Poster Communication Abstract – 2A.61

HORSE MITOCHONDRIAL GENOME ANALYSES TO DEFINE THE ORIGIN OF ANCIENT HUMAN POPULATIONS

LANCIONI H.*, CAPOMACCIO S.**, FELICETTI M.**, CAPPELLI K.**, SILVESTRELLI M.**, VERINI SUPPLIZI A.**, ACHILLI A.*

*) Dip. Biologia Cellulare e Ambientale, Università di Perugia, Via Pascoli 1, 06123 Perugia (Italy)
**) Dip. Patologia, Diagnostica e Clinica Veterinaria, Università di Perugia, Via S.Costanzo 4, 06126 Perugia (Italy)

Maremmano breed, mitochondrial genome, phylogenetic analysis

Since the use of horses was profoundly connected to human activities in both pre-historical and historical times, detailed molecular and phylogenetic analyses of equine mtDNA can increase our knowledge on both horse domestication and ancient human populations. In this species, genetic association studies are also favoured by the availability of studbooks with pedigrees and racing records. Maremmano's studbook could be traced back to 4 stallions and 440 mares. The Maremmano is an Italian warmblood horse mostly bred in the provinces of Grosseto and Viterbo (Central Italy). It is believed that this breed originated in Tuscany from ancient local populations living along the Tyrrhenian coast during the Etruscan time and was influenced by ages of crossing with other horse breeds. In order to investigate this theory from a genetic point of view, following the approach recently used to analyze humans (modern Tuscans) and bovines (Maremmana and Chianina breeds), we evaluated the mitochondrial DNA variation of 73 unrelated horses preselected on the bases of an accurate genealogical analysis of the maternal lines. Control region sequencing (nps 15491-16100) revealed 47 different haplotypes, ascribable into 12 major haplogroups. Particular interest was arisen from samples belonging to A4, (relatively abundant with 11.0 % of frequency) because this haplogroup clearly shows a frequency peak in the Near East. On the basis of these preliminary data, in order to avoid redundancies and to achieve a good representation of the entire equine "natural" mtDNA variation, we selected 20 samples for complete sequencing of the entire mitochondrial genomes. Excluding ambiguous sites and the 16129-16360 short tandem repeat, 20 different haplotypes were identified in the sequences and evolutionary history was inferred by a parsimony approach.

The resulting data show a peculiar phylogenetic connection between the Maremmano horse and some typical eastern breeds.