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**GENETIC DIFFERENTIATION OF MAINLAND AND ISLAND POPULATIONS
IN EASTERN LINEAGE OF THE STRIPED FIELD MOUSE (*Apodemus agrarius*):
A STUDY OF 5 MICROSATELLITE LOCI**

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The striped field mouse inhabits a wide geographical area from the central Europe to the Pacific coast of Asia including nearest islands. The species range is subdivided into two allopatric parts (European-Siberian- Kazakh versus Russian Far Eastern-Chinese-Korean) with disjunction in Transbaikalia. Using a fragment analysis of 5 microsatellite loci (GTTDS8, GATAE10A, CAA2A, GTTF9A and GSADT7), it was shown that allelic diversity in the western lineage is lower than in the eastern one (Frisman et al. 2016). Perhaps, for *A. agrarius*, this was due to much longer period of living in the Eastern Palearctic than in Siberia and Europe. It was found that the affinity of continental populations within each lineage is higher, and genetic differentiation between these lineages is larger (Frisman et al., 2016).

The aim of this study was to compare differentiation of mainland and island populations within the eastern lineage. A total of 205 animals were caught in five continental localities as well as on two islands in the Peter the Great Bay (Sea of Japan). To perform the fragment analysis we used the same microsatellite markers as before. GTTDS8 locus was monomorphic in all the samples except for one population in the southern Primorye (Khasan district) where the second allele was found. The number of alleles in continental populations were higher than in populations on the islands. The smallest number of alleles was found in population on the Bolshoi Pelis Island.

The highest genetic similarity was revealed within both groups of populations "Middle Priamurye" and "Primorye" ($D_{Nei1978} < 0.06$). There was somewhat lower similarity between populations in these groups ($D_{Nei1978} 0.074-0.092$). Island populations presented higher differentiation both among themselves and when compared to continental ones ($D_{Nei1978} 0.109-0.382$). It suggests the importance of genetic drift in formation of their genetic structure.

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