Abstract of Joanna's Grzegorczyk doctoral dissertation entitled:

"Characteristics of the population structure and identification of the unique features of the White Kołuda geese® genome."

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The goose breeding in Poland has become an important and constantly developing branch of the poultry industry. Currently, the goose is an economically significant farm animal, and its breeding is widespread all over the world, thanks to the excellent properties of meat and feathers. In Poland, geese are covered by the national program for the protection of animal genetic resources and kept in 14 conservation breeds. Moreover, one of the most important commercial breeds, breed in Poland is the White Kołuda goose®, originally bred at the National Research Institute of Animal Production, which currently constitutes 98% of the geese population in Poland. However, geese genetic profile and variability within it have not been thoroughly investigated, and the capabilities of the most commonly used molecular tools are strongly limited in non-model organisms (no reference genome sequence), such as the goose. Therefore, it could be concluded that the Polish geese population is an interesting material for research on the genetic diversity and population genetics, which is moreover a reservoir of still undiscovered genetic resources. In order to characterize the Polish population of geese, two molecular methods were selected using: microsatellite loci and single nucleotide polymorphism (SNP- single nucleotide polymorphism) markers. These methods have proved to be valuable tools for determining population structure, phylogenesis, and species diversity. In the first stage, a panel of 15 microsatellite loci was tested, confirming the polymorphism of selected markers, demonstrating usefulness in terms of population genetics. It was also the first time that the geese population was tested using the Structure software, which showed a high degree of differentiation in the studied population but no clear racial distinctiveness. Then, an innovative method of genotyping by sequencing (GBS) was used for the first time to identify SNP polymorphisms that could be possible genetic markers allowing for the interspecies distinction of geese. Our research has proven that GBS is a useful population genetics tool for detecting

SNPs and analysing the genetic diversity of non-model species. The results reveal that SNPs obtained from GBS analysis have a greater potential than microsatellite markers for detecting genetic diversity of Polish geese. Some patterns of variation are captured that can be assessed based on the geographic origin of the breed, body weight and color of the plumage. Nevertheless, the conducted research did not allow for the identification of the unique features of the genome of the White Kołuda® geese, and on the contrary indicated the lack of racial distinctiveness at the genetic level. Presumably, with the progress of breeding works, the differences at the genetic level between the White Kołuda® breed and other breeds will become more and more clear. Markers identified in the research: 791 new high-quality SNPs, including polymorphisms in the EDAR gene - which is responsible for the development of feathers, will be useful in the future genetic monitoring of the geese population in Poland.