

Radiation Dose Rates Estimation and Allozyme Variability in the Population of the Northern Red-Backed Vole (*Clethrionomys rutilus*) from the East-Ural Radioactive Trace

M. V. Modorov

Institute of Plant and Animal Ecology, Ural Branch, Russian Academy of Sciences, Yekaterinburg, 620144 Russia

e-mail: mmodorov@gmail.com

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Abstract—The paper estimates the external (due to radionuclides accumulated in the soil) and internal (due to incorporated radionuclides) exposure of rodents that live in the head of the East Urals Radioactive Trace (EURT). It is shown that in the last decades the dose rates were lower than the values that lead to a doubling the number of mutations in the allozyme loci in mammals. The variability of the eight allozyme loci in populations of northern red-backed voles from the EURT zone and their neighboring plots, as well as the territories of the Urals and Trans-Urals with background levels of radioactive contamination, are analyzed. No differences in the pattern and frequency of allozymes that would distinguish the EURT samples from a number of other populations of the Urals, were found. In the control sample “Sysert”, “unique” for the Ural populations of northern red-backed voles, alleles of the loci *Got* and *Sod* were marked, conspecific to a closely related species—the bank vole. This fact can be regarded as evidence of recent cross-species hybridization.

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INTRODUCTION

In September 1957, there was a major radiation accident (total emission of radioactive waste 74 PBq) at the production association “Mayak” (Southern Urals). A territory with contamination of ^{90}Sr over 74 kBq/m^2 was called the East-Ural Radioactive Trace (EURT); its area was 997 km^2 with a width of 8–9 km [1]. Ecological and genetic studies of small mammals of EURT began in 1962 and still continue. A number of data points to the fact that the potency of at least two factors determining the genetic structure of animal populations has changed as a result of radioactive contamination of the territory: the mutation process [2–4] and natural selection [5]. It is of interest to analyze the consequences of such changes. Perhaps they have led to a shift in the frequency of alleles and an increase in the genetic diversity parameters or were compensated.

Previously, we analyzed the allozyme variability of the Ural field mouse that inhabits the EURT zone [6]. It was shown that the pattern and frequencies of allozymes in animals caught in the impact and control areas are similar. Unsubstantiated extrapolation of this result to other rodent species, in our opinion, is unjustified, since there are interspecific differences in radiosensitivity, habitat preferences, and migration activity. In this paper, we analyze the allozyme variability of the northern red-backed vole *Clethrionomys rutilus* Pallas, 1779, which, like the Ural field mouse, is one of the most frequently used objects for studying the

EURT biota [2, 5, 7, 8]. To assess the impact of the radiation factor on the rate of the mutation process, we calculated radiation doses received by rodents that live in the contaminated area.

MATERIALS AND METHODS

Sites and Methods of Trapping

The animals were caught using live traps in snow-free periods of 2005–2011 at nine sites. The impacted areas are located on the central axis of EURT on the southern shores of the lakes Berdenish ($55^{\circ}46' \text{ N}$, $60^{\circ}52' \text{ E}$) and Uruskul' ($55^{\circ}49' \text{ N}$, $60^{\circ}55' \text{ E}$). The sites “Metlino” ($55^{\circ}48' \text{ N}$, $60^{\circ}00' \text{ E}$) and “Druzhnyi” ($55^{\circ}48' \text{ N}$, $61^{\circ}20' \text{ E}$) lie in areas adjacent to the eastern boundary of the trace. As control samples, we used animals caught in the territory of the Urals with a background level of radioactive contamination. The sites “Serga” ($56^{\circ}30' \text{ N}$, $59^{\circ}15' \text{ E}$), “River Uy” ($54^{\circ}01' \text{ N}$, $60^{\circ}59' \text{ E}$) and “Sysert” ($56^{\circ}36' \text{ N}$, $61^{\circ}01' \text{ E}$) are at a distance of more than 90 km from the test grounds. In the Kurgan region, the animals were caught in the vicinity of the village Zverinogolovskoe ($54^{\circ}28' \text{ N}$, $64^{\circ}51' \text{ E}$) and the village Uspenka ($54^{\circ}47' \text{ N}$, $66^{\circ}22' \text{ E}$). Moreover, as an external control, we used bank voles (*Clethrionomys glareolus* Schreber, 1780) from the sites “Sysert” and “Serga”.

