Systematic Characterization of Glycosyltransferases Involved in Plant Cell Wall Biosynthesis

Henrik Vibe Scheller[*1], Ai Oikawa[a], Lan Yin[1,2], Eva Knoch[1,2], Naomi Geshi[2], Carsten Rautengarten[1], Yuzuki Manabe[1], Chithra Manisseri[1]

[1] Feedstocks Division, Joint Bioenergy Institute, Emeryville, California.

[2]Department of Plant Biology and Biotechnology, University of Copenhagen, Denmark

*hscheller@lbl.gov

www.jbei.org

The goals of the project are to provide a detailed understanding of the enzymes that are responsible for biogenesis of the plant cell wall and develop a knowledgebase to enable generation of crop plants with improved properties as feedstocks for biofuel production.

Plant cell walls are composed mainly of polysaccharides and production of biofuels from biomass requires decomposition of the polymers. Many of the polymers are recalcitrant to degradation and they are composed of sugars that are not optimal for fermentation. Better understanding of the biosynthesis of the cell wall polysaccharides may enable development of crops with improved properties as biofuels feedstocks. Despite rather detailed information on the structure of the cell wall polysaccharides, little is known about their biosynthesis. The key enzymes are glycosyltransferases (GTs) and plants need a large number of GTs to synthesize the complex polysaccharides present in the walls. However, only a few GTs have had their activity demonstrated. In Arabidopsis thaliana, approximately 450 GT genes have been identified based on their sequence and deposited to the CAZy database (www.cazy.org). We have cloned a large number of these GTs in Gateway vectors in order to heterologously express the GTs and characterize their activity. Systematic analysis of the GTs is in progress and results will be presented. Agrobacterium-mediated transient expression in Nicotiana benthamiana has a high success rate for expression of GTs.

An alternative way to elucidate the function of GTs and other biosynthetic enzymes is to study the effect of downregulating or inactivating the corresponding genes. This approach is often hampered by the overlapping function of many GTs. Generation of mutants that are affected in several homologous genes can overcome this limitation. In other cases, GTs are functioning in complexes that contain several different polypeptide subunits. The CslD family of proteins provides examples of both redundancy in function and of protein complexes.