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Identification of Genomic Regions Related to pH in Nellore Beef Cattle

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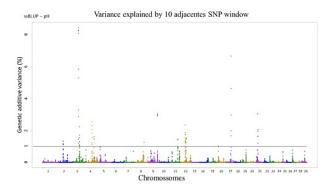
Objectives

The aim of this study was to identify genomic regions that potentially have association with pH in Nellore cattle.

Materials and Methods

Post mortem muscle metabolism (pH) was measured on samples of Longissimus thoracis muscle collected 24 h post mortem using a portable pHmeter (Hanna HI9963) from 1208 feedlot Nellore steers slaughthered at 2 yr of age. Genotypic data of all animals was used for genome wide association studies through the ssGWAS method. Those animals were genotyped with the Illumina Bovine beadchip HD GGPi (74K). Based on another Nellore population genotyped for Illumina beadchip BovineHD (777K), genotypes were imputed using the FImpute software. Analyses were performed using a pedigree composed by 6276 animals. Single step analyses were performed using the Blupf90 family of programs considering windows of 10 markers to estimate the SNP effects. This procedure enables the identification of regions associated with pH along the chromosomes. After quality control (MAF < 0.05%, call rate < 90%), 463,995 SNPs in autosomal chromosomes were used in the association analyses.

Results

The current investigation revelead 15 regions located in 10 different chromosomes (2, 3, 4, 8, 9, 11, 12, 16, 17, and 21), which explained more than 1% of the additive variance (Fig. 1). Gene identification was performed using the BioMart do Ensembl Genome Browser tool (www.ensembl.org). The following genes were identified in 6 distinct regions: WD repeat, sterile α motif and U-box domain containing 1; palmdelphin; insulin like growth factor binding protein 1; Bos taurus charged multivesicular body protein 7; tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain; rho-related BTB domain-containing protein 2; spectrin repeat containing nuclear envelope protein 1 e ubiquitin specific peptidase like 1.

Conclusion

The ssGWAS method, using high density panel, allowed the identification of regions and genes related to pH in Nellore beef cattle. Further investigation combining information of the reported genes and its biological pathways is required to better evaluate their importance for meat quality traits.