
Artificial and natural selection in livestock is expected to leave unique footprints on their genomes. Goat breeds in Kenya have evolved for survival, breeding, and production in various harsh ecological areas, and their genomes are likely to have acquired unique alleles for adaptation to such diverse production environments and other traits of economic importance. To investigate signals of selection for some selected goat breeds in Kenya, Alpine ($n = 29$), Galla ($n = 12$), Saanen ($n = 24$), and Toggenburg ($n = 31$) were considered. A total of 53,347 single-nucleotide polymorphisms (SNPs) generated using the Illumina GoatSNP50 BeadChip were analyzed. After quality control, 47,663 autosomal single-nucleotide polymorphisms remained for downstream analyses. Several complementary approaches were applied for the following analyses: integrated Haplotype Score (iHS), cross-population-extended haplotype homozygosity (XP-EHH), hapFLK, and FLK. A total of 404 top genomic regions were identified across all the four breeds, based on the four complementary analyses. Out of the 16 identified putative selection signature regions by the intersection of multiple-selective signal analyses, most of the putative regions were found to overlap significantly with the iHS and XP-EHH analyses on chromosomes 3, 4, 10, 15, 22, and 26. These regions were enriched with some genes involved in pathways associated directly or indirectly with environmental adaptation regulating immune responses (e.g., *HYAL1* and *HYAL3*), milk production (e.g., *LEPR* and *PDE4B*), and adaptability (e.g., *MST1* and *PCK*). The results revealed few intersect between breeds in genomic selection signature regions. In general, this did not present the typical classic selection signatures as predicted due to the complex nature of the traits. The results support that some various selection pressures (e.g., environmental challenges, artificial selection, and genome admixture challenges) have molded the genome of goat breeds in Kenya. Therefore, the research provides new knowledge on the conservation and utilization of these goat genetic resources in Kenya. In-depth research is needed to detect precise genes connected with adaptation and production in goat breeds in Kenya.
