

Selection signature analyses revealed multiple genomic regions associated with milk production in Girgentana breed

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The Girgentana goat is an ancient Sicilian breed with distinctive morphological, adaptive and production traits. In this study, the integrated haplotype score (iHS) was used to detect within-population selection signatures in a sample composed of 205 Girgentana animals. Then, the haplotypes from these individuals were compared with those from other Italian goat breeds (5 from Southern and 8 from Northern Italy) to detect genomic regions under divergent selection, using Rsb approach. After editing, 536 animals and 48,744 SNPs were available. Multidimensional scaling and the individuals' Neighbor joining tree revealed a clear separation of three major clades coinciding with Girgentana, the Northern and Southern Italian breeds. A total of 14 genomic regions were detected: three within the Girgentana (iHS) and eleven from the comparisons Girgentana vs Northern and Girgentana vs Southern breeds (Rsb). The largest overlap between the two approaches was on chromosomes 1 (110 – 112 Mb) and 5 (38 – 40 Mb). Among the several selection sweeps, worth noting the region on chromosome 6 mapping to the casein genes (CSN2, CSN1S1, CSN3) known to be involved in milk quality. Other selection signatures mapped genes associated with body size, reproduction, and immune resistance. The results presented here provide a foundation for detecting mutations that underlie genetic variation of economic important traits for breed.

Genomic analysis of longevity with productive and reproductive traits in Girolando cattle

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The objective of this study was to estimate (co)variance components, heritability and genetic associations between different measures of longevity, productive and fertility traits in Girolando cattle using genomic selection. Phenotypic, pedigree and genotype records were obtained from the Brazilian Association of Girolando Breeders. A sample of 24,993 animals was genotyped with chips of different densities. Longevity measures related to the productive life of the cow, as well as productive and fertility traits were evaluated. The analyses were carried out using the AIREMLF90 software. Heritability estimates for measures of longevity, productive and reproductive traits ranged from 0.06 to 0.31, 0.06 to 0.13 and 0.03 to 0.03, respectively. Genetic correlations between longevity measures and productive traits ranged from 0.02 to 0.31, while genetic correlations between longevity measures and reproductive traits ranged from 0.00 to 0.13. Productive traits showed a greater genetic association with longevity measures compared to reproductive traits, suggesting that genetic improvements obtained in milk production can lead to longer retention of cows in the herds. Longevity measurements were found to be significantly influenced by the environment, indicating a low potential for response to selection. Therefore, they should be combined with other traits in an index to achieve greater genetic gains.