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Modern Achievements in Population, Evolutionary, and Ecological Genetics : International Symposium, Vladivostok – Vostok Marine Biological Station, September 1–10, 2015 : Program & Abstracts. – Vladivostok, 2015. – 84 p. – Engl. ISBN 978-5-7442-1563-7

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SPONSORS:

*Russian Foundation for Basic Research, Khimexpert Agency,
GenoTek Company, SkyGene Company*

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Современные достижения в популяционной, эволюционной и экологической генетике : Международный симпозиум, Владивосток – Морская биологическая станция «Восток», 1–10 сентября 2015 : Программа и тезисы докладов. – Владивосток, 2015. – 84 с. – Англ. ISBN 978-5-7442-1563-7

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INTRASPECIES GENETIC DIFFERENTIATION OF NORTHERN RED-BACKED VOLE POPULATIONS INHABITING THE URALS BASED ON mtDNA

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The northern red-backed vole (*Clethrionomys rutilus*, Pallas, 1779) is a wide-ranging Holarctic species encompassing 20 subspecies, designated based on variation in the color of the fur, body size and craniological features. Among them, hardly more than eight-ten subspecies fall into real taxonomic categories (Gromov, Erbaeva, 1995). A broad overlap of values in morphological traits, used to identify a subspecies, hampers subspecies differentiation, in particular, if information about a geographical sampling site is absent. Within the Urals and neighboring territories, the following zones are defined: steppe, forest-steppe, forest, forest-tundra and tundra along with distinct altitudinal belts. Therefore, the Urals might be a habitat for a few northern red-backed vole subspecies (Bolshakov, 1972). Genetic analysis of *C. rutilus* samples from different geographical zones is very important as, unlike morphological analysis, it is based on the variability of genetic markers, which are significantly less affected by environmental factors.

We conducted genetic studies of *C. rutilus*, based on the nucleotide variability of mtDNA cytochrome b (*cyt b*) fragment (866 bp) of 44 voles from eight localities within Polar (near Labytnangi town), Middle (Sverdlovsk region) and Southern (Chelyabinsk region, Bashkortostan) Urals along with Southern Yamal (the Yerkuta River). Phylogenetic analysis of *cyt b* sequences were conducted employing the Bayes method (program MrBayes 3.2). The evaluation of phylogenetic tree parameters was conducted with the help of Tracer v 1.6 program. The sequences of *C. rufocanus cyt b*, obtained from GenBank, were used as an outgroup.

Among 44 analyzed nucleotide sequences of *cyt b* gene of *Cl. rutilus* we revealed 23 haplotypes including 17, which are not found in the GenBank database. The obtained phylogeographic data, however, do not point to the existence of a separate subspecies of the *C. rutilus* group within the Urals. According to the obtained phylogenetic tree of *C. rutilus*, representatives from different subspecies do not fall into separated monophyletic groups, and even voles from the same locality also do not group together. To conduct further, more specific phylogenetic analysis of *C. rutilus*, inhabiting the Urals, it is necessary to use a higher amount of samples per locality, include more sampling sites and employ new DNA markers, in particular nuclear gene(s).

Consequently, the obtained data on genetic variability of *cyt b* point to the absence of a distinct phylogeographic structure of *C. rutilus* inhabiting the Urals in the geographic gradient from the north to the south.

This study was supported by the Russian Foundation for Basic Research (projects nos. 14-04-00614 and 13-04-00847).