Application of 12 STR markers for the evaluation of genetic variation in sheep.

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It is important to study and monitor changes in genetic structure of small old sheep breeds. Microsatellite markers are widely used for estimating genetic diversity within and differentiation among populations. For the study we used the following set of 11 polymorphic STR markers: CSRD247, ETH152, INRA005, INRA006, INRA063, INRA172, MAF065, MAF214, McM042, McM527, OarFCB20 and AMEL locus.

The objective of the research was to study the genetic structure of 3 breeds included into the sheep genetic resources conservation programme in Poland (Wielkopolska - 100, Old Type Polish Merino - 93 and Olkuska - 88) and to determine genetic differentiation between them based on polymorphism of 12 STR markers.

Genetic analyses was performed in an ABI 3130xl sequencer and the results were analysed using GeneMapper Software 4.0. The identified alleles were used to estimate observed (Ho) and expected heterozygosity (H_E), polymorphic information content (PIC) and genetic distance D_N according to Nei (1987).

There were identified 101 alleles in 12 microsatellites loci with a mean of 6.87 alleles per locus. A range of H_0 and H_E were from 0.2903 to 0.8710 and 0.3307 to 0.8370, respectively. All the markers were highly polymorphic. PIC values for each marker were high and exceeded 0.5 except for INRA172 locus in Merinos (PIC=0.3171) and ETH152 locus in Olkuska (PIC=0.4781). The highest polymorphism was observed in INRA63 of Merino Sheep where PIC and Ho were 0.8710 and 0.8181 respectively. The estimated coefficient of genetic distance, calculated based on all markers, was low and ranged from D_N =0.0836 between Merino and Wielkopolska to D_N =0.2187 between Merino and Olkuska sheep. It can be concluded that each race gain a genetic distinction.

Keywords: ovine, microsatellite, genetic variation, native breed