

FEATURES OF THE DYNAMICS OF THE GENETIC STRUCTURE OF POPULATIONS OF SPECKLED GROUND SQUIRREL (*SPERMOPHILUS SUSLICUS* GÜLD.) IN THE RIGHT-BANK VOLGA REGION

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Abstract. *Background.* Long-term isolation of populations leads to a restriction of gene flow, a decrease in the level of heterozygosity, an increase in the level of inbreeding and a loss of genetic diversity. This often leads to the complete extinction of populations or a strong restructuring of their structure. The latter process is associated with the overcoming of populations of the "bottleneck" state or the restoration of density with a limited number of migrants. The aim of the article was to study in a model colony of the speckled ground squirrel (*Spermophilus suslicus* Güld.) the features of the long-term dynamics of the genetic structure of the population due to strong isolation and wave-like changes in density against the background of existing sympatry with the russet (*S. major* Pall.) ground squirrel. *Materials and methods.* Analytical samples for genetic analysis were: 8 specimens – the population of *S. suslicus* of the village of Trubetchina (Tr1) in 2016; 20 specimens – the population of *S. suslicus* of the village of Trubetchina (Tr2) in 2021-2022. Tissue samples were collected in vivo (biopsy on the auricle) by non-invasive methods, taking into account Directive 2010/63/EU of the European Parliament and the Council of the European Union on the protection of animals used for scientific purposes (Articles 9 and 42) and the recommendations of ASAB/ABS, Guidelines for the treatment of animals in behavioral research and teaching. The variability of two mtDNA markers was analyzed: the control region (C-region, D-loop) and the Cyt *b* gene. Microsatellite DNA was also studied at 4 loci – Xm C10, Xm D116, Igs-bm and Ssu 17. Fragments of the mtDNA control region (n = 13) and the Cyt *b* gene (n = 16), as well as fragments of microsatellite DNA (n = 33) were sequenced using an ABI 3500 sequencer (Applied Biosystems). The nucleotide sequences were analyzed using the programs BioEdit 7.0, Mega 7.0.21, PopArt and DnaSP 5.10.01. Sequences of isolated mtDNA haplotypes (D-loop and Cyt *b*) were placed in GeneBank NCBI (OP896081–OP896085; OP896086–OP896090). All results were verified by statistical tests (STATISTICA 13.3). *Results.* The peculiarities of changes in the genetic structure of the speckled ground squirrel population of the village of Trubetchina by mitochondrial markers indicate that it has overcome the "bottleneck" state (a change in the frequency ratio of alleles), and a new genetic structure of the population has been formed with the participation of migrants (the appearance of new alleles in the population). Analysis of the dynamics of the genetic structure of the temporal states of speckled ground squirrel populations by more evolutionarily "fast" microsatellite markers confirms the obtained mtDNA data. *Conclusions.* Genetic studies have revealed slow restructuring of the speckled ground squirrel population structure, which indicate low plasticity of the species and its susceptibility to depression. Such vulnerability of the speckled ground squirrel to the actions of external factors explains its unfavorable state within the eastern part of its range and the extinction of a large number of modern colonies. Therefore, the study of the genetic condition of the preserved colonies of this species is important in the framework of measures for its protection. Such studies are especially relevant when studying the dynamics of contact areas of sympatric zones of hybridizing closely related species.

Keywords: speckled ground squirrel, genetic structure of the population, temporal dynamics, variability, mitochondrial markers, right-bank Volga region

Acknowledgments: the study was supported by the Russian Science Foundation grant № 22-24-00108. URL: <https://rscf.ru/project/22-24-00108/>

For citation: Titov S.V., Kartavov N.A., Simakov M.D., Chernyshova O.V., Kuzmin A.A. Features of the dynamics of the genetic structure of populations of speckled ground squirrel (*Spermophilus suslicus* Güld.) in the right-bank Volga region. *Russian Journal of Ecosystem Ecology*. 2022;7(3). (In Russ.). Available from: <https://doi.org/10.21685/2500-0578-2022-3-1>