

New technique offers glimpse at human evolution in action

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Credit: Winslow Homer

In research published in *Science*, a Stanford-led international team used a new analytic technique to map recent evolution. The technique relies exclusively on the DNA sequences of modern humans, yet it can reveal rapid changes in the prevalence of different gene variants over the last 2,000 to 3,000 years.

The team was motivated to understand how [natural selection](#) works in humans and was able to draw on the genomes of 3,195 Britons stored in a database of 10,000 UK genomes, said the paper's senior author, Stanford geneticist and biologist Jonathan Pritchard, PhD. The lead author was Yair Field, PhD, a postdoctoral scholar in Pritchard's lab.

Previous approaches lacked the resolution to look at periods of time less than 10,000 to 20,000 years, Pritchard said. But their approach could recognize very recent and very strong selection, he said. "Our work shows that selection has continued until very recently, probably within the past 500 years or so," said Pritchard.

Tracking changes in the population wide frequencies of different versions, or alleles, of a gene allows researchers to watch microevolution in action. They found several cases of rapid evolution, including the gene that regulates whether we make the enzyme lactase, which allows us to digest milk sugars, which is one of the best understood examples of this small-scale evolutionary change.

Infants make lots of lactase so they can digest milk. Most mammals turn off the lactase gene after weaning. Once lactase is turned off in adults, if

they drink milk, they get a stomach ache and diarrhea. But in some human populations, up to 80 percent of people carry a mutation that allows them to continue making lactase and drink milk as adults. Populations with a high prevalence of the lactase-persistence gene are more likely to raise animals that produce milk, such as cows and goats.

Since dairy farming is only a few thousand years old, it was no surprise that the lactase-persistence gene has become more prevalent, evolving rapidly and recently among the Britons, the study found.

Most traits, however, are influenced not by one or two genes but by hundreds that are scattered across our 23 pairs of chromosomes. For example, nearly 700 genes are known to influence height in humans. And northern Europeans are known to possess more height-promoting alleles than southern Europeans.

The current study concluded that in the last 2,000 to 3,000 years, natural selection has caused an increase in the prevalence of 551 gene alleles associated with being taller among the Britons in the sample.

What selective forces might cause the changes is still unknown. For natural selection to occur, individuals with the selected traits would have to consistently have more children over the 2,000-year period of the study.

I asked Pritchard how he knows that the changes in allele frequency are due to natural selection rather than chance. He said that although the genome is constantly changing, the new technique allows researchers to pick out alleles whose frequency is changing faster than that of other alleles.

"If most of the genome is not under strong selection, it's all kind of drifting along at the same rate. The amount of drift is the same," he said.

"So if you see something different—like a change in frequency that's 10 times or 100 times than what you'd expect from drift—then it's much more likely that what your seeing it due to natural selection."

More information: Y. Field et al. Detection of human adaptation during the past 2000 years, *Science* (2016). [DOI: 10.1126/science.aag0776](https://doi.org/10.1126/science.aag0776)

Provided by Stanford University

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