

Abstract of the doctoral thesis of mgr inż. Tomasz Szmatoła entitled: „Charakterystyka ciągów homozygotyczności u wybranych ras bydła”. Supervisor of the thesis: dr hab. Tomasz Ząbek prof. IZ. Co-supervisor of the thesis: dr inż. Artur Gurgul.

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Runs of homozygosity (ROH) are defined as long homozygous regions of the genome that arise as a result of inheriting two identical haplotypes from both parents. It has been shown that the analysis of runs of homozygosity in terms of their length, quantity and frequency of occurrence in the genome allows for inference about population history, inbreeding level and determination of the selection signals.

In this study, BovineSNP50 microarrays (Illumina) were used to determine runs of homozygosity in the genomes of 11 cattle breeds maintained in Poland. These cattle breeds represent three basic utility types: milk (HO, RW, SM, MO), meat (HH, CH, LM) and bi-directional (BG, RP, ZB, ZR). Analysis of runs of homozygosity allowed to assess the level of autozygosity within each breed, in order to determine the genomic inbreeding coefficient ( $F_{ROH}$ ), as well as to identify regions of the genome with a high frequency of ROH occurrence, which may reflect traces of directional selection left in their genomes.

During the research, visible differences in the length and distribution of runs of homozygosity in the genomes of the analyzed cattle breeds were observed. The highest mean number and mean sums of lengths of runs of homozygosity were characteristic for Hereford cattle, intermediate for Holstein-Friesian Black-White (HO), Holstein-Friesian Red-White (RW), Simentaler, Limousine, Montbeliarde and Charolaise breeds. Lower values, however, were observed for cattle of conserved breeds RP, BG, ZR and ZB.

In addition, cattle breeds differed in the level of inbreeding estimated using the  $F_{ROH}$  coefficient. The highest mean  $F_{ROH}$  values were observed in the Montbeliarde, Hereford and Holstein-Friesian Black-White cattle, suggesting a relatively high degree of relatedness between animals and a lower level of genetic variation in these breeds. Intermediate values of the  $F_{ROH}$  coefficient were noticed for the remaining commercial breeds (RW, SM, LM, CH), while lower values were characteristic for conserved cattle breeds (RP, BG, ZR and ZB).

In regions of the genome with high frequency of ROH occurrence, which may reflect the impact of selection pressure, many genes have been observed to be potentially related to the production traits that are under selection in each breed and type of cattle. The most important of these genes were: *GHR*, *MSTN*, *DGATI*, *FABP4* or *TRH* with a known influence on the milk and meat traits of the studied cattle breeds.

