GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Random regression models in the evaluation of the growth curve of Simbrasil beef cattle

R.R. Mota[1], L.F.A. Marques[2], P.S. Lopes[1], L.P. da Silva[1], A.M. Hidalgo[3], C.D.S. Leite[1] and R.A. Torres[1]

[1]Departamento de Zootecnia, Universidade Federal de Viçosa, Viçosa, MG, Brasil
[2]Departamento de Zootecnia, Centro de Ciências Agrárias, Universidade Federal do Espírito Santo, Alegre, ES, Brasil
[3]Animal Science Department, Wageningen University, Wageningen, The Netherlands

Corresponding author: R.R. Mota
E-mail: rreismota@hotmail.com

Genet. Mol. Res. 12 (1): 528-536 (2013)
Received January 30, 2012
Accepted October 18, 2012
Published February 27, 2013
DOI http://dx.doi.org/10.4238/2013.February.27.2

ABSTRACT. Random regression models were used to estimate the types and orders of random effects of (co)variance functions in the description of the growth trajectory of the Simbrasil cattle breed. Records for 7049 animals totaling 18,677 individual weighings were submitted to 15 models from the third to the fifth order including as fixed effects sex, contemporary group, feeding regimen, and type of reproduction and as random effects additive direct genetic effect, animal permanent environment, maternal additive genetic effect, and maternal permanent environment. The best-fit model presented order five to additive direct genetic effect, animal permanent environment, and maternal additive effect, with 6 classes of residual variances, and the maternal permanent environment effect was not significant, likely owing to the low average number of calves per cow. However, the model chosen for the growth curve presents three classes of residual variances, because even not showing the best fit

it is more parsimonious, in addition to promoting a more realistic estimate of heritability.

Key words: (Co)variance functions; Residual variance; Heritability

