GENETIC STRUCTURE AND DIVERSITY OF RED DEER (CERVUS ELAPHUS) POPULATIONS IN LITHUANIA

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The genetic structure of European red deer populations is influenced by both natural and anthropogenic factors, including historical and recent introductions. These processes may increase the risk of interspecific hybridization and contribute to uncertainty regarding the genetic status of local populations. Due to limited genetic monitoring, data on the genetic status and diversity of local red deer populations remain scarce in many regions. This study was aimed at assessing the genetic diversity of red deer (Cervus elaphus) in Lithuania using molecular genetic markers and identifying possible signs of heterogeneity in genetic origin.

In this study, molecular genetic markers were used, including an intron fragment of the Y-chromosome zfy gene and mitochondrial DNA sequences. Samples from red deer and individuals of unknown genetic origin were analyzed. The obtained sequences were compared with reference sequences available in the GenBank database, and phylogenetic analyses were performed using MEGA software.

The genetic data of Lithuanian red deer individuals showed close similarity to other European populations, including individuals from Scotland and Norway that have traditionally been classified as different subspecies (Cervus elaphus scoticus, C. e. atlanticus). Meanwhile, the genetic data of individuals of unknown origin exhibited higher genetic variability, possibly indicating a different genetic origin.

Overall, these preliminary results suggest that Lithuanian red deer are genetically similar to other European populations; however, more extensive sampling and additional genetic markers are required for a comprehensive assessment of population genetic structure and origin.