

Manipulating Lignin Biosynthesis to Maximize Ethanol Production from *Populus*

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Statement of Problem:

High gasoline prices, global warming, national security, and the limitations of global petroleum resources have reinvigorated worldwide interest in renewable resources as a feedstock for liquid transportation fuels, particularly those derived from cellulose. As a perennial woody plant, hybrid poplar (genus *Populus*) offers several advantages with regard to cellulosic biofuel production including rapid growth rates, the ability to cycle nutrients, a wide geographic distribution, genetic diversity, amenability to genetic engineering, and abundant genomic resources. The phenolic cell wall polymer lignin constitutes a significant barrier to biomass conversion but, at the same time, it is essential to normal plant growth and development. Recent advances in our understanding of how lignin monomers are synthesized provide us with an opportunity to modify the content and composition of the lignin polymer. The research to be conducted will enable us to rationally assess the cost savings that could result from using genetically engineered poplar, instead of corn, as a feedstock for producing biofuels.

Current Activities:

The expression of four enzymes in the lignin biosynthetic pathway will be up- and/or down-regulated. For each DNA construct, poplar cDNA has been synthesized from young shoot RNA using reverse transcriptase and PCR-amplified with gene-specific primers developed based on conserved regions within the genes' sequences identified from the poplar genome, the *Arabidopsis* genome, and other plant sequences. All constructs are now being transformed into clone NM-6 (*Populus nigra* x *P. maximowiczii*) using an *Agrobacterium*-mediated transformation protocol.

Goals:

1) Generation of transgenic poplar up- or down-regulated for four enzymes known to impact lignin quantity and quality; 2) Development of metabolic profiling methods for poplar and their application to greenhouse- and field-grown wild-type and transgenic plants; 3) Morphometric analysis of transgenic lines grown in field plots; and 4) Cell wall deconstruction analysis of wild-type and lignin-modified transgenic lines.