Molecular Genetics of Cellulose Synthesis in Developing Wood of Loblolly Pine

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Cellulose is a major component of wood and wood fiber. The quantity, quality and deposition of cellulose in the secondary cell wall of vascular tissues determine a number of important wood fiber properties and consequently the suitability of wood and wood fiber for various uses. Recent progress in model plant systems has identified a number of genes necessary for cellulose synthesis, however, our knowledge of the molecular and cellular control of cellulose synthesis remains incomplete. Three genes or gene families directly involved in cellulose synthesis have been identified. These include the genes encoding the catalytic subunits of the cellulose synthesis complex, a membrane bound cellulase, and sucrose synthase.

The *CesA* multi-gene family encodes the catalytic subunits of the cellulose synthesis complex in plant cells. In angiosperms, two different groups, each containing three genes, are necessary for cellulose synthesis in the plant primary and secondary cell wall, respectively. The three secondary cell wall *CesA* genes are functionally non-redundant paralogs and all three are required for normal cellulose synthesis in vascular tissues as demonstrated by analysis of cellulose deficient mutants in *Arabidopsis*. Comparative analysis of the *CesA* gene families from monocot, herbaceous dicot, and woody perennial dicot species indicates that the secondary cell wall *CesA* genes in angiosperms are orthologous and functionally conserved. A specific member of the γ subfamily of the cellulase (endo-β-1,4-glucanase) multi-gene family, which contains a putative trans-membrane domain, is necessary for normal cellulose synthesis. A gene encoding this enzyme, *KORRIGAN*, was first identified in cellulose deficient mutants of *Arabidopsis*. Sucrose synthases are also encoded by a multi-gene family and are believed to supply the substrate, UDP-glucose, to the cellulose synthesis complex.

We have cloned full-length cDNA sequences representing three *CesA* genes from developing xylem of loblolly pine (*Pinus taeda* L.). Phylogenetic analysis indicates that these genes are orthologous to the secondary cell wall *CesA* genes of angiosperms. These three genes are co-expressed in loblolly pine tissues and higher levels of expression are correlated with tissues undergoing secondary cell wall biosynthesis. These data are consistent with conservation of functional roles for orthologous secondary cell wall *CesA* genes in angiosperms and gymnosperms, suggesting that the gene family and their functional roles evolved prior to the divergence of extant seed plant lineages. We have also isolated full-length cDNA clones for putative orthologs of the membrane bound cellulase and sucrose synthase from developing xylem of loblolly pine. Phylogenetic analysis indicates that these genes are orthologous to those implicated in cellulose synthesis of angiosperms. Preliminary data for expression of these genes are consistent with conserved functions for these components of cellulose biosynthesis in the secondary cell wall of loblolly pine during wood formation. These full-length cDNA clones will facilitate functional analysis and are potentially useful in developing markers for genetic selection strategies and/or cellulose modification through direct gene transfer.

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