Taxonomy Genetics

Multiple mitochondrial pseudogenes in the nuclear genome in two species of mole voles (*Ellobius*, *Cricetidae*)

Kristina V. Kuprina[1], Olga V. Bondareva[2], Antonina V. Smorkatcheva[1], Nataliya Abramson[2], Svetlana A. Galkina[1]

[1]Saint Petersburg State University, Saint Petersburg, Russia, cuprum.ru@gmail.com
[2]Zoological Institute RAS, Saint Petersburg, Russia

Within the last decades, mitochondrial molecular markers have been widely used for phylogeographic and phylogenetic studies. They are most suitable markers when estimating genetic divergence between natural fragmented populations. However, the presence of numerous nuclear mitochondrial copies (numts) may severely complicate such studies. The mole voles, genus *Ellobius*, are specialized subterranean rodents with highly fragmented range. In our earlier study of the Northern mole vole population, *Ellobius talpinus*, we uncovered high nucleotide diversity of the mitochondrial control region fragment (Kuprina et al., 2016). Here we suggest that one of two predominating haplotypes which have been assigned to the mitochondrial control region actually represents a nuclear pseudogene (numt) of the control region. Moreover, the subsequent cloning of control region and cytochrome b fragments of the Northern mole vole and the Zaisan mole vole (*Ellobius tancrei*) showed the presence of different variants of these putative numts within the genome of each individual. To reveal an approximate time of various mitochondrial-nuclear translocations we conducted a phylogenetic analysis using the control region fragment of different taxa of subfamily *Arvicolinae* including pseudogenes of *Ellobius talpinus* and *Ellobius tancrei* obtained in this study. Our results emphasize the importance of testing for numts in every phylogenetic and phylogeographic study using mt markers. Technical and financial support: Chromas and MCT RRCs of SPbSU, RFBR (projects 16-04-00479, 18-04-00730) research theme № AAAA-17-1170 424 10 167-2 and Program of Presidium RAS “Dynamics of gene pools in natural populations” and “Development of vital and biosphere processes”.

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Editors:
Jens Jacob[1] and Jana Eccard[2]
[1]Julius Kuehn Institute, Federal Research Centre for Cultivated Plants,
Institute for Plant Protection in Horticulture and Forests, Vertebrate Research,
Toppheideweg 88, 48161 Münster, Germany
[2]University of Potsdam, Institute of Biochemistry and Biology,
Animal Ecology Group, Maulbeerallee 1,
14469 Potsdam, Germany

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