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Realized accuracies of Genomic Selection for volume growth in tropical Eucalyptus: marker assisted selection coming to reality in forest trees

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Genomic selection (GS) involves selection decisions based on genomic breeding values estimated as the sum of the effects of genome-wide markers capturing most QTLs for the target trait(s). GS is revolutionizing breeding practice for complex trait in domestic animals. The same approach and concepts can be readily applied to forest tree breeding. Trees also have long generation times and late expressing traits. However the application of GS in forest trees has additional advantages: (1) large even-aged "discovery" populations can be easily assembled and accurately phenotyped; and (2) effective population sizes (N_e) can be tailored to specific breeding programs. Differently from association genetics that aims at dissecting complex traits in their discrete components, GS precludes the discovery of individual marker-trait associations and focuses on prediction of performance. We initially carried out a deterministic study to assess the impact of linkage disequilibrium (modeled by N_e and inter-marker distance), the size of the training set, trait heritability and the number of QTL on the predicted accuracy of GS (Grattapaglia and Resende, 2010). Results indicate that GS has the potential to radically improve the efficiency of tree breeding. The benchmark accuracy of conventional BLUP-based phenotypic selection (0.68) is reached by GS even at a marker density ~2 markers/cM when Ne ≤30, while up to 10 markers/cM are necessary for larger Ne. Shortening the breeding cycle by 50% with GS provides an expected increase ≥100% in selection efficiency. To validate these results we then carried out a large multi-population proof-of-concept study of GS in tropical *Eucalyptus*. De-regressed breeding values for height and DBH and genotypes at 3,129 DArT markers (a marker density of 2.4 marker/cM) were collected for 856 trees randomly sampled from a progeny trial with 58 full sib-families and N_e = 11. Discovery and validation were carried out with 700 and 156 individuals respectively. Average realized selection accuracies of 0.67 for height and 0.69 for DBH were obtained. Recent results from the analysis of a second independent population with a larger N_e (N_e=120), second generation hybrid composition, genotyped for >3,500 DArT markers, confirmed these very encouraging results. Realized accuracies of 0.60 were obtained for growth traits and wood density. In this scenario, gain in selection efficiency evaluated as the ratio of GS and phenotypic selection exceeds 350% by reducing breeding generation time from 8 to 2 years with early flower induction. To our knowledge these are the first experimental results of GS in forest trees and among the first public ones in plants in general. With the technological advances and declining costs of genotyping methods, our cautiously optimistic outlook is that GS has true potential to be implemented operationally and revolutionize tree breeding practice.