Redesigning the plant cell wall for conversion of biomass to biofuels and high-value products

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Cellulose, xylan and lignin are the principal macromolecules of lignocellulosic biomass in bioenergy crops, such as grasses and fast-growing trees. Optimization of biomass yield and quality is predicated by the ability of these plants to capture partially reduced carbon from these macromolecular structures and convert it to biofuels and high-value chemicals. Lignin abundance is considered to be a major barrier to the enzymatic digestion of cellulose from biomass to fermentable sugars, contributing greatly to the general property of recalcitrance. Genetic redesign of the lignin networks simplifies its cell wall architecture to enable facile catalytic disassembly and conversion of aromatics. However, our analysis of biomass from maize represented in populations that capture the large range of natural genetic diversity, show that lignin abundance or quality is not strictly correlated with increased saccharification yields. We have identified several candidate genes that contribute to cell wall architecture beyond those related to lignin deposition. Recalcitrance is also conferred by the crystallinity of cellulose microfibrils. A deuterium-tagging method will be described that determines the size of microfibrils and the amount of amorphous cellulose in genetic variants and in the type of biomass pretreatment employed. Our efforts towards solving the 3-dimensional structure of plant cellulose synthase proteins will permit new ideas about molecular re-design of cellulose less recalcitrant to processing.

Supported by the Center for Direct Catalytic Conversion of Biomass to Biofuels (C3Bio), an Energy Frontier Research Center funded by the U.S. Department of Energy, Office of Science, Office of Basic Energy Sciences, Award Number DE-SC0000997