

## ABSTRACT

Nowadays, an adequately selected and balanced diet is considered one of the most critical factors determining human health. Particular importance is attached in particular to the content of vitamins and trace elements in the diet. One of them is selenium (Se). The multiple functions it performs inside the body are primarily related to the presence of selenoproteins. A deficiency of selenium in the diet means that enzymes that require its incorporation cannot be produced or are produced, but their function is impaired. Hence, selenium deficiency may manifest in disorders at various levels of the body's functioning. The Se content in natural food is closely related to its geographical location. Unfortunately, the soil in Poland is poor in selenium, which also translates into deficiencies of this element in the organisms of Poles. Considering the commonly occurring selenium deficiencies, ensuring an adequate supply of selenium in the diet becomes a problem. Animal products are the primary source of Se. Currently, pork is analyzed in terms of gene polymorphisms, the protein products of which are essential for its quality, including health-promoting properties. One of the essential proteins is selenoprotein P (SeP). This protein is involved in the storage and transport of selenium.

**Objective of the work.** The research aims to detect polymorphisms in the gene coding for selenoprotein P (*SEPPI*) in the domestic pig (*Sus Scrofa domestica*) and to establish possible relationships between the genotypes of the analyzed gene fragments and the performance characteristics of pigs (fattening and slaughter), selected parameters of meat quality and selenium content in the *musculus longissimus dorsi*.

**Research hypothesis.** Genetic variation within the *SEPPI* gene may affect the production characteristics of pigs and the selenium content in the *musculus longissimus dorsi*.

**Materials and methods.** The study included 722 pigs belonging to 3 breeds: Polish Large White, Polish White Landrace, and Pulawska. The Genomic Mini (A&A Biotechnology) and Sherlock AX (A&A Biotechnology) kits were used to isolate genomic DNA from a fragment of the *musculus longissimus dorsi* tissue. The following methods were used to detect the variability and then genotype-selected fragments of the *SEPPI* gene: PCR-HRM, Sanger sequencing, PCR-ACRS, PCR-RFLP, and fragment size analysis using the CEQ8000 capillary sequencer (Beckman Coulter). Selenium content in 163 selected samples was determined by the spectrofluorimetric method using 2,3-diaminonaphthalene. The statistical analysis of the results was performed with the SAS ver. 8.02 program, using the GLM (General Linear Model) procedure.

**Results.** As a result of the analyses carried out within the selenoprotein P gene, the presence of 11 mutations was identified. The frequency of five polymorphic changes and their influence on pigs' production characteristics and the selenium content in the examined tissues of the *musculus longissimus dorsi* were determined. The identified polymorphisms significantly influenced fattening characteristics (feed consumption per kilogram of gain, daily gain), slaughter traits (e.g., slaughter yield, loin weight, percentage of meat in the carcass), and pork quality (e.g., water absorption of meat, pH of loin and ham).

**Conclusions.** Combining the numerical values for meat characteristics with the identified polymorphic variants of the *SEPP1* gene revealed their influence. Individual polymorphisms in the *SEPP1* gene have the potential to be used as a selectable marker for standard production traits, one of which is predisposed to a novel approach to increase selenium levels in pork.

01.09.2022 r.  
Agnieszka Korpala