Agrociencia Uruguay 2023 | Volume 27 | Number NE2 | Article e1264
DOI: 10.31285/AGRO.27.1264
ISSN 2730-5066

IUFRO Conference 2023

Genomic-enhanced Markov causal models for predicting breeding values in forest trees

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Received *11 Aug 2023*
Accepted *09 Sep 2023*
Published *20 Nov 2023*

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Traditionally, in forest genetic evaluations, the pedigree-based individual-tree mixed model (ABLUP) has been utilized to identify individuals with the highest breeding value (BV). The ABLUP is considered a Markov causal model as the BV of an individual is independent of all its non-descendants, conditional to including the BV of its parents. Under this model, an individual's BV is expressed as a linear regression on parental BVs, along with a Mendelian sampling term. The availability of genome-wide marker panels has led to the development of a technique known as genomic selection (GS). In forest tree breeding, the most widespread GS method is the GBLUP model, which replaces the pedigree-based genetic covariance matrix with a marker-based relatedness matrix (G-matrix) derived from genotyped individuals. The GBLUP model has demonstrated improved BV accuracy compared to the ABLUP model. However, the use of Markov causal models incorporating genomic information remains unexplored in forest tree breeding. Therefore, the objective of this study was to develop and apply two new Markov causal models that substitute the “path coefficient” of the ABLUP model (which is 0.5) with an alternative coefficient, calculated using genomic information. Subsequently, we compared the performance of these new two causal models with the classical causal ABLUP and non-causal GBLUP models in terms of their predictive ability (PA) for BVs. Our investigation focused on a fourth-generation population of *Eucalyptus grandis* (Hill ex Maiden), comprising 3,082 genotyped trees with 14,033 single-nucleotide polymorphism markers. The study assessed six growth and wood quality traits in 1,219 trees spanning the first three generations. Progeny validation was conducted to evaluate PA, where individuals from generations 1 and 2 comprised the training set, and individuals from generation 3 constituted the validation set. Overall, the GBLUP model exhibited slightly superior predictive performance compared to the Markov causal models for most analyzed traits (with an average PA of 0.24 for causal models compared to 0.27 for GBLUP). However, when analyzing BVs of individuals from generation 4 in the greenhouse, without phenotypic data, the GBLUP model displayed greater dispersion in predicted BVs compared to those obtained through the genomic Markov causal models. The Markov causal models developed in this study appear to be more “stable”, and, due to their lower computational burden, represent a potential alternative to classical non-causal GBLUP GS model employed in forest breeding programs.

Keywords: forest genetic evaluations, genomic selection, causal model, Eucalyptus grandis

Jurcic E, Dutour J, Villalba PV, Centurión C, Cantet RJC, Munilla S, Cappa EP. Genomic-enhanced Markov causal models for predicting breeding values in forest trees. Agrociencia Uruguay [Internet]. 2023 [cited dd mmm yyyy];27(NE2):e1264. Doi: 10.31285/AGRO.27.1264.