

Genome wide association analysis for birth and weaning weight in Canchim beef cattle

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Genome-wide association studies (GWAS) are becoming a powerful tool for the animal breeding industry as technology and research advances. The basic concept of GWAS is to find regions in the genome that affect (or could affect) the productive performance of animals. Productive performance can be interpreted as disease resistance, milk yield and fat percentage, meat and carcass quality, growth rate, cow's fertility, and many other economically important traits. In Brazil, traditional breeding programs have had successful results by using growth traits (e.g. weight measurements) in selection indexes that aim to improve beef production. However, with the advent of genomic information, genome regions could be studied to further knowledge of which genes are acting on phenotype expression. Furthermore, this information could be used to identify genetically superior animals at younger ages. The aim of this study was to apply the Generalized Quasi-Likelihood Score method to assess genome wide associations with birth weight (BW) and weaning weight (WW) in a Brazilian synthetic breed. Canchim beef cattle are a synthetic breed developed at the facilities of Brazilian Agricultural Research Corporation (Embrapa). In this study we used animals from the Canchim breed (62.50% Charolais and 37.50% Zebu composition) and from the "MA" genetic group (65.60% Charolais and 34.40% Zebu composition). Genotype data from 400 individuals was collected for high density genotyping (BovineHD - Illumina® bead chip). Single nucleotide polymorphism (SNP) from Canchim (285 animals), MA (114 animals), and Charolais (1 animal), 195 males and 205 females born between 1999 and 2005 were analyzed. For the genome wide association the Generalized Quasi-Likelihood Score method was used. This method uses a logistic regression model to link the individual's information (i.e. breeding value) of the trait (treated as a covariate) with the genotype (treated as a response variable). Genotype quality control excluded the following: sexual chromosomes, SNP with calling score lower than 0.15, call rate for animals and SNP lower than 0.85, SNP with deviations of the Hardy-Weinberg equilibrium ($P < 10^{-5}$), SNPs with excess of heterozygosity ($< 15\%$), and minor allele frequency lower than 5%. The false discovery rate ($FDR \leq 10\%$) was used for corrections for multiple testing in significant SNP. We found 4 and 12 SNPs associated with BW and WW, respectively. SNPs were located in the intron of the DPP6 (*dipeptidyl-peptidase 6*, for BW and WW) gene; in the promoter region of the FARSB (*phenylalanyl-tRNA synthetase beta chain*, for WW) gene; and in the intergenic region of the MANEA (*mannosidase, endo-alpha*, for BW), LOC783932 (*small ubiquitin-related modifier 1-like*, for BW), KCNIP4 (*Kv channel-interacting protein 4*, for WW), RALGDS (*ral guanine nucleotide dissociation stimulator*, for WW), and GTF3C5 (*general transcription factor 3C polypeptide 5*, for WW) genes. The SNP rs43421095 was found significant for both BW and WW. This SNP is located in the DPP6 gene, which acts in proteolysis and in the physiological processes of the central nervous system. This pleiotropic effect seems to be important for animal's development. Other genes were found to be related to cell maintenance, ion transporters, and energy carriers. GWAS points to promising candidate SNP (or genes) for BW and WW improvement. Selection of growth traits could be enhanced by using genomic information in this breed. The genes identified here appear to have an important role in the growth and maintenance in Canchim animals.

Keywords: alleles, beef cattle, genes, genomic selection, SNP

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