

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

ASSESSING GENETIC ARCHITECTURE AND SIGNATURES OF SELECTION OF DUAL PURPOSE GIR CATTLE POPULATIONS USING GENOMIC INFORMATION

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Gir is one of the main cattle breeds for livestock systems in tropical South American countries. Strong artificial selection through its domestication resulted in increased diversity among the recent populations. Over these last years, genomic studies in Gir have become more common. However, studies of population structure and the signatures of selection in divergent Gir populations are scarce and need more attention to better understanding the genetic differentiation, gene flow and the genetic makeup of the recent populations. The genotypes of 173 animals selected for growth traits and 273 females selected for milk production were used for the study. Clear genetic differentiation between the beef and dairy populations was identified, what is consistent with their history. Different criteria led to genetic divergence and difference in the allele frequencies between the two populations. Segregation of genes in within each population was forced by artificial selection, promoting the isolation and genetic variation between them. The results showed evidence of selective forces in different regions of the genome. 488 SNPs were relevant loci as evidence of signature of selection identified through the fixation index (F_{st}), a measure of genetic differentiation between populations. The within population method, integrated haplotype score (iHS) test, revealed 82 and 129 SNPs harbored signatures of selection in beef and dairy populations, respectively. iHS test revealed the most significant SNP mapped to BTA6 and BTA16 for the beef and dairy populations, respectively. The investigation of genes and pathways showed traces associated to fertility, milk production, beef quality, and growth were involved in the process of specialization of these populations. These results would support further investigations in the Gir breed.

Keywords: fixation index, genetic differentiation, gene, haplotype, pathways

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