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(AccuPower-South Korea) was used to amplify the gene. Polymerase chain reaction (PCR) was performed for amplification of 94 pairs of games using a pair of proprietary initiators. The fragment was digested by PCR-RFLP by KPN2I restriction enzyme. Statistical data was analyzed using POPGENE software version 1.32 . The genotype of each animal was determined by using RFLP method and 3% agarose gel and ethiodium bromide staining. For digestion of PCR products, 1 unit KPN2I enzyme was used at 37 Â° C for 6 hours. The frequency of T and C alleles were 0.53 and 0.47, respectively, and the TT and CT and CC genotypes were 0.397, 0.266 and 0.337, respectively. Chi square test showed that the studied population was not in Hardy Weinberg equilibrium ($p < 0.05$). The relationship between the polymorphisms and traits was evaluated by SAS software. The Duncan test was used to compare the average of milk production traits. The polymorphism of the leptin gene was not significantly correlated with the traits of the milk yield, fat content, and milk protein content and percentage ($P > 0.05$). There was a significant relationship between the leptin polymorphism and the level of S.C.C ($P < 0.05$) the highest mean of somatic cell count was related to TT genotype. This suggests the possible role of the leptin gene in the regulation of immune responses and the occurrence of mastitis.

Keywords: Polymorphism, Leptin Gene, Holstein Cow, PCR-RFLP

P-15: The Effect of Fetal Bovine Serum on Differentiation of Ovine Myogenic Satellite Cells

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Satellite cells are a population of adult muscle stem cells that play a key role in mediating muscle regeneration. The established muscle-derived satellite cells model can be used to study the genes associated with muscle development, and as seed cells for animal biotechnology related studies. Sheep satellite cells have a greater similarity to human satellite cells with regard to metabolism, life span, proliferation and differentiation, than satellite cells of the rat and mouse; from this feature, can be used as an animal model for the treatment of human diseases. These cells are precursors of myoblast cells. The purpose of this study was to determine the effect of the Fetal Bovine Serum (FBS) content on the process of satellite cells growth rate and differentiation. The satellite cells were isolated from Semimembranosus and Semitendinosus Muscle tissues of 50 to 60-day-old Kurdi sheep fetuses. After Enzymatic digestion, a combination of satellite and non-myogenic cells was cultured on the flask. Flasks were replaced after 3 hours to isolate non-myogenic cells, such as fibroblasts. After 6 days, the cells differentiated. Then the cell growth were evaluated by counting for 8 continuous days in media containing 0, 5 and 10% of FBS. The analysis of cell growth showed that the differentiation of satellite cells was significantly higher in enriched medium with 10% FBS ($P<0.05$).

Keywords: Satellite cells, Sheep, Fetal bovine serum, Differentiation

P-16: Transcriptomics pathway analysis with cellular signaling pathways as a key tool to improve marbling in beef cattle

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Background: Red meat is as an important dietary source that provides part of the nutritional requirements such as proteins, minerals, B-complex vitamins and essential fatty acids. Intramuscular fat is located throughout skeletal muscles. It is responsible for the marbling seen in certain cuts of beef. Marbling is a trait of major economic relevance that positively influences sensory quality aspects, including flavor, juiciness and tenderness of meat.

Objectives: the objective of this study was to identify cellular signaling pathways regulating muscle marbling in beef cattle using microarray gene expression data.

Methods: publicly available preprocessed transcriptomics data (E-GEOD-46411) from a study by Sadkowski et al was used. They measured gene expression in skeletal muscle of well-marbled beef and lean-marbled beef using Agilent microarrays. Pathway analysis was performed with the pathway visualization and analysis tool, PathVisio.

Results: The regulation of marbling is possibly the result of interaction of signaling pathways in muscle, fat and intramuscular connective tissue, identifying these processes with pathway analysis can help to decipher the key marbling processes. Pathway analysis revealed 17 pathways that showed differences in expression (z-score > 1.96) between well-marbled and lean marbled beef. MAPK (WP998) and P38 MAPK (WP1037) signaling, two pathways well known two affect lipid metabolism, were enriched in the well marbling breed. In addition, the signaling pathways â€œhypertrophy modelâ€-, â€œmicroRNAs in cardio myocyte hypertrophyâ€- and â€œphysiological and pathological hypertrophy of the heartâ€- that play a role in tissue development were affected. Interestingly, the analyses also demonstrated that pathways related to immune response (IL signaling, TCR signaling and Toll-like receptor signaling pathways) and insulin signaling, mitochondrial gene expression and Vitamin D metabolism were enriched and might act together with the pathways related to lipid metabolism.

Conclusion: The present study shows that regulatory pathways of marbling in Bos taurus muscle are regulated not only for pathways related to lipid metabolism and muscle development but also for pathways involved in energy metabolism, protein synthesis and immune response.