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PROCEDURES FOR QUALITY CONTROL OF GENOTYPES USED IN GENOMIC EVALUATIONS OF HEREFORD AND BRAFORD CATTLE IN BRAZIL[1]

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The objective of this study was to apply different quality control criteria to determine which samples and/or loci had to be removed from a final dataset which will be analyzed for generating genomic predictions for tick resistance. Blood samples were collected with MGM cards from a total of 2,161 Hereford and Braford bulls and heifers evaluated by the Delta G Connection breeding program. DNA was extracted from two 6 mm discs with standard lab protocols and each sample was genotyped with the Illumina BovineSNP50 v2 BeadChip (Illumina Inc., San Diego, CA) for a total of 54,609 single-nucleotide polymorphisms (SNP). Samples with call-rates below 90% (41 samples) and outliers (± 3 standard deviations) for average heterozygosity (21 samples) were removed; however, in total 50 samples were excluded, because 12 failed both criteria. SNPs with call-rates below 90% (548 in total) as well as SNPs fixed or with little information content (minor allele frequencies < 3%, 6,774 SNPs) were removed. Finally, a total of 3,378 SNPs were discarded for showing extreme Hardy-Weinberg disequilibrium (± 4 standard deviations). The total number of SNPs eliminated by all three criteria was 9,877, since 823 failed more than one criterion. A total of 44,732 SNP and 2,111 samples were considered of high quality and informativeness and will be used for genome-wide association studies and genomic selection for tick count and other production traits on this population.