BIOMASS BIOLOGY

Understanding the regulation of secondary cell wall synthesis in Arabidopsis

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While cellulosic ethanol may have potential as a long term sustainable source of biofuels with low net CO_2 emissions there are formidable technological barriers to realising its potential. A recent report divides the process into three parts: generation and composition of the starting material (feedstock), breaking down this material to efficiently and cheaply to release the constituent sugars (deconstruction) and the generation and separation of the ethanol (fermentation/recovery). There are two particular problems to the efficient utilisation of plant cell wall material. Firstly, the heterogeneous starting material that contains a mixture of complex polysaccharides and cross-linked phenolic compounds limit accessibility to compounds such as cellulose. Secondly, all different stages of feedstock composition, deconstruction and fermentation are all intimately linked. Given the complexity of the process it would obviously be preferable to make only carefully selected alterations in cell wall composition and use this information to make informed choices about pre-treatment, wall digestion and processing.

Plant secondary cell walls (SCWs) constitute the majority of plant biomass, they represent more than 70% of the dry weight of the plant even in small perennials such as Arabidopsis and a much higher proportion in woody species such as willow, poplar and pines. SCWs are dominated by three major components: cellulose microfibrils, hemicellulose (usually xylan) and phenolic (including lignin). Although a number or targets for improved feedstock composition have been identified, the problem is an astonishing lack of understanding of what regulates cell wall biosynthesis. We do not know what controls the amount of cellulose a plant makes, what controls the frequency of polysaccharide branching, which enzyme catalyse the addition of acetate groups to what extent phenolics other than lignin are important for cell wall integrity and how changes in cell wall composition affect the mechanical properties of the wall and their ability to function within the plant. To address these problems we have been using a combination of expression profiling and reverse genetics using Arabidopsis. While it is easy to identify several hundred genes expressed during secondary cell wall formation we only know the function of a very few of them. We are currently using a combination of reverse genetics, metabolic fingerprinting and cell wall analysis to group these genes into different metabolic pathways, understand the function of these pathways and understand how these pathways are interrelated. Answering these questions will facilitate a more rationale approach to engineering cell wall composition for optimal utilisation as biofuels. Our progress in addressing these issues will be illustrated with examples from the xylan and cellulose biosynthesis pathways.