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PALAEOGENETICS

Genomes reveal mammoth history

Nature 520, 589 (30 April 2015) | doi:10.1038/520589d
Published online 29 April 2015

Subject terms: Genomics · Palaeontology

Genome sequences from two woolly mammoths provide a rare look at the genetic events leading up to extinction.



Nat. Hist. Mus., London/SPL

Eleftheria Palkopoulou and Love Dalén at the Swedish Museum of Natural History in Stockholm sequenced the genomes of a woolly mammoth (*Mammuthus primigenius*; artist's impression pictured) that roamed Eurasia roughly 45,000 years ago, and of one that lived on a remote island some 4,000 years ago, just before the animals went extinct. Using the genomes to infer population trends, the team found that mammoths declined around 300,000 years ago, then recovered until about 12,000 years ago when mainland populations went extinct, leaving just a few hundred island-dwelling animals.

The island mammoth showed decreased genetic diversity, which could have contributed to extinction, the team says, adding that this kind of genetic analysis could help conservation biologists to assess how much diversity has been lost from endangered species today.

Curr. Biol. <http://doi.org.ezproxy.lib.utah.edu/34d> (2015)

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Image credit: Zachary Canepari/NYT/Redux/eyeview

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18 October 2015 — 22 October 2015
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