

Preliminary studies for identification of SNPs associated with ribeye area in Canchim cattle.

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**Abstract:**

Brazil has the largest commercial cattle herd in the world. However, zebu breeds, which are mainly used in the country due to their adaptation to tropical climates, have low meat quality when compared to European breeds. In order to remain competitive, the Canchim composite breed (5/8 Charolais + 3/8 zebu) was bred to combine the adaptative traits of zebu to the higher muscle deposition of the Charolais breed. The Ribeye area (REA) is an important measure to evaluate carcass quality of cattle. Studies that aim to identify molecular markers, such as single nucleotide polymorphisms (SNP), associated with REA may be helpful to implement this trait in Canchim breed genomic selection programs. A genome wide-association study (GWAS) was performed with 400 animals with extreme phenotypes for REA, using the RandomForest methodology. From this analysis, 7 SNPs in the 3,4989,224 to 3,689,224 interval of chromosome 27 (UMD 3.1) were identified as associated. Another association analysis based on a case-control approach was performed using the Plink software in the same region and 193 SNPs were also found as being significant ( $P < 0.001$ ). Least square mean for estimated breeding values of one selected SNP (BovineHD2700010242) located within the SRFP1 gene (A/C) were: AA (n=78):  $-0,929 \pm 0,35$ ; AC (n=198) :  $-0.518 \pm 0,22$  and CC (n=114):  $0.866 \pm 0,29$  with the genotypes AA and AC being significantly different from the CC genotype. These genotypic means suggest an additive effect, but should be interpreted with caution, since estimates are possibly biased due to sampling of extreme phenotypes. The least square mean value indicate that CC genotype for the BovineHD2700010242 SNP is related to higher breeding values for REA. Further studies including more animals will help to estimate accuracy of this effect before this information could be applied in a selection program for REA.