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Isozyme structure of the *Ixodes persulcatus* Schulze (Acari: Ixodidae) tick populations in the Baikal Region

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ABSTRACT. We have studied 13 enzyme systems encoded by 15 lo*ci of the I. p*ersulcatus tick populations from two suburban areas of the city of Irkutsk. We have identified a high intrapopulation heterogeneity and insignificant differences between the two populations. This indicates a high rate of gene migration.

Keywords: ticks, isozyme analysis, proportion of polymorphic loci, average heterozygosity, genetic distances

The number of ticks, their infestation with pathogens and the incidence of tick-borne infections in the Irkutsk Region is higher than the average in Russia. Ticks differ in the infestation degree and reaction to the presence of pathogens in infected individuals. Thereby, they ensure the preservation of the diversity of pathogen genotypes and cause the replacement of one types of pathogens with others. This detemines the phenotypic and genetic differences in ticks. In this regard, the studies of heterogeneity of tick populations will provide the assessment of the characteristics of their migration, interactions, kinship, and evolution.

The aim of the study was to assess the genetic variability of natural populations of the taiga ticks at sites with different anthropogenic pressure by methods of isozyme analysis of proteins.

In the Irkutsk Region, ticks were collected in forest area along Baikal (BH) and Goloustnoye (GH) highways in 2018 (BH-1, n = 30 and GH-1, n = 20) and 2019 (BH-2, n = 30 and GH-2, n = 20). The collection area extended over more than 500 m.

Preparation of samples (Jensen et al., 1999) and electrophoresis analysis (Davis, 1964; Peacock et al., 1965) were carried out by standard methods. To separate proteins, two running buffers were used: Tris-glycine buffer and Tris-borate-EDTA buffer. We studied 13 enzyme systems. Proteins were stained according to the instructions of Aebersold et al. (1987). Analysis of allozyme variation and test for homogeneity of allele frequencies between samplings were carried out using the BIOSYS-2 program (Black, 1997).

We studied 13 enzyme systems encoded by 15 loci, among which 8 loci were polymorphic in the BH-1 sampling, 11 – in BH-2, 7 – in GH-1, and 8 – in GH-2. The distribution of phenotypes over all isoloci in all investigated samplings corresponded to the Hardy-Weinberg equilibrium. We identified a high level of variation for all polymorphic loci. The average heterozygosity was 47.06% for BH-1, 64.7% for BH-2, 41.18% for GH-1, and 47.08% for GH-2, and the polymorphism level was 11 ± 0.04%, 12 ± 0.03%, 8.1 ± 0.025, and 13.5 ± 0.02%, respectively. Analysis of allele frequencies in polymorphic loci using a homogeneity test revealed reliable differences in six loci between the BH-1 and BH-2 samplings, in three loci between the GH-1 and GH-2 samplings and in two loci between the BH (1 + 2) and GH (1 + 2) samplings. We did not identify alternative fixed alleles. Genetic distances (DN) between samplings were 0.02 for BH-1 and BH-2, 0.07 for GH-1 and GH-2 as well as 0.04 for BH and GH, which slightly exceeds the previously determined level of differences between BH and GH (0.011) (Dzhioev et al., 2009).

The data on allozyme analysis of the tick samplings in 2018 and 2019 confirmed our conclusions (Dzhioev et al., 2009) about the high heterogeneity of tick samplings at the same site as well as about no differences between the samplings at different geographical sites.

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References

Aebersold P., Winans D., Teel G. et al. 1987. Manual for starch gel electrophoresis: a method for the detection of genetic variation. NOAA Technical Report NMFS 61, U.S. Department of Commerce.

Black W.C. 1997. BIOSYS-2. A computer program for the analysis of allelic variation in genetics. Department of Microbiology of the Colorado State University, Fort Collins, Colorado.

Davis B.J. 1964. Disk-electrophoresis. 2. Method and application to the human serum proteins. Annals of the New York Academy of Sciences 121: 404-427. DOI: 10.1111/j.1749-6632.1964.tb14213.x

Dzhioev Yu., Yakhnenko V., Revizor A. et. al. 2009. Electrophoretic identification of allozyme variation in natural population of ticks *Ixodes perculatus* Schulze (Acari: Ixodidae) in Irkutsk suburbs. Environmental Biotechnology 5(2): 81-86.

Jensen P.M., Kaufmann U., Smirnova L. 1999. Diurnal activity of *Ixodes ricinus* in Denmark: aspects of physiological age and genotypic variation. Heredity 130: 325-330. DOI: 10.1111/j.1601-5223.1999.00325.x

Peacock A.C., Bunting S.L., Queen K.G. 1965. Serum protein electrophoresis in acrylamide gel: patterns from normal human subjects. Science 147(3664): 1451-1452. DOI: 10.1126/science.147.3664.1451