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New data on genetic differentiation of allopatric lineages of Striped field mouse (*Apodemus agrarius*): study based on fragment analysis of 5 microsatellite markers

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The Striped field mouse inhabits a wide geographical area from central Europe to the Pacific coast of Asia. The species range is subdivided into two allopatric lineages (European-Siberian – Kazakh versus Russian Far Eastern-Chinese-Korean) with disjunction in Transbaikalia. Here we analyzed variation of 5 microsatellite markers in the data set of 230 individuals to investigate the genetic differentiation of continental and island isolates. The Striped field mice of the western lineage from 14 geographic locations were combined in two samples: "European Russia" and "Western Siberia + Kazakhstan." Animals of the eastern lineage were caught in four continental populations from the south of the Russian Far East as well as on two islands of the Peter the Great Bay (Sea of Japan). With the fragment analysis we used following microsatellite markers GTTDS8, GATAE10A, CAA2A, GTTF9A and GSADT7 (Makova et al., 1998).

GTTDS8 locus was monomorphic in all the samples except one population of the southern Primorye where the second allele was found. GATAE10A, CAA2A, GTTF9A and GSADT7S loci were highly polymorphic. Allelic diversity in the western lineage was lower than in the eastern one. Perhaps this is due to the much longer period of *A. agrarius* inhabiting in the Eastern Palearctic than in Siberia and Europe. It was found higher affinity of continental populations within each of the lineages and somewhat greater genetic differentiation between these lineages.

The numbers of alleles in the continental populations were higher than in the island ones. The island populations differ more significantly both from each other and from the mainland western and eastern ones.

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