

## Predictive ability and genotype frequencies of a set of SNPs for backfat thickness in Canchim

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Canchim is a beef cattle breed that has fared well in Brazilian production systems, however its backfat thickness (BFT) deposition is still suboptimal. In a previous genome wide association study for backfat thickness in Canchim beef cattle, a set of 21 single nucleotide polymorphisms (SNPs) was selected as being the most informative, with an ability to predict up to 53% of the deregressed estimated breeding value (dEBV). The objectives in this study were to determine the predictive ability of this set of 21 SNPs for estimated breeding values (EBVs) and to verify the genotype frequencies associated with extreme EBVs for backfat thickness. The predictive ability of the set of SNPs for backfat thickness EBVs was evaluated by fitting a regression model that included the whole population. The population was formed a total of 396 animals divided between males and females, with EBVs for BFT and genotyped by Illumina<sup>®</sup> BovineHD BeadChip (700kb). For determining the genotype frequencies and association of these SNPs, a sample with 100 extreme EBVs (50 lowest and 50 highest EBVs) was selected and tested as a case-control in a 2x3 contingency table using Fisher's exact test. The 50 lowest EBVs were coded as "0" (zero) and the 50 highest EBVs were coded as "1" (one). The analyses were done using the SAS/STAT 9.3 software. The predictive ability of the 21 SNPs was quite high with an adjusted  $R^2 = 0.68$  for the EBVs; showing an even better performance than for estimating dEBVs. From the 21 SNPs, just one SNP on chromosome (chr) 10 was not significant in the model ( $p=0.0812$ ), two SNPs (chr 8 and chr 9) had a p-value between 0.01 and 0.05, while all the other 18 SNPs had a p-value  $< 0.001$ . For the genotype frequencies, even though these SNPs were previously selected by an association analysis to BFT, three of them (located on chromosome 09, 13, and 16) were not confirmed by Fisher's exact test using 100 extreme EBVs for backfat thickness. All remaining 18 SNPs were highly associated by Fisher's exact test, and most of them were possible to verify by demonstrating a clear trend among the genotypes. Also, there were 5 SNPs where the favorable homozygous genotype had less than 5% frequency, which could make selection of these SNPs more difficult. Overall, the set of 21 SNPs previously selected shows good EBV predictive ability, and may be of interest for implementation in a future genomic selection program for Canchim beef cattle.

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