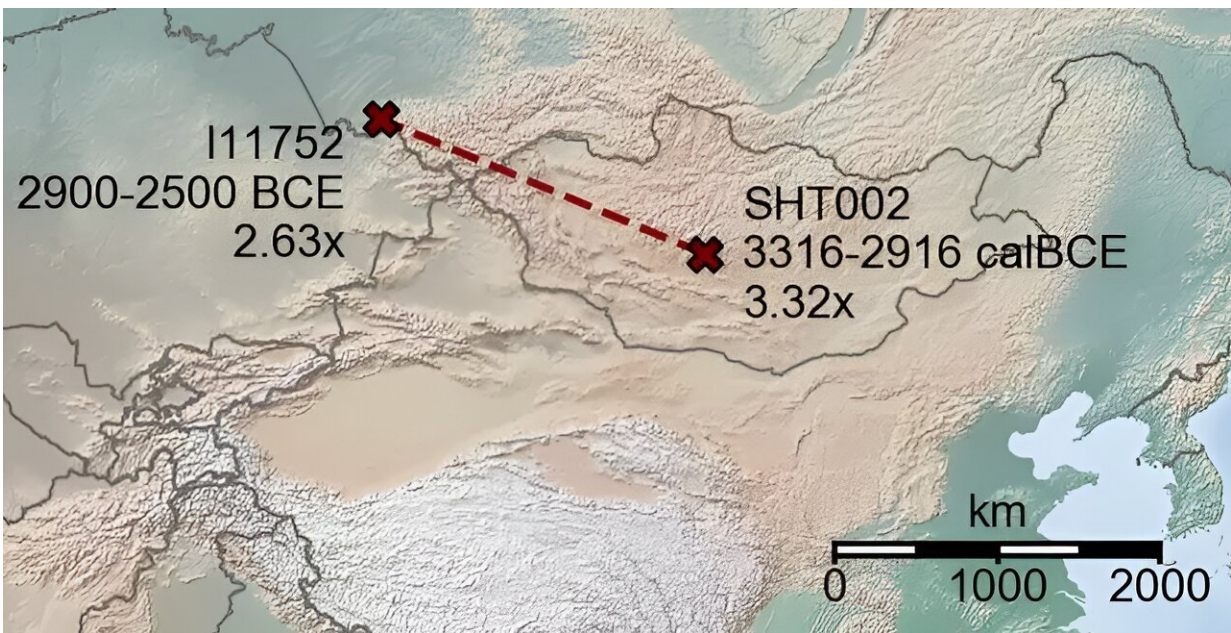


Revealing close and distant relatives in ancient DNA with unprecedented precision

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When screening ancient Eurasian individuals for IBD segments, the researchers detected a pair of biological relatives whose remains were buried 1,410 kilometers apart, one in central Mongolia and one in southern Russia. Credit: *Nature Genetics* (2023). DOI: 10.1038/s41588-023-01582-w

If two persons are biologically related, they share long stretches of DNA that they co-inherited from their recent common ancestor. These almost identically shared stretches of genomes are called IBD ("Identity by Descent") segments. Up to the sixth-degree relatives—such as second to

third cousins would be, or a great great great great grandparent—the two relatives even share multiple IBD segments. Personal genomics companies such as 23andme or Ancestry detect those segments routinely in DNA of their customers, and use this signal to distinctively reveal biological relatives in their databases.

In a [new study](#) published in *Nature Genetics*, researchers from the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany, and Harvard University, U.S., has now developed a powerful new tool named "ancIBD" to extract these IBD segments also in genomes of humans who lived hundreds, thousands, or even tens of thousands of years in the past.

The critical challenge was that such ancient genomes are often very degraded and therefore of much worse quality than modern DNA, so the authors had to come up with an innovative trick to fill in gaps in ancient genomes using modern reference DNA panels.

This advance unlocked completely new ways to analyze ancient DNA data. "By precisely measuring the regions of shared [genome](#) we can now detect pairs of up to sixth-degree relatives also in ancient genomes, while previous aDNA methods using genomic average similarities were limited to detecting only up to third-degree relatives," explains Yilei Huang, a first author of the study and Ph.D. researcher at the Max Planck Institute for Evolutionary Anthropology.

Researchers identified hundreds of new pairs of relatives

The authors then applied their new tool to a dataset of 4,248 previously published ancient genomes from across Eurasia and the last 50,000 years and were able to identify hundreds of previously undetected pairs of

relatives. In some fascinating cases, the two relatives were buried a large distance apart, which directly revealed the mobility of past people.

In one such case, the authors detected a pair of two Early Bronze Age nomads from Central Asia who lived ca. 5,000 years ago and were fifth-degree relatives who were buried ca. 1,500 kilometers apart from each other. These individuals, or their immediate ancestors, must have moved hundreds of kilometers between being born and being buried.

The new tool allowed the authors to also investigate even more [distant relatives](#) with unprecedented precision. Not all such relatives beyond the tenth degree share long IBD, but the authors could measure the average rate of sharing long DNA between groups of ancient people. These signals revealed previously unknown connections.

"We found exciting links between ancient cultures, and the signal of long shared segments allowed us for the first time to specifically demonstrate [close relationships](#) between important ancient cultures, sometimes over vast spaces over the order of only a few hundred years," says Harald Ringbauer from the Max Planck Institute for Evolutionary Anthropology, the lead researcher of this study.

The new method to screen ancient DNA for parental relatedness gives researchers a versatile new computational tool. Looking forward, the field of ancient DNA is quickly developing, with thousands of [ancient genomes](#) being produced every year. By revealing close and distant biological relatives, the new tool will allow researchers to shed new light on the lives of our ancestors, both on the small scale, relevant to understanding the life stories of people and their relatives, and on the macroscale, relevant to large-scale cultural-historical events.

More information: Harald Ringbauer et al, Accurate detection of identity-by-descent segments in human ancient DNA, *Nature Genetics*

(2023). [DOI: 10.1038/s41588-023-01582-w](https://doi.org/10.1038/s41588-023-01582-w)

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