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GENERAL  
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## Common Voles of the *Microtus arvalis* Group in the Urals: Genome Instability and Chromosomal Polymorphism

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The chromosomal sibling species common and eastern European voles (*Microtus arvalis* sensu stricto Palas, 1779 and *M. rossiaemeridionalis* Ognev, 1924) have been widely used in evolutionary and ecological studies for a long time. Despite significant differences in chromosomal and molecular genome organization [1, 2], they are characterized by a high phenotypic similarity and ecological specialization, because of which they coinhabit many areas where their ranges overlap. Nevertheless, multivariate analysis shows that sibling species differ in some biochemical [3] and immunohematological [4] parameters, as well as in a set of morphological traits [5–7].

The subject of this study was various aspects of chromosomal variation in the common and eastern European voles, including genome instability in somatic cells and intrapopulation polymorphism.

Genome instability (the mutation rate) was estimated from the frequency of structural and numerical chromosomal mutations in metaphases of bone marrow cells. True breaks were differentiated from chromatid gaps on the basis of the standard criteria (a shift with respect to the chromatid axis and/or the presence of a space exceeding chromatid width). Chromosomal aberrations were studied in sibling species from four localities of the Middle and Southern Urals and from the Middle Volga region. In all cases, *M. arvalis* and *M. rossiaemeridionalis* inhabited adjacent localities; hence, the effects of mutagenic environmental factors were similar. It can be seen from Table 1 that, in all habitats, the parameters of chromosomal instability of the eastern European vole were higher than those of the common vole. Three-way log-linear analysis with the factors *species*, *locality*, and *the proportion of cells with chromosome aberrations* showed highly significant interspecific differences with respect to aberrations and gaps. Animals of the same species but from different populations also significantly differed in these parameters, which was especially pronounced in the eastern European vole. The concentrations of heavy metals (copper, zinc, cadmium, and lead) in the liver and the

content of some radionuclides (K-40, Sr-90, Cs-137, Ra-226, and Th-232) in the bone and muscular tissues were similar in animals from all localities studied, although, in some cases, the effects of other mutagens could not be excluded. For example, the Kristalka village is located in the affected zone of the Totskii radioactive trail, where the plutonium content of soil is increased [8]. The site of vole trapping in a Ioshkar-Ola suburb was in the immediate vicinity of a motor depot, which suggests the effects of organic chemical pollutants, which are known to be potent mutagens. In this locality, pathogens were apparently important clastogenic agents. Many of them, primarily viruses (including persistent ones), are primarily capable of inducing chromosome mutations [9]. Changes in the immune system of both species, which were correlated with the frequencies of chromosomal aberrations and were more pronounced in *M. rossiaemeridionalis*, suggest that infectious agents play a role in the induction of chromosome mutations in voles [4]. Similarly, among the animals from the Bainy village, the immune system was more stressed in the eastern European vole [4]. The latter species may be more sensitive to infections, which at least partly explains its higher mutability compared to the common vole.

Intrapopulation polymorphism is inherent in both sibling species, especially in *M. arvalis* [1]. Many populations of the form *obscurus* were found to be polymorphic with respect to a pericentric inversion in chromosome 5 pair, namely, two morphological variants (subtelocentric and acrocentric). The frequency of acrocentrics varied in different localities of the area and was low as a rule, although in some places (in Armenia and the Volga region), this parameter reached 30–40% [1, 10, 11]. Opinions on the selective role of chromosome 5 polymorphism in common voles vary largely, from denial [10] to recognition [1]. Both random and selective factors seem to support this polymorphism, depending on the situation. For example, Akhverdyan *et al.* [10] have with reason suggested the leading role of isolation in the high frequency of the acrocentric variant in voles from highland Transcaucasian regions. The situation was different in the populations studied in this work.

To date, we found 19 localities inhabited by common voles in the Urals. They cover an area from 51°08'

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**Table 1.** Frequency of chromosome aberrations in sibling species of the *M. arvalis* group

