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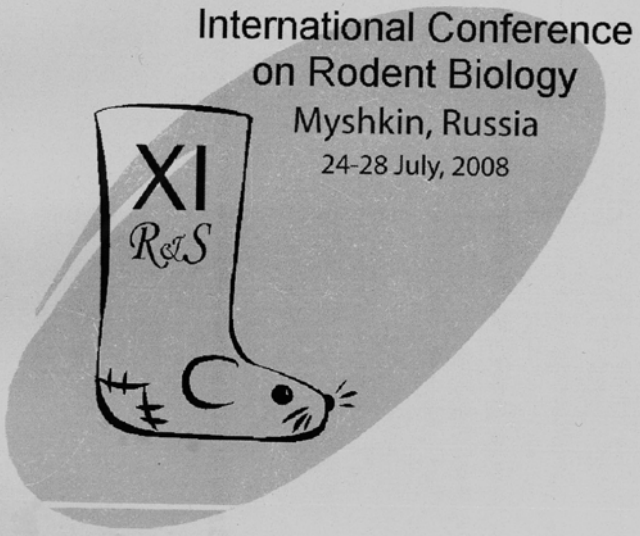
on Rodent Biology



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Abstracts
List of Participants

Grey voles (*Microtus* Schrank, 1798) of Russian Far East: Geographical or chromosomal speciation model

Frisman L., Kartavtseva I., Korobitsyna K., Sheremetyeva I.

Institute of Biology and Soil Science FEB RAS, 159, Stoletia str., Vladivostok 690022, Russia
frisman@ibss.dvo.ru

A formation of reproductive isolation in a case of geographical (allopatric) model of speciation is a long-term process accompanied by the accumulation of the significant interspecific allozymic distinctions. There are hiatus between the small intraspecific distances and significant interspecific ones as a rule.

A chromosomal speciation (Vorontsov, 1960) is generally quick process. The differentiated karyomorphs can fail to have distinctions on other taxonomically significant characteristics (morphological, allozymic) by the moment of occurrence of reproductive isolation. In other words, the relation of karyological and allozymic differentiation is a measure of evolutional history of taxon.

There are known grey vole species within *Microtus* subgenus distinguished extremely poorly morphologically, but well-marked karyologically. They are as follows *M. oeconomus* ((2n=30; NF^a=56) *M. fortis* (2n=52; NF^a=62-64) and *M. sachalinensis* (2n=50; NF^a=60); *M. mujanensis* (2n=38; NF^a=46-48) *M. evoronensis* (2n=38-40; NF^a=51-54) and *M. maximowiczii* (2n=36-44; NF^a=52-58) (Mejer et al., 1996). The present study focuses on tree subspecies of *M. maximowiczii* (85 individuals from 5 localities), on 23 individuals *M. fortis* from 3 localities, on 10 individuals *M. sachalinensis*, on one individual of *M. evoronensis*, 14 individuals *M. mujanensis* and on *M. oeconomus* (19 individuals from two localities) for which estimates of intraspecies and interspecies genetic differentiation were derived from electrophoretic variation of proteins. Additionally one hundred and eighty four individuals of *M. oeconomus* from 10 Kuril Islands and two mainland sides were analyzed for intraspecific differentiation. Twenty one loci coding for 11 enzymatic systems (Ldh-1, Ldh-2, Ldh-reg, Aat-1, Aat-2, Idh-1, Idh-2, Sod-1, Sod-2, Sdh, G6pd, Gpd, Pgd, Mor-1, Mor-2, Mod-1, Mod-2, Pgm and three another proteins (Alb, Hb, Trf) were examined. Three hierarchical levels of contribution to overall diversity were computed: between populations within subspecies, between subspecies within species and between species.

Genetic differentiation between *M. maximowiczii ungurensis* populations is equivalent to that between *M. m. maximowiczii* populations (unbiased genetic distances 0.016 and 0.01 respectively). The similar level of differentiation was found between populations of *M. fortis pelliceus* (unbiased genetic distances 0.029) and between *M. oeconomus kamtschaticus* populations (unbiased genetic distances 0-0.034). The average unbiased genetic distance for population level of that species is 0.008.

Genetic differentiation between *M. m. ungurensis* and *M. m. maximowiczii* is equivalent to that between *M. o. kamtschaticus* and *M. o. koreni* (unbiased genetic distances 0.04-0.042 and 0.021-0.053 respectively). The average unbiased genetic distance for subspecies level is 0.04.

Genetic differentiation between *M. m. gromovi* and the rest subspecies of *M. maximowiczii* is equivalent to that between *M. maximowiczii* and *M. fortis* and *M. sachalinensis* and *M. oeconomus* (unbiased genetic distances 0.260-0.305 and 0.153–0.375 respectively). If chromosomal changes were "the starting mechanism" in the process of speciation of the species group, then this event is so old, that for the expired period the allozymic distinctions had enough time to be accumulated.

We have observed another picture at *M. maximowiczii, M. mujanensis* and *M. evoronensis* group species. Allozymic distinctions between them (unbiased genetic distances 0.016-0.029 and average value is 0.023) do not exceed intraspecific ones.

The group of *M. mujanensis M. evoronensis* and *M. maximowiczii* can be considered as an example of chromosomal model of speciation.