
Taxonomy Genetics

Taxonomic structure and evolutionary history of mountain voles (*Alticola*, subgenus *Aschizomys*) in north-eastern Asia

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Two species of Asian mountain voles assigned to subgenus *Aschizomys*, of the genus *Alticola*, namely, *Alticola macrotis* and *Alticola lemminus* inhabit mountain areas from Altay range at the south to Korytski Range and Chukotka peninsula in northeast Siberia. The distribution of both species is highly fragmented. The certain borders of their distribution, taxonomic status of isolated populations and phylogenetic interrelationships are obscure. We examine patterns of lineage diversification, phylogenetic and population genetic history analyzing mitochondrial *cytb* and three nuclear markers: partial *BRCA*, *GHR* and *LCAT* from specimens covering a large portion of species' ranges. We tested the hypothesis of hybridization between two species with JML software. The obtained results support the hypothesis of ancestral polymorphism and incomplete lineage sorting rather than interspecies hybridization. Genetic differentiation within both species as inferred from the *cytb* tree including museum type specimens is consistent with current species delimitations. The current intraspecies taxonomy correctly reflects evolutionary relationships. The nuclear genes species tree supports monophyly of the subgenus and included species. Further, we combine results of the phylogeographic analysis with species niche and distribution modelling with MAXENT software and use these combined results to reconstruct possible ancestral area and species distribution history from LGM to present. This study was conducted under research theme № AAAA-17-1170 424 10 167-2 and RFBR grant № 15-04-04602 and Program of Presidium RAS "Dynamics of gene pools in natural populations" and "Development of vital and biosphere processes".

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Book of Abstracts



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