Szkoła Główna Gospodarstwa Wiejskiego

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Zależność między genami kandydującymi a kształtowaniem się potencjału oksydacyjnego mięsa wołowego

Relationship between candidate genes and the shaping of oxidative potential in beef

Rozprawa doktorska

Doctoral thesis

Rozprawa doktorska wykonana pod kierunkiem:

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Summary

The research was part of the project "*ERA NET SUSAN:* Increasing productivity, resource efficiency and product quality to increase the economic competitiveness of forage and grazing based cattle production systems." The project was carried out within the consortium of scientific units of Newcastle University, Institute of Genetics and Animal Biotechnology of the Polish Academy of Sciences in Jastrzębiec, Swedish University of Agricultural Sciences, Research Institutes of Sweden, Kiel University, University of Padova. The results of the research were published as 1 review (publication P1) and 3 research papers based on 5 cattle breeds with a total of 237 animals, including experiment 1 (publication P2): Polish Holstein-Friesian (16), Limousine (18), Charolaise (17), Hereford (16); experiment 2 (publication P3): Holstein-Friesian (45) and F1 crossbred Charolaise×Holstein-Friesian (60); and experiment 3 (publication P4); Hereford (65).

The first publication (P1) reviewed the literature on the impact of genes commonly used in beef cattle breeding programs. The aim of the study was to discuss the importance of single nucleotide polymorphism in achieving genetic progress based on the literature based on the widely studied and described 4 candidate genes such as myostatin (MSTN), thyroglobulin (TG), calpain (CAPN) and calpastatin (CAST). The literature review included 130 positions in the field of beef cattle breeding, gene polymorphism, their impact on shaping beef quality and animal health. The literature review showed the important role of variation in the polymorphism of the genes in question in modern cattle breeding by considering their impact on production differences and meat quality traits. In the case of the gene encoding MSTN, its association with muscle hypertrophy was pointed out, which determines the trait known as double muscling. It influences an increased proportion of muscle in the carcass and better growth rates, but can increase the proportion of difficult births. The TG gene polymorphism was also found to be related to the degree of meat marbling and the proportion of fat in the carcass. Meat with higher intramuscular fat content has better tenderness, juiciness and palatability, which are important organoleptic traits. A literature review of the calpain-calpastatin gene system showed their significant influence on meat quality traits. Polymorphic forms of both of these genes showed varying degrees and rates of post-mortem changes, which shapes meat tenderness, juiciness and palatability. The genes discussed are important determinants of meat quality, which is particularly important in beef cattle breeding. The use of knowledge of the polymorphism of the discussed genes in breeding work can significantly improve its quality traits, carcass conformation and the rate of post-slaughter transformation.

The second publication (P2) investigated the nutritional value and antioxidant status of beef from three leading beef breeds (Limousine, Charolaise, Hereford) kept in Poland compared to the most popular dairy breed used in the country (Polish Holstein-Friesian), using the same feeding program. The aim of the study was to analyse differences in the antioxidant potential of meat, taking into account the activity of protective mechanisms against antioxidant stress. The study was conducted on semimembranosus muscle and blood samples collected from 67 bulls, including 18 Limousine (LM), 17 Charolaise (CH), 16 Hereford (HH) and 16 Polish Holstein-Friesian (PHF). These samples were subjected to detailed analyses including basic chemical composition, fatty acid profile, fat-soluble vitamin content, levels of bioactive components of the protein fraction and oxidative stress indices (DAP, TAS, MDA). The results indicated the advantages of meat breeds in the formation of the protein content of the analysed muscle and lower collagen content. The highest fat content was shown in the HH breed. Analysis of functional fatty acids and vitamins showed the highest levels in the LM and CH groups, suggesting their higher antioxidant potential. A similar relationship was also shown for the formation of TAS and DAP. In addition MDA concentrations were lowest in LM and CH. Analysis of the 6 bioactive components of the protein fraction, in each case, showed a better predisposition of meat breeds toward PHF, indicating a significant relationship between breed and antioxidant potential and nutritional value of beef.

The third publication (P3) presents the results of a study on the effect of single nucleotide polymorphisms in five genes: DGAT1, LEP, SCD1, SREBF1, and TG, on beef quality traits. The study was conducted on semimembranosus muscle and blood samples taken from 105 bullocks, including 45 Holstein-Friesian (HF) and 60 Holstein-Friesian×Charolaise (HF×CH). The aim of the study was to determine the relationship between candidate genes (DGAT1, LEP, SCD1, SREBF1 and TG) and traits related to meat quality such as degree of marbling, color, pH and flavor. We hypothesized the influence of these genes on meat quality traits. Genetic analyses were performed using RFLP and PCR methods. The results indicated that polymorphisms in the SCD1, LEP, TG and DGAT1 genes were associated with carcass conformation and meat quality traits. SREBF1 was also shown to be associated with carcass fatness.

The fourth publication (P4) presents the results of a study on the effect of single nucleotide polymorphisms in three candidate genes (DGAT1, LEP, SCD1) on the level of oxidative stress markers. The purpose of the study was to determine the relationship between candidate genes and the antioxidant potential of beef, including oxidative stress markers.

The research hypotheses included the influence of these genes on the levels of selected oxidative stress markers, such as superoxide dismutase (SOD), glutathione peroxidase (GPx), glutathione reductase (GR) and malondialdehyde (MDA), as well as on the antioxidant content of the protein fraction. The study was conducted on semimembranosus muscle and blood samples collected from 65 hereford bulls. The parameters analysed included basic chemical composition, the content of bioactive components of the protein fraction and measures of oxidative stress. Genetic analyses were carried out using RFLP and PCR methods. The results indicated that the TT genotype in the DGAT1 gene was correlated with elevated levels of MDA, suggesting increased lipid peroxidation and oxidative damage. Moreover, the increased activity of antioxidant enzymes such as GluRed and GPx in this group suggests the activation of compensatory mechanisms in response to oxidative damage. In addition higher concentrations of taurine, carnosine and anserine in the TT genotype may indicate their role in protection against oxidative stress, highlighting adaptive defence mechanisms. In the case of the LEP gene, the highest SOD activity was shown in the CT genotype, while the highest TAS level was in the TT genotype. These differences may suggest that different variants of LEP genotypes affect the regulation of the antioxidant response differently, possibly through differences in the localization and function of SOD isoforms. In contrast, SCD1 analysis showed that the AA genotype had the highest GluRed, GPx and SOD activities. The higher activities of these enzymes in the AA genotype indicate an increased ability to effectively neutralize and manage oxidative stress.

In summary, the results of the study showed that polymorphisms in the DGAT1, LEP, SCD1, SREBF1 and TG genes have significant effects on meat quality parameters and the regulation of the body's response to oxidative stress. Significant correlations were identified between different genotype variants and levels of oxidative stress markers and antioxidant enzyme activity.

Keywords: beef cattle, beef quality, oxidative stress, candidate genes