QTL MAPPING IN *EUCALYPTUS* USING PSEUDO-TESTCROSS RAPD MAPS, HALF AND FULL-SIB FAMILIES.

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ABSTRACT

The genus *Eucalyptus* includes the most widely used tree species for plantation establishment in tropical and subtropical regions of the world. Associations between molecular markers and quantitative trait loci (QTL's) could become a powerful tool in tree breeding to shorten breeding cycles, guide recombination and selection procedures. Particularly in *Eucalyptus*, linkage disequilibrium generated by hybridization coupled to high selection intensities and clonal propagation are conditions that would greatly favour the use of such strategies.

A pseudo-testcross mapping strategy was applied in conjunction with the high polymorphism detecting power of the RAPD (Random Amplified Polymorphic DNA) assay to construct linkage maps for single trees of two *Eucalyptus* species. At a LOD threshold of 5.0 the two maps have 242 markers on 14 linkage groups and 259 markers on 11 linkage groups respectively for *E. grandis* clone 44 and *E. urophylla* clone 28 (n=11 in *Eucalyptus*). A subset of evenly spaced markers that could be ordered at a 1000:1 odds established a framework map covering an estimated 96% of the genome at an average density of 11 cM.

One hundred and twenty individuals of the full-sib family used for map construction were clonally propagated and planted in a replicated trial in two locations. Height growth at 6 months and "in vitro" micropropagation ability will be evaluated in this population. A maternal interspecific half-sib family of the mapped *E. grandis* clone was analyzed at rotation age (6.5 years) in two locations in Brazil. The genetic architectures of traits with varying heritabilities are under investigation. These are wood specific gravity, volume growth and cellulose yield displaying high (0.9), medium (0.7) and low (0.4) broad sense heritabilities respectively. Simulations were used to determine statistical power for QTL detection under varying heritabilities, magnitude of QTL effect and sample sizes. A total of 1000 trees were measured for volume growth and harvested in each location. Disks at the DBH were taken on 400 trees for wood specific gravity and cellulose yield determination. Marker/Q ^{T}L, search is being carried out by a sequential approach including multiple bulks segregant analysis, selective individual genotyping and co-segregation analysis.

This within-half-sib approach for QTL mapping using diploid individuals is analogous to the analysis of haploid megagametophytes in conifers. Half-sibs are screened/genotyped for evenly spaced framework markers heterozygous on the maternal map. However, in the pedigree under study this approach is made even more powerful since our results show that the maternal markers are absent in the paternal pollen pool due to the genetic divergence of the two species. The pseudo-testcross mapping strategy and the approach to QTL search described should be widely applicable to any hardwood species with sufficient genetic heterogeneity. This project aims to test the feasibility of dissecting commercially important quantitative traits in fast growing *Eucalyptus* and determining the potential utility of molecular markers as a breeding tool for forest trees.