

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

GENETIC PARAMETERS ESTIMATES FOR COOKING LOSS AND WARNER-BRATZLER SHEAR FORCE INCLUDING OR NOT GENOMIC INFORMATION

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The objective of the present study was to evaluate the effect of different structures of the relationship matrix (**A** and **H**) on the estimation of genetic parameters for cooking loss (CL) and Warner-Bratzler shear force (WBSF) of Nelore cattle. Animals from DeltaGen, CRV Paint and Cia de Melhoramento breeding programs were used, considering 12,314 animals in the pedigree, 4,785 observations for CL, 4,866 observations for WBSF and 5,922 genotypes. The animals were genotyped using the BovineHD BeadChip (777,962 SNPs) and GeneSeek (74,677 SNPs) imputed to the HD panel. For quality control of the SNPs, SNP non-autosomes, with GenCall score lower than 0.92, SNP at the same genomic position, with minor allele frequency < 0.02, Hardy-Weinberg equilibrium deviation not highly significant ($P > 10^{-5}$) and call rate < 0.90 were excluded. Samples with call rate < 0.90 were also eliminated. After quality control, 476,582 SNP remained. The contemporary groups (CG) were formed by year of birth, farm and management group at yearling. Analyses were performed by Bayesian inference and consisted of a chain of 1,000,000 cycles, with burn-in period of 200,000 cycles and a thinning interval of 50 cycles, using GIBBS2F90 software. Systematic effects of CG and age at slaughter were considered as covariate for both traits. The heritability estimates for CL (0.012 - 0.030 using **A** and **H** matrices, respectively) and WBSF (0.113 - 0.114 using **A** and **H** matrices, respectively) obtained with the 2 methods were similar and of low magnitude. Genetic correlations estimated between CL and WBSF ranged from moderate (0.293 using matrix **A**) to high (0.736 using matrix **H**) values. One explanation for this finding is the higher proportion of multiple sires as parents of animals with meat quality measures in the evaluated pedigree, which leads to impoverishment of the **A** matrix and makes it difficult to obtain estimates of genetic covariances. In addition, the **H** matrix improves the relationship coefficients and, consequently, additive-genetic relationships.

Keywords: Bayesian inference, genetic correlation, heritability, meat quality, Nelore cattle

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