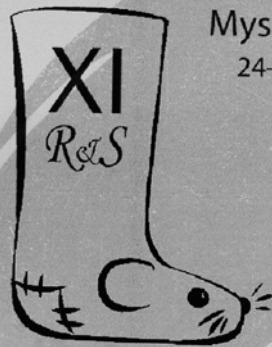


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Abstracts
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Morphological and genetic characteristics of *Microtus maximowiczii gromovi* Vorontsov, Boeskorov, Lyapunova et Revin, 1988

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The vole *Microtus maximowiczii* Schrenck, 1858 is a widely distributed species inhabiting humid biotopes of the forest zone in East Asia. This species is the central representative of the so-called "maximowiczii" group of the genus *Microtus* Schrank 1798 – an intensively disputed systematic group. This group includes three karyologically related species: *M. maximowiczii*, *Microtus mujanensis* Orlov et Kovalskaya, 1978, and *Microtus evoronensis* Kovalskaya et Sokolov, 1980 (Meyer et al., 1996). All are similar by morphological properties but highly variable within each species. Consequently, taxonomic rank of these forms remained unclear. Besides of two subspecies described for *M. maximowiczii* - *M. m. maximowiczii* Schrenck, 1858 and *M. m. unguensis* Kastchenko, 1913, recently a new subspecies from South-East of Yakutia, at the eastern shore of Bolshoe Toko lake was described: *M. maximowiczii gromovi* Vorontsov, Boeskorov, Lyapunova et Revin, 1988 (Vorontsov et al., 1988). The description of this subspecies has been based on one young individual only, by using characteristics of its karyotype ($2n=44$, $NF=60$), the complexity of M^3 shape and the lack of skull crest as diagnostic criteria. Later, however, Meyer with co-authors (1996) pointed out that the description of this subspecies has been done incorrectly, since a large geographic variability of the first two indicators not allowed to use them as characteristic for this subspecies, and the latter characterized age variability only.

The aim of the present study was to examine morphological and genetic data of *M. maximowiczii* from its whole distribution range in Russia, especially with respect to the taxonomic status of *M. m. gromovi*.

We conducted morphological (7 samples), karyological (3 samples), allozyme (3 samples) analyses and sequence analysis of the mitochondrial control region (4 samples) of *M. m. gromovi*, which have been trapped in the mouth of Nelkanka river, 5 km to the South of Ayan settlement in Khabarovskii Region (Russian Far East).

In the UPGMA analysis of the morphological data using multidimensional scaling axis as variables and standard Euclidean distance, samples of *M. m. gromovi* clustered separately from the other subspecies of *M. maximowiczii*. In average, *M. m. gromovi* proved to be considerably smaller than the other *M. maximowiczii*. The majority (i.e., 6 of 7) individuals studied from vicinities of the Ayan village, as well as specimens found on the coast of Lake Bolshoe Toko (Vorontsov et al., 1988), revealed a complicated shape of M^3 . Numbers of crests on the lingual and angle-labial sides was 5/4 for the animals from this population. The exception was one specimen whose M^3 had a simplified form - 4/3. The most common morphotypes of M^3 in *M. maximowiczii* were 4/3 and 4/4. In Transbaikalia and Mongolia, the portion of the 4/3 morphotype was 68% and 71%, respectively. In the Amur River basin, the content of 4/3 and 4/4 was almost equal to 38% in the both cases, in Manchuria it was about 20% and 70%, respectively. More complicated morphotypes 5/3 and 5/4 at *M. maximowiczii* can be met very rare (<7%). Thus, *M. m. gromovi* differs considerably from the other subspecies of *M. maximowiczii* by portion of morphotypes in the third upper molar.

The number and morphology of chromosomes in all animals investigated were stable and equal: $2n=44$, $NF=60$. G-banding of *M. m. gromovi* chromosomes allowed identifying each chromosome pair. Comparison of G-banded chromosomes of *M. m. gromovi* with those of *M. maximowiczii* from Buryatiya ($2n=44$; $NF=58$), published earlier (Meyer et al., 1996), has shown, that, despite of the identical formula of a chromosomal set ($2n=44$, $NF=60$), the animals from various regions differ by morphology of several chromosomes. So, distinctions are revealed in three pairs of autosomes. Differences in the first and 4th pairs of chromosomes are caused by pericentric inversions. Distinction in the 10th pair is connected with additional euchromatin and formation of a short arm.

Allozyme analysis showed that among 23 loci assayed, *M. m. gromovi* and the remaining *M. maximowiczii* are differentiated at Mod-2 and Gpd, possessing no common alleles in these two loci. At the G6pd locus Hb, the *M. m. gromovi* allele was found only in two individual of the other *M. maximowiczii* studied (82 individuals). The resulting values for Nei's unbiased genetic distance are in the range of interspecific distances within the genus *Microtus*. An mtDNA sequence analysis showed that the samples of *M. m. gromovi* and the remaining *M. maximowiczii* form two independent clades with high level (up to 9%) of p-distance.

Summarizing, the results confirm a distinct taxonomic position of *M. m. gromovi*. Besides pronounced differences in morphology, allozymes and DNA sequences, especially the karyological characteristics allow to propose species status for this taxon.