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ANALYSIS OF LONG-TERM DYNAMICS OF CHROMOSOMAL INSTABILITY IN THE BANK VOLE POPULATION

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Assessment of the mutation process dynamics in natural populations is a complex and multifactorial problem. In particular, it is unclear to what extent the frequency of mutations in germ and somatic cells are modified by population-demographic processes, that can also lead to significant changes in metabolism and reproductive system (Chernyavskii et al., 2003).

In this paper we analyze the results of the unique long-term observations (1999–2014 years) of the dynamics of chromosome mutation frequency in the model cyclic populations of bank vole (*Myodes glareolus*) from the territory of the Middle Urals ($57^{\circ}15' N$, $58^{\circ}44' E$), reported to be exposed to a background level of anthropogenic pollution (Gileva et al., 2006). The rate of structural chromosomal aberrations (CA) in the bone marrow of voles was used as an indicator of mutation intensity. We used general linear model with different combination of predictors, including sex, year of capture, relative abundance, age and reproductive status. The analysis of association between the frequency of cells with CA and demographics parameters showed no gender differences between animals in terms of frequency of cells with structural chromosome mutations ($G = 6,55 \times 10^{-8}$, $df = 1$; $p = 0,99$), and pointed to a significant interannual differences in cytogenetic parameter ($G = 126,32$; $df = 15$; $p < 0,11 \times 10^{-9}$). Age effect was tested only on a group of reproductive voles because reproduction affects mutagenesis intensity (Gileva et al., 2006). The frequency of cells with CA did not significantly correlate with age ($G = 1,98$, $df = 1$, $p = 0,16$). The impact of vole reproductive status was assessed only on the young-of-the-year voles as several studies showed a significant effect of age on the level of chromosomal instability (Gileva et al., 2006). We found that the frequency of cells with CA was significantly higher in reproductive animals ($G = 4,97$, $df = 1$, $p = 0,026$) compared to non-reproductive young-of-the-year, and it peaked with the medium population density. The contribution of mature animals (both overwintered and young-of-the-year), the percentage of which is significantly reduced at the maximum density of rodents, to the variability of mutation rates at the chromosomal level, apparently was associated with the reproduction intensification in the population growth period and the influence of sex hormones. Clastogenic effect of the latter was repeatedly described in the experimental conditions (Liehr, 2000).

We also demonstrated significant association of CA cells with population density ($G = 21,88$, $df = 2$, $p = 0,00002$). Besides, several periods of chromosomal instability increase, which were not directly related to the population density (in 2001–2003, 2006–2007 and 2010–2013) were identified. During these periods genomic instability increased, and we observed the cells with numerous damages of chromatid type, which served as markers of persisting viral infections, whereas in the remaining research years such cells were not detected. In addition to the functional and physiological state of animals in different phases of population cycle, a significant contribution to the mutation process in *M. glareolus* cyclic population was due to the spread of pathogens, which (in the first place, viruses) were known to have a distinct mutagenic effect (Buzhievskaya, 1984).

Thus, in rodents there is a complex dynamic association of the level of genomic instability and population-demographic parameters, with the lowest frequencies of cells with CA observed at a maximum population density (more than 40 ind./100 trap-days).

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