



IUFRO Conference 2023

Genomic prediction across generations in a *Eucalyptus grandis* breeding population

Rodríguez Raffo, M. V. ¹; Dutour, J. ²; Cappa, E. P. ³; Quezada, M. ¹

¹ Universidad de la República, Montevideo, Uruguay

² UPM Forestal Oriental, Paysandú, Uruguay

³ Instituto Nacional de Tecnología Agropecuaria (INTA), Buenos Aires, Argentina

Received 16 Aug 2023

Accepted 10 Sep 2023

Published 20 Nov 2023

Correspondence

María Virginia Rodríguez Raffo,
virginiarodriguezraffo@gmail.com

Forest genetic breeding programs are intricate, long-term, and costly processes. To overcome these limitations, genomic selection emerges as an important tool to enable shorter cycles through early selection and to increase breeding value accuracies. Genomic selection is based on a predictive model derived from a training population (TP), integrating genotypic, phenotypic, and pedigree data to predict breeding values on selection candidates (SP) based on genomic information. As breeding generations advance, the relatedness between the TP and SP decreases, with the reduction of the prediction ability. The objective of this study is to optimize the TP for a *Eucalyptus grandis* breeding population across four consecutive generations (G1, G2, G3, and G4). A population of 66,221 individuals (from four generations) resulting from cross-breeding and open-pollination were measured for diameter at breast height (DBH) and total tree height (HT). Wood quality traits were determined for 16,068 trees and assessed using Near-Infrared Spectroscopy (NIRS). A total of 3,221 individuals from the four generations were genotyped using the EUCHIP60K or the Euc72k Axiom Eucalyptus Genotyping Array. We compared the prediction ability using all the previous generations in the TP as opposed to only including the previous generation. Single-step GBLUP (ssGBLUP) models were evaluated in three phenotypic traits: volume, pulp yield, and wood density. The inclusion of all the previous generations provides a higher predictive ability of 0.40 and 0.54 for volume and pulp yield, respectively, in the target generation G4. When only the previous generation G3 was used as a TP, no significant differences in predictive abilities were observed for volume, and there was a slight decrease in pulp yield. In contrast, for wood density, the predictive ability was highest (0.37) in the G4 when the model was training with only the G3, while including all preceding generations decreased to 0.33. Our results provide insight into the optimization of TP across generations, encouraging the implementation of genomic selection in the *Eucalyptus* breeding program.

Keywords: genomic selection, training population, generations