Table 1. Content and activity concentrations of ^{90}Sr and ^{137}Cs at sites “Berdensh” and “Uruskul” in 2007 (according to data from [18])

Parameter	Nuclide	Site	
		Berdensh	Uruskul
Activity concentration of radionuclide in soil layer of 0–10 cm, Bq/kg*	^{90}Sr	138200	98210
	^{137}Cs	5465	5571
Radionuclide content in soil layer of 0–10 cm, kBq/m ^{2**}	^{90}Sr	8033	2780
	^{137}Cs	317	204
Radionuclide content in soil layer of 0–45 cm, kBq/m ²	^{90}Sr	12851	7625
	^{137}Cs	427	225
Ratio of radionuclide content in soil layer of 0–10 cm to content in soil layer of 0–45 cm	^{90}Sr	0.63	0.36
	^{137}Cs	0.74	0.91

* Indicator was obtained by averaging values given for soil layers of 0–5 and 5–10 cm.

** Indicator was obtained by adding values given for soil layers of 0–5 and 5–10 cm.

Calculation of Radiation Doses

In the first years after the accident, the radiation dose rates in EURT were conditioned by medium-lived isotopes: ^{144}Ce , ^{95}Zr , ^{106}Ru . After their decay (after 1–4 years), the absorbed doses decreased sharply and at the present time are determined by ^{90}Sr [9]. In 1967, the head part of EURT received additional radioactive contamination as a result of the spread of radioactive silt and sand from the shores of the Lake Karachay [10, 11]. This led to the emergence of a large number of ^{137}Cs in the ecosystems.

The radiation doses received by the animals in the first months after the accident were taken from [9]. It has been shown that the dose absorbed by the rodents in autumn–winter of 1957–1958, per 1 MBq $^{90}\text{Sr}/\text{m}^2$, averaged for 1–2 Gy, whereas the maximum values of the parameter reached 100 Gy. Calculation of the radiation doses received by rodents after 1958 was carried out in a program ERICA Tool [12] using Tier 3. Creation of a model suitable for analysis required considering a number of parameters, which were obtained based on the following publications:

1. *Size and weight of the animal.* We took average values of the parameters for the samples of the northern red-backed vole from the sites “Berdensh” and “Uruskul”: body length was 86 mm, weight was 17.2 g. The width and height of the animal were set to 25 mm.

2. *Time spent by the animal in a hole and on the surface of the soil.* We assumed that the animal spends 20% of the time on the surface of the soil and 80% in the hole. On the basis of [13], we found that vole holes are located in the upper soil layer (0–10 cm).

3. *Activity concentrations of ^{90}Sr and ^{137}Cs in the rodent body (Bq/kg).* The data are taken from [14–17]. In [14–16], the authors calculated the total beta activity of $^{90}\text{Sr} + ^{90}\text{Y}$, so we divided the values of activity concentration of radionuclides cited in the publications into two.

4. *Contents and activity concentrations of ^{90}Sr and ^{137}Cs in the soil.* It was assumed that the entire ^{90}Sr entered the territory of EURT in 1957, and the entire ^{137}Cs entered in 1967. The parameter values obtained in 2007 were taken from [18]. The data used are summarized in Table 1.

The content of ^{90}Sr in the soil in 1957 (Bq/m²) was calculated according to the law of radioactive decay. For the calculation of activity concentration of ^{137}Cs in the soil (Bq/kg) during 1967–2007, we used the formula

$$A = N_0 100 / (N_{0-10} / N_{0-45}) \%,$$

where A is the specific activity of a radionuclide, N_0 is the concentration of ^{137}Cs in the soil layer of 0–10 cm in the analyzed year, N_{0-10} is the concentration of ^{137}Cs in the soil layer of 0–10 cm in 2007, N_{0-45} is the content of ^{137}Cs in the soil in 2007.

