

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

## GENOME-WIDE ASSOCIATION STUDY FOR BODY SIZE TRAITS IN SANTA INÊS SHEEP

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Genome-wide association studies (GWAS) allows the identification of regions in the genome that are associated with phenotypes. A limited number of related GWAS have been performed sheep breeds and identified genomic regions associated to body size. The purpose of this study was to identify genomic regions and pathways associated with body size traits in Santa Inês sheep. Pedigree data from 428 animals registered by the Brazilian Association of Sheep Breeders and raised in the states of Piauí and Maranhão were used. The studied dataset contained 152 records for body weight (BW), 267 for body length (BL), 256 for height at the withers (HW), 267 for thoracic circumference (TC), 267 for leg length (LL), and 267 for leg perimeter (LP). A high-density panel (Illumina Ovine SNP50K BeadChip) was used for genotyping 271 animals. After genomic data quality control, 43,164 SNPs were available. The genome-wide association analysis for each trait was performed using the single-step GWAS approach (ssGWAS). The results were presented by the proportion of variance explained by each window of 50 SNPs with average of 594 Kb. The chromosome segments that explained more than more than 1.0% of the additive genetic variance were selected to explore and determine possible quantitative trait loci. The Map Viewer tool of ovine genome was used for identification of genes, available at the National Center for Biotechnology Information database. The classification of genes according to its biological function and identification of metabolic pathways was performed using the Database for Annotation, Visualization and Integrated Discovery tool v6.7. On chromosome 6 (OAR6), 19, 21, and 18 genes were identified in three different associated windows, respectively for BW, LL, and LP. For TC trait, 14, 30, and 22 genes were identified on OAR4, OAR7, and OAR13, respectively. On OAR4, 28 and 11 genes were also identified respectively for HW (in two different windows) and BL traits. Candidate genes (e.g. BMP3, BMPR1B, DMP1, SPP1, HGF, and CACNA2D1) related to bone formation and development, carcass, and growth traits were found. The results presented in this study should help to better understand the genetic and physiologic mechanisms regulating the body size traits of sheep. The identification of candidate genes should contribute for Santa Inês sheep breeding programs in order to consider body size traits as selection criteria in their genetic evaluation.

**Keywords:** body weight, genomic regions, meat sheep, morphometric traits, SNP

Promoção e Realização:

Apoio Institucional:

Organização: