

## IDENTIFYING PROTEIN-DNA INTERACTIONS INVOLVED IN WOOD DEVELOPMENT IN POPLAR

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Trees are unique among plants since they have extremely long life spans and have the ability to generate large quantities of woody biomass resulting from the formation of secondary xylem formed by the vascular cambium. The composition of xylem and the arrangement of cell types determine the physical and structural properties of wood. Gene-specific transcription factors (TFs) are DNA-binding regulatory proteins capable of either activation or repression by binding to a specific region of DNA, normally located in the 5-prime upstream region of the gene. These Protein-DNA interactions are responsible for gene expression during plant growth and development. One method for altering lignin composition is by manipulation of TFs involved in lignin biosynthesis. By using data from tissue specific *Populus trichocarpa* micro-arrays, TFs expressed 4 fold or greater in a xylem-biased manner are being used to screen for interactions with specific promoter sequences. The 1700-bp promoter region for the lignin biosynthesis enzymes caffeic-acid methyl transferase (COMT), and hydroxycinnamoyl transferase (HCT) were screened against a mini-library composed of 40 xylem-biased TFs in a Gateway-Compatible Yeast One-Hybrid (Y1H) assay to screen for Protein-DNA interactions. Results indicate transcriptional regulation by TFs from both the MYB and Zinc-finger families are involved in regulation of lignin biosynthesis. Subsequent transient assays in *Nicotiana benthamiana* have resulted in confirmation for some of these interactions based upon reporter GUS staining level when compared to background. Novel interactions are currently being characterized *in planta* by ectopic expression and RNAi mediated gene-silencing.