Locality	Species	The number of animals (cells)	Average proportion of cells, %		
			with chromo- some aberrations	with aneu- and polyploidy	with gaps
Botanical Gardens, Ural Division, Russian Academy of Sciences, Yekaterinburg, 56°48' N, 60°40' E	<i>M. arvalis</i>	6 (300)	0.67	0.33	2.00
	<i>M. rossiaemeridionalis</i>	12 (600)	2.17	0.50	2.83
Bainy village, Sverdlovsk oblast, 56°42' N, 62°08' E	<i>M. arvalis</i>	34 (1700)	1.12	0.41	2.00
	<i>M. rossiaemeridionalis</i>	51 (2550)	1.84	0.51	2.94
Starikovo village, Sverdlovsk oblast, 56°10' N, 61°25' E	<i>M. arvalis</i>	14 (700)	1.29	0.29	2.57
	<i>M. rossiaemeridionalis</i>	5 (250)	3.20	0.40	2.80
Kristalka village, Orenburg oblast, 53°00' N, 53°28' E	<i>M. arvalis</i>	7 (350)	0.86	0.86	1.43
	<i>M. rossiaemeridionalis</i>	22 (1125)	3.56	0.98	5.42
Ioshkar-Ola, Mari El Republic, 56°40' N, 48°00' E	<i>M. arvalis</i>	39 (1950)	2.51	0.36	2.67
	<i>M. rossiaemeridionalis</i>	28 (1400)	6.00	0.71	7.64
Species ( <i>df</i> = 5)	G		44.604	2.461	60.923
	P		<0.0001	0.7824	<0.0001
Locality ( <i>df</i> = 8)	G		64.544	4.808	55.179
	P		<0.0001	0.7779	<0.0001

**Table 2.** The frequencies of acrocentric chromosome 5 variant and of females with karyotype 45, XO in common voles in the Urals

The region of trapping		Year	Number of animals		
			total studied	heterozygous for chromo- some 5 pair	females with karyotype XO
Predural'e reserve, Perm' oblast, 57°20' N, 57°09' E	The right bank of the Sylva River	1998	6	1 (0.08)*	
	The right bank of the Sylva River	2000	31	1 (0.02)	
	The left bank of the Sylva River		31	1 (0.02)	
	The right bank of the Sylva River	2001	36	3 (0.04)	
	The left bank of the Sylva River		56	8 (0.07)	
Shigaevovillage, Sverdlovsk oblast, 57°15' N, 58°44' E		1999	28	1 (0.02)	1
Southwestern district, Yekaterinburg, 56°48' N, 60°40' E		2003	16	1 (0.03)	
Bainy village, Sverdlovsk oblast, 56°42' N, 62°08' E		2000	14	1 (0.04)	
		2001	74	1 (0.01)	3
		2004	20		
Biological Station of the Ural State University, Sverdlovsk oblast, 56°37' N, 61°08' E		1995	13	1 (0.04)	
		1997	12	1 (0.04)	
		2002	14	1 (0.04)	
Starikovo village, Sverdlovsk oblast, 56°10' N, 61°25' E		2003	23	2 (0.04)	1
		2004	14		
The region of Eastern Ural Reserve, Chelyabinsk oblast, 55°47'–55°50' N, 60°55'–61°00' E		1994	23	1 (0.02)	1
Arkaim reserve, Chelyabinsk oblast, 52°37' N, 59°33' E		1996	5	1 (0.10)	
		2002	17	1 (0.03)	
Total			433	26 (0.03)	

\* The frequency of acrocentric chromosome 5 variant is indicated in parentheses.

to 57°20' N and from 53°28' to 62°08' E. Fourteen out of them have been described in [12]; the remaining localities are listed in Tables 1 and 2. In addition, 18 *M. arvalis* were trapped near the Kurmanka village (Sverdlovsk oblast), at 56°50' N, 61°20' E. Six localities are coinhabited by *M. arvalis* and *M. rossiaemeridionalis* (Table 1; see also [12]). The acrocentric chromosomes 5 were found at low frequencies in eight populations; no significant differences between populations or variation from year to year were observed ( $\chi^2 = 3.72$ ,  $df = 15$ ,  $P = 0.999$ , calculated by the Bartlett method for low frequencies [13]) (Table 2). As few as three samples were characterized by a frequency exceeding 5%; however, in two cases, the samples included no more than six animals, whereas in the third case (the left bank of the Sylva River, 2001) most acrocentric carriers seem to originate from the same litter. Five localities were under observation for as long as several years, and there were no significant changes in the frequency of acrocentrics. Thus, a stable chromosomal polymorphism is characteristic of the common vole in the Urals, the frequency of the minor variant being extremely low. It is difficult to assume that random processes underlie this type of polymorphism maintained for a long time in numerous populations. Selective factors, including oppositely directed ones, are most likely to determine this polymorphism. Mitotic drive may also promote selection, which is confirmed by a high frequency of X monosomy in females, which was found previously in Central Europe [14] and now in Ural populations (Table 2). Further studies on *M. arvalis* under laboratory conditions will be helpful in the analysis of these factors.

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