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Screening for Single Nucleotide polymorphisms in MYOD1 gene and its association with meat tenderness in cattle

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The MYOD1 (Myogenic Differentiation 1) gene is located at bovine chromosome 15 in a QTL region associated with meat tenderness. Meat tenderness is a major quality required by meat consumers. A candidate gene approach was initiated to search for Single Nucleotide Polymorphisms (SNPs) associated to meat tenderness in animals with extreme phenotypes for shear force (SF) measured at 24 hours postmortem. A statistical model was used to correct the phenotype to environmental variations and the residues were obtained. The mixed model included fixed effects of contemporary group and genotypes, age of the animal at the time of measurement and the pH as a covariate. A total of 137 animals of Nelore cattle were evaluated and 14 extreme animals were chosen using this methodology. The genotypic data was obtained by sequencing the MYOD1 gene by Sanger method. The sequences were further analyzed with Phred, Phrap, and Consed programs. Ten SNPs were found at 686, 960, 1285, 1383, 1533, 1733, 2571, 2597, 2745, 2871 bp, according to the MYOD1 sequence available in the Ensembl database. These SNPs will be further denominated as SNP1, SNP2, SNP3...SNP10, respectively. SNP1 is located in exon one and is an insertion of an Adenine base (-/A) and showed Minor Allele Frequency (MAF) = 0.077. SNP2 (C>T, MAF 0.077), SNP3 (T>G, MAF 0.038), and SNP4 (G>A, MAF 0.03) are also located in exon one and change the amino acids coding of Arginine to Cysteine; Isoleucine to Serine and of Glycine to Serine, respectively. The SNP5 (T>C, MAF 0.115) and SNP6 (C>A, MAF 0.083) are located at intron one. SNP7 (G>C, MAF 0.115), SNP8 (G>A, MAF 0.153), SNP9 (A>C, MAF 0.192) and SNP10 (C>G, MAF 0.041) are located in exon three. The SNPs identified in this study are not deposited in the public database NCBI yet. No significant association between any SNP of MYOD1 gene described in this work and SF ($P \leq 0.05$) was found, according to the fisher test analysis performed by the SAS software. An extended association study in the entire population is needed to confirm the real effect of these markers on meat tenderness.