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# Weighted genomic prediction for growth and disease resistant traits in a *Eucalyptus globulus* breeding population

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Genomic selection is becoming an efficient and effective tool to increase genetic gain per unit time in forest tree breeding. The single-step genomic best linear unbiased prediction (ssGBLUP) method has been widely used in forest trees because it can use the complete phenotypic and pedigree data, with the genotypic information of a subset of the population. However, ssGBLUP assumes that all single nucleotide polymorphisms (SNP) explain the same amount of genetic variance, which is unlikely for traits whose major genes are segregating. The weighted ssGBLUP (WssGBLUP) method allows the use of unequal variance or weights for SNP in the construction of the genomic relationship matrix. The purpose of this study was to improve the accuracy of ssGBLUP by using the WssGBLUP, which gives more weight to relevant markers, for growth (tree height and diameter at breast height) and disease resistance traits (defoliation, leaf spot severity, and change to adult foliage) in a *Eucalyptus globulus* population. The weights were obtained iteratively by a nonlinear method that resembles Bayes A (nonlinear A). This weighting procedure was evaluated and compared with the unweighted ssGBLUP. The data comprised 3,853 individuals from 194 open-pollinated families, 975 of them were genotyped using the EUChip60K SNP chip. A random fold validation strategy was performed to evaluate the predictive ability of each model. Thus, a random sample of 10% of the genotyped trees (partial set) was removed and they were predicted based on the remaining data. This procedure was repeated 100 times. The predicted ability was estimated as the ratio of accuracies, defined as the Pearson correlation between the average prediction of the complete data and the partial set. For all traits, the ratio of accuracies of the weighting method was higher than that of the unweighting procedure. The average ratio between accuracies using ssGBLUP varied from 0.52 to 0.73 and 0.69 to 0.85 for growth and disease-related traits, respectively. These ratios were further increased from 0.59 to 0.76 for growth traits, and from 0.73 to 0.87 for disease related-traits by using the nonlinear A method under the WssGBLUP model. Our findings indicate that WssGBLUP has the potential to increase predictive abilities in genomic evaluations of *Eucalyptus* breeding programs.

**Keywords**: genomic selection, WssGBLUP