Abstract of the doctoral thesis of MSc Igor Jasielczuk entitled:

“The use of SNP markers for breed assignment in cattle”

Supervisor of the thesis: dr hab. Tomasz Ząbek, prof. IZ.

Co-supervisor: dr hab. Artur Gurgul, prof. UR.

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With the increasing occurrence of food crises (e.g. the bovine spongiform encephalopathy, avian and swine influenza, African swine fever) and attempts of fraud in the labeling of valuable quality products of animal origin, there is an increasing demand for molecular (including genetic) methods enabling identification of individuals or their breed of origin. One of the tools providing high-quality data on genetic markers are single nucleotide polymorphism (SNP) microarrays, but their disadvantage is the cost and time-consuming nature of both preparation and subsequent computational analysis, which significantly limits the possibility of their use in routine tests of animal products. Nevertheless, the data obtained with the use of microarrays can be used to develop a minimal set of SNP markers enabling breed identification that could be effectively used in breeding practice and identification of the breed identity of some unprocessed animal products.

In this study, using selected marker selection methods and genotypic data obtained with the use of Illumina Bovine SNP50 BeadChip for individuals belonging to ten cattle breeds, the reduced panels containing the most informative SNP markers were developed. Suitability of selected SNP panels for the effective and reliable assignment of the studied individuals to the breed of origin was checked by three allocation algorithms implemented in the GeneClass 2 program. The studied breeds included both Polish native breeds under the genetic resources conservation programs as well as highly-productive breeds with a global range. For all of the tested marker selection methods (delta and two F_{ST} variants), two separate methodological approaches of markers assortment were used and three marker

panels were created with 96, 192 and 288 SNPs respectively, to determine the minimum number of markers required for an effective differentiation of the studied breeds. For all created SNP panels, a characterization of the localization of the selected SNPs in the genome and the share of SNPs common to all created panels was made. Moreover, the usefulness of the most effective panels of markers to assess the population structure and genetic diversity of the analyzed breeds was examined.

By means of all three algorithms enabling the allocation of individuals to the breed of origin, it was shown that the marker assortment method developed in this study made it possible to identify SNPs with a greater discriminatory power of the analyzed cattle breeds than the marker selection approaches used so far. All three tested algorithms enabling the allocation of individuals to the breed of origin worked effectively on the basis of the developed sets of markers. In relation to Polish conservative breeds, highly-productive breeds were more efficiently assigned to the breed of origin and achieved higher values for all the applied indicators of the allocation efficiency assessment. The conducted analyzes of genomic distribution of selected markers showed that the chromosome six of cattle is characterized by definitely the largest share of SNP markers with the highest discriminatory power among the analyzed cattle breeds. Moreover, a large proportion of common SNP markers was observed between all panels selected by most of the tested methods. The analysis of the usefulness of the created sets of markers, on the basis of which the most effective allocation methods worked, for determining the genetic diversity within and between the tested cattle breeds, showed that for most of the parameters tested, the obtained results were satisfactory and comparable with the whole genomic panel of SNP markers.

In conclusion, the conducted analyzes showed the possibility of using SNP subsets from medium density genotypic microarrays to distinguish breeds of cattle kept in Poland and to analyse their genetic structure. Studies have also shown that the results obtained are largely dependent on the degree of breed consolidation and are distorted by recent gene flow between discriminated populations.