

Mitochondrial sequence variation in ancient horses from the Carpathian Basin and possible modern relatives

Katalin Priskin

Institute of Genetics, Biological Research Center, Hungarian Academy of Sciences, Szeged, Hungary

Whatever the place, ethnic changes always leave their footprint in the local culture and genetic makeup and the same applies to the different types of horses moving with their owners. This thesis is concerned with the mitochondrial control region genotypes of ancient and modern horses from the Carpathian Basin, where in the late 9th century the incoming pagan Hungarian tribes permanently changed the population.

Studies of mitochondrial DNA have shown that modern horses are descended from at least 77 different wild mares, with a last common ancestor over 300,000 years ago, and so probably inhabiting very different regions. Despite this matrilineal genetic diversity, correlations between modern breeds of horses and mitochondrial genotype are often uncommon. This is probably because horse-trading and horse-stealing, sometimes over long distances, have been popular and profitable for a long time.

To determine genetic diversity and origin of horse populations in the Carpathian Basin at the time of the Avars and of the Hungarian Conquest, mitochondrial DNA analysis was undertaken on 31 archaeological horse remains, excavated from authentic, well-dated Avar and pagan Hungarian burial sites. Based on a supposed relationship, modern Hucul and Akhal Teke horses were included in the analysis. To reveal relationships to other ancient and recent breeds, mtDNA sequences from 79 breeds representing 913 individual specimens were combined with our sequence data. Sequences were aligned and truncated to a length of 247 bp to accommodate published short sequences (nucleotide positions 15495-15740 of reference sequence X79547).

Estimation of standard diversity measures, such as haplotype diversity (h) and nucleotide diversity (π) were performed in DnaSP 4.50.2.

To compare our samples with other modern and ancient horse sequences, 921 previously published equine mtDNA CR sequences with fully overlapping standard 247 bp lengths were obtained from the database (<http://www.ncbi.nlm.nih.gov/Genbank>).

Median-joining network was constructed using the NETWORK 4.5.1 software (Fluxus Technology Ltd. at www.fluxus-engineering.com) to reveal approximate genealogical relationships among the haplotypes found in our ancient and recent breeds and the haplogroup-indicating sequences.

Both genetic distances and haplotype-based methods indicate a clear separation between horses of the Avar and Hungarian leading nobles. Avar sequences were genetically heterogeneous, closely related to Eastern breeds; (with Mongolian and north Russian Vyatskaya groups). This Asian relationship can also be seen in the genetic distance matrix and the haplotype network.

By contrast, beside the great heterogeneity and unique haplotypes, the ancient Hungarian horses showed a relatively close relationship with the Turkoman Akhal Teke and Norwegian Fjord. It confirms the assumption of Hecker (1955) and is an admixture to the clew up of the Hungarian origin. After a short communication of Bjørnstad (2003), different distance measures suggest genetic associations between northern European horse breeds and the Mongolian native horse. By all means, the high variability of Hungarian horse haplotypes may be connected with the well-attested, continent-wide raiding habits of the ancient Hungarians. The Hucul data show no such relationship. Our results show that the ethnic changes induced by the Hungarian Conquest in the late 9th century were accompanied by a similar change in the stables of the Carpathian Basin.

Supervisor: Raskó István
e-mail: priskin@brc.hu

Isolation and characterization of bacterium and phage isolates which have biocontrol ability against *Pseudomonas* strains pathogenic to *Pleurotus ostreatus*

Enikő Sajben

Department of Microbiology, University of Szeged, Szeged Hungary

Pleurotus ostreatus is one of the most extensively cultivated mushrooms in the world; however significant loss of crop and quality arises from bacterial diseases causing by different bacterial pathogens. The yellowing of *Pleurotus ostreatus* and the brown blotch disease of *Agaricus bisporus*, caused by *Pseudomonas tolaasii* is well known (Lee and Cha 1998). The bacterium produces the toxins tolaasins that disrupt the cellular membrane by forming pores (Rainey et al. 1992).

Ps. tolaasii can be identify easily, with tolaasin toxin gene specific primers. This method is much more reliable than the white line test. The *Ps. tolaasii* is able to make a phenotypic switch; this variant form is nonpathogenic and differs from the wild type in a range of biochemical and physiological characteristics (Cutri et al. 1984).