



Estimation of genetic parameters for growth evaluation of the Tabapuã cattle created in Brazilian Northeast region using Random regression models¹

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Abstract: This study aimed to compare different Random regression models (RRM) and determine the most appropriate to describe changes in bovine growth assessment parameters Tabapuã created in Northeastern Brazil. Was evaluated 1,505 weight records taken at different ages. Five different Random regression models were used in which contained the fixed effects contemporary group and the covariate age of cow at calving and the random additive genetic effects, direct and maternal. These models were compared using the Log-likelihood function and the Akaike information criterion and Schwarz Bayesian. The MRA45-5 model with five classes of residual variance were defined as the best fit. Estimates of direct additive and maternal genetic variance increased with age. But the maternal additive genetic variance showed birth of growing up close to 420 days. This result differs from the commonly reported with Zebu animals, because the maternal variance values should be more expressively in the period surrounding birth to weaning. Estimates of direct heritability showed increased birth to the following ages, with a slight decrease after 120 days. Maternal heritability presented birth of growing up close to 300 days, when he showed a fall to the later ages. Response to selection for getting heavier animals will be effective when performed at a later age at weaning.

Keywords: breeding, covariance functions, growth curve, Legendre polynomials, livestock

Estimação de parâmetros genéticos para avaliação do crescimento de bovinos Tabapuã criados no Nordeste brasileiro, utilizando Modelos de regressão aleatória

Resumo: Objetivou-se comparar diferentes Modelos de regressão aleatória (MRA) e determinar o mais adequado para descrever mudanças nos parâmetros de avaliação do crescimento de bovinos Tabapuã, criados no Nordeste brasileiro. Foram avaliados 1.505 registros de peso em diferentes idades, utilizando-se cinco Modelos de regressão aleatória, nos quais continham os efeitos fixos de Grupo de contemporâneo e covariável idade da vaca ao parto, além dos efeitos aleatórios genéticos aditivos, direto e materno. Os modelos foram comparados com o Logaritmo da função de verossimilhança e os critérios de Informação de Akaike e Bayesiano de Schwarz. O modelo MRA45-5 com cinco classes de variância residual foi definido como o de melhor ajuste. As estimativas de variâncias genéticas aditivas, direta e materna, aumentaram em função da idade do animal. Porém, as variâncias genética aditiva materna mostraram crescimento do nascimento até próximo a 420 dias de idade. Este resultado difere do comumente apresentado por animais zebuínos, cujos valores tendem a ser mais expressivos do nascimento até a desmama. As estimativas de herdabilidade direta mostraram tendência de aumento nas idades seguintes ao nascimento, mas com leve decréscimo após os 120 dias. A herdabilidade materna apresentou crescimento do nascimento até próximo aos 300 dias, seguido de queda nas idades posteriores. Resposta à seleção para obtenção de animais mais pesados será eficiente quando realizada em idades posteriores ao desmame.

Palavras-chave: curva de crescimento, funções de covariância, melhoramento genético, pecuária, polinômios de Legendre

Introduction

Brazil is one of the largest food producers in the world, mainly due to favorable climate and soil conditions. In this context, emphasis should be given to the production and export of animal protein. Genetic improvement is a key technology to increase the meat production in Brazil, mainly beef, considered the most produced and exported by the country. Among the various methods available for the genetic evaluation of livestock, the use of Random regression models in the evaluation of the growth curve is efficient by eliminating the need of pre-settings and the possibility to use all the information of individuals weighing (Malhado et al., 2008). To adjust the Random regression models the use of an array of infinite dimensional covariance is necessary, being the covariance



functions an efficient alternative (Sousa Júnior et al., 2010). This study aimed to compare different Random regression models and determine the most appropriate to describe changes in the valuation parameters of Tabapuã cattle growth created in Northeastern Brazil.

Material e Methods

Were analyzed 3,172 Tabapuã cattle weight records with ages ranging from birth to 660 days of age, born between the years 1984 and 2004. This information was originated from herds of three states in Northeastern Brazil (Alagoas, Maranhão and Sergipe) and provided by the Brazilian Association of Zebu Breeders (ABCZ). After the data consistency analysis and restrictions carried out with the help of SAS® software (Statistical Analysis System 9.0) (SAS, 2003), the set of final data contained 1,505 records. Animals with less than three records of weight and / or contemporary groups with less than three animals were eliminated. Were used as criteria for the formation of contemporary groups, sex, month and year of birth and weighing, farm of birth and rearing condition (the pasture breeding system). To better evaluation of the data, were created 118 age classes. The weights measured at different ages were modeled using five different Random regression models with five residual variance classes (M45-5, M45-5, M45-5, M46-5 and M56-5) each model contained the fixed effects of a Contemporary group and the covariate age at calving (under quadratic effect) and random effects, additive genetic (direct and maternal). Legendre Orthogonal polynomials from fourth to sixth order were used in the modeling of random effects mentioned above. These models were compared and evaluated by the Log-likelihood function, in addition to the Information criteria of Akaike and Bayesian Schwarz.

