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The Runs of Homozygosity (ROH) are continuous homozygous segments which are common in all individuals and populations. The aim of this study was to identify and characterize ROH segments in the Gyr cattle genome. A total of 585 sires comprising the progeny test program from the National Program for Improvement of Dairy Gyr were genotyped with the BovineHD BeadChip (Illumina Inc.). Eight sires were removed due to low call rate (0.1); 7,411 markers were excluded based on HWE test ($p \leq 0.00000001$); 14,351 SNPs failed on missing genotype rate; and 286,289 SNPs failed on MAF test ($MAF < 0.05$), totaling 438,193 SNPs and 577 animals in the dataset. The ROH were identified in every individual using PLINK v1.07. Regions of homozygosity were extracted just in autosomes. The parameters set to perform ROH analyses were: homozyg-window-snp 50, homozyg-window-het 1, homozyg-window-missing 5, homozyg-snp 100, homozyg-gap 500, homozyg-kb 1000, homozyg-density 50. There were identified 26,292 ROH segments in the overall samples. Total length of ROH was composed mostly of high number of shorter ROH segments (1-2 Mb) totaling 53.32% of the observed segments. The average ROH number per animal was 45.57 ± 9.17 , and ranged from 23 to 88. Overall, ROH length varied from 1.00 Mb to 104.82 Mb. The number of ROH per chromosome was greatest for BTA5 (1,790 runs across 553 animals), with on average, 9.93% of the chromosome within a ROH. The average genome coverage by ROH was 162.52 (6.5%) Mb and was higher than previously reported for other indicine cattle breeds. The less and most autozygous individual showed 1.75% and 24.8% of its genome covered by ROH, respectively. All animals comprising the dataset showed ROH patterns in their genome. Therefore, a deeply insight in those homozygous regions can increase the understanding of biological and genetics mechanisms underlying population structure, selection pressure, and the occurrence of deleterious variants throughout the genome, since these events tend to be expressed as ROH.

Key words: autozygosity, Bos Taurus Indicus

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Exploring runs of homozygosity patterns in Gyr cattle

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