

GENETIC FEATURES OF THE POPULATION STRUCTURE OF THE RUSSET GROUND SQUIRREL (*SPERMOPHILUS MAJOR* PALL.) DUE TO POPULATION DYNAMICS OVER TIME

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Abstract. Relevance and goals. Spatial subdivision and temporary isolation of populations, as a rule, lead to limited gene flow, a decrease in the level of heterozygosity, an increase in the level of inbreeding, and a loss of genetic diversity. In some cases, both their complete extinction and radical restructuring of their structure are possible due to the passage of populations of the "bottleneck" state or of the formation process from a limited number of early settlers. In the conditions of such a contradictory and undirected population dynamics in the area, structural population changes are constantly taking place. Under the conditions of sympatric habitation of closely related species at certain points of contact, situations arise in which sympatric species overcome isolation barriers and interspecific hybrids appear in random contacts of non-specifics [11, 12]. The goal of this work was the study in model settlements of the russet ground squirrel (*Spermophilus major* Pall) of the peculiarities of the dynamics of the genetic structure of populations in connection with deep isolation and wavelike changes in numbers against the background of the existing sympatry with the spotted souslik (*S. suslicus* Güld). **Materials and methods.** Analytical samples for genetic analysis were as follows: *S. major* population near the village of Chirikovo, 2005–2010, 43 individuals, and 2018–2019, 34 individuals; *S. major* population on the island of Paltsinsky (2011) – 10 individuals. The analysis of intrapopulation polymorphism and genetic differences of two model populations of the russet ground squirrel was carried out using the results of the analysis of two mtDNA markers variability – the control region (C-region, D-loop) and the Cyt *b* gene, in two directions: by the nature of DNA mitotypes distribution in them and by identifying haplotype variability of the analyzed samples for the used markers. Fragments of the mtDNA control region ($n = 32$) and the Cyt *b* gene ($n = 44$) were sequenced on an ABI 3500 sequencer (Applied Biosystems) using reagent kits BigDye® Terminator v 3.1 Cycle Sequencing Kits during the initial sample preparation in the SimpliAmp™ Thermal Cycler amplifier. Nucleotide sequences were studied using the BioEdit 7.0 Mega7.0.21 PopArt and DnaSP 5.10.01 programmes. The obtained sequences of the isolated mtDNA haplotypes (D-loop and Cyt *b*) were placed at GeneBank NCBI (MW398128-MW398138; MW398139-MW398148). All the results were verified by statistical tests (Microsoft Office Excel 2010, STATISTICA 10.0). **Results.** Analysis of the variability of the fragments of the control region D-loop and the Cyt *b* gene of mtDNA showed that the analyzed populations of the russet ground squirrel are well differentiated and differ from each other. The analysis of two temporal states of the population near the village of Chirikovo revealed significant differences between them, despite the fact that the search for these differences is complicated by a well-marked mitotypic structure. Testing sequences of two time samples of a russet ground squirrel population near the village of Chirikovo by the degree of their differentiation showed that the Tajima indices ($T's D$) have positive values for both mtDNA markers. In this case, the indices have values indicating the effect of stabilizing selection after a rapid increase in numbers, which, according to observational data, took place after a strong depression and the passage of the population of the "bottleneck" state. **Conclusions.** The conducted genetic studies of dynamically changing and reliably isolated populations of the russet ground squirrel showed that the use of mtDNA markers allows studying their genetic structure quite accurately and recreating the history of settlement formation. Such studies are especially relevant when studying the dynamics of contact areas of sympatric zones of hybridizing closely related species. As our studies have shown, it is in those points of the range where an explosive demographic situation associated with the passage of the populations of the "bottleneck" state and the restoration of numbers is observed, as well as the presence of a sympatric species occurs, that cases of interspecific hybridization of the russet ground squirrel with other representatives of the r. *Spermophilus* are recorded.

Key words: russet ground squirrel, genetic structure of the population, temporal dynamics, variability, mitochondrial markers, Volga region.

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