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High Realized Accuracies Of Genomic Selection For Volume Growth And Wood Density In *Eucalyptus* Breeding Populations With Contrasting Effective Sizes

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Genomic Selection (GS) will likely cause a paradigm shift in tree breeding due to the prospects of radically increasing gain per unit time and improving selection accuracy. Deterministic simulations show GEBV (Genome Estimated Breeding Values) accuracies matching or exceeding phenotypic BLUP-based-accuracy (0.68) even with low-density marker panels (2-3 markers/centiMorgan) in breeding populations with effective sizes $Ne \leq 60$. Furthermore, a GS-based reduction in breeding cycle time by 50% should provide a gain $\geq 100\%$ in selection efficiency for low heritability traits (Grattapaglia&Resende, 2010; DOI: 10.1007/s11295-010-0328-4). We now report on experimentally realized accuracies of GS for three key traits in *Eucalyptus* in two breeding populations (CEN and FIB) with contrasting effective sizes ($Ne= 11$ and $Ne= 120$). Genotypes at ~3,500 DArT markers and de-regressed phenotypes for Height (H), Diameter at Breast Height (DBH) and wood density (WD) (age 4yr.) were obtained for 783 and 920 random trees from CEN and FIB respectively. Sets of 700 and 838 trees for CEN and FIB were used for training and the remaining trees for validation in a jackknifing scheme. Realized GEBV accuracies for H, DBH and WD were 0.67,0.69 and 0.54 for CEN and 0.62,0.54 and 0.53 for FIB respectively. Accuracies matched and slightly surpassed expectations from simulations for FIB, possibly due to its hybrid composition. GEBV accuracies were low (zero to 0.18) across populations suggesting that population specific GS models will be necessary. These are the first experimental results of GS in forest trees and among the first public ones in plant breeding.