GENOMICS TOOLS IN *Eucalyptus grandis*: DArT, SSR AND SNP FOR MAPPING AND BREEDING

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Genomic selection strategies, information coming from Quantitative Trait Loci (QTL) analysis and relatedness estimation were evaluated in *Eucalyptus grandis*. Genotyping was performed with panels of 15-20 SSRs (Simple Single Repeats), 384 SNPs (Single Nucleotide Polymorphisms) and 7680 DArTs (Diversity Array Technology). Phenotyping included physical and chemical properties of wood by Near Infrared reflectance and conventionally measurements of growth.

Genomic selection (Bayes Lasso) and multiple lineal regressions analysis (MLR) using significant QTL linked markers to growth and wood density were analyzed in a full-sib progeny trial of *E. grandis* for their prediction capability. For wood density BL performed better than MLR capturing other regions that QTL analysis did not. Also, a comparison of the performance of regression algorithms (reproducing kernel Hilbert space, RHKS and Random Forest regression, RFR) with classification methods (Random Forest Classification (RFC) and Support Vector Classification) were applied for separating two classes (best and worst candidates). For wood density RFC performed better than SVC-lin.

On the other side, the three different molecular markers were used to estimate relatedness between individuals in a small open pollinated progeny trial of *E. grandis* with limited pedigree information and/or few available parents instead of using pedigree matrix information. Estimated relatedness could be accurately inferred from co-dominant or sufficiently dense dominant molecular markers.