118. Candidate Gene Discovery and Validation by Analysis of Natural Variation for Cell Wall Compositional Traits in Maize

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Goals: The main goal of this project is to utilize naturally occurring genetic variation in maize as a gene discovery tool to identify novel genes that are associated with cell wall compositional traits and therefore potentially reduce plant biomass recalcitrance.

Maize is a relevant source of biomass for biofuel production in the near term, and also an important model for other biofuel feedstock grass species. Our project exploits naturally occurring phenotypic variation for non-grain biomass traits in maize coupled with extensive genetic information to identify novel genomic regions that can reduce biomass recalcitrance. We have evaluated cell wall bound glucose and pentose release from cores taken from the second lowermost stalk internode of 563 diverse maize inbred lines using an automated digestibility platform. These inbred lines were evaluated in 2010, 2011 and 2012 in field experiments with a randomized complete block design and two replications per year. Three representative plants per genotype and field replication were sampled each year.

We observed significant genetic variation for both traits ranging from 4.1 to 20.2 % of sugar per mg dry biomass for glucose and 1.2 to 9.02 for pentose release across genotypes. The genetic basis of these traits was analyzed using a set of 438,222 single nucleotide polymorphisms in a genome wide association study. We identified natural alleles of different genes that are promising candidates to alter biomass digestibility. Based on their biological relevance and expression profiles, genes were prioritized for validation. These candidates are annotated as having a role in xylan biosynthesis and nuclear processes that relate to cell wall biosynthesis. Our current focus is on using transgenic plants and transposon alleles to further explore the potential of these genes in reducing biomass recalcitrance.

This work was funded by the Department of Energy Great Lakes Bioenergy Research Center (DOE BER Office of Science DE-FC02-07ER64494).