MOLECULAR CHARACTERIZATION OF A HYBRID POPLAR CLONE TRANSFORMED WITH A TYROSINE-RICH CELL WALL GENE FOR IMPROVED SUGAR RELEASE

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To facilitate lignin removal and potentially advance the utilization of woody biomass as a biofuel feedstock, we previously transformed a hybrid poplar clone with a hydroxyproline-rich glycoprotein encoding gene from parsley. While our previous results suggested that the TYR transgenic plants had no significant change in total lignin content or overall morphological characteristics when compared to the wild types, a number of transgenic lines released more polysaccharides with protease digestion, and in addition were more flexible than wild type plants, as measured by storage modulus assays. In this report, gene expression studies were conducted using whole genome DNA microarrays to examine the molecular basis for the flexibility and digestion phenotypes observed in the previous study. Microarray data revealed a total of 102 differentially expressed transcripts in transgenic lines. All 102 transcripts were decreased in expression in TYR plants. The lignin biosynthetic pathway was most affected, with four genes encoding three enzymes (cinnamoyl CoA reductase, hydroxycinnamoyl-CoA transferase, and laccase) being significantly down-regulated. Transgenics also showed reduced expression of genes involved in other branches of phenylpropanoid metabolism, amino acid metabolism, and defense. Transcription factors, as well as genes involved in macromolecule catabolism, reassembly, and polysaccharide synthesis were also repressed in expression. Validation experiments by qRT-PCR indicated an average of 72% of the 20 genes chosen were down regulated in three transgenic lines used in the microarray experiments. Our results provide the first gene expression evidence for the basis of the flexible and degradable cell wall phenotype obtained in the transgenic poplar plants.