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High-Density Diversity Arrays Technology (DArT) Genotyping For Cost-Effective Mapping And Genome-Wide Selection In *Eucalyptus*

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In spite of the recent advances in the theory and practice of association genetics in forest trees, the few marker-trait associations described are still too modest to impact breeding. It is thus becoming clear that single gene-trait association discovery will hardly be sufficient to improve complex traits. Future applications for complex traits improvement will likely focus on predictive methodologies. At the same time, genotyping is becoming cheaper than phenotyping. Opportunities abound for increasing gain per unit time in operational tree breeding. Genome-wide, high-throughput, and cost-efficient marker systems on a per sample rather than on per data-point basis are needed. In *Eucalyptus*, such systems could allow genome-wide selection approaches in dedicated hybrid breeding populations, focusing purely on prediction of performance, precluding gene-trait association discovery overall. To this end we have advanced towards an optimized DArT marker array for *Eucalyptus*. A first “discovery array” with 14,592 clones derived from 11 representations revealed 5,033 high quality markers, polymorphic between and within main plantation species and over 3,000 within a species. A total of 1,547 markers fitted a 1:1 pseudo-testcross segregation in a *E. grandis* x *E. urophylla* pedigree resulting in a first high density DArT linkage map for *Eucalyptus*. A preliminary redundancy analysis based on between-markers distance revealed 50% of apparently redundant score signatures. Validation by sequencing polymorphic DArT markers is underway, together with screening of new representations. These results indicate that the optimization of genome-wide DArT arrays for *Eucalyptus* species with several thousand polymorphic, non-redundant, sequenced and mappable markers is a feasible target.