

Application of plant genomics to enhance ethanol production from biomass crops

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There has been a growing interest in the production of transportation fuels from renewable resources as a result of political and environmental concerns. In the United States the majority of fuel ethanol is currently produced from microbial fermentation of sugars derived from the enzymatic hydrolysis of corn starch. Grain supplies will, however, be insufficient to meet anticipated demands of ethanol. Alternative crops that can be used for ethanol production include species that produce sugar such as sugar cane, sweet sorghum, and sugar beet, as well as crops that produce large amounts of vegetative biomass. Vegetative biomass, such as corn and sorghum stover, consists largely of plant cell walls. The plant cell walls is a complex matrix that contains the polysaccharides cellulose and hemicellulose, as well as the phenolic polymer lignin, hydroxycinnamic acids, pectin, and proteins. Enzymatic hydrolysis of lignocellulosic biomass results in the formation of monomeric sugars that can be fermented by microorganisms to ethanol or other chemical feedstocks. While production of so-called cellulosic ethanol from stover is feasible from an energy balance perspective, its production is currently not economically competitive. Along with improvements in bioprocessing, enhancing the yield and composition of the biomass has the potential to make ethanol production considerably more cost-effective.

In order to enhance biomass crops, it will be necessary to obtain a better understanding of how cell wall composition and structure affect the efficiency of enzymatic hydrolysis. It will also be necessary to identify and develop traits that enhance biomass conversion efficiency and increase biomass yield. This process can be expedited through the development of rapid screening protocols to evaluate biomass conversion efficiency.

Several genetic resources are available to improve corn and sorghum as sources of lignocellulosic biomass. This includes the use of existing mutants, forward and reverse genetics to obtain novel mutants, and transgenic approaches in which the expression of genes of interest is modified. Plant breeding can be implemented to improve biomass yield, biomass quality, and biomass conversion efficiency, either through selection among progeny obtained by crossing parents with desirable traits, or as a way to enhance the agronomic performance of promising mutants and transgenics.

This presentation will focus on the identification of novel cell wall mutants of corn. A high-throughput screen aimed at the identification of changes in chemical composition was developed to evaluate a large population of genetically uniform corn families in which mutations were introduced through the action of transposable elements. A set of 39 mutants with so-called spectrotypes, but otherwise no distinct visual phenotype were identified, and some of these mutants look promising with respect to cellulosic ethanol production.

This presentation will also focus on the development of *brown midrib* sweet sorghum as a dual-source feedstock for ethanol production. Under this scenario sugar-rich juice from the stalk will be directly processed into ethanol through microbial fermentation, while the sorghum bagasse is processed for the production of cellulosic ethanol. The *brown midrib* trait enhances the yield of cellulosic ethanol because hydrolysis of the resulting bagasse yields more fermentable sugars. We are using comparative genomics approaches and the recently released sorghum genome sequence to identify and isolate the genes underlying these useful traits. The genetic variation is then exploited for the development of allele-specific molecular markers that can expedite plant breeding efforts.