Title: Genetic differentiation in *Cricetulus migratorius* Pallas, 1773 (Rodentia, Cricetidae)

Authors: Vladimir Lebedev, Natalia Poplavskaya, Anna Bannikova, Georgy Ryurikov, Alexey Surov

PII: S1616-5047(17)30422-6
DOI: https://doi.org/10.1016/j.mambio.2018.05.001
Reference: MAMBIO 41010

To appear in:

Received date: 24-12-2017
Accepted date: 2-5-2018

Please cite this article as: Lebedev V, Poplavskaya N, Bannikova A, Ryurikov G, Surov A, Genetic differentiation in *Cricetulus migratorius* Pallas, 1773 (Rodentia, Cricetidae), *Mammalian Biology* (2010), https://doi.org/10.1016/j.mambio.2018.05.001

Genetic differentiation in *Cricetulus migratorius* Pallas, 1773 (Rodentia, Cricetidae)

Vladimir Lebedev[1], Natalia Poplavskaya[2], Anna Bannikova[3], Georgy Ryurikov[2], Alexey Surov[2]

1 - Zoological Museum of Moscow State University, 2, Bolshaya Nikitskaya Str., Moscow, 125009 Russia

2 – A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, 33, Leninskij prosp., Moscow, 119071, Russia

3 - Department of Vertebrate Zoology, Moscow State University, 1-12, Leninskie Gory, Moscow, 119991, Russia

E-mails:

Lebedev V., corresponding author: wslebedev@gmail.com

Poplavskaya N.: nata.poplavskaja@gmail.com

Bannikova A.: hylomys@mail.ru

Ryurikov G.: cricetulus@mail.ru

Surov A.: allocricetulus@gmail.com

Abstract

The grey hamster *Cricetulus migratorius* is the most widespread and ecologically opportunistic species among Palearctic hamsters. Genetic diversity across most of its range was examined by using cytochrome b (*cytb*) and cytochrome oxidase I (*coI*) gene sequences. Phylogenetic analyses revealed three well-differentiated allopatric lineages. The western lineage is distributed in Ukraine, Central and South Russia, Caucasus and Anatolia; the eastern lineage occupies Kazakhstan, Turan, Mongolia, West China and some mountain areas in western Central Asia. The Lower Volga valley may act as the barrier between these two phylogroups. The third lineage is found only in the Qurama Mountains (Uzbekistan). Mitochondrial data are in good agreement with the results of previous craniometric and allozyme studies, suggesting a subdivision into *migratorius* (eastern) and *phaeus* (western) subspecies groups.

Keywords: phylogeography, mtDNA, Palearctic hamsters, steppe fauna, Pleistocene

Phylogeographic studies of wide-range species can provide important insights into the tempo and mode of evolutionary diversification, the range dynamics through major climatic shifts and the nature of biogeographical boundaries. The Quaternary history of species associated with temperate forest zone has