Genetic diversity of the harvest mouse (*Micromys minutus*): new data of the mtDNA cyt b and control region from central part of North Eurasia and Far East

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The harvest mouse (*Micromys minutus* P., 1771) is the smallest rodent of the family Muridae of Eurasia, whose range occupies a significant part of the forest and forest-steppe zones of the Palaearctic from northern Spain and Great Britain to the Korean Peninsula, as well as the islands of Japan and Taiwan. The species inhabits a wide variety of open habitats, including gardens and arable land, drainage ditches, and grain or rice paddies. One of the main conditions for successful *M. minutus* existence is the presence of habitats with high and dense herbage. For the island (Great Britain, Japan) and Central European populations, a decrease in number and a fragmentation of the range has been noted, caused by anthropogenic impact. At the same time, a number of captures of *M. minutus* beyond the eastern boundary of the distribution area of the species have been explained by the broadening of the range as a result of climate change. In this context, understanding of the processes underlying the formation of the intraspecific genetic structure, the assessment of the genetic diversity of populations and the degree of relationship between them are very important. A number of studies are devoted to the intraspecific genetic variability in *M. minutus*, phylogeny and phylogeography of the genus *Micromys*. However, there is not much data on the central part of Northern Eurasia and almost no data on the Far East. Therefore, cyt b (1140 bp) and control region (CR - 851 bp) sequences of 26 specimens of *M. minutus* from 15 localities in the East European Plain, Urals, Eastern and Western Siberia, and the Far East were analysed. For cyt b, CR and concatenated sequences of both markers 16, 15 and 19 haplotypes, respectively, have been described. Phylogeographic analysis with the inclusion of new data has revealed the existence of four new mitochondrial lineages: Central Eurasia (from the central part of the East European Plain to Altai in the southeast and Yakutia in the northeast), Eastern Siberia (Cis-Baikal Region) and two Far East linages. Three other lineages, namely Europe (from Great Britain to the northwest part of the East European Plane), Taiwan (Taiwan Island) and Japan-Korea (Japanese islands and Korean Peninsula) have been described previously. The genetic diversity and demographic analysis of *M. minutus* allowed to suggest that the modern species genetic structure and the species range have been formed during the Late Pleistocene - Holocene period under the global climate change, the dynamics of physical and geographical conditions of the regions, and, possible, anthropogenic influence.

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