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Genetic diversity and structure of Iranian horses' population based on mitochondrial marker

N. Hedayat Evrigh^{1*}, M. Omri¹, A. Boustan¹, R. Seyedsharifi¹ and V. Vahedi¹

1. Department of Animal Science, Faculty of Agricultural and Natural Resources, University of Mohaghegh Ardabili, Ardabil, Iran.

2. Department of animal science, Moghan College Of Agriculture & Natural Resources, University of Mohaghegh Ardabili, Ardabil, Iran.

* nhedayat@uma.ac.ir

Abstract

The source and history of horse domestication have been studied for decades in biology and archeology. The aim of this study was to evaluate the genetic structure and the genetic relationship between six breeds of native horses' using mitochondrial D-loop region. Blood samples were collected from 96 horses. Total DNA was extracted and 430 bp of D-Loop region (hyper variable) were amplified and sequenced using Sanger sequencing methods. The analysis of data led to identify 48 polymorphic sites that create 52 haplotypes. The plotted phylogenetic tree for haplotypes of Iranian native horses is placed in the 11 haplogroups including A, B, C, E, G, I, L, M, N, P and Q. Genetic and haplotype diversity values obtain 0.0233 and 0.980 respectively. Nucleotide diversity (Pi) observed between 0.0172 to 0.0242 in populations. In addition, the average number of nucleotide differences (k) ranged from 6.0 (DAH) to 8.5 (KOH) with an average value of 7.8. The highest and lowest genetic differentiate was observed between KOH and DAH ($f_{st}=0.193$) and between NWH and CLH ($F_{st}= 0.003$), respectively. Tajima D

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