

Abstract of the doctoral thesis of mgr Agnieszka Bieniek entitled:

Genetic characterization of chosen horse breeds using microsatellite sequence polymorphism and SNP markers

Supervisor: dr hab. Anny Radko, prof. IZ

Date of abstract preparation: 29.06.2023

Dissertation was done at the National Research Institute of Animal Production.

The equine parentage verification is presently based on microsatellite markers (STRs), and their analysis is not error-free, for example, due to the mutations. Therefore, polymorphism and genetic variation within breeds or populations should be verified and monitored. Native breeds may be vulnerable to reductions in biodiversity and genetic variability. For this reason, native breeds included in the genetic resources conservation program, such as the Hucul horse, the Polish Konik, the Malopolski horse, the Polish Coldblood Sokolski and Sztumski types, should be subject to monitoring of the variability and the utility of the STR set used for horse parentage testing.

The livestock genome sequencing project, including the horse, has provided a vast amount of information about polymorphic DNA variants, where single nucleotide polymorphisms (SNPs) are particularly noteworthy. Currently, global trends in research on individual identification and parentage testing of many animal species are focused on the search for alternative and complementary methods based on the usage of SNP markers in replacing the currently used STR markers.

STR markers in the parentage testing may be replaced by SNP markers in the future, or a panel of these markers may become a supplementary panel in doubtful cases of putative pedigree. The aim of the proposed research was to determine the genetic polymorphism and evaluate the effectiveness of the currently used set of microsatellite markers for chosen horse breeds, test a panel of 53 SNPs and design the

own set of SNP markers, and determine their usefulness relative to STR markers for selected horse breeds.

The high genetic variability of the 17 STRs set in the tested breeds showed their usefulness for usage in the native breeds parentage testing , which was also the basis for determining the level of variability and potential usefulness of the designed SNP marker set s. The results for SNP markers showed the feasibility of genotyping with OpenArray, using the QuantStudio 12KFlex instrument, and the analysed SNP sets (set of SNP 53 JPN System and own marker set) showed polymorphism in the Polish horse breeds tested.