

Horse Domestication



Wildlife Ecology Essay

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Purpose

The purpose of this study was to investigate not so much the exact date of domestication of the horse, moreover what are the Origin of the domesticated horse and what is its relationship with the Wild horse of prehistoric times.

Background

Since the process of domestication inherently takes many generations over a long period of time, and the spread of breed and husbandry techniques is also slow, it is not meaningful to give a single "date of domestication".

There are claims for Horse Domestication as early as 4,500 BC in Iberia and the Eurasian Steppe. The earliest undisputed evidence is chariot burials dating to from 2000BC from Krivoe Ozero. (Sintashta – Petrovka Culture) on the Ural Steppe. Here horses were found accompanied by artefacts in graves – artefacts we would associate with riding or traction. (Levine, 1999)

Various different theories have been postulated as to best estimate the earliest date of domestication. Uerpuann (1990) investigated the domestication of the horse in the West and Middle Europe. He concluded that a decreasing size and an increase in Heterogeneity are taken as proof of domestication. However Levine (2006) disputed that the anatomy of the Equines has remained the same. Furthermore the large wild herds of horses that existed during the late Pleistocene in Europe, Asia and North America also exhibited heterogeneity. (Kavor and Dovic, 2008). Another weak theory was that increased relative abundance of horses(and horse remains) could indicate domestication. On the otherhand it could merely explained by increased hunting.

Tooth morphology alone was considered an important analytic method. Horse teeth remains were studied at 2 Eneolithic sites, Botai in Northern Kazakhstan and Dereivka in the Ukraine (Year 35000-3000 BC).

Bevelings on the anterior part of the lower P2 masticatory surface were found (Levine, 1999). However this does not clearly indicate horses were ridden at this time. In fact the horses can be ridden without bits and also the upper 2nd premolar can cause abnormal occlusions on the lower 2nd premolar tooth. Therefore teeth occlusions alone does not provide enough information.



The Tarpan and the Przewalski

Only 2 subspecies of wild horses survived to historic times in Eurasia; The Tarpan (*Equus ferus ferus*) and the Przewalski horse (*Equus ferus przewalskii*). Sadly the last Tarpan went extinct in 1918 or 1919 in Poland. It was assumed that the Tarpan was the progenitor of the domesticated horse.

Przewalski horses can still be found in captivity. They were brought to Europe in the 20th century after being captured in the Mongolian Steppes. The chromosomal pattern differs in the domesticated horse (2n=64) and the Przewalski horses (2n=66), therefore the Przewalski horses are considered as a sister taxon of wild progenitors of domestic horses.



Horses in Kazakhstan and Mongolia

In ancient times horses were hunted for meat and then horse taming was a secondary phenomenon. Levine (1999) reviewed Interviews carried out in Cambridge in 1989 and 1990 of 5 men, 2 of whom grew up in Mongolia and practised traditional horse husbandary. One of the men herded horses at a village near Botai, one man was born and brought up at Botai aul and the 5th man represented a region in North Kazakhstan. Very useful information was obtained from the 5 men. Horseflesh was considered very important to Kazakhs and Mongols when they had to travel or in winter. Horses were usually slaughtered between the ages of 1 or 3 years, when their meat was very tender or else over the age of 20 when they were not useful for working or breeding. In Kazakhstan horse fat had a medicinal value for treating Tuberculosis. Ulcers, gastric diseases, typhoid fever, plague, fever and cancer of the gullet was said to be cured by Horse sweat. The importance of the horse in Mongol and Kazakh life was large. (Levine, 1999)

Genetic Studies

Equine Genetic Data has provided much needed information regarding the debate if horses were domesticated from one or several ancestral horse populations (Jansen et al, 2002) and also information regarding the genetic relationships between domesticated and wild horses. (Kaver and Dovic, 2008)

Methods and Results:

Jansen et al (2002) extracted hair roots from 318 unrelated horses of 25 Breeds and varieties in the USA, Spain, Austria, Britain and Germany. The mitochondrial DNA of modern Equids was compared with the osteological tree of modern and fossil Equids. Interestingly Comamara ponies were included in the study. The mt DNA (mitochondrial DNA) was used to determine the minimum number of mares domesticated from the wild. The results showed that 77 breeding mares is a minimum estimate for the number of wild mares ever domesticated. The wild horses had a lower individual genetic diversity compared to the domesticated horse who's demonstrated a greater diversity in mtDNA.

More recently (Kaver and Dovic, 2008) reviewed the genetic data of both mares and stallions, namely the mtDNA and the Y chromosome markers respectively. Firstly there were interesting results in the mtDNA haplotypes of Ancient Domestic and Wild Horses. A large amount of North American haplotype (late Pleistocene horses) did not survive domestication since they'r haplotypes were not found in Domestic horses. Thus the wild horses of the American prairies were not involved in domestication since they extinct before the process of domestication.

The population bottleneck theory is a very useful way of explaining the reduced matrilineal diversity of horses. The matrilineal diversity of domestic horses is less than the overall diversity of domesticated and wild horses. The constricted end of the bottle represents the stages in history when horse populations did not survive. The matrilineal diversity was reduced 10,000 years ago by the mass extinction of horses and other large body animals due to dramatic climatic changes. The second population bottleneck was 6,000 years ago which is considered to be as a result of Domestication. The halotypes and their derivatives which survived the two bottlenecks are found in Domestic horses, 100 halotypes are known.

However regarding the Y chromosome sequence in the males, only a single haplotype was detected, indicating that only a few patriline took part in horse domestication. The population bottleneck appears to have had a much larger effect on the male horse population. It was concluded from the study that a high number of wild (and tamed) horse were domesticated and that Domestication may have started when the appropriate stallion was obtained by selection or found.

Conclusion

From the above discussions the Intermediate model of domestication which was postulated by Clutton-Brock is probably the best explanation of horse domestication. The domesticated mare of today with her pre-existing haplotype diversity, arises from different wild stock spread over a moderately extensive geographical region. Domestication probably occurred in multiple locations simultaneously rather than just at one location. Needless to say it would be very difficult to put an exact date on horse domestication given the wide geographical spread of the Horse.

References:

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