



# Genome-wide transcriptional profiling reveals molecular signatures of secondary xylem differentiation in *Populus tomentosa*

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**ABSTRACT.** Wood formation occurs via cell division, primary cell wall and secondary wall formation, and programmed cell death in the vascular cambium. Transcriptional profiling of secondary xylem differentiation is essential for understanding the molecular mechanisms underlying wood formation. Differential gene expression in secondary xylem differentiation of *Populus* has been previously investigated using cDNA microarray analysis. However, little is known about the molecular mechanisms from a genome-wide perspective. In this study, the Affymetrix poplar genome chips containing 61,413 probes were used to investigate the changes in the transcriptome during secondary xylem differentiation in Chinese white poplar (*Populus tomentosa*). Two xylem tissues (newly formed and lignified) were sampled for genome-wide

transcriptional profiling. In total, 6843 genes (~11%) were identified with differential expression in the two xylem tissues. Many genes involved in cell division, primary wall modification, and cellulose synthesis were preferentially expressed in the newly formed xylem. In contrast, many genes, including *4-coumarate:cinnamate-4-hydroxylase (C4H)*, *4-coumarate:CoA ligase (4CL)*, *cinnamyl alcohol dehydrogenase (CAD)*, and *caffeoyl CoA 3-O-methyltransferase (CCoAOMT)*, associated with lignin biosynthesis were more transcribed in the lignified xylem. The two xylem tissues also showed differential expression of genes related to various hormones; thus, the secondary xylem differentiation could be regulated by hormone signaling. Furthermore, many transcription factor genes were preferentially expressed in the lignified xylem, suggesting that wood lignification involves extensive transcription regulation. The genome-wide transcriptional profiling of secondary xylem differentiation could provide additional insights into the molecular basis of wood formation in poplar species.

**Key words:** Wood formation; Affymetrix microarrays; Secondary xylem differentiation; Lignified xylem; Vascular cambium; Newly formed xylem