

Inbreeding Study Using Runs of Homozygosity in Nelore Beef Cattle

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Abstract : The best linear unbiased predictor (BLUP) is a method commonly used in genetic evaluations of breeding programs. However, this approach can lead to higher inbreeding coefficients in the population due to the intensive use of few bulls with higher genetic potential, usually presenting some degree of relatedness. High levels of inbreeding are associated to low genetic viability, fertility, and performance for some economically important traits and therefore, should be constantly monitored. Unreliable pedigree data can also lead to misleading results. Genomic information (i.e., single nucleotide polymorphism - SNP) is a useful tool to estimate the inbreeding coefficient. Runs of homozygosity have been used to evaluate homozygous segments inherited due to direct or collateral inbreeding and allows inferring population selection history. This study aimed to evaluate runs of homozygosity (ROH) and inbreeding in a population of Nelore beef cattle. A total of 814 animals were genotyped with the Illumina BovineHD BeadChip and the quality control was carried out excluding SNPs located in non-autosomal regions, with unknown position, with a p-value in the Hardy-Weinberg equilibrium lower than 10^{-5} , call rate lower than 0.98 and samples with the call rate lower than 0.90. After the quality control, 809 animals and 509,107 SNPs remained for analyses. For the ROH analysis, PLINK software was used considering segments with at least 50 SNPs with a minimum length of 1Mb in each animal. The inbreeding coefficient was calculated using the ratio between the sum of all ROH sizes and the size of the whole genome (2,548,724kb). A total of 25.711 ROH were observed, presenting mean, median, minimum, and maximum length of 3.34Mb, 2Mb, 1Mb, and 80.8Mb, respectively. The number of SNPs present in ROH segments varied from 50 to 14.954. The longest ROH length was observed in one animal, which presented a length of 634Mb (24.88% of the genome). Four bulls were among the 10 animals with the longest extension of ROH, presenting 11% of ROH with length higher than 10Mb. Segments longer than 10Mb indicate recent inbreeding. Therefore, the results indicate an intensive use of few sires in the studied data. The distribution of ROH along the chromosomes showed that chromosomes 5 and 6 presented a large number of segments when compared to other chromosomes. The mean, median, minimum, and maximum inbreeding coefficients were 5.84%, 5.40%, 0.00%, and 24.88%, respectively. Although the mean inbreeding was considered low, the ROH indicates a recent and intensive use of few sires, which should be avoided for the genetic progress of breed.

Keywords : autozygosity, *Bos taurus indicus*, genomic information, single nucleotide polymorphism

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