

Human evolution: The Neanderthal in the family

Thirty years after the study of ancient DNA began, it promises to upend our view of the past.

Ewen Galloway

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An equine oddity with the head of a zebra and the rump of a donkey, the last quagga (*Equus quagga quagga*) died in 1883. A century later, researchers published¹ around 200 nucleotides sequenced from a 140-year-old piece of quagga muscle. Those scraps of DNA — the first genetic secrets pulled from a long-dead organism — revealed that the quagga was distinct from the mountain zebra (*Equus zebra*).

More significantly, the research showed that from then on, examining fossils would no longer be the only way to probe extinct life. “If the long-term survival of DNA proves to be a general phenomenon,” geneticists Russell Higuchi and Allan Wilson of the University of California, Berkeley, and their colleagues noted in their quagga paper¹, “several fields including palaeontology, evolutionary biology, archaeology and forensic science may benefit.”

A million-year-old genome

Ludovic Orlando, an evolutionary biologist at the University of Copenhagen, had low expectations when he started sequencing DNA from a 560,000-to-780,000-year-old horse leg bone. His colleague, Eske Willerslev, had discovered the bone buried in the permafrost of the Canadian Yukon in 2003. Then he had chucked it into a freezer, waiting for technological improvements that would allow the bone's degraded DNA to be read. (Freezers in ancient-DNA labs brim with such 'wait and see' samples.)

On a Sunday evening in 2010, Willerslev called Orlando to say that the time had come. Orlando was unconvinced: “I started the project with the firm intention of proving that it was not possible,” he says.

Sequencing ancient DNA is a battle against time. After an organism dies, the long strands of its DNA fissure into ever shorter pieces, helped along by DNA-munching enzymes. Low temperatures slow this process, but eventually the strands become so short that they contain little information.

To read the horse's genome, Orlando needed to shepherd useful DNA fragments through the harsh enzymatic treatments used to extract them and ready them for sequencing. Orlando and his team found that the preparation lost vast quantities of fragments. But with a few tweaks to the experimental protocol, such as reducing the extraction temperature, the researchers captured ten times more scraps of DNA than before — and produced a draft of the oldest genome on record².

References:

¹ Higuchi, R. Bowman, B., Freiberger, M., Ryder, O. A. & Wilson, A. C. *Nature* **312**, 282–284(1984).

² Orlando, L. et al. *Nature* **499**, 74–78 (2013).

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HIDDEN HERITAGE

The study of ancient DNA is revealing connections between archaic humans — and the traces they left behind in modern genomes.



Homo antecessor may be related to a ghost population that bred with archaic humans called Denisovans.



Researchers hope to push the limits of technology to tackle *Homo erectus* fossils found in relatively warm climates.



Fossils in Spain show an unexpected kinship with Denisovans found thousands of kilometres away.



Modern humans from Oceania share 3–6% of their DNA with Denisovans.

