A Dominant Approach to Reduce Xylan in Bioenergy Crops

Andrew G. Brandon*[1,2] (abrandon@lbl.gov), Devon Birdseye[2], **Henrik V. Scheller**[1,2]

[1]Department of Plant and Microbial Biology, University of California, Berkeley, CA 94720, USA ; [2]Feedstocks Divison, Joint BioEnergy Institute, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA

http://www.jbei.org

Project Goals: Increase the C_6:C_5 sugar ratio and improve the quality of biomass by suppressing xylan biosynthesis in a wild-type background

Xylan is the most abundant non-cellulosic polysaccharide in plant biomass and one of the most abundant biopolymers on earth. The xylan backbone is a homopolymer of β-(1,4)-linked xylose, decorated at regular intervals with GlcA, 4-*O*-MeGlcA and acetyl groups. As a hemicellulose, xylan coats and crosslinks cellulose microfibrils, promoting their crystallinity. Indeed, xylan is critical for the overall health and mechanical strength of the plant. Xylan biosynthesis mutants are severely dwarfed due to cell wall collapse in the water-conducting xylem vessels. While important, the relatively high amount of xylan in plant biomass creates several problems for the development of advanced biofuels. Xylose, a 5-carbon sugar, is poorly utilized by microorganisms and strongly inhibits the fermentation of 6-carbon sugars like glucose. Additionally, the acetate released from the xylan backbone creates a toxic environment for microbial growth. Any way to reduce the amount of xylan in plant biomass will significantly reduce the cost and enhance the efficiency of conversion to biofuel and bioproducts. Since few mutants of important biomass crops exist, the ideal approach would act as a dominant suppressor of xylan biosynthesis. This has been accomplished by identifying potential catalytic residues in the xylan biosynthetic enzyme IRX10 and mutating them. Overexpression of the mutated IRX10 outcompetes the native form of the enzyme, suppressing the biosynthesis of the polymer.