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GENETIC ANALYSIS OF MORPHOLOGICAL AND MANAGEMENT TRAITS IN GYR DAIRY CATTLE

ANALISE GENÉTICA DE CARACTERÍSTICAS MORFOLÓGICAS E DE MANEJO NA RAÇA GIR LEITEIRO

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The study of genetic components involved in phenotype expression of morphological traits (functional type) in dairy cattle is justified by the known relationship between productive and reproductive traits. Gyr dairy cattle are widely bred in tropical environments, where pronounced environmental challenges compromise aspects related to health, reproduction and longevity. The objective of this study was to estimate components of variance and genetic parameters for morphological and management traits in Gyr dairy cattle. A database containing a total of 4,989 observations for 17 traits related to morphology and management was analyzed. The evaluated traits were: rump height (RH), hoof angle (HA), rump angle (RA), rump length (RL), rear teat length (RTL), milking ease (ME), rump width (RW), legs side view (LSV), udder depth (UD), temperament (TP), body length (BL), front teat length (FTL), navel length (NL), rear udder width (RUW), ischia width (IW), thoracic perimeter (TP), legs rear view (LRV). Variance components were estimated by univariate animal models using a Bayesian approach. Inference about the results was based on the posterior distributions of the parameters. The model proposed for the analyses considered the fixed effects of herd-year of birth of the animal, classifier, cow age (covariate); and random effects of animal, permanent environment and residual. A Markov chain containing 850,000 samples was created, with *burn-in* of 250,000 samples and storing only 100 sample intervals (thinning), resulting in a posterior distribution of 6,000 samples. The posterior means (and confidence intervals; 0.05 - 0.95) for the heritability of the studied traits were: RH= 0.52 (0.41 – 0.62), HA= 0.09 (0.03 – 0.14), RA= 0.21 (0.09 – 0.33), RL= 0.20 (0.13 – 0.28), RTL= 0.47 (0.37 – 0.57), ME= 0.08 (0.02 – 0.14), RW= 0.20 (0.12 – 0.28), LSV= 0.24 (0.11 – 0.36), UD= 0.08 (0.003 – 0.15), TP= 0.11 (0.05 – 0.17), BL= 0.11 (0.05 – 0.18), FTL= 0.47 (0.36 – 0.56), NL= 0.52 (0.33 – 0.71), RUW= 0.17 (0.05 – 0.30), IW= 0.16 (0.09 – 0.22), TP= 0.23 (0.13 – 0.33), LRV= 0.01 (0,00 – 0.05). Low, medium and high heritabilities were observed depending on the evaluated trait. The results indicate that different aspects of morphology and management respond differently to selection and should be analyzed independently. However, due to the large number of traits considered, joint selection may be essential for the practical application of results from genetic evaluations. The formation of indices composed of different traits can help to compile results more efficiently, improving their usability by breeders. Studies evaluating the magnitude and direction of the genetic correlation between analyzed traits, as well as involving morphological, productive and reproductive traits are important to guide decision making.

Keywords: Bayesian inference, type traits, zebu.

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