

## Abstract

Nowadays, intensive research is conducted to improve the quality of pork. The quality of meat is a set of features that determine its utility value and features that determine its nutritional value for a consumer. However, for a modern consumer, among the numerous parameters that characterise meat, the most important are: colour, tenderness, juiciness, as well as taste and smell, i.e. organoleptic parameters. The reasons for the above phenomenon are multi-faceted and include both environmental and genetic aspects. Understanding them in terms of association with the quality of pork may, in the future, enable the selection of animals with a preferred genetic variant, whose meat will be characterised by more favourable meat quality parameters. This is a priority issue for pig farmers and producers. In this context, the analysis of polymorphic variants of the *HK2* gene in terms of the performance characteristics of pigs and pork quality parameters can be considered justified due to the biological role in the regulation of the glycolysis process, as well as due to the molecular nature of the mechanism indicating the variability of the encoded proteins.

**The aim of this dissertation.** The aim of this study was to detect polymorphisms in the gene encoding hexokinase 2 (*HK2*) in domestic pig (*Sus scrofa domestica*) and to determine the potential relationships between the genotypes of the analysed gene fragments and the performance characteristics of pigs (fattening and slaughter) and selected parameters of meat quality.

**Materials and methods.** The research covered 722 pigs of 3 breeds: Polish Landrace, Polish Large White and native breed Puławska. The animals were kept at Pig Tests Stations (National Research Institute of Animal Production) in Balice, Poland. Feeding and housing conditions were consistent for all animals. Genomic DNA was isolated from *longissimus dorsi* muscle with the use of A&A Biotechnology (Poland) sets: Sherlock AX and Genomic Mini. In the first phase of the research, exons in the gene *HK2* had to go through PCR-HRM method. Fragments of PCR amplification selected by this technique, and the obtained products were sequenced using the Sanger method. 15 mutations were found in the analysed *HK2* gene fragments. For two identified polymorphisms, SNP type located in the splicing region of exon 7 (g.68177052A> G) and in exon 12 (g.68167661C> T), an appropriate molecular method was developed (PCR-RFLP and PCR-ACRS, respectively) allowing to determine the frequency of selected mutations on a larger group of animals. Statistical analysis was performed using the SAS / STAT software.

**Results.** The obtained frequencies of the polymorphic variants of the analysed gene show that there is variability within the *HK2* gene. The identified polymorphisms show a significant association with selected fattening and slaughter characteristics as well as meat quality in pigs of various breeds.

**Conclusions.** The *HK2* gene may be a candidate gene for a genetic marker gene of selected fattening traits.

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