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Functional Variability Of Candidate Genes Involved In The Lignification Process In Eucalyptus

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Lignin quantity and quality (S and G monomers) are two major components of wood quality. Optimizing these traits for charcoal and pulp production in Eucalyptus can have enormous economical impact. In this context, our objective is to establish an efficient early selection procedure of superior trees for these two highly heritable traits using gene based markers. To this end, we first described the landscape of nucleotide diversity of structural and regulatory genes of the lignification pathway including CCR, CAD2, COMT2, C4H, F5H, 4CL, Myb2, and RAC1, in a sample of unrelated Eucalyptus urophylla and camaldulensis genotypes. Emphasis was given to the CCR gene for which 7 overlapping amplicons were cloned and sequenced to obtain the full length CDS. Results showed an important level of variability and a rapid decrease of linkage disequilibrium in both species. Second, association mapping was carried out in a factorial design comprising 300 progenies of E. urophylla. A significant association (controlled for multiple testing) between one SNP in the CCR gene and S/G ratio was obtained using a mixed-model.