

New analysis provides fuller picture of human expansion from Africa

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A new, comprehensive review of humans' anthropological and genetic records gives the most up-to-date story of the "Out of Africa" expansion that occurred about 45,000 to 60,000 years ago.

This expansion, detailed by three Stanford geneticists, had a dramatic effect on [human genetic diversity](#), which persists in present-day populations. As a small group of modern humans migrated out of Africa into Eurasia and the Americas, their [genetic diversity](#) was substantially reduced.

In studying these migrations, genomic projects haven't fully taken into account the rich archaeological and anthropological data available, and vice versa. This review integrates both sides of the story and provides a foundation that could lead to better understanding of [ancient humans](#) and, possibly, genomic and medical advances.

"People are doing amazing [genome sequencing](#), but they don't always understand human [demographic history](#)" that can help inform an investigation, said review co-author Brenna Henn, a postdoctoral fellow in genetics at the Stanford School of Medicine who has a PhD in anthropology from Stanford. "We wanted to write this as a primer on pre-[human history](#) for people who are not anthropologists."

This model of the Out of Africa expansion provides the framework for testing other anthropological and [genetic models](#), Henn said, and will allow researchers to constrain various parameters on [computer](#)

[simulations](#), which will ultimately improve their accuracy.

"The basic notion is that all of these disciplines have to be considered simultaneously when thinking about movements of ancient populations," said Marcus Feldman, a professor of biology at Stanford and the senior author of the paper. "What we're proposing is a story that has potential to explain any of the [fossil record](#) that subsequently becomes available, and to be able to tell what was the size of the population in that place at that time."

The anthropological information can inform geneticists when they investigate certain [genetic changes](#) that emerge over time. For example, [geneticists](#) have found that genes for lactose intolerance and gluten sensitivity began to emerge in populations expanding into Europe around 10,000 years ago.

The anthropological record helps explain this: It was around this time that humans embraced agriculture, including milk and wheat production. The populations that prospered – and thus those who survived to pass on these mutations – were those who embraced these unnatural food sources. This, said Feldman, is an example of how human movements drove a new form of natural selection.

Populations that expand from a small founding group can also exhibit reduced genetic diversity – known as a "bottleneck" – a classic example being the Ashkenazi Jewish population, which has a fairly large number of genetic diseases that can be attributed to its small number of founders. When this small group moved from the Rhineland to Eastern Europe, reproduction occurred mainly within the group, eventually leading to situations in which mothers and fathers were related. This meant that offspring often received the same deleterious gene from each parent and, as this process continued, ultimately resulted in a population in which certain diseases and cancers are more prevalent.

"If you know something about the demographic history of populations, you may be able to learn something about the reasons why a group today has a certain genetic abnormality – either good or bad," Feldman said. "That's one of the reasons why in our work we focus on the importance of migration and history of mixing in human populations. It helps you assess the kinds of things you might be looking for in a first clinical assessment. It doesn't have the immediacy of prescribing chemotherapy – it's a more general look at what's the status of human variability in DNA, and how might that inform a clinician."

More information: The study is published in the current edition of the *Proceedings of the National Academy of Sciences*.

intl.pnas.org/content/early/20.../1212380109.abstract

Provided by Stanford University

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