Haplotype tree of MYOD1 gene in Bos indicus beef cattle

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Haplotype trees are used to estimate the evolutionary history of the genetic variation. This kind of study may also be used to test hypotheses about the evolutionary significance of genetic variation and to identify mutations that are associated to phenotypes. We initiated a haplotype tree study for a candidate gene supposed to influence meat tenderness in cattle. The MYOD1 (Myogenic Differentiation 1) gene is involved in muscle organ development, positive regulation of skeletal muscle, tissue regeneration, myoblast differentiation, positive regulation of muscle cell differentiation, skeletal muscle tissue development, skeletal muscle fiber adaptation and development, among others processes. Samples from 14 animals of Nelore breed were selected for sequencing, characterized as extremes for Warner â Bratzler shear force measured at 24 hours postmortem. These animals were chosen based on the residues obtained from a statistical model used to correct phenotype to environmental variations. The genotypic data was obtained by sequencing the MYOD1 gene by Sanger method. The sequences were further analyzed with the Phred, Phrap, and Consed programs. Ten SNPs located at 686 (-/A), 960 (C>T), 1285 (T>G), 1383 (G>A), 1533(T>C), 1733 (C>A), 2571 (G>C), 2597 (G>A), 2745 (A>C), 2871 (C>G) bp, according to MYOD1 sequence available in Ensembl database were found. The Haplotype tree of these genetic variations was constructed using the TCS v1.21 software. This analysis detected ten different haplotypes and inferred additional three. The haplotypes detected were: i) -CTGTCGGAC; ii) -TTGTCGGAC; iii) ACTGTCGGAC; iv) -CTGTCGAAC; v) -CTGTCGGCC; vi) -CTGTCCGCC; vii) -CGATCCGAC; viii) -CTGCAGGCC; ix) -TTGCAGGCC and x) -CTGGC?GGCG. The three inferred haplotypes were: xi) -CTATCGGAC, which arose from i haplotype; xii) -CGATCGGAC, which arose from xi haplotype and xiii) -CTGTAGAAC, which arose from v haplotype. The haplotypes inferred may not have been detected because of the small sample size analyzed. The most ancestral haplotype detected was âCTGTCGGAC (i); this sequence showed consensus nucleotide for all variation analyzed. Although the ancestral haplotype should be the most frequent genotype observed, that was not the case, probably because of extreme phenotype sample bias. The haplotype iv was found in four animals, three of which were in the same extreme phenotype class. The fisher test showed a significant (P â¤ 0.0012) prevalence of this haplotype in the animals with major residues for shear force. Further studies should be performed to test the association