Results and Discussion

Among the five Random regression models evaluated, the M45-5 model was defined as being the best fit for describing the estimates of variance and heritability of the growth characteristics of animals evaluated. Estimates of direct additive genetic variance increased with age (Figure 1), supporting the study of Martínez Niño et al. (2012) showing that there is satisfactory genetic variability to weight gain when selection is made at a later age at weaning phase. On the other hand, the maternal genetic additive estimative, showed an increase from birth until close to 420 days of age, when decreased until the 660 days. This result differs from the commonly reported in studies with Zebu animals, because maternal variance values should be more significant in the time of birth until weaning phase, which on average is made at 205 days of age.

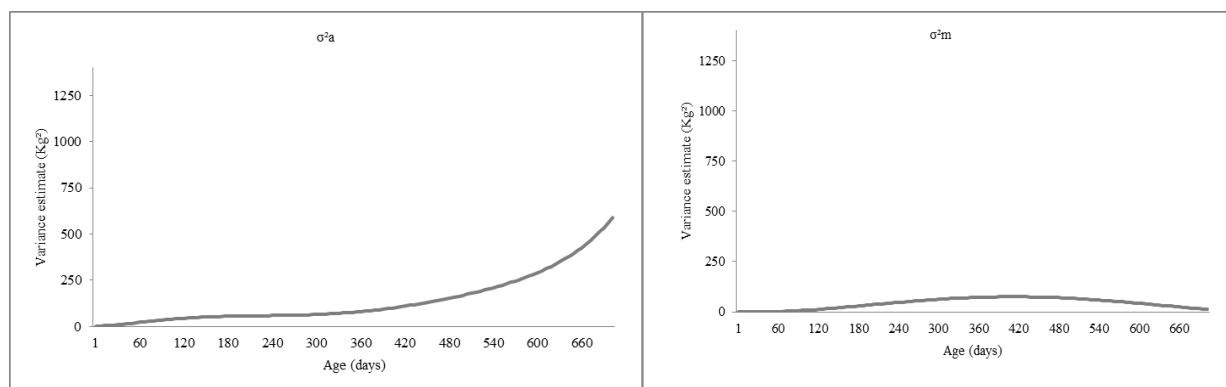


Figure 1. Estimates of direct additive genetic variance (σ^2_a) and maternal (σ^2_m) from birth weights at 660 days of age Tabapuã cattle.

Estimates of direct heritability, in general, showed increased birth at the following ages, however, there was a downward trend after 120 days, remaining stable until the 600 days when it returned to grow until the end of the study period (Figure 2). Laureano et al. (2011) reported that in studies that found high levels of direct heritability yearling weight, not included in the model the maternal genetic effect, and that this fact may have caused overestimation in additive genetic variance. In general maternal heritability presented growing of birth up close to 300 days, when it showed a fall till the later ages. Dias et al. (2006) found different heritability values to this work, in which the highest maternal heritability values were found before weaning, around 150 days of age in Tabapuã cattle. The found results suggest that there may be good response to selection of the feature maternal ability, when it is carried out based on weights before weaning, due to largest mother's influence on offspring's.

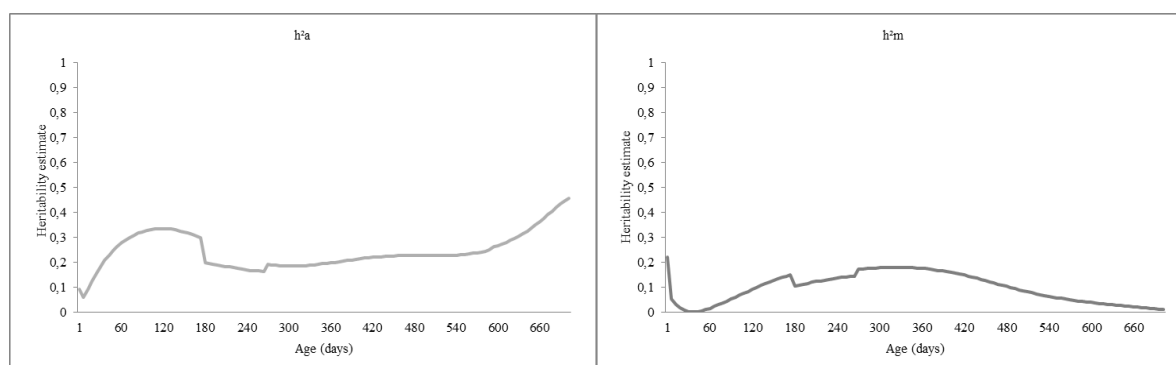


Figure 2. Heritability estimates direct (h^2_a) and maternal (h^2_m) from birth weights at 660 days of age Tabapuã cattle.

Conclusions

The M45-5 model was the best fit for description of estimates of variance and heritability of growth characteristics of animals evaluated.

When evaluating the growth curve of cattle through the interpretation of genetic parameters is possible to identify and select animals with higher growth rate which makes it possible to define those who are able to slaughter early.

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