Inclusion of cytoplasmic lineage effect and direct-maternal genetic covariance for genetic evaluation of growth traits in Nellore cattle

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ABSTRACT. We evaluated the impact of cytoplasmic lineage effects (Lc) for growth traits on genetic evaluation, including the genetic covariance between direct and maternal effects (σ_{am}). Pedigree data from 496,190 Nellore animals and observations on birth weight (BW, N = 243,391), weaning weight (WW, N = 431,681), and post-weaning weight gain adjusted to 345 days (PWG, N = 172,131) were analyzed. Four univariate models were used to obtain estimates of (co)variance components using the restricted maximum likelihood method in the BLUPF90 program. Model 1 included Lc and σ_{am}. Model 2 included Lc and σ_{am} was set to zero. Model 3 did not include Lc. Model 4 did not include Lc and σ_{am} was set to zero. These models considered the effects

of the Lc as random. Phenotypic variance obtained through cytoplasmic lineage effects was determined for all traits, ranging from 0.07 to 0.15, 0.15 to 0.03, and 0.05 to 0.03% for BW, WW, and PWG, respectively, for models 1 and 2. Correlations between direct and maternal genetic components were positive for WW and negative for BW and PWG. No differences were observed for genetic parameter estimates or animal ranking with the inclusion of σ_{am}. For BW, the likelihood ratio suggested that model 1 best fits the data, while model 4 was the most appropriate for WW and PWG. Thus, these models are recommended for genetic evaluations. Despite the low magnitude of cytoplasmic lineages, this effect could predict breeding value and improve the selection of animals for BW in this Nellore population.

Key words: Cytoplasmic lineage effect; Direct-maternal covariance; Growth traits; Mitochondrial DNA; Nellore