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## Scythian horses shed light on animal domestication

**By studying the genome of Scythian horses, an international team of researchers is outlining the relations that these nomads from Iron Age Central Asia had with their horses—and lifting the veil on some of the mysteries of animal domestication. Published in the journal *Science* on April 28, 2017, this research was led by Ludovic Orlando, CNRS senior researcher at the Laboratory of Molecular Anthropology and Image Synthesis (CNRS/Université Toulouse III – Paul Sabatier/Université Paris Descartes) and professor at the Natural History Museum of Denmark.<sup>1</sup>**

Nomadic Scythian herders roamed vast areas spanning the Central Asian steppes during the Iron Age (from approximately the ninth to the first century BCE (Before Common Era)). They were known for their exceptional equestrian skills, and their leaders were buried with sacrificed stallions at grand funerary ceremonies. The genomes of a few of these equids were fully sequenced as part of this study, so as to form a better understanding of the relations that the Scythian people developed with their horses. The researchers sequenced the genomes of thirteen 2,300–2,700-year-old stallions from the Scythian royal burial tombs of Arzhan (Russian Republic of Tuva, in the outer reaches of Mongolia) and Berel' (Kazakh Altai Mountains). They also sequenced the genome of a mare from an older culture, found in Chelyabinsk (Russia), and which is 4,100 years old.

By studying the variants carried by certain specific genes, they were able to deduce a large diversity in the coat coloration patterns of Scythian horses, ranging from bay to black by way of chestnut. Their analysis also revealed a total of 121 genes selected by Scythian breeders, most of which are involved in the development of forelimbs—the Scythians seem to have had a preference for horses with a robust morphology—but also in the development of mammary glands, which corroborates the view that mare's milk has been used for millennia.

The study therefore contributes to shedding light on a whole swathe of animal domestication. The researchers have identified the genomic regions in which adaptive mutations were concentrated during the first three millennia of horse domestication (begun some 5,500 years ago). These regions often carry genes linked to a population of cells in the embryo known as the neural crest, which gives rise to many of the organism's tissues. This provides some of the first experimental evidence in favor of the "neural crest hypothesis", which aims to explain why all domestic animals, despite independent lineages, have converged toward common physical and behavioral characteristics. As the neural crest gives rise to many tissues, the reprogramming of this group of cells over the course of development can lead to the co-

<sup>1</sup> Researchers from other French laboratories contributed to this research, at the Institut Jacques Monod (CNRS/Université Paris Diderot), the Archéozoologie, archéobotanique : sociétés, pratiques et environnements laboratory (CNRS/MNHN) and the Archéologies et sciences de l'Antiquité laboratory (CNRS/Université Paris 1 Panthéon-Sorbonne/Université Paris Ouest Nanterre La Défense/Ministère de la Culture et de la Communication).



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appearance of a host of traits of interest. The overrepresentation of genes linked to the neural crest among genes carrying adaptive mutations suggests the importance of this structure for domestication.

By comparing the genetic diversity of these ancient horses with that of modern-day horses, the authors discovered that a demographic collapse has occurred over the last 2,300 years, leading to a fall in the genetic diversity of horses. This is due to breeding practices, which use an increasingly limited number of stallions in reproduction, to such an extent that, today, almost all domestic horses share the same Y chromosome, unlike Scythian horses. These phenomena have been accompanied by an accumulation of deleterious mutations. The relatively recent accumulation of these deleterious mutations—found in all domestic animals—contradicts the so-called “cost-of-domestication” hypothesis, which holds that this accumulation occurs from the earliest stages of domestication.

As part of the ERC Pegasus project led by Ludovic Orlando, the researchers will now extend their paleogenetics research to other human cultures in order to understand how the domestication of horses has influenced the destiny of civilizations.

A video by the Natural History Museum of Denmark is available at: <https://youtu.be/PLwJDB94LMI>

For further details on the ERC Pegasus project, see: <http://orlandoludovic.wixsite.com/pegasus-erc>



**Modern Kazakh horse domesticates**

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**Przewalski's horses (wild), Seer reintroduction reserve, Mongolia**

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**Excavation of the Kurgan Arzhan 2 site (Tuva, Siberia), 7th century BCE.**

Tomb 16. View of 14 exhumed horse skeletons.

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**Excavated tomb at the Alaas Ebé archaeological site, Churapchinsky District, Yakutia, Russia.**

Mission archéologique française en Sibérie orientale (MAFSO).

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Other photos available upon request.

## Bibliography

**Ancient genomic changes associated with domestication of the horse**, Pablo Librado, Cristina Gamba, Charleen Gaunitz, Clio Der Sarkissian, Mélanie Pruvost, Anders Albrechtsen, Antoine Fages, Naveed Khan, Mikkel Schubert, Vidhya Jagannathan, Aitor Serres-Armero, Lukas F. K. Kuderna, Inna S. Povolotskaya, Andaine Seguin-Orlando, Sébastien Lepetz, Markus Neuditschko, Catherine Thèves, Saleh Alquraishi, Ahmed H. Alfarhan, Khaled Al-Rasheid, Stefan Rieder, Zainolla Samashev, Henri-Paul Francfort, Norbert Benecke, Michael Hofreiter, Arne Ludwig, Christine Keyser, Tomas Marques-Bonet, Bertrand Ludes, Eric Crubézy, Tosso Leeb, Eske Willerslev, Ludovic Orlando. *Science*, April 28, 2017.

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