A SIMULATION STUDY TO EVALUATE THE EFFECT OF RESPONSE VARIABLE ON GENOMIC PREDICTION ACCURACIES IN BEEF CATTLE

Gerardo Alves Fernandes JÚNIOR*[1,2], Roberto CARVALHEIRO[1,2], Diogo Osmar SILVA[1], Lucia Galvão de ALBUQUERQUE[1,2]

*corresponding author: gerardojjunior@yahoo.com.br
[1]School of Agricultural and Veterinarian Sciences – FCAV/UNESP, Jaboticabal, São Paulo, Brazil
[2]National Council for Scientific and Technological Development (CNPq), Brasília, Brazil

Phenotype adjusted for fixed effects (Y*) has been used as the response variable in genomic selection studies for difficult to measure traits where, usually, most animals present both genotypic and phenotypic information. In this case, the genomic prediction accuracies are obtained by dividing the correlation between Y* and direct genomic value (DGV) by the square root of the trait heritability. Other types of response variable, such as the pedigree-based estimated breeding values (EBV) and deregressed EBV (dEBV) have also been used to attain prediction equations. In order to investigate the effect of using different pseudo-phenotypes on real accuracy (correlation between direct genomic value (DGV) and true breeding value (TBV)) two complex and sex limited traits with heritabilities (h^2) of 0.30 and 0.50, respectively, were simulated. Fixed effects of contemporary groups (CG) and age of animal were also simulated. All animals (3,032 males randomly selected from the last three of fifteen simulated generations) had phenotypic and genotypic information. Genotypes were simulated with 777k SNP markers and 80K QTL, being both biallelic and randomly distributed across 29 autosomes. The pseudo-phenotypes (Y*, EBV and dEBV) were obtained considering a traditional pedigree-based additive genetic model including fixed effects of CG and age of animal as covariable. For genomic analyses, considering the Bayesian ridge regression model, the animals from the generations 13 e 14 formed the training population and those from the generation 15 formed the validation population. In practice, the genomic prediction accuracies are measured as the correlation between DGV of the validation population and the respective response variable (Y*, EBV and dEBV) used in the analysis. Based on this criterion, EBV provided higher prediction accuracies (0.75 and 0.76, respectively for traits with h^2 of 0.30 and 0.50) than Y* (0.54 and 0.64) and dEBV (0.53 and 0.61). Considering the real accuracy [r(DGV,TBV)], the results obtained using EBV (0.54 and 0.67) or dEBV (0.55 and 0.68) were similar and higher than those from Y* (0.50 and 0.65), for both traits. Therefore, for some scenarios, in which all animals present both, genotypic and phenotypic information, the phenotype adjusted for fixed effects may not be the best response variable for genomic predictions.

Keywords: direct genomic value, genomic selection, true breeding value