PROCEEDINGS OF IV. INTERNATIONAL AGRICULTURAL, BIOLOGICAL , LIFE SCIENCE CONFERENCE AGBIOL 2022

29-31 AUGUST, 2022

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A RESEARCH ON DETERMINATION OF FASN GENE POLYMORPHISMS IN TURKISH HOLSTEIN BULLS

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ABSTRACT

Meat is the most important nutrient in human nutrition in terms of proteins, fats, vitamins, and minerals. Meat, which has an important place in nutrition with its high biological value and satiety, contains essential amino acids required for metabolism. There are many factors that affect the quality of meat. One of these factors is the marbling score of the fat accumulated between the muscle fibers of the meat. However, the marbling score alone is not effective on meat quality. The fatty acid composition that forms the marbling score has an effect on both the meat quality and the flavor of the meat. For this reason, the fatty acid composition of the intramuscular tissue of red meat has an important place in the red meat industry. In recent years, researchers have been studying the genetic effects of animal species and breeds on the fatty acid compositions in meats, as well as the effects of the ration contents used in animal nutrition to manage the fatty acid composition in meat and meat products. In particular, studies have focused on the SNPs of genes such as CAST, CALP, LEP, SCD, FABP4 and FASN, which are associated with meat quality and fat content. The fatty acid synthase gene (FASN) is a multifunctional enzyme complex that regulates the de novo biosynthesis of long-chain fatty acids. FASN is an important candidate gene influencing the fatty acid composition of meat due to its role in de novo lipogenesis in mammals. The beef of Turkish Holstein Bulls (THB) is the most consumed beef in the Marmara region of Turkey. In our study, sample meats collected from the Logissimus muscal dorsi (MLD) muscle of 90 male THBs of 17 months old were studied. The aim of the current research is to contribute to the improvement and standardization of the beef quality of THBs before slaughter. It is desired that THBs will contribute to the production of better quality and healthy meat products for those who will be used in butchery production. In the FASN gene of THBs, exons 34, 35 and 36, and introns 34 and 35 were completely sequenced, and introns 33 and 36 were partially sequenced (Beckman Coulter GenomeLab GeXP). The 839 bp (the between 50791309th and 50792147th position) on bovine chromosome 19 (19q22) has been sequenced. As a result of DNA sequencing, 2 single nucleotide polymorphisms (SNPs) (rs208645216 G>A and rs209734560 C>T) were determined in our samples. Bioedit and Chromas programs were used. It was observed that both loci of SNPs identified in the FASN gene of THBs were polymorphic. It has been determined that THBs have a potential in determining the relationships between FASN gene variants and fatty acid composition. Whether it has potential as a genetic marker in marker assisted selection studies should be evaluated with new studies.

Keywords: Bovine, FASN gene, SNP, Fatty acid composition

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