

Genome wide association study for beef tenderness in Polled Nellore cattle.

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The aim of this study was to identify genomic regions associated with meat tenderness in a Polled Nellore cattle population. The dataset was provided by the Guaporé Pecuária S/A (OB Ranch) and Embrapa Cerrados, and contained 1102 animals in which 436 of them had records of tenderness measured approximately at 2 years of age. A total of 609 animals were genotyped either with BovineHD BeadChip (Illumina Inc.) or GGP-Indicus HD (GeneSeek Inc.), remaining 600 genotyped animals and 375,668 SNPs available for analysis after the genomic quality control. SNP solutions were estimated by genome-wide association using a single-step genomic BLUP procedure (ssGWAS). Variance components were estimated for tenderness traits using an animal model under Bayesian inference. The model included fixed effects of sex, slaughter group, age at slaughter (covariate), and direct animal random effect. Variances were calculated for windows of 1 Mb. The regions that accounted for more than 1% of additive genetic variance were used to search for candidate genes. The Map Viewer of bovine genome (UMD3.1 version) and Ensembl Genome Browser were used for gene identification, and its biological function was identified on GeneCards. The results indicated a total of 19 windows explaining more than 1% of the genetic variance for tenderness. Among those windows, genes related to intracellular lipid receptors and fatty acid binding proteins were identified, such as OSBPL1A (BTA24) and FABP7 (BTA9), respectively. The gene CAPZA1 (BTA3) which regulates growth of actin filament and that had been previously associated with leaf fat in swine was also identified. A gene which has been previously related to marbling content in cattle (TAGLN2) was found on BTA3. The study revealed genes related to muscle weakness, such as KLHL41 and CASQ1. Calcium ion binding and calcium-dependent phospholipid binding gene (MCTP1) was observed on BTA7. The MYO3B gene that encodes class III myosins was found on BTA2. The CAST gene was found close to the region with the highest genetic variance for tenderness. The CAST gene is considered important functional candidate for meat tenderness in livestock. Results found in this study should help to better understand the genetic and physiologic mechanism associated with tenderness in beef cattle.

Key words: Meat Quality, Candidate gene, Livestock