

**Archaeogenetic analysis of the avar and the early  
hungarian horses from the Carpathian Basin**

**Summary of Ph.D Thesis**

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**2010**

## Acknowledgement

First of all, special thanks to **Prof. Dr. István Raskó**, who gave me the chance to do my doctoral work. Furthermore, thanks to **Dr. Gyöngyvér Tömöry, Dr. Erika Bogácsi-Szabó, Dr. Bernadett Kovácsné Csányi, Réka Eördögh, Anita Szécsényi, Dr. Ágnes Czibula, Dr. Mónika Mórocz, Mária Radóné Dudás** and **Istvánné Lehócz** for the professional advice and technical support. I am very grateful to **Krisztián Szabó** for providing assistance with the statistical analysis and **Prof. Dr. C. Stechen Downes** to the valuable critical reviewing. Many thanks to **Dr. István Vörös, Dr. Ferenc Horváth, Dr. Béla Kürti, Dr. Attila Lőrincz, Dr. Balázs Gusztáv Mende, Dr. Péter Langó, Dr. László Költő** and **Dr. József Szentpéteri**, for the archaeological materials and professional support in the historical background.

Additionally, thanks to **Dr. Sándor Mihók, András Szontagh** and **József Nyéki** for the hucul and the akhal teke samples.

My special thanks to my **parents** and my **husband** to the huge patience and backing.

## **Introduction**

The possible genetic relationship between the avars and the early hungarians is a controversial question of the hungarian history. The comparative anthropological analysis of the avar and early hungarian ethnic groups showed high similarity of the two populations (Éry 1994; Szathmáry 1996). Settlements of the two groups inlay in a mosaic-like pattern. The plentiful arhaeozoological materials of the Carpathian Basin gave us the possibility to examine this question by the horse stock of the two ethnical groups.

Avars and early hungarians, like most of their nomadic predecessors on the steppes buried their dead with weapons, jewelry and, most importantly, with their horses. Whatever the place, ethnic changes always leave their footprint in the local culture and genetic makeup and the same applies to the horses moving with their owners. On examination of exclusively morphological data, only the phenotypic and not the genotypic parameters can be observed.

Analysis of morphological data from these burials suggested that the hungarian horse stock was not homogeneous. Contrarily, in the case of the avar horses morphological homogeneity can be observed. In addition, most known horse skeletons originate from burials of warriors and other leading people, and these people rode a selected set of animals (Bartosiewicz 2006). According to Vörös (1997) horses from pagan Hungarian burials may have a common ancestry with hucul horses, a small stocky breed from the eastern Carpathian Mountains, which may be closely related to the tarpan, the eastern European wild horse that became extinct in the Ukraine in the late nineteenth or early twentieth century (Mihók et al. 2007).

Ancient Hungarian horses have also been suggested to be derived from the turkoman breed, the ancestors of the modern akhal teke (Hecker 1955) and perhaps of all 'hot blooded' breeds of horse (Szontagh 2005), bred in the area of today's Turkmenistan, Uzbekistan, and south Kazakhstan. The northern parts of this region are on the probable trajectory of the ancestors of the hungarians, in their travel from western Siberia to the Carpathian Basin (Hecker 1955).

Phylogenetic relationships among horse mtDNA control region haplotypes were estimated using both genetic distance and the non-dichotomous network method.

## **Aims**

This study is concerned with the mitochondrial (mtDNA) control region genotypes of ancient horses from the Carpathian Basin, where the incoming pagan hungarian tribes permanently changed the population in the late 9th century AD. The aims of our research were as follows:

- to test the used method by extracting ancient DNA from much older samples. (iron age schytian horses and late neolithic aurochs)
- to determine genetic diversity and origin of horse populations in the Carpathian Basin at the time of the avars and of the hungarian Conquest
- to reveal relationships to other ancient and recent breeds, especially modern hucul and akhal teke and mtDNA sequences from 76 breeds representing 851 individual specimens
- to estimate the genetic diversity of the hucul, that is involved in a conservation genetic program since 2002

## **Materials and methods**

Mitochondrial DNA is a usable tool for population genetic studies. One of the most informative ways to study ancestry and history of populations is to examine ancient DNA from the biological remains of the populations. DNA analysis was undertaken on 31 archaeological horse remains, excavated from avar and pagan hungarian burial sites. To reveal relationships to other ancient and recent breeds, modern hucul and akhal teke samples were also collected, and mtDNA sequences from 76 breeds representing 851 individual specimens were combined with our sequence data.

