



Identification of genes associated with seminal volume and its correlation with reproductive traits of Dairy Gyr bulls

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Genomic wide association studies (GWAS) allow genes identification with greater effects, related to traits of interest, enabling to integrate this information into the genetic evaluation. Also, the aim was to estimate the heritability and evaluate the correlations between volume and reproductive traits in this population. The data were collected from eight editions of pre-selection tests for the Progeny Test of the Brazilian Association of Dairy Gyr Breeders (ABCGIL) and the Brazilian Agricultural Research Company (EMBRAPA – Dairy Cattle), that occurred between 2012 and 2019. It was used 676 information from 545 bulls with an average age of 26.6 months. The covariance components used to determine the heritability of seminal volume were estimated through the REMLF90 application of BLUPF90 software. The statistical model included the animal random effect, and month of collection, year of the test, in addition to scrotal perimeter, linear and quadratic age, as covariates. For the phenotypic correlation between volume, test year, semen collection month, age, scrotal circumference (SC), swirling, motility, vigor and sperm concentration, it was used Pearson's correlation test (with 5% significance level), through the Studio Version of R software. A sample of 677 animals was genotyped with chips of different densities, and the Illumina BovineHD chip (777K) was defined as standard. The SNPs of the other chips were extracted and/or imputed to the 777K chip, and the analyzes started with a total of 735,293 SNPs. Subsequently, the following criteria were used to exclude SNPs: allele frequency ≤ 0.02 , maximum difference between observed and expected allele frequency for Hardy-Weinberg equilibrium of 0.15, GenCall score ≤ 0.70 , call rate ≤ 0.98 and SNPs with correlation between them > 0.995 . Samples with genotyping efficiency (call rate) ≤ 0.90 were also excluded. For the GWAS analyses, an additive model was used, through the SVS 8.3.0 software (Golden Helix Inc.), and a total of 403,498 SNPs were mapped in 29 autosomes of mount *Bos taurus* ARS-UCS 1.2. Different genetic models were tested (codominant, dominant, recessive, superdominant and log-additive) and the R/WGstats function was used to provide P values for the likelihood ratio association test. The heritability estimated for volume was 0.18 ± 0.12 . Seminal volume was evaluated, with a positive correlation, with age (0.19), SC (0.16) and sperm concentration (0.15). In the other evaluated traits, no correlation was verified ($P > 0.05$). No major effect gene was found for seminal volume in dairy Gyr bulls. However, the heritability of the trait and its correlation with sperm concentration indicate that the use of volume as a selection criteria, associated with fertility traits, may have positive long-term effects on the reproductive performance of bulls in the population evaluated.

Keywords: Fertility, GWAS, Genetic parameters, Semen production, Zebu.