



Genomic prediction for additive and dominance effects of censored traits in pigs

V.S. Santos¹, S. Martins Filho¹, M.D.V. Resende², C.F. Azevedo¹,
P.S. Lopes³, S.E.F. Guimarães³ and F.F. Silva³

¹Departamento de Estatística, Universidade Federal de Viçosa,
Viçosa, MG, Brasil

²Empresa Brasileira de Pesquisa Agropecuária,
Centro Nacional de Pesquisa de Florestas, Colombo, PR, Brasil

³Departamento de Zootecnia, Universidade Federal de Viçosa,
Viçosa, MG, Brasil

Corresponding author: V.S. Santos
E-mail: 2santosvinicius@gmail.com

Genet. Mol. Res. 15 (4): gmr15048764

Received May 5, 2016

Accepted August 30, 2016

Published October 17, 2016

DOI <http://dx.doi.org/10.4238/gmr15048764>

Copyright © 2016 The Authors. This is an open-access article distributed under the terms of the Creative Commons Attribution ShareAlike (CC BY-SA) 4.0 License.

ABSTRACT. Age at the time of slaughter is a commonly used trait in animal breeding programs. Since studying this trait involves incomplete observations (censoring), analysis can be performed using survival models or modified linear models, for example, by sampling censored data from truncated normal distributions. For genomic selection, the greatest genetic gains can be achieved by including non-additive genetic effects like dominance. Thus, censored traits with effects on both survival models have not yet been studied under a genomic selection approach. We aimed to predict genomic values using the Cox model with dominance effects and compare these results with the linear model with and without censoring. Linear models were fitted via the maximum likelihood method. For censored data, sampling through

the truncated normal distribution was used, and the model was called the truncated normal linear via Gibbs sampling (TNL). We used an F_2 pig population; the response variable was time (days) from birth to slaughter. Data were previously adjusted for fixed effects of sex and contemporary group. The model predictive ability was calculated based on correlation of predicted genomic values with adjusted phenotypic values. The results showed that both with and without censoring, there was high agreement between Cox and linear models in selection of individuals and markers. Despite including the dominance effect, there was no increase in predictive ability. This study showed, for the first time, the possibility of performing genomic prediction of traits with censored records while using the Cox survival model with additive and dominance effects.

Key words: GBLUP; Censored data; Mixed model; Survival models