Agrociencia Uruguay 2023 | Volume 27 | Number NE2 | Article e1250
DOI: 10.31285/AGRO.27.1250
ISSN 2730-5066

IUFRO Conference 2023

Genomic selection comes to life: Unraveling its potential in an advanced four-generation *Eucalyptus grandis* population

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Received *08 Aug 2023*
Accepted *01 Sep 2023*
Published *20 Nov 2023*

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Genomic selection (GS) in tree breeding utilizes genomic information to accelerate genetic gains by reducing breeding cycle duration and concurrently minimizing the costs associated with phenotyping. By utilizing genomic predicted breeding values (GEBVs) to select young unphenotyped candidates, GS eliminates the need to wait for phenotypic observation of quantitative traits like yield, which typically take three to four years to mature in *Eucalyptus* breeding programs. The potential of GS in forest trees has been frequently assessed through measures as prediction accuracy or predictive ability, and evaluated by cross-validation analysis on available generations. However, it is crucial to validate predictions through experimental trials that examine the phenotypic values of genomically selected trees. Only then can accurate conclusions be drawn regarding the realized GS gain achieved. In this study, we validate the GEBVs for growth, wood density (WD), and pulp yield (PY) traits in a four-generation *Eucalyptus grandis* population. Utilizing the single-step genomic BLUP approach, we compared the GEBVs with conventional pedigree-based genetic values obtained from observed phenotypes (i.e., phenotypic selection, PS). Our training population consisted of three generations, including approximately 49,770 trees with recorded three-year growth traits, 10,579 trees with recorded wood quality traits, and 1,915 genotyped trees with 12,695 SNPs from the EUChip60K and Axiom Euc72K chips. Subsequently, we made predictions of GEBVs for 825 untested four-generation full-sib greenhouse trees (validation population). Among the top 11% trees with the highest GEBVs using GS (90 trees), 13 (14%) for growth, 14 (16%) for WD, and 33 (37%) for PY were correctly classified based on corresponding phenotypic traits (PS). However, among the top 18% (10 out of 55) full-sib families with the highest GEBVs, four families (40%) were identified and selected based on the respective phenotypes using PS. Moreover, out of the total 90 trees, which included the top nine trees from each of the top 10 GS families, the GS approach exhibited high selection rates. Specifically, the selection rates were 58% for growth, 71% for WD, and 67% for PY, resulting in the selection of 52, 64, and 60 trees, respectively. Despite challenges in accurately classifying individual trees, GS demonstrated its effectiveness in identifying and selecting high-performing full-sib families, as well as the best trees within these families. These results provide evidence of the potential of GS in tree breeding, and emphasize the importance of validating predictions through experimental trials across multiple generations to assess phenotypic values of genomically selected trees.

Keywords: realized genomic selection, breeding cycle duration, genomic breeding values, Eucalyptus grandis

Duarte D, Dutour J, Jurcic EJ, Villalba PV, Centurión C, Cappa EP. Genomic selection comes to life: Unraveling its potential in an advanced four-generation *Eucalyptus grandis* population. Agrociencia Uruguay [Internet]. 2023 [cited dd mmm yyyy];27(NE2):e1250. Doi: 10.31285/AGRO.27.1250.