

# 'Game-changing' research could solve evolution mysteries

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A *Stephanorhinus* skull from Dmanisi. Credit: Mirian Kiladze, Georgian National Museum

An evolution revolution has begun after scientists extracted genetic information from a 1.7 million-year-old rhino tooth—the largest and oldest genetic data to ever be recorded.

Researchers identified an almost complete set of proteins, a proteome, in the dental enamel of the rhino and the [genetic information](#) discovered is one million years older than the oldest DNA sequenced from a 700,000-year-old horse.

The findings by scientists from the University of Copenhagen and St John's College, University of Cambridge, are published today (September 11) in *Nature*. They mark a breakthrough in the field of ancient biomolecular studies and could solve some of the biggest mysteries of animal and human biology by allowing scientists to accurately reconstruct evolution from further back in time than ever before.

Professor Enrico Cappellini, a specialist in Palaeoproteomics at the Globe Institute, University

of Copenhagen, and first author on the paper, said: "For 20 years ancient DNA has been used to address questions about the evolution of extinct species, adaptation and [human migration](#) but it has limitations. Now for the first time we have retrieved ancient genetic information which allows us to reconstruct molecular evolution way beyond the usual time limit of DNA preservation.

"This new analysis of ancient proteins from dental enamel will start an exciting new chapter in the study of molecular evolution."

DNA data that genetically tracks human evolution only covers the last 400,000 years. But the lineages that led to modern humans and to the chimp—the living species genetically closest to humans—branched apart around six to seven million years ago which means scientists currently have no genetic information for more than 90 per cent of the evolutionary path that led to [modern humans](#).

Scientists also don't know what the genetic links are between us and extinct species such as *Homo erectus*—the oldest known species of human to have had modern human-like body proportions—because everything that is currently known is almost exclusively based on anatomical information, not genetic information.



Left lower Stephanorhinus molar from Dmanisi. Credit: Natural History Museum of Denmark

Researchers have now used ancient protein sequencing—based on ground-breaking technology called mass spectrometry—to retrieve genetic information from the tooth of a 1.77 million year old Stephanorhinus—an extinct rhinoceros which lived in Eurasia during the Pleistocene. Researchers took samples of dental enamel from the ancient fossil which was discovered in Dmanisi, Georgia, and used [mass spectrometry](#) to sequence the ancient protein and retrieved genetic information previously unobtainable using DNA testing.

Tooth enamel is the hardest material present in mammals. In this study researchers discovered the set of proteins it contains lasts longer than DNA and is more genetically informative than collagen, the only other protein so far retrieved from fossils older than one million years.

Professor Jesper V. Olsen, head of the Mass Spectrometry for Quantitative Proteomics Group at the Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, and co-corresponding author on the paper, said: "Mass spectrometry-based protein sequencing will enable us to retrieve reliable and rich genetic information from mammal fossils that are millions of years old, rather than just thousands of years old. It is the only technology able to provide the robustness and accuracy needed to sequence tiny amounts of [protein](#) this old."

Professor Cappellini added: "Dental enamel is extremely abundant and it is incredibly durable, which is why a high proportion of fossil records are teeth.

"We have been able to find a way to retrieve genetic information that is more informative and older than any other source before, and it's from a source that is abundant in the fossil records so the potential of the application of this approach is extensive."

Lead author on the paper Professor Eske Willerslev, who holds positions at St John's College, University of Cambridge, and is director of The Lundbeck Foundation Centre for GeoGenetics, Globe Institute, Faculty of Health and Medical Sciences, at the University of Copenhagen, said: "This research is a game-changer that opens up a lot of options for further evolutionary study in terms of humans as well as mammals. It will revolutionise the methods of investigating evolution based on molecular markers and it will open a complete new field of ancient biomolecular studies."

This rearranging of the evolutionary lineage of a single species may seem like a small adjustment but identifying changes in numerous extinct mammals and humans could lead to massive shifts in our understanding of the way the world has evolved.

The team of scientists is already implementing the findings in their current research. The discovery could enable scientists across the globe to collect the genetic data of ancient fossils and to build a bigger, more accurate picture of the [evolution](#) of hundreds of species including our own.

**More information:** Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny, *Nature* (2019). [DOI: 10.1038/s41586-019-1555-y](#) , [nature.com/articles/s41586-019-1555-y](#)

Provided by University of Cambridge

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