

While it's not usually something I talk about on this podcast, the distribution and history of humans is a question of interest to many people and scientists such as anthropologists. Normally the methods for answering this question come from archaeology, linguistics—studying the distribution of different but related languages—or genetics, comparing common sequences, such as from mitochondria, from different human populations.

But in this study, published this July in PLoS ONE, scientists used a different technique to figure out how human populations spread through continental Southeast Asia: by comparing the genetics of a particular human stomach microbe!

*Helicobacter pylori* is a bacterium found in the stomachs of a significant proportion of humans. Sometimes it can cause ulcers and very occasionally, stomach cancer, but most of the time it is fairly harmless.

The researchers analyzed *H. pylori* samples that had been taken from 66 men in Cambodia over the past few years, by growing them up and sequencing a number of genes that each strain possessed.

Then, by comparing the sequences with other sequences obtained from people around the world, they made a tree to model how the population of Cambodia relates to other peoples.

They found that people fell into two distinct groups, either similar to Europeans or to East Asians. The Europe group was a mix of two older groups, from central Asia and northern Africa. Both the Europe and East Asia groups seemed to have swapped genetic material with each other, indicating that they had been living together for quite a while.

The scientists thought the European grouping may have resulted from colonization by the French, but they found that the proportion in the Europe group in Thailand, which had not been colonized, was higher than places that had been. So it's possible that the European-seeming bacteria in Southeast Asia came from a migration from Europe that took place much earlier than more recent European colonizations. It seemed likely that they could have come from migrations into India around 2000-8000 BC and from there into Southeast Asia around 1000 BC.

Other studies, using mitochondrial DNA, suggested that there weren't any migrations into Southeast Asia after the first one, so this study is the first to suggest something different. Using bacterial DNA to determine human history is another method we can use in addition to the ones we already have to figure out where we came from. The more different, independent methods that agree with each other, the more we can trust that what they're showing is the truth.

There is a lot more to the paper than what I mentioned, and the news article I linked to is also very good, so check them out.

*H. pylori* is a good choice for this kind of study, because being found almost exclusively in the stomach, there is not much crossover of genes very quickly between bacteria in different people. Humans and their bacteria basically evolve together.

This is a creative use of our relationship with microbes to learn about our history, sorta similar to using finger bacteria left behind on keyboards to determine who had touched an object last, as I mentioned in full episode 9. It's pretty cool!