

Preliminary validation study for SNPs associated to rib eye area in Canchim beef cattle

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The discovery of polymorphisms associated with economically important traits are in demand for the modern beef cattle industry. Canchim is a composite beef cattle breed (3/8 *Bos indicus* x 5/8 Charolais) which was developed in the 1960's in Brazil with the purpose of being used for production of high-quality meat. The objective in this study was to validate four single nucleotide polymorphisms (SNPs) which were previously associated with rib eye area REA, a trait related to meat quality, in Canchim animals by a genome-wide association analysis using the RandomForest methodology. For association, a sample of 400 Canchim animals with extreme values for REA was genotyped using *Illumina® BovineHD Beadchip*. After quality control processing, 708,641 SNPs and 396 animals remained in the analysis. The RandomForest genome-wide association was performed in a two-step approach, where the top 1% SNPs in each chromosome were selected, and then combined together and analyzed again to retain only the top 1% SNPs among all chromosomes. After that, four of the top SNPs were selected based on a biological annotation analysis for validation using a population of approximately 700 animals. One SNP was on chromosome 4 (SNP4) in the histone deacetylase 9 gene (*HDAC9*), the SNP on chromosome 10 (SNP10) was in the actinin, alpha 1 (*ACTN1*) gene, while the SNP on chromosome 22 was in the CKLF-like MARVEL transmembrane domain containing 7 gene (*CMTM7*), and SNP27 was in an intergenic region on chromosome 27. The process of SNPs validation was done by including the SNP genotype as a fixed effect into an animal model using the Wald F Statistic for testing the association. SNP4 was significantly associated with REA at a p-value of 0.05; SNP10 was significantly associated with REA at a p-value of 0.005; SNP22 was significantly associated with REA at a p-value of 0.007; while SNP27 was not determined to be significantly associated with REA (p-value of 0.701), unlike the previous study. The next steps in this validation analysis include the estimation of additive and dominance effects, epistasis among SNPs, as well as determination of allelic substitution effects. SNP4, SNP10, and SNP22 seem to be promising markers to be included in future programs for genetic improvement of Canchim beef cattle. Supported by: CAPES.



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