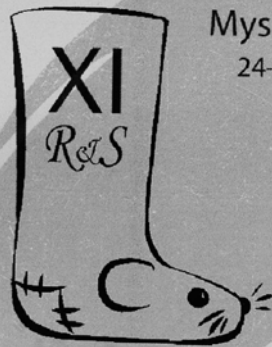


**11<sup>th</sup> International Conference**  
***Rodens et Spatium***  
**on Rodent Biology**

International Conference  
on Rodent Biology  
Myshkin, Russia  
24-28 July, 2008



**Myshkin, Russia**  
**July 24-28, 2008**

**Abstracts**  
**List of Participants**

## Chromosomal polymorphism of *Microtus maximowiczii* Schrenck, 1858 (Rodentia, Cricetidae)

Kartavtseva I.V. (1), Korobitsina K.V. (1), Sheremetyeva I.N. (1), Nemkova G.A. (1),  
Konovalova E.V. (1), Korablev V.P. (1), Kryukov A.P. (1), Voita L.L. (2)

(1) Institute of Biology and Soil Science, Far East Branch of Russian Academy of Sciences,  
Vladivostok, 690022 (Russia)

Irina-kar52@rambler.ru

(2) Institute of Natural Resource, Siberian Branch of Russian Academy of Sciences, Chita, 672014 (Russia)

The vole *Microtus maximowiczii* Schrenck, 1858 is widely distributed species inhabiting humid biotopes of the forest zone in East Asia: Russia (Transbaikalia and Amur region), Mongolia and NE China. The polymorphism in number and morphology of chromosomes ( $2n=36-44$ ;  $NF=52-60$ ) for this species has been reported before for 134 animals from 19 local populations (Kovalskaja, 1977; Kovalskaja et al., 1980, Golenizhev, Radjably, 1981; Mejer et al., 1996).

We investigated 69 animals from 14 populations not surveyed before in Chita and Amur regions and 10 animals from two the same populations in Buryatia: Istomino vil. and Romanovka vil., all trapped from 2003 to 2007. The  $2n$  of investigated animals was 38-43,  $NF=54-59$ . We tracked the same and different karyotype variants according to literature data ( $2n$ ,  $NF$ ) and distributed all animals into 5 geographical regions: three in Transbaikalia (1. Selenga river estuary, 2. Vitimskoe plateau 3. Chita area and Mongolia) and two in the Russian Far East (4. Amur region, 5. South part of Yakutia and north part of Khabarovsk territory).

The *M. maximowiczii maximowiczii* Schrenck, 1858 and *M. maximowiczii unguensis* Kastchenko, 1913 are characterized by polymorphism on fusion of two middle sized pairs of metacentrics ( $m1/m1$ ,  $m2/m2$ ) to forming of large metacentric -  $M1$  ( $m1+m2$ ). This reorganization can be found both in homozygous [ $M1$  ( $m1+m2$ )/ $M1$  ( $m1+m2$ )] and in heterozygous condition ( $M1$  ( $m1+m2$ );  $m1$ ;  $m2$ ). The large metacentric was absent only in two of 203 voles investigated with remaining  $m1/m1$ ,  $m2/m2$ . Besides, the karyotypes differ also by 4 Robertsonian rearrangements and 3 pericentric inversions in various combinations as in homozygous, as in a heterozygous condition. Only in one population from Chita region (Podoinicino vil.) we trapped 12 animals with stable karyotype:  $2n=42$ ,  $NF=56$ , X - middle A, Y - small A, 4 ST, 2 M ( $M1/M1$ ), 8 middle M and 26 A. This kind of karyotype was typical for Chitinskaja Obl. and Hankin-gol in Mongolia.

For 33 animals from the Amur region, variability of three variants of chromosomal rearrangement was found: 1.  $M1$  ( $m1+m2$ ) /  $M1$  ( $m1+m2$ );  $M1(m1+m2)$ ;  $m1$ ;  $m2$ ; 2. Robertsonian rearrangements ( $a+a$ ) with variants of karyotypes  $a/a$ ;  $a/sm$ ;  $sm/sm$ ; 3. Pericentric inversions (variants  $st/st$ ,  $st/a$ ,  $a/a$ ). Interestingly, that animals from Amur region, Norskii Reserve ( $n=28$ ), Arhara town ( $n=1$ ), Aur vil. ( $n=1$ ) and Leninskoe vil. ( $n=3$ ) had the following two variants of chromosome sets:  $M1$  ( $m1+m2$ )/ $M1$  ( $m1+m2$ );  $sm/sm$ ;  $st/st$  and  $M1$  ( $m1+m2$ );  $m1$ ;  $m2$ ;  $sm/sm$ ;  $st/st$ . Such variant of a combination of chromosomal reorganizations was found only in population from the Amur region. The G-, C- banding of chromosomes was applied for voles from Norskii Reserve and Arhara which permitted to determine the pairs involved to the rearrangements mentioned above.

The karyotype of *Microtus maximowiczii gromovi* Vorontsov, Boeskorov, Lyapunova et Revin, 1988 has no big metacentrics and differs from the simple chromosomal variant ( $2n=44$ ,  $NF=60$ ) by pericentric inversions on three St pairs of chromosome including one large St pair (G banding was applied), which in *M. m. maximowiczii* and *M. m. unguensis* we can meet all time in constant size and morphology. Instead, in *M. m. gromovi* this pair is presented by large acrocentric.

Thus, the analysis of available data allows assuming that in various populations there is a fixing of various types of chromosomal rearrangements. Using of methods of differential staining of chromosomes will allow clearing up character of these rearrangements in the set of geographical populations.

This work was partly supported by the grants of RFBR № 06-04-48969, 07-04-10175 and FEB RAS 06-III-A-06-473.