Mammuthus sp. (Early and Middle Pleistocene Mammoths)

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Lessons Learned
Mammoths, *Mammuthus* sp., are iconic megafauna species that came to symbolize the Ice Age. However, the typical Late Pleistocene forms, which we know as the woolly and Columbian mammoths, were only the youngest offshoots on the mammoth evolutionary tree. The time window during which mammoths acquired traits that made them adapted to the cold environment has now become clearer thanks to genomic data from three Early and Middle Pleistocene mammoths. Two of these, identified as steppe-mammoths and called Krestovka and Adycha, lived >1 million years ago (Mya) and represent two independent genetic lineages. The third mammoth, Chukochya, is a 650 000-year-old early representative of the woolly mammoth, which descended from the Adycha lineage.

Analyses of gene variants, previously identified as underlying cold adaptation in the woolly mammoth, showed that more than 80% of these were already present in the Adycha genome, that is, before woolly mammoths evolved. This includes genes potentially involved in thermal sensation, hair growth, and circadian rhythms.

Fun fact about the Genome
One of the key genes in the evolution of the mammoth lineage is *TRPV3*, which encodes a temperature-sensitive transient receptor channel. The *TRPV3* gene was essential for cold adaptation due to its pleiotropic action, affecting at the same time thermosensation, hair growth, and build-up of fat deposits. Previous studies showed that mice

Figure 1. (A) Map showing the locations of the samples analysed in van der Valk et al. (2021). (B) A timeline showing the age of ancient genomic data published to date. (C) Tooth morphology of the Krestovka and Chukochya samples. (D) A phylogenetic tree showing the relationships among the analysed samples, built in FASTME using pairwise genetic distances and assuming balanced minimum evolution. Node labels indicate bootstrap support and blue dots highlight the Early and Middle Pleistocene samples. Silhouettes were obtained from PhyloPic and were made by Scott Hatmann and Zimices under the Creative Commons Attribution-ShareAlike 3.0 Unported license (http://creativecommons.org/licenses/by-nc/3.0/), no modifications were made. Abbreviations: Kya, thousand years ago; M. columbi, Mammuthus columbi, Mya, million years ago.

**GENOME FACTS:**
These three *Mammuthus* sp. specimens represent the oldest DNA sequenced to date (~1.15 Mya, ~1.1 Mya, and ~0.65 Mya).

A total of 49 million, 884 million and 3671 million bp of genomic data were generated for the Krestovka, Adycha, and Chukochya specimens.

Early and Middle Pleistocene mammoth DNA displays higher fragmentation and greater postmortem damage at CpG sites than Late Pleistocene mammoths.

By comparing the relative number of DNA sequences aligned to the autosomes and to chromosome X, all three *Mammuthus* sp. specimens were identified as males.

**SPECIES FACTS:**
Asian elephants are the closest living relatives of mammoths.

Just like present-day elephants, mammoths had a matriarchal social system, meaning that herds consisted of related adult females and juveniles. Adult males either lived alone or within small bachelor groups.

During the past Ice Age, the mammoth’s distribution stretched from Western Europe to Siberia and across North America.

One of the most notable morphological adaptive changes in the mammoth lineages through time is the evolution of their molar teeth characterized by an increase in the number of enamel ridges, corresponding to a shift in diet from browsing to grazing.
with TRPV3 knockout prefer colder temperatures. Interestingly, of the four substitutions observed in the TRPV3 gene in the Late Pleistocene woolly mammoths, we observed only two in the early woolly mammoth (Chukochya) and its ancestor (Adycha).

Declaration of Interests
There are no interests to declare.

Literature