

# Woolly mammoth genomes offer insight into their history and extinction

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Eleftheria Palkopoulou is with a mammoth tusk in the ancient DNA lab at the Swedish Museum of Natural History. Credit: Love Dalén

Before the world's last woolly mammoth took its final breath, the iconic animals had already suffered from a considerable loss of genetic diversity. These findings, based on a comparison of the first complete genome sequences isolated from two ancient mammoth specimens, are reported in the Cell Press journal *Current Biology* on April 23.

One of those mammoths, representing the last population on Russia's Wrangel Island, is estimated to have lived about 4,300 years ago. The other specimen, from northeastern Siberia, is about 44,800 years old. The younger of the two specimens showed much lower genetic variation, including large stretches of DNA with no variation whatsoever - the mark of living in a very small population in which related individuals unavoidably mate with each other.

"We found that the genome from one of the world's last mammoths displayed low [genetic variation](#) and a signature consistent with inbreeding, likely due to the small number of mammoths that managed to survive on Wrangel Island during the last 5,000 years of the species' existence," says Love Dalén of the Swedish Museum of Natural History.

Sequencing ancient genomes is no easy feat, explains Dalén and Eleftheria Palkopoulou. In most cases, the DNA is damaged, highly fragmented, and contaminated by DNA from microbes and sediments. After considerable screening, the researchers managed to find two samples with exceptionally well-preserved mammoth DNA.

Because an individual's genome is a mosaic of bits and pieces of DNA inherited from a large number of its ancestors, a single genome contains a vast amount of information about a species' population history. Taking advantage of this, the researchers inferred that [woolly mammoth](#) populations suffered a blow in the Middle or Early Pleistocene, some 250,000 to 300,000 years ago, for reasons that aren't at all clear. That more ancient and temporary loss in numbers was followed by a more

severe decline at the end of the last glaciation, from which the woolly mammoth never recovered.



A mammoth tusk by a river on the Taimyr Peninsula in Siberia. Credit: Love Dalén

"Only by generating high-quality genomes could we discover population-size changes far back in time, revealing two significant population crashes in the mammoth's history," Palkopoulou says.

The study is a result of an international collaboration that involved researchers from Sweden, the United States, Canada, and Russia. The researchers say that they plan to continue sequencing genomes representing different time points in order to further investigate the woolly mammoth's evolutionary history.





Love Dalén is with mammoth bone found on the Taimyr Peninsula in Siberia.  
Credit: Ivar Benediktsson

"Sequencing the genomes from extinct animals will not only help us better understand the biology and history of these species, but can also provide important information on how and why species become extinct in general," Dalén says.

**More information:** *Current Biology*, Palkopoulou et al.: "Complete genomes reveal signatures of demographic and genetic declines in the woolly mammoth" [dx.doi.org/10.1016/j.cub.2015.04.007](https://doi.org/10.1016/j.cub.2015.04.007)

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