variation. Such associations will likely have to be "harvested" at the genome-wide level for multiple traits for translational genomics to effectively materialize. Genome-wide methodologies, precluding information on discrete marker-trait associations but instead incorporating all marker information into predictive models, have a greater probability of application, as biased marker effect estimates are avoided and variation due to small-effect loci is captured. Genomic Selection (GS) was introduced by Meuwissen *et al.*, and involves the simultaneous selection for thousands of markers so that most of the relevant genomic regions are expected to be in linkage disequilibrium (LD) with markers or haplotypes of markers. To validate GS in *Eucalyptus* we have initiated a proof-of-concept study involving three discovery populations, with effective population sizes (Ne) varying from 13 to 50 so that different extents of LD are evaluated, while adequate amounts of variation are maintained for sustained gains. Genotyping is carried out with DArT at a density <0.5 cM, targeting several silvicultural and wood quality traits. Our simulation studies indicate that for traits with h^2= 0.2, 50 loci controlling the trait(s), Ne=20 and genotyping density at <0.5 cM, selection accuracies ~80% are anticipated. The expectation is that GS in *Eucalyptus* could significantly reduce the time necessary to release elite clones.

Quantitative Genetics and Breeding

From phenotype dissection to genomic selection in *Eucalyptus* breeding

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Despite the major advances of forest tree genomics, its ultimate goal of contributing to a faster release of improved clones or populations is still a promise. Although an increasing number of marker-trait associations have been discovered, they typically explain only modest portions of the quantitative