On that score amplification was carried out by using two sets of overlapping primers designed to amplify a 254 bp fragment from the most variable segment of the horse mtDNA control region (NCBI GenBank X79547; Xu 1994). DNA was extracted from archeological samples with standard precautions to minimize risk of exogenous DNA contamination, with methods routinely in use in our laboratory.

Phylogenetic relationships among horse mtDNA control region haplotypes were estimated using both genetic distance and the non-dichotomous network method.

## **Results and discussion**

Both methods indicate a clear separation between horses of the avar and hungarian leading nobles. The phenotypical differences that are written in the scientific literature are proven also in molecular genetic way. Despite the fact, that avar sampling has more significant chronological heterogeneity, avar sequences were genetically less heterogeneous, than the early hungarian horses. Beside the great heterogeneity, the genetic separation of the two groups confutes the avar-early hungarian continuity, at least, in

case of the horse husbandry. If the avars had assimilated into the hungarian mass, avars would have changed the lifestyle and also the economy. We can't exclude the possibility, that the reason of this genetic differency is the diverse cultural habit of the horse sacrifice. Beside the mostly similar cultural habits, avars sacrificed the 4-7 year old, most valuable horses. Contrary to the early hungarians, who sacrificed 2-15 year old, diverse value horses. Consequently, archaeological material is a highly selective group of samples. The investigated horses are just the small part of the whole horse stock. Different social groups used supposedly different kind of horses, too. The results don't support the genetic relationship between the two ethnical groups.

Ancient hungarian horses showed a relatively close relationship with the akhal teke breed, indicating an eastern ancestry. By all means, the high variability of hungarian horse haplotypes may be connected with the well-attested, continent-wide raiding habits of the early hungarians. In contrast with the early hungarians, avar horses show great distance from the akhal teke horses. There are four identical haplotypes between the avar and the akhal teke horses, and two identical haplotypes between the akhal teke and the early hungarian horses. The haplotype network shows some closely related sequences between akhal tekes and early hungarian horses in the cases of the unique haplotypes. In both samplegroup, half of the haplotypes grouped into the haplogroup A. The ancestor of the akhal teke, the turanian horse has been used as military horse for thousands of years by steppe nomads. Due to its extreme physical performance, this breed was in request by the nomad tribes, like early hungarians, especially the leading nobles.

The hucul data represented 22 mare family, that involve 80% of the european hucul stock. Despite of the two bottleneck-effects in the breed's history, it shows relatively high genetic diversity. The high significance level of the genetic distance values between hucul and the other breeds can't allow taking it on trust. The sequence similarities show some mare families that are

possibly important in the breed history. In addition, testing the mtDNA showed some error in the registration in the hucul studbook. These data can be very important in the genetic conservation of the breed.

Our results suggest that the geographical and historical origin of horse breeds cannot be traced through mitochondrial haplotypes, but the relationships between breeds can to some extent. The ancestry of commoners' horses remains beyond conjecture; though in conquest period burials, a clear distinction between the mitochondrial genotypes of low-status and more asian high-status hungarians has been established. But at least at the level of high quality horses, our results show that the ethnic changes induced by the Hungarian Conquest in the late 9<sup>th</sup> century were accompanied by a similar change in the stables of the Carpathian Basin. Therefore genetic characterization of horse remains from that particular geographic region might be misleading without the proper knowledge of the genetic origin of populations which bred them.

As the genetic variance is much higher within the groups, than among the groups, it doesn't allow revealing the exact genealogical relationship between the breeds. Moreover, genealogical history of horse breeds is often highly complex, showing great genetic divergence within breeds. Therefore, population genetic methods can give false results. As in the case of the human mitochondrial haplotipization, where coding markers are also necessary to the exact determination of the maternal lines, the horse breeds need additional mitochondrial and nuclear markers to better understand the breeds' history.

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Summary of impact factors: 8,003

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