

Genome wide association study for production traits in canchim breed

Gustavo G. Santiago; UFMS
Fabiane Siqueira; Embrapa Gado de Corte
Luciana C. A. Regitano; Embrapa Pecuária Sudeste
Fernando F. Cardoso; Embrapa Pecuária Sul
Maury D. S. Júnior; ABCCAN/Genepplus
José F. Garcia; UNESP
Anna B. R. Ferreira; Embrapa Gado de Corte
Isabella M. Z. Blecha; UEMS
Roberto A. A. T. Júnior; Embrapa Gado de Corte
Corresponding author e-mail: gustavo_garciasantiago@hotmail.com

Abstract:

The Canchim breed was developed with the objective to unite zebu's rusticity and adaptability to reproductive efficiency, meat quality and economic yield of european cattle. The main traits of Canchim are: precocity in weight gain, at sexual maturity, muscling and high carcass yield. Know the molecular basis of phenotypic variation can increase the understanding of the metabolic and genetic control of economically important traits. The large scale use of molecular information in the genetic improvement of cattle it became possible following the development of genotyping platforms single nucleotide polymorphism's (SNPs) covering all genome. In this context, statistical and bioinformatics tools show that genome wide association studies (GWAS) allow the identification of SNPs that are in linkage disequilibrium with chromosomal regions controlling phenotypes. Therefore, the discovery of genetic markers associated with production traits allow the inclusion of this information in genetic evaluations, resulting in more accurate predictions. The objective is to identify genomic regions, candidate genes and metabolic ways associated with production traits in Canchim breed through genome wide association study using the Illumina® BovineSNP50 BeadChip. Phenotypic data have been collected from 500 animals in tests of performance evaluation, performed in feedlot, in 2011 and 2012. The animals were ranked according to important traits for the production and meat quality such as weight gain, final weight, slaughter conformation, rib eye area, marbling and fat thickness. With around eight months of age, the animals were confined, presenting an average initial weight of 230 kg, staying for a total period of 154 days, being 42 days for adaptation and 112 days for evaluation of average daily weight gain. Blood samples were collected for genomic DNA extraction and subsequent genotyping with the Illumina® BovineSNP50 BeadChip. Thereafter, genotypes will pass through stages of quality control, verification of population substructure, statistical association and confirmation through analysis of functional enrichment. Is expected identify chromosomal regions and metabolic ways that are associated with phenotypic characteristics measured. Furthermore, selecting the most informative SNPs aiming at the development of a low density panel's markers to be used for selection of superior animals. The identification of chromosomal regions influencing economically important traits in beef cattle will allow the inclusion of molecular markers in genetic evaluation utilized in animal breeding programs. Moreover, this information will contribute to the understanding of biological mechanisms and the genetic architecture of the trait, As such how many genes are involved in its expression, the effect of each gene and the interaction between them in the phenotypic manifestation.