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Genome-wide association study of navel length in Dairy Gir cattle

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Reproductive complications, such as acroposthitis and preputial infections, are commonly observed in male cattle with excessively long navels. Frequent contact between the reproductive organs and the ground or vegetation facilitates contamination by pathogenic agents, triggering infectious processes. Investigating the genetic architecture underlying this trait is essential to gain deeper insights and guide genetic improvement. In this context, the objective of this study was to identify genomic regions associated with navel length in Dairy Gir cattle, through a single-step genome-wide association study (ssGWAS). Data was obtained at the National Dairy Gir Cattle Breeding Program (PNMGL), a technical cooperation between Embrapa Dairy Cattle and the Brazilian Association of Dairy Gir Cattle Breeders (ABCGIL). The dataset included 10,975 phenotypic records and 193,408 pedigree records. Additionally, 6,913 animals were genotyped using single nucleotide polymorphisms (SNP) chips of various densities. The Illumina BovineHD (777K) chip was defined as the reference, and genotypes from other chips were imputed to approximately 420,000 SNPs. Quality control procedures were applied to the genotypic data, including the removal of SNPs with a call rate below 0.90, a minor allele frequency (MAF) less than 0.05. After filtering, 399,168 SNPs remained in the data set. An animal model was implemented, considering the contemporary group as a combination of evaluator, year of evaluation, and herd. Season, age, and quadratic age were also included as fixed effects, along with the random effects of permanent environment and animal. The association analysis was performed using the BLUPF90 software suite. SNPs with false discovery rate (FDR)-adjusted p-values ≤ 0.05 , according to the Benjamini-Hochberg procedure, were deemed significant. The analysis identified nine significant SNPs on chromosome 5, located between 47,456,260 and 47,687,668 base pairs (bp). Notably, these markers are located in proximity to genes involved in immune system processes, suggesting a potential association between genetic control of navel length and immunological mechanisms. These findings represent an important advancement in understanding of the genetic basis of navel length in Dairy Gir cattle and offer a valuable foundation for future studies. Subsequent research should aim to study the candidate genes within this region and functionally validate their roles in the biological mechanisms underlying this trait. Such knowledge will be fundamental for the development of more effective selection strategies.

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