

Research Project

Genetic signatures in wild and domestic horses (*Equus* sp.) during 40'000 years BC in Switzerland in comparison with present-day horse breeds

Third-party funded project

Project title Genetic signatures in wild and domestic horses (*Equus* sp.) during 40'000 years BC in Switzerland in comparison with present-day horse breeds

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Organisation / Research unit

Departement Umweltwissenschaften / Archäozoologie (Schibler)

Department

Project start 01.08.2008

Probable end 31.12.2017

Status Completed

The aim of the project is to unravel the complex history of horses by combining different research disciplines: archaeology, archaeozoology, archaeogenetics and modern animal genetics. The project will help to understand the transition of wild to domestic animals and the developments leading to current variation in horses. The focus is on archaeological horse finds in Switzerland and on present-day rare horse breeds.

The domestication of horses is complex and involves several domestication events from yet unknown, extinct wild horse populations. Archaeozoologically at least three morphological types of wild horses with different geographic distribution were suggested. No extant wild ancestral horse populations are known and knowledge on the developments that led to the current variation in modern horse breeds is limited. Both modern genetics and archaeogenetics offer the possibility to genetically investigate extinct species including horse, to shed light on the past population history of animals or search for selection signatures. The high mitochondrial d-loop variation in horses, commonly explained by high mobility of men and their horses obscured clear geographic patterns or the inference of domestication areas. However evidence for regional patterns in horses was recently published.

With the reasonable expectation, that original patterns are more likely preserved in regional either ancient horses or extant horse breeds than in today's widespread breeds, geographically restricted wild and domestic horse populations from archaeological sites in Switzerland will be genetically characterized. Any presence and subsequent "evolution" of patterns will be detected by mitochondrial d-loop variation obtained from wild Palaeolithic to domestic Celtic horses according to their position within phylogenies and networks of published horse sequences.

To measure the effect of domestication nuclear coat colour loci will be investigated as these are among the most obvious to be under early human selection. All chosen markers have the advantages of being well known in present-day breeds, which facilitates comparison and the embedding of results to extend current knowledge. Regional present-day rare horse breeds will be included in the study for comparison with ancient samples, and which may serve as a potential model for conditions at the time of early agriculture.

Keywords ancient DNA, archaeozoology, domestication, *Equus*, mitochondrial DNA, genetic diversity, coat colour

Financed by

Add publication

Add documents

Specify cooperation partners

ID	Kreditinhaber	Kooperationspartner	Institution	Laufzeit - von	Laufzeit - bis
102585	Schlumbaum, Angela	Archaeological Services of the Cantons	Archaeological Services of the Cantons	01.08.2008	31.07.2011
102588	Schlumbaum, Angela	Poncet, P.-A.	Haras national Suisse	01.08.2008	31.07.2011
102591	Schlumbaum, Angela	Leeb, Tosso	Universität Bern	01.08.2008	31.07.2017
3715513	Schlumbaum, Angela	Ludwig, Arne	Leibniz-Institute for Zoo- and Wildlife Research	01.08.2014	31.12.2022
3715822	Schlumbaum, Angela	Hofreiter, Michael	Universität Potsdam	01.08.2014	31.12.2022
3715835	Schlumbaum, Angela	Orlando, Ludowig	Centre of Geogenetics	01.08.2014	31.12.2022