

Wood formation in loblolly pine: Characterizing gene function in xylem morphogenesis

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The expansion of genomic resources for loblolly pine (*Pinus taeda*), and other plant species, enables comparative and functional genomic approaches for characterizing genes involved in xylem development. Comparative approaches using model plant species such as *Arabidopsis* and *Populus* can be used to identify candidate genes in loblolly pine. We conduct transcript profiling in developing xylem of loblolly pine by quantitative real-time RT-PCR (qRT-PCR) for preliminary validation of candidate genes. Unigene assemblies of genes that are expressed in xylem are used to design qRT-PCR arrays and conduct transcript profiling in loblolly pine tissues, including paired xylem and phloem samples. We employ comparative phylogenetic analysis to infer homology between pine genes and members of the corresponding gene families in other plant taxa, including relationships to clades within gene families that have been implicated in specific functions during plant development. We have identified homologs in loblolly pine of glycosyl transferases (GT) and glycoside hydrolases (GH) implicated in plant cell wall biosynthesis as well as transcription factors implicated in vascular development and characterized their expression in developing xylem. A subset of the identified GTs and GHs exhibit patterns of expression that are consistent with a role in cell wall biosynthesis during xylem development and profiles of genes encoding transcription factors are consistent with a role for specific gene family members in vascular tissue development. Orthologous relationships between specific pine genes and genes from *Arabidopsis* can also be inferred from gene phylogenies. These include genes for which specific functions in cell wall biosynthesis have been demonstrated in other species and therefore are candidates for functional studies examining wood formation in conifers. One such gene, *FRA8*, a member of the GT47 family is necessary for normal xylan synthesis in cell walls of *Arabidopsis*. A loblolly pine ortholog of *FRA8*, *PtaGT47c*, transformed into the *Arabidopsis fra8* line complements the mutation and restores normal levels of xylan in stem cell walls. These observations indicate that some orthologous genes are functionally conserved in conifers and angiosperms. These studies also demonstrate that heterologous angiosperm systems have potential applications for functional characterization of loblolly pine genes and dissecting gene function in wood formation.

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