This formula takes into account the decay of the radionuclide. Furthermore, because of the low migration of ^{137}Cs within soil horizons (see Table 1), we made an assumption that prior to 2007 the entire radionuclide was in the soil layer of 0–10 cm. The activity concentration of ^{90}Sr in the soil (Bq/kg) during the period of 1957–2007 was calculated similarly to ^{137}Cs .

Allozyme Analysis

We analyzed 216 individuals of *C. rutilus* and 13 individuals of *C. glareolus*. The method of obtaining the specimen and carrying out electrophoresis was described previously [6]. We analyzed eight enzyme systems: 6PGDH (E.C. 1.1.1.44), GPDH (E.C. 1.1.1.8), GOT (E.C. 2.6.1.1), G6PDH (E.C. 1.1.1.49), LDH (E.C. 1.1.1.27), SOD (E.C. 1.15.1.1), PGM (E.C. 2.5.7.1), PGI and (E.C. 5.3.1.9). The enzyme system G6PDH (one locus) showed no variability. The enzyme system LDH is represented by two loci, of which only one (LDH-1) can be interpreted correctly.

Table 2. External dose rates T (cGy/year) received by rodents from sites “Berdensh” and “Uruskul’,” caused by ^{90}Sr and ^{137}Cs , in 1957–2007

Year	Berdensh		Uruskul’	
	^{137}Cs	^{90}Sr	^{137}Cs	^{90}Sr
1957		8.1×10^{-5}		10.1×10^{-5}
1967	4.3	6.3×10^{-5}	3.6	7.9×10^{-5}
1977	3.4	5.0×10^{-5}	2.8	6.2×10^{-5}
1987	2.7	3.9×10^{-5}	2.2	4.8×10^{-5}
1997	2.1	3.0×10^{-5}	1.8	3.8×10^{-5}
2007	1.3	1.5×10^{-5}	1.3	1.1×10^{-5}

Table 3. Dose rates received by rodents that live at site “Berdensh,” from incorporated ^{90}Sr and ^{137}Cs

Species	Years*	Dose-forming radionuclide	Activity concentration of rodent body, Bq/g	Dose rates, cGy/year	Data source
<i>Microtus arvalis</i> s.l.	1987–1995	^{90}Sr	40–100	20.1–50.4	[17]
<i>Apodemus uralensis</i>	1987–1996	^{90}Sr	25–50	12.6–25.1	
	1988	^{90}Sr	43	21.7	
	1995	^{90}Sr	22	11.1	
	1996	^{90}Sr	16	8.1	
<i>A. agrarius</i>	1988	^{90}Sr	25	12.6	
	1995	^{90}Sr	18	9.1	
	1996	^{90}Sr	15	7.6	
<i>M. arvalis</i> s.l.	1992	^{90}Sr	9.5–30.3	4.7–15.3	[15]
<i>M. gregalis</i>		^{90}Sr	20.0–52.0	10.0–26.2	
<i>M. arvalis</i> s.l.	1986–1993	^{137}Cs	1.0	0.13	[17]
<i>A. uralensis</i>	1986–1993	^{137}Cs	0.9	0.12	

* Indicates period in which catches may have been carried out.

We calculated the following standard indicators of variability: the frequency of alleles, the proportion of polymorphic loci at 95 and 99% nominal significance criteria ($P_{95\%}$, $P_{99\%}$), the effective (N_e) and average (N_a) number of alleles per locus, the fixation index (F) and its standard error (SE_F). Accordance of the observed distribution of genotypes with the distribution that follows from the Hardy-Weinberg equilibrium was assessed using the criterion χ^2 . In assessing the genetic subdivision of the samples (F_{ST}), the calculated value of the parameter was compared with zero, and the genetic differentiation was considered significant at $p < 0.05$. Processing of the data was carried out using GenAlex 6.1 [19].

