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Mitochondrial D-loop sequence variation among autochthonous horse breeds in Croatia

A. Ivanković, J. Ramljak, M. Konjačić, N. Kelava, P. Dovč, P. Mijić

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Genetic variation in three Croatian coldblood horse populations was analysed using a sequence analysis of the proximal part (nt 15 498–15 821) of the D-loop region of mtDNA. Twenty unrelated horses were chosen from the Posavina horse and the Croatian Coldblood breeds and fifteen horses from the Murinsulaner horse population. Sequencing of the proximal part of the mtDNA D-loop region revealed 26 polymorphic sites representing thirty haplotypes which were clustered into eight haplogroups. A wide variety of mitochondrial haplotypes of the analysed horse breeds were clustered into eight different haplogroups. Two haplogroups (D and F) were specific to Posavina horse, five haplogroups were shared among the Croatian Coldblood and Murinsulaner horse, the fact that can be explained by selection strategy at the beginning of the 20th century and possible gene flow between the two populations. These results indicate the presence of many ancient maternal lineages with high diversity in mtDNA. The genetic information based on mtDNA typing has a great importance for the future breed conservation strategy, especially for the critically endangered breed such as Murinsulaner horse.

Keywords:

mtDNA; genetic diversity; horse; conservation genetics

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