC statistics to reconstruct and date the migrations of Siberian *H. pylori* (and their human hosts) across Siberia and to the Americas."

Originally, all [modern humans](#) came from Africa. About 60,000 years ago small groups of hunter-gatherers left Africa on foot and made their way into Eurasia where they settled. These were the world's first human immigrants. Astonishingly, by the end of the ice age some 50,000 years later, modern humans had already reached the American continent which, if travelling over land, is almost as far away from Africa as it is possible to get.

These ancient human migrations took place during the last glacial period,

or ice age, which lasted from 115,000 to 11,700 years ago. At that time, most of northern Eurasia, also known as Siberia, would have been a frozen wasteland, and presumably inhospitable to long-term human settlement. So how then, did humans manage to migrate across this vast region and find their way to North America? This is one of the most important, and as yet unanswered, questions in human prehistory, because it would explain how humans were able to colonise the whole world from an African origin, in such a short space of time.

The team took the unusual approach of using the DNA of a human stomach bacterium named *Helicobacter pylori* as a biomarker for ancient human migrations. They successfully collected, sequenced and analysed bacterial strains from indigenous people across Siberia and the Americas. The bacterial DNA sequence database they generated suggested that, remarkably, some groups of humans, known as ancient northern Eurasians, did manage to reside in Siberia throughout the bitter ice age. Yet, other human groups who originally inhabited warmer latitudes in Asia, colonised Siberia after the end of the ice age, leading to the complex mix of human populations we see in that region today.

The team also used their bacterial data set to model human migration into the Americas. It is important to remember that during the ice age, much more water was frozen at the earth's poles, making the sea level at that time over 100 metres lower than the present-day sea level, thus exposing a land bridge between Eurasia and North America and allowing [human](#) migration. The team showed that one small group of ancient northern Eurasians managed to successfully cross this land bridge about 12,000 years ago, and this population subsequently expanded to give rise to the indigenous Americans we see today.

**More information:** Yoshan Moodley et al., "Helicobacter pylori's historical journey through Siberia and the Americas," *PNAS* (2021). [www.pnas.org/cgi/doi/10.1073/pnas.2015523118](http://www.pnas.org/cgi/doi/10.1073/pnas.2015523118)

Provided by University of Warwick

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