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Abstracts List of Participants

## Genomic instability in the cyclic bank vole population

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Genomic instability in relation to population dynamics and demographic parameters was studied for nine years (1999-2007) in a bank vole (*Clethrionomys glareolus* Schreber, 1780) population in the Middle Urals. Studies were performed with the population of bank voles living near the village of Shigaevo, Shalinskii raion of Sverdlovsk oblast (57°15 N, 58°44.E). Anthropogenic load on this area is at the background level for the Urals. Metaphase chromosome preparations of bone marrow cells were stained with azure–eosin and studied under a microscope to count structural chromosome aberrations, and the numbers of aneuploid and polyploid cells. As a rule, 25–100 cells (in some cases, up to 250 cells) per animal were analyzed. A total of 419 voles were included in the study. Animal abundance was estimated from the capture rate per 100 trap-days over the first two days, as the catch was sometimes greater on the second than on the first day. In all animals, sex, reproductive status (reproductive and nonreproductive) and age (overwintered and young of the year) were identified. Animal age was determined from the degree of root development in the second upper molar. Our purpose is to analyze probable correlations of the levels of genomic instability with these parameters and with fluctuations of animal abundance.

The average frequencies of chromosome mutations in males and females were similar. No significant difference between individual samples corresponding to different combinations of values (grades) of the examined factors was revealed in any of the pairwise comparisons for both cytogenetic indices for different years (for structural aberrations:  $\chi^2 = 0.00 - 2.93$ ; df=1; P=0.09-1,00; for numeric chromosome mutations:  $\chi^2$ =0.00-1.98; df=1; P=0.32-1.00), which allowed us to pool the data on males and females for further analysis. The dependence of the level of chromosome instability on animal age was estimated in reproductive voles using three-way log-linear analysis with factors "year," "age," and "frequency of cells with chromosome mutations." The analysis was performed with pooled data on males and females (overwintered animals and reproductive young of the year) over the period from 1999 to 2003, and from 2005 to 2007, as no reproductive young of the year were caught in 2004. Nonreproductive animals were not considered, because they were represented by only one age group (young of the year). The rate of structural aberrations was not associated with age of animals (G=2.12; df=1; P=0.145), but the proportion of an euploid and polyploid cells increased with the age of voles (G=14.6; df=1; P=0.0001). The subsequent analysis spent by means of the generalized linear model with «year of capturing», «phase of a population cycle» and «reproductive status» as factors in different combinations, which optimality was determined by means of information criterion Akaike (Akaike, 1983). After nine years of observations on the frequency structural and numeric chromosome mutations in the bank vole from a cyclic population, significant differences between years have been found for both types of mutations (G=49.74; df=8; P=4.58xE-08 and G=17.94; df=8; P=0.022, respectively). The level of structural chromosome aberrations in different years varied from 0.72 % and up to 2.87 %, and numerical disturbances from 0.25 % and up to 1.21 %. In searches of the causes of these distinctions we investigated connection of mutability with the phase of population cycle and participation of animals in the reproduction. Animal abundance in different years varied from 2.5 and up to 69.0 ind./100 trap-days. Phases of population cycle (depression, growth and peak of number) were identified based on density and structure of population. It was not revealed significant connection population density and the frequency of aneuploid and polyploid cells for all three groups divided on age taking into account of reproductive status (G=0.43-3.67; df=2; P=0.160-0.805), in contrast to the frequency of cells with structural chromosome mutations. There was significant influence both phase of population cycle and reproductive status for them (G=6.44; df=2; P=0.040 and G=6.08; df=1; P=0.014, respectively).

Thus, the aberration frequency displayed a clear connection with phase of population cycle, at that maximal value being arrived during growth of number. Mainly mature animals contributed to this effect, apparently as a result of augmented activity of hormones (both sexual and stressing ones). Strengthening mutation processes can increase the genetic diversity, compensating its possible loss after phases of low numbers.

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