Tailoring Biomass for Catalytic Conversion to Biofuels and Bio-based Products

Nicholas C. Carpita¹ and Maureen C. McCann²

¹Department of Botany & Plant Pathology, and ²Department of Biological Sciences, Purdue University, West Lafayette, Indiana, U.S.A. 47906-2054

Second-generation biofuels will be derived from lignocellulosic biomass using biological catalysis to convert carbon in plant cell wall polysaccharides to ethanol or other biofuels. However, fermentation processes are both carbon- and energy-inefficient, and the lignin interferes with the access of hydrolytic enzymes to the polysaccharides. The Center for Direct Catalytic Conversion of Biomass to Biofuels (C3Bio), a DOE-funded Energy Frontier Research Center, comprises an interdisciplinary team of plant biologists, chemists and chemical engineers who are developing processes to enable the catalytic transformation of cellulose, xylans and lignin into biofuels and bio-based products. By integrating biology, chemistry and chemical engineering, we are learning how to use genetic resources to tailor biomass for physical and chemical conversion processes. Grass species hold the highest potential as annual feedstocks for biofuel production. We have classified the major genes and gene families of maize and sorghum involved in cell wall biology. Analysis of transcripts generated by deep sequencing for cell wall genes in developing maize stem revealed distinct expression patterns within families and at specific stages of development corresponding to cell division, cell elongations, secondary wall deposition and lignification. Dynamics of small regulatory RNA profiles representative of these stages reveal genes of common regulation. We also high throughput means to quantify relative abundance of characteristic carbohydrate and aromatic constituents of the grass cell walls in recombinant inbred lines to identify quantitative trait loci corresponding abundance of pentose and hexose residues, acetylated xylans, hydroxycinnamic acids, and G:S lignin. We are extending this study to the nested association mapping (NAM) populations to capture the broadest diversity of maize for optimizing quantity and quality of lignocellulosic biomass that is readily translatable to other closely related energy grasses. Thus, gene discovery of biomass traits in bioenergy grasses serve as the knowledge base for the tailoring of biomass for catalytic conversion to high-value bio-based products.

Supported by U.S. Department of Energy, Office of Science, Office of Basic Energy Sciences and Biological and Environmental Research programs, and the National Science Foundation, Emerging Frontiers in Research and Innovation program This document was created with Win2PDF available at http://www.win2pdf.com. The unregistered version of Win2PDF is for evaluation or non-commercial use only. This page will not be added after purchasing Win2PDF.