RESULTS

Radiation Dose Rates

The dose rates received by rodents living at the sites “Uruskul’” and “Berdensh” in the period of 1957–1958 amounted to 26–88 Gy. Beyond the EURT boundaries (that is, the territory with the level of post-accident contamination by ^{90}Sr less than 74 kBq/m²), they do not exceed 0.07–0.14 Gy.

The external dose rate in the rodents living at the sites “Berdensh” and “Uruskul’” in 1967 didn’t exceed 4.4 cGy/year, and by 2007 it decreased to 1.3 cGy/year (Table 2). It was determined by ^{137}Cs by more than 99%.

The internal dose rates in the small mammals living at the site “Berdenish” in the period 1986–1996 were 4.7–50.4 cGy/year (Table 3). The contribution of ^{90}Sr into the dose rate exceeded 99%.

On the basis of [14, 16, 17], one can track the dynamics accumulating ^{90}Sr in the bone tissue of the Ural field mouse from the site “Berdenish” over 40 years. The specific activity of the radionuclide was 426 Bq/g in 1962–1967 [14], 140 Bq/g in 1986–1993 [17], and 80 Bq/g in 2001 [16]. Thus, for 25–30 years (from 1962–1967 to 1986–1993), the specific activity of ^{90}Sr in the bone tissue of the animals declined by about three times, and over the next 10–15 years by another factor of 1.5. The dose rate received by rodents in this area from incorporated ^{90}Sr has decreased, probably by about the same extent.

The levels of accumulation of ^{90}Sr by rodents caught outside EURT are tens or hundreds of times lower than the levels seen at the site “Berdenish” in the same period. It can be assumed that such a low specific activity of the radionuclide did not lead to a significant accumulation of radiation exposure.

Rate of Mutation

In [20], the doses that lead to a doubling of the frequency of spontaneous mutations of allozyme loci of mammals were substantiated. It was shown that the rate of spontaneous mutation of man is $(2.95 \pm 0.64) \times 10^{-6}$ events per gene per generation. The dose of chronic low intensity irradiation that results in a doubling of this level (the doubling dose) in mice is 0.82 ± 0.29 Gy. We assume a linear relationship “dose–effect.”

Thus, in the first months after the accident, the levels of radiation exposure received by animals in the areas “Berdenish” and “Uruskul” significantly exceeded not only the doubling dose, but also the average half-lethal dose of acute radiation of the northern red-backed vole, which is 9.6 Gy [5]. In the period of 1962–1967, the annual radiation dose of the animals from the site “Berdenish” apparently exceeded the doubling dose by more than two times. Since 1986 to the present time, it is below the doubling dose by more than 1.5 times, that is, irradiation induces the appearance of no more than two mutations at a particular locus in a million individuals. Outside EURT in the first months after the accident, the dose rates were five times less than the doubling dose.

Allozyme Variability in Populations of Northern Red-Backed Vole

The parameters of allozyme variability of the animals are shown in Table 4. In populations of the northern red-backed voles, from one to five loci show variability. The average number of alleles per locus ranges from 1.125 to 1.750, and the effective number of alleles per locus ranges from 1.123 to 1.292. No alleles unique

to the EURT populations were observed. The parameters of allozyme variability in the sample from the site “Berdenish” most contaminated by ^{90}Sr are at a minimum level for the region. In the sample from the impacted area “Uruskul”, the values of these parameters are within the limits of the regional norm. The fixation index values (F) in the samples of EURT are negative. In four of the five control samples, values of this parameter are below zero (Table 4). In almost all the cases, the observed ratio of genotypes did not differ from that expected from Hardy–Weinberg. Statistically significant differences ($p < 0.05$) were found in the sample “Uruskul” by the locus *Ldh* (an excess of heterozygous genotypes was observed) and the sample “Zverinogolovskoe” by the locus *Gpdh* (an excess of homozygous genotypes was marked). In general, these deviations are not of unidirectional nature.

