

Scientific study sheds new light on human evolution

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A new study shows that modern humans (*Homo sapiens*) inherited DNA from two previously unidentified extinct populations for which there is currently no known fossil evidence. The remarkable discovery was made possible by the ability of scientists to identify complete human genomes and examine them in exquisite detail using advanced computational tools.

The results deepen our scientific understanding of how interconnected and complex human evolution was.

The research, led by Priya Moorjani's laboratory at the University of California, Berkeley in the US, with graduate student Yulin Zhang and Johns Hopkins postdoctoral researcher Arjun Biddanda as co-first authors, was published in the journal *Science* on July 30, 2026.

It builds on more than a decade of prior genomic research establishing that the modern human genome contains DNA inherited from Neanderthals and Denisovans, our closest known extinct relatives, following landmark 2010 studies that first sequenced their genomes and proved ancient interbreeding had occurred.

Neanderthal are well known as the stockier cousin of modern humans. They lived in Europe and went extinct about 40,000 years ago.

Once thought to have disappeared due to lack of intelligence compared to *Homo sapiens* which outcompeted and even killed them, Neanderthal are now understood to have been highly complex socially and culturally. They were as technologically advanced as *Homo sapiens* of a similar age, and there is evidence that Neanderthal practiced burial rights and decorative crafts.

It is now believed that, rather than simply being wiped out by *Homo sapiens*, Neanderthal were outcompeted but also assimilated into the modern human population through interbreeding.

Denisovans, our closest relatives who lived in Asia, died out about 30,000 years ago. They too did not vanish completely, leaving traces of their DNA in modern humans, particularly those living in the Pacific Islands today.

The new study extends these established findings by

showing this pattern of ancient mixing was even more extensive than previously known.

Analysing genomes from 503 people worldwide, the researchers identified two previously unknown archaic hominin lineages that had interbred with the ancestors of modern humans.

The first, which the team calls a “ghost” lineage, split from the human line about 800,000 years ago and interbred with human ancestors in Africa at some point more than 50,000 years ago—before the major migration of *Homo sapiens* out of the continent. This ghost DNA is present in every population studied, comprising roughly 0.5 to 1 percent of the genome of every living person, comparable in scale to Neanderthal ancestry.

Yulin Zhang emphasised in a UC Berkeley news release that the ghost lineage “is in all modern humans, not only in Africans.”

The second, so-called “super-archaic” lineage that diverged some 1.8 million years ago, never interbred with humans directly. Instead, it mixed with Denisovans in Eurasia, who later passed a trace of that ancient DNA on to modern humans through further interbreeding, primarily detectable today in the genomes of modern Pacific Islander populations. Altogether, roughly 2 percent of the modern human genome now appears to derive from archaic hominins previously unknown to science.

The finding has been received with considerable interest, alongside calls for careful, ongoing verification.

Moorjani stressed the importance of rigour in interpreting such findings in a media statement on *EurekAlert!*: “The increasing scale and complexity of genomic datasets make transparency, reproducibility, and open methods more important than ever. Continued efforts to share data, software, and benchmarking frameworks, together with careful validation across independent datasets, will help ensure that new discoveries are both robust and reproducible.”

Yale computational biologist Patrick Reilly, who was not involved in the study, echoed this caution in comments

published in the *Scientific American*, noting that “as with any method, there will always be false positives,” and that confirmation through independent methods and future fossil evidence will be needed.

Previous discoveries of archaic ancestry relied on comparing living human DNA against ancient DNA physically extracted from Neanderthal and Denisovan fossils. That approach cannot work for populations that left no recoverable bones.

Until recently, palaeontologists and archaeologists have had to develop all of their understanding of human evolution on scant fossil evidence. For more than a decade after their 2010 discovery, for example, Denisovans were known only from a finger bone and a few teeth—no skull was confirmed until 2025.

Over the last two decades, scientists have added DNA to tools they can use to explain how the human story developed over millions of years. Even this, though, has required specimens which are well-preserved enough to have genetic material that has not degraded over thousands of years.

The Berkeley team’s tool, called TRACE, requires no ancient DNA and no fossils at all.

The human genome is a tangle of many family trees carrying within it a complex history of ancient mixing. The researchers built the computer program TRACE to comb through this genetic tangle and pick out the pieces that signal ancient lineages.

The method was first tested against the known Neanderthal genome and Denisovan-linked regions, successfully rediscovering both, before being applied to search for entirely new, unknown lineages.

The study exemplifies how advances in computing power and genomic sequencing have transformed evolutionary science over the past two decades. Where earlier researchers were confined to whatever bones happened to survive and be discovered, geneticists can now look at hundreds of human genomes at the same time.

Through this remarkable capability scientists have inferred the existence, approximate age, and population history of two extinct human relatives despite possessing not a single fragment of their physical remains.

Given how sparse and geographically uneven the fossil record remains—particularly in tropical Africa, where organic remains decay rapidly—this computational approach may prove indispensable for filling gaps that fossils alone may never resolve.

The findings also add a new layer to the “Out of Africa” model of human dispersal.

From the 1980s until the 2010s, this model competed with a rival “multiregional” theory, which held that modern humans evolved simultaneously across Africa, Europe and

Asia from earlier populations, rather than solely in Africa. Genetic evidence, beginning with the 1987 “Mitochondrial Eve” study, gradually settled this debate in favour of Out of Africa, which is now the accepted model.

The standard theory holds that *Homo sapiens* evolved in Africa and later migrated into Eurasia around 50,000 to 70,000 years ago, encountering Neanderthals and Denisovans there.

The new study shows that even before that migration occurred, the population that would eventually leave Africa had already absorbed DNA from an unrelated, unknown hominin group within the continent itself.

The researchers are careful to state only that this African admixture predated the migration out of the continent; they do not claim to have determined the exact number of separate mixing events, their precise dates, or the specific location within Africa where they occurred, leaving those details as open questions for future research.

Taken together with two decades of fossil discoveries—the diminutive *Homo floresiensis* found in Indonesia in 2003, the genetically defined Denisovans identified in Siberia in 2010, and *Homo naledi* and *Homo luzonensis* unearthed in South Africa and the Philippines respectively—this research reinforces a fundamental shift in how scientists understand human evolution.

The old image of a single evolutionary ladder, with modern humans as its final, inevitable rung, has been replaced by something far more complex: a landscape in which multiple related human populations lived side by side for hundreds of thousands of years, repeatedly meeting, mixing and exchanging genes across vast stretches of time and geography.

Moorjani described this shift directly in the UC Berkeley news release: “We often think of human evolution as a branching tree, but new genomic data and analytical methods reveal a much more interconnected history—more like a complex web of populations connected by repeated episodes of migration and mixing.”

This reflects a materialist understanding of evolution as a dynamic process, shaped by chance encounters, migration and environmental pressure rather than a fixed march toward a single, inevitable outcome.



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