Breeding value accuracy estimates for growth traits using random regression and multi-trait models in Nelore cattle

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ABSTRACT. We quantified the potential increase in accuracy of expected breeding value for weights of Nelore cattle, from birth to mature age, using multi-trait and random regression models on Legendre polynomials and B-spline functions. A total of 87,712 weight records from 8144 females were used, recorded every three months from birth to mature age from the Nelore Brazil Program. For random regression analyses, all female weight records from birth to eight years of age (data set I) were considered. From this general data set, a subset was created (data set II), which included only nine weight records: at birth, weaning, 365 and 550 days of age, and 2, 3, 4, 5, and 6 years of age. Data set II was analyzed using random regression and multi-trait models. The model of analysis included the contemporary group as fixed effects and age of dam as a linear and quadratic covariable. In

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the random regression analyses, average growth trends were modeled using a cubic regression on orthogonal polynomials of age. Residual variances were modeled by a step function with five classes. Legendre polynomials of fourth and sixth order were utilized to model the direct genetic and animal permanent environmental effects, respectively, while third-order Legendre polynomials were considered for maternal genetic and maternal permanent environmental effects. Quadratic polynomials were applied to model all random effects in random regression models on B-spline functions. Direct genetic and animal permanent environmental effects were modeled using three segments or five coefficients, and genetic maternal and maternal permanent environmental effects were modeled with one segment or three coefficients in the random regression models on B-spline functions. For both data sets (I and II), animals ranked differently according to expected breeding value obtained by random regression or multi-trait models. With random regression models, the highest gains in accuracy were obtained at ages with a low number of weight records. The results indicate that random regression models provide more accurate expected breeding values than the traditionally finite multi-trait models. Thus, higher genetic responses are expected for beef cattle growth traits by replacing a multi-trait model with random regression models for genetic evaluation. B-spline functions could be applied as an alternative to Legendre polynomials to model covariance functions for weights from birth to mature age.