Association of SNPs and haplotypes in µ-calpain and calpastatin genes with Warner-Braztler Shear Force in a crossbred Brahman-Angus population

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Tenderness results from proteolysis of key structural muscle sarcomere proteins, and is modulated by the calpain-calpastatin system. A total of 581 crossbreed Angus-Brahman steers with average slaughter weight of 537.94±55.31 kg at 17.31±1.23 months were used in this study. One steak of 2.54 cm of *Longissimus dorsi* aged for 14 days was used for Warner-Bratzler Shear Force (WBSF). Genotypes for 37 SNPs in µ-calpain and calpastatin genes from 250K Bovine SNP BeadChip were used. An association test was performed with each polymorphic SNP and haplotypes based on linkage disequilibrium (LD) analysis. One LD block was predicted in µ-calpain; for calpastatin three LD blocks were predicted. The third block is located in the seven final exons of calpastatin, including the 3'UTR. Only one individual SNP in calpastatin, ARSUSMARC116 was associated with WBSF. Similarly, the LD block 3, harboring ARSUSMARC116, was significantly associated with WBSF. The CG-CG diplotype (4.82±0.16 kg) was different from TA-CG (4.40±0.08 kg), and both of them were different from TA-TA (4.21±0.05 kg) and TG-CG (3.85±0.23 kg). A bioinformatic analysis of all reported SNPs in the associated block was performed. JAVA was used in the screening, substitutions, transcription and translation of sequences. From 6,787 SNPs located in calpastatin, only 786 SNPs located in the third block were included in this analysis. The wild DNA sequence was analyzed with MATCHTM in order to predict Transcription Binding Sites (TBS). The motives of those TBS were analyzed in each DNA sequence with JAVA and compared with the wild type prediction. Each mRNA sequence was analyzed with RNAFold for prediction of ΔG and folding. A protein analysis was performed with Swiss Model server and Compute PI/MW tool. Twelve SNPs were found to modify TBS and 8 SNPs were found to change the ΔG value and mRNA folding. At protein level, 13 SNPs were able to change the value of isoelectric point, 4 SNPs can modify structure, surface and electrostatic field of this protein.