MICROSATELLITE VARIATION IN THE BALTIC SHEEP BREEDS

Ilma Grigaliūnaitė¹, Miika Tapio², Haldja Viinalass³, Ziedonis Grislis⁴, Juha Kantanen², Ilona Miceikienė¹ ¹Lithuanian Veterinary Academy, Tilžės 18, 3022 Kaunas, Lithuania; ²Agrifood Research Finland (MTT), 31600 Jokioinen, Finland; ³Institute of Animal Science of Estonian Agricultural University, Kreutzwaldi 1, 51014 Tartu, Estonia; ⁴Latvian University of Agriculture, Liela str. 2, 3001 Jelgava, Latvia.

Summary. The history of sheep farming in the Baltic countries began around 2700 BC. In the modern era the western breeds have influenced heavily the improvement of the Baltic sheep breeds. Lithuanian Coarsewooled, Lithuanian Blackface, Latvian Darkheaded, Estonian Ruhnu, Estonian Whitehead, Estonian Blackhead and Estonian Saaremaa breeds were studied to evaluate the usefulness of the microsatellite markers for parentage testing in sheep breeds and to demonstrate the presence of within–population variation. 195 individuals were genotyped for 15 unlinked microsatellite markers. Allele numbers, observed (H_{obs}) and expected (H_{exp}) heterozygosities were calculated. All microsatellite loci were found to be polymorphic, with 4.4 to 10.9 alleles per locus in average. The mean number of alleles, calculated from all 15 microsatellites, varied from 3.9 (in Estonian Ruhnu) to 8.3 (in Estonian Whitehead) and supported the possible use of studied markers for paternity testing even in rare Baltic sheep breeds. The average H_{exp} values compared to the average H_{obs} values did not show big differences in the studied populations, only in Estonian Saaremaa population the observed heterozygosity was substantially lower than expected. Among studied populations, Estonian Ruhnu breed demonstrated lowest genetic diversity. Indications of recent decrease in effective population size in breeds were investigated by applying a bottleneck test with a Wilcoxon sign–rank test and a qualitative graphical method. Only Estonian Ruhnu population showed a slight mode–shift distortion in the distribution of allele frequencies, indicating possible recent reduction in effective population size.

Keywords: sheep, microsatellites, genetic diversity, genetic bottleneck.