



PRESS RELEASE

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Genome of extinct Siberian human sheds new light on modern human origins.

The sequencing of the nuclear genome from an ancient finger bone from a Siberian Cave shows that the cave dwellers were neither Neandertals nor modern humans.

An international team of researchers led by Svante Pääbo of the Max Planck Institute for Evolutionary Anthropology in Leipzig (Germany) has sequenced the nuclear genome from a finger bone of an extinct hominin that is at least 30,000 years old and was excavated by archaeologists from the Russian Academy of Sciences in Denisova Cave in southern Siberia, Russia, in 2008.



Image 1:
Excavation works inside the East Gallery of the Denisova cave where archaeologists found part of a finger bone in 2008. (Copyright: Max Planck Institute for Evolutionary Anthropology).

Earlier this year the team showed that the mitochondrial DNA from the finger bone displayed an unusual sequence suggesting that it came from an undescribed ancient hominin form. Using techniques the researchers developed to sequence the Neandertal genome, they have now sequenced the nuclear genome from the bone. They find that the individual was female and comes from a group of hominins that shared an ancient origin with Neandertals, but subsequently had a distinct history. They call this group of hominins Denisovans. Unlike Neandertals, Denisovans did not contribute genes to all present-day

Eurasians. However, Denisovans share an elevated number of genetic variants with modern-day Papuan New Guinean populations, suggesting that there was interbreeding between Denisovans and the ancestors of Melanesians. In addition, a Denisovan tooth found in the same cave shows a morphology that is distinct from Neandertals and modern humans and resembles much older hominin forms. Bence Viola, a scientist at the Max Planck Institute of evolutionary Anthropology comments: “The tooth is just amazing. It allows us to connect the morphological and genetic information”.



Image 2:

The morphology of this Denisovan molar differs from the morphology of a Neandertal or a modern human molar. (Copyright: Max Planck Institute for Evolutionary Anthropology)

David Reich, an Associate Professor at Harvard Medical School who led the population genetic analysis, says: “The fact that Denisovans were discovered in Southern Siberia but contributed genetic material to modern human populations from New Guinea suggests that Denisovans may have been widespread in Asia during the Late Pleistocene.”

Svante Pääbo of the Max Planck Institute of evolutionary Anthropology remarks: “In combination with the Neandertal genome sequence, the Denisovan genome suggests a complex picture of genetic interactions between our ancestors and different ancient hominin groups”. (Nature, December 23, 2010).

This study also involved contributions from researchers at the Broad Institute of Harvard and MIT (Massachusetts, USA), the University of California both Santa Cruz and Berkeley (California, USA), the University of Tübingen (Germany), Emory University (Georgia, USA), the University of Montana (Montana, USA), the University of Washington (Washington, USA), the Institute of Evolutionary Biology (Barcelona, Spain), the Institute of Vertebrate Paleontology and Paleoanthropology of the Chinese Academy of Sciences (Beijing, China), the

University of British Columbia (Vancouver, Canada), and the Institute of Archaeology & Ethnography, Russian Academy of Sciences, Siberian Branch (Novosibirsk, Russia).

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Original paper:

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