

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

IDENTIFICATION OF RUNS OF HOMOZYGOSITY ISLAND IN A GYR DAIRY CATTLE POPULATION

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Runs of Homozygosity (ROH) are contiguous homozygous regions in the genome generated by the transmission of identical haplotypes by descent (IBD) segments. A particular SNP can be precisely determined as part of a ROH with the use of high-density SNP chip information. Uniform regions of high frequency of autozigosidade are called ROH islands. The aim of the present study was to analyze the length and distribution of ROH islands in Gyr dairy cattle. A total of 292 animals were used this study. Genotypes were imputed to 777K SNPs. ROH was calculated considering different lengths of the genome: >2 Mb, >4 Mb, >8 Mb, >16 Mb and <16 Mb. The ROH islands were classified using PLINK v1.07 with the ROH regions in frequency higher than >50% in the samples. Traits such as milk production, milk composition (fat and protein), somatic cell count, handling (e.g., ease of milking and temperament), and conformation (e.g., ligament last udder, rear udder height, rear udder width, length and diameter of the teats) were included in the breeding program for the selection of animals. Short segments of ROH were present in all the animals indicated by ROH >2. This suggested genetic variability among ancestors and different selection pressures in the herd. Variety in the long levels of ROH was observed by ROH <16, indicating differences in frequencies among the animals, probably due to inbreeding. The presence of long homozygous segments indicates that inbreeding occurred due to the intensive and recent selection through the use of breeding and reproductive biotechnology. Eight ROH islands were identified. They were located in the chromosomes BTA3, BTA5, BTA11, BTA13, BTA16, and BTA26. Genomic regions associated with important traits were found within ROH island. The genes that overlapped with ROH islands are related with traits that were under selection in this population. ROH approach was consistent in this study.

Keywords: Genomic regions, inbreeding, selection pressures.

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