The genetic differentiation of the samples “Berdenish”, “Uruskul”, “Metlino”, “Druzhnyi”, “Serga”, and “River Uy” is not pronounced; the value of F_{ST} is not significantly different from zero. The samples “Zverinogolovskoe” and “Uspenka” are statistically differentiated from the samples “Druzhnyi” and “Uruskul” ($F_{ST} = 0.036–0.053$, $p = 0.01–0.05$). The differentiation of all these samples and animals from the site “Sysert” is statistically significant ($F_{ST} = 0.077–0.144$, $p < 0.05$). The interspecific genetic differentiation is $F_{ST} = 0.808$ ($p < 0.01$).

DISCUSSION

In the northern red-backed vole populations, like in the populations of Ural field mouse, no differences in the pattern and frequencies of allozymes were detected that would distinguish the samples from radioactively contaminated sites from a number of other populations of the Urals. For an explanation of the reasons for such a result, we will analyze factors, the combined effect of which determine the genetic structure of the population, namely, mutations, migrations, genetic drift, and natural selection [21].

Mutation of genes. The manifold increase in the rate of the mutation process in the populations of rodents from the EURT zone with respect to spontaneous levels occurred only in the most contaminated sites, and only in the first years after the accident. The contemporary speed of mutagenesis of allozyme loci in the animals from the sites “Berdenish” and “Uruskul” is only slightly above the spontaneous level. In the analysis of the sample of 52 individuals, only those mutant forms can be identified that occurred several generations before the catches, the frequency of which was increased because of genetic drift or natural selection. Since the genetic variability parameters of samples from the EURT zone are not increased relative to the control values, it is impossible to speak about an accumulation of the mutant forms of alleles in the population inhabiting the impacted territory.

Table 4. Allele frequencies and parameters of genetic variability in samples of *Clethrionomys rutilus* and *C. glareolus*

Locus	Allele	<i>Clethrionomys rutilus</i>									<i>C. glareolus</i>
		EURT territory		sites adjacent to EURT		territory with background to Urals level of radioactive contamination					
		1	2	3	4	5	6	7	8	9	
<i>6Pgdh</i>	1	0	0.060	0	0.033	0	0	0	0	0	0
	2	1	0.940	1	0.967	0.987	1	1	1	1	1
	3	0	0	0	0	0.013	0	0	0	0	0
<i>Got</i>	1	0	0	0	0	0.026	0	0	0.125	0	0
	2	0	0.012	0.023	0.017	0.013	0.145	0.019	0	0.062	0
	3	1	0.988	0.977	0.983	0.961	0.855	0.981	0.875	0.688	0
	4	0	0	0	0	0	0	0	0	0.250	1
<i>Gpdh</i>	1	0	0.012	0.045	0.017	0	0	0	0	0	0
	2	0	0	0	0	0.013	0.032	0.037	0	0	0.192
	3	1	0.988	0.932	0.983	0.947	0.919	0.944	1	1	0.808
	4	0	0	0.023	0	0.039	0.048	0.019	0	0	0
<i>Ldh-1</i>	1	0.450	0.381	0.477	0.350	0.408	0.500	0.556	0.313	0.375	1
	2	0.550	0.619	0.523	0.650	0.592	0.500	0.444	0.687	0.625	0
<i>Pgi</i>	1	0	0	0.091	0.017	0	0	0	0	0	0
	2	1	1	0.909	0.983	1	1	1	1	1	1
<i>Pgm</i>	1	0	0	0	0	0	0	0	0	0	1
	2	0	0	0	0	0	0	0	0.063	0	0
	3	1	1	1	1	1	0.952	0.907	0.875	1	0
	4	0	0	0	0	0	0.048	0.093	0.063	0	0
<i>Sod</i>	1	1	1	1	1	1	1	1	1	0.750	0
	2	0	0	0	0	0	0	0	0	0.250	1
<i>N</i>		10	42	22	30	38	31	27	8	8	13
<i>N_a</i>		1.125	1.500	1.625	1.625	1.750	1.625	1.625	1.500	1.500	1.125
<i>N_e</i>		1.123	1.133	1.174	1.126	1.144	1.201	1.167	1.166	1.292	1.056
<i>P_{95%}</i>		12.5	25.0	37.5	12.5	25.0	37.5	37.5	37.5	37.5	12.5
<i>P_{99%}</i>		12.5	50.0	50.0	62.5	50.0	50.0	50.0	37.5	37.5	12.5
<i>F</i>		-0.010	-0.125	-0.045	0.051	-0.058	0.173	-0.054	-0.234	-0.430	0.257
<i>SE_F</i>		0.065	0.068	0.015	0.057	0.021	0.075	0.012	0.068	0.052	0.040

