

GENETIC POLYMORPHISM AND TAXONOMIC STATUS OF ROE DEER (ARTIODACTYLA, CERVIDAE, CAPREOLUS GRAY, 1821) OF THE PENZA REGION ACCORDING TO THE RESULTS OF mtDNA ANALYSIS

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Abstract. It has now been established that two species of roe deer live in Eastern Europe – the European (*Capreolus capreolus* Linnaeus, 1758) and the Siberian (*C. pygargus* Pallas, 1771). At the same time, as a result of artificial and natural colonization, a zone of sympatric habitat with a possible blurred "hybrid zone" was formed in the area from the Right Bank Volga to Eastern Poland. The purpose of the article was to study the genetic status and polymorphism of mitochondrial DNA of roe deer (*Capreolus* sp.) caught in the Penza region. The material for the article was collected in the hunting grounds of the Penza region with the direct participation of the Department for the Protection, Supervision and Regulation of the Use of Wildlife of the Ministry of Forestry, Hunting and Nature Management of the Penza Region. The analytical sample consisted of 18 individuals from different regions of the Penza region. An analysis of the variability of two mtDNA markers was carried out: the control region (CR) and the Cyt *b* gene. Sequencing of fragments of the CR mtDNA (*n* = 18) and the Cyt *b* gene (*n* = 18) was performed on an ABI 3500 sequencer (Applied Biosystems). Nucleotide sequences were studied using BioEdit 7.0, Mega7.0.21, PopArt and DnaSP 5.10.01 software. All results were verified by statistical tests (STATISTICA 13.3). Analysis of the nucleotide sequences of fragments of the control region (CR) and a fragment of the Cyt *b* gene of roe deer from the Penza region using the ML method indicates that they all correspond to the mtDNA of the Siberian roe deer (*C. pygargus*). Only 2 samples of the cytochrome *b* gene fragment form a separate haplogroup, without a direct association with samples of the European roe deer (*C. capreolus*). Comparison of genetic distances of formalized groups of Siberian roe deer (CP), European roe deer (CC) and roe deer from the Penza region (CPR) shows that for the control region the distance of the Penza roe deer group is minimal with the *C. pygargus* group, and for the Cyt *b* gene – with group of *C. capreolus*. The identified genetic spatial groupings of roe deer in the region are not spatially determined. The obtained positive values of the T'sD indicator (1.221) reveal the process of weak fluctuations in the total number associated with the uneven intensity of hunting exploitation of roe deer populations and reproduction activities. Of the entire sample of roe deer in the Penza region, 6 CR mtDNA haplotypes (33.3 %) and 6 haplotypes of the Cyt *b* gene (42.8 %) are regionally specific. The analysis of species identity based on two mitochondrial markers of roe deer from the Penza region, which most reliably identifies them as Siberian, can hardly be called definitive. We are probably faced with cases of interspecific crossing of two species of Eurasian roe deer or the fact of widespread introgression of *C. pygargus* mtDNA into the aboriginal population of *C. capreolus*. To clarify this situation, it is necessary to conduct additional genetic studies using nuclear markers, including microsatellite DNA markers.

Keywords: *Capreolus capreolus*, *Capreolus pygargus*, variability, mitochondrial DNA, Penza region

For citation: Titov S.V., Schvychkova I.N., Ilyin V.Yu., Kuzmin A.A. Genetic polymorphism and taxonomic status of roe deer (Artiodactyla, Cervidae, *Capreolus* Gray, 1821) of the Penza region according to the results of mtDNA analysis. Russian Journal of Ecosystem Ecology. 2023;8(4). (In Russ.). Available from: <https://doi.org/10.21685/2500-0578-2023-4-1>