

## More light shines on Pleistocene extinction event with possible discovery of new genus of horse

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Credit: AI-generated image (disclaimer)

A group of North American Pleistocene horses was previously identified as different species. Now, mitochondrial and partial nuclear genomic studies support the idea that there is only one species, which belongs to a new genus.



Meet Haringtonhippus, a possible new genus of horse covering the extinct New World stilt-legged (NWSL) equids, which, until now, have been thought of as multiple species. Prior to this study, these thinlimbed, lightly-built horses were believed to be related to the Asiatic wild ass or onager, or simply a separate species within the genus Equus, which includes all living horses, asses, and zebras. The fossil record shows how the ancestors of these animals evolved from dog-sized, three-toed browsers to larger, one-toed grazers over a period of about 55 million years. Along the way many species became extinct.

The current mitochondrial DNA (mtDNA) -based phylogenetic model suggests that the stilt-legged morphology arose independently in the New and Old Worlds. The thought is that the two may have converged in the face of the need to adapt to arid climates and habitats. But the researchers, supported in part by the EU through the PEGASUS project, point out that this is based on two questionable sources: an unreliable data type and mitochondrial genome sequences that are incomplete or otherwise problematic.

As they explain in their recently published paper, "A <u>new genus</u> of horse from Pleistocene North America," they used their phylogenetic framework and comparisons between specimens identified by palaeogenomics and/or morphology, to try to determine the taxonomy of middle-late Pleistocene NWSL equids.

The fossil record of the horse family is robust but more recently, from around 2.5 million years ago, things get a bit confused. This is the Pleistocene and it is not clear how horses of this period relate to each other. The downside of this abundant <u>fossil record</u>, say the researchers, is that many dubious fossil equid taxa have been erected, a problem especially acute within Pleistocene Equus of North America.

They have been classed into two groups, stout-legged and stilt-legged



horses, both of which became extinct in North America towards the end of the period. Based on their anatomy, many scientists suggested that stilt-legged horses were most closely related to modern-day asses living in Asia. But other studies using ancient DNA placed the stilt-legged horses closer to the stout-legged horses.

There appears to be a discrepancy between the rates of extirpation between NWSL equids south and north of the <u>continental ice sheets</u>. This implies that their populations responded variably to demographic pressures in different parts of their range, which is consistent with results from some other megafauna, report the researchers. To test this hypothesis, the team analyses 26 full mitochondrial genomes and 17 partial nuclear genomes from late Pleistocene NWSL equids.

"This revealed that individuals from both eastern Beringia and southern North America form a single well-supported clade that falls outside the diversity of Equus and diverged from the lineage leading to Equus during the latest Miocene or early Pliocene," they explain. This, they claim, warrants the recognition of NWSL equids as a distinct genus, which they name "Haringtonhippus."

Their results suggest that populations of stilt-legged Haringtonhippus and stout-legged caballine Equus were sympatric both north and south of the continental ice sheets, through the late Pleistocene and became extinct at roughly the same time. The near synchronous extinction of both horse groups across their entire range in North America suggests that similar causal mechanisms may have led each to their demise.

Tracing morphology can be complex: this case underlines a recurrent problem in systematic biology, which is how best to discriminate authentic relationships within groups, such as Neogene equids, that were prone to what the researches refer to as 'rampant convergence." The solution they present in their paper utilised both palaeogenomic and



morphometric information to reframe the position of Haringtonhippus, which, they assert, now clearly emerges as the closest known outgroup to all living Equus.

Proteins may persist significantly longer than ancient DNA and collagen proteomics may come to play a key role in characterising affinities. "A reciprocally informative approach like the one taken here holds much promise for lessening the amount of systematic noise, due to oversplitting, that hampers our understanding of the evolutionary biology of other major late Pleistocene megafaunal groups such as bison and mammoths," they say.

The 5,500-year-long history of horse domestication and management, which transformed the natural evolutionary trajectory of wild horses into the more than 625 domestic breeds living today, is difficult to reconstruct from archaeology, history and modern genetics alone. PEGASUS (The makeup of the modern horse: a history of the biological changes introduced by human management) set out to build on the latest advances in the analysis of ancient DNA molecules to gather new genomic, epigenomic and metagenomic information from ancient horses.

More information: Project website: cordis.europa.eu/project/rcn/206440\_en.html

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