N, sample size. Sites: 1, Berdenish; 2, Uruskul'; 3, Metlino; 4, Druzhnyi; 5, Serga; 6, Zverinogolovskoe; 7, Uspenka; 8, River Uy; 9, Syser't. For remaining symbols, see Materials and Methods.

Natural selection. Most of the newly emerged mutations in some degree reduce the viability of organisms [22]. Consequently, natural selection will increase the likelihood of elimination of carriers of mutations. However, the same process can lead to a rapid increase in the incidence of traits that increase fitness. There were no statistically significant differences of allele frequencies in samples from the EURT zone ("Berdenish", "Uruskul'") and sites adjacent to it ("Metlino", "Druzhnyi"). Therefore, selection of individuals in the EURT zone by the loci analyzed is either absent or very weak.

Genetic drift. Random changes in allele frequencies and thus a decrease in the genetic variability parameters occur because of the finite size of any real-life population. The intensity of these changes will be the stronger, the smaller the effective population size. Genetic drift leads to genetic differentiation of subpopulations for which migration is low or absent [21].

For rodents of the head of the EURT zone, at least two factors that could affect the effective population size can be distinguished. The first is associated with high dose rates in 1957–1958. It can be assumed that a con-

siderable proportion of the animals that lived in the area of the greatest contamination died or had disturbed reproduction. The second factor is the fires that occurred in this area in recent years. Previously, on the example of the field mouse, it was shown that there are no small mammals at recently burned areas [8]. The number of individuals in the burned areas can be restored, either by surviving individuals (in this case, there will be a genetic drift) or by migrants from the surrounding areas. Taking into account the small width of the site of the impacted subpopulation, it can be suggested that the migrants are those animals that live in areas with low levels of radioactive contamination.

Migration of genes. Migration leads to equalization of allelic frequencies between the interacting subpopulations. The signs of migration of genes between subpopulations of the impacted (“Berdensh”, “Uruskul”) and territories adjacent to it (“Metlino”, “Druzhnyi”) consist of the absence of genetic differentiation of the samples and the presence in loci *6Pgdh* and *Gpdh* of alleles unique only to the voles from this region. In favor of migration, interactions between populations of EURT and adjacent territories speak of the comparable distances of the trace width (9 km), the maximum daily run of red-backed voles of 1.5 km [23], and the medium-range dispersal of animals, which is more than 500 m [24].

Based on the above, one can distinguish the following reasons for the absence of genetic features in terms of frequencies and forms of allozymes in populations of small mammals of EURT:

1. The low rate of mutation process of allozyme loci at the present time; the short duration and remoteness in time of the period in which the mutation rate was much higher than the spontaneous level; a small area of contamination.

2. A decrease in viability of carriers of the majority of mutations, which leads to elimination of mutant forms.

3. High levels of animal migration caused by both the small width of the contamination zone and the frequent fires, which lead to a decrease in the density of animals in the burnt areas of EURT.

The allozyme variability of the animals from the site “Sysert” is especially interesting, namely the presence in loci *Got* and *Sod* of “unique” for the Ural populations of red-backed voles alleles conspecific to the bank vole (Table 4). In the remaining samples that we analyzed, these alleles (respectively 4, 2) are missing in red-backed voles. These alleles were also not described in other studies of allozyme variability of the studied species [25–27]. It can be assumed that the presence of “unique” alleles is associated with the interspecific hybridization of red-backed and bank voles that took place earlier. The possibility of such hybridization in the Urals was pointed out earlier in [28, 29].

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