Genetic and Environmental Contributions to Switchgrass Biofuel Traits

Acer VanWallendael[1,2,*] (vanwaax07@gmail.com), Rebecca G. Ong,[3] Laura E. Bartley,[4] Li Zhang,[5] Jason Bonnette,[5] Robert B. Mitchell,[6] Thomas E Juenger,[5] and **David B. Lowry[1,2]**

[1]Great Lakes Bioenergy Research Center, Michigan State University, East Lansing, MI; [2]Department of Plant Biology, Michigan State University, East Lansing, MI; Department of Chemical Engineering, Michigan Technological University, Houghton, MI; [4]Department of Microbiology and Plant Biology, University of Oklahoma, Norman, OK; [5]Department of Integrative Biology, The University of Texas at Austin, Austin, TX; [6] USDA-ARS Wheat, Sorghum, and Forage Research Unit, University of Nebraska, Lincoln, NE

Project Goals:

1. Quantify traits associated with biofuel yields from switchgrass across environmental conditions.
    a. Using controlled digestion, quantify the yield of glucose and pentose sugars from three clonally replicated field plantings in Texas, Missouri, and Michigan
    b. Using Near-infrared spectroscopy (NIRS), estimate several key compounds in switchgrass biomass for switchgrass planted in eight field sites in Texas, Oklahoma, Missouri, Nebraska, Kansas, and Michigan.
2. Elucidate the genetic architecture of biofuel traits.
    a. Using quantitative trait locus (QTL) mapping, identify loci associated with important biofuel traits across field sites.
3. Evaluate the degree to which traits vary across different environmental conditions.
    a. Quantify how QTL effects for biofuel traits vary across space to evaluate genotype x environment (GxE) interactions.

Abstract

A key to successful bioenergy production will be economically efficient decomposition and conversion of biomass to liquid fuels. Unfortunately, recent research suggests that environmental variation in growing conditions can alter biomass in way that can interfere with decomposition and conversion. Therefore, it will be necessary to understand how both genotype and environmental variation in feedstock crops contributes to variation in traits associated with cell wall digestibility as well as influences downstream decomposition and conversion processes.

In this study, we evaluated digestibility and cell wall traits for a switchgrass genetic mapping population planted at multiple locations throughout the central United States, from Texas to Michigan. We used two complementary techniques to evaluate key traits of switchgrass biomass collected from each site. The first technique, digestibility analysis, involved controlled digestion of switchgrass biomass followed by the quantification glucose and pentose sugar yields. The second technique, NIRS (Near-infrared spectroscopy), uses calibrated spectral data from NIR light to infer chemical composition of a sample for a number of important compounds, including nitrogen, ethanol, calcium, and several types of sugars. For each of the quantified traits, we

conducted QTL mapping to understand the genetic architecture underlying variation in each trait. Because traits had been scored at multiple field sites, we were also able to identify QTL x Environment interactions contributing to trait variation. We performed controlled digestion for plants at three sites and NIRS analysis at eight field sites.

For the digestibility analyses, we identified one QTL for glucose yield, and three pentose yield QTLs, all three of which had significant interactions with the environment. For the NIRS analysis, we faced challenges in the calibration of several compounds. Using the measure of divergence between spectra (global H), traits deviated significantly from switchgrass biomass calibrations ($H > 3.0$). Therefore, we used the general calibrations for forage biomass to calculate compound concentrations. Overall, we mapped twenty NIRS QTLs for biomass collected in the middle of the season, and 27 for biomass collected at the end of season. Importantly, nearly all of the QTLs had significant GxE. Further, while several traits showed significant QTLs at both mid- and end-season timepoints, the majority only were detected at one of the two time points. This suggests that phenology plays an important role in the chemical composition of switchgrass biomass.

Overall, our results indicate that there is significant genotype, environment, and genotype x environment effects on key traits that will influence decomposition and conversion of switchgrass feedstocks to liquid fuels. Thus, researchers using switchgrass biomass should expect geographic and genetic variation in chemical composition that may impact downstream biofuel yields. We are currently in the process of determining the extent to which these sources of variation contribute to those downstream decomposition and conversion processes.

Funding statement:

This work is supported by the Great Lakes Bioenergy Research Center, U.S. Department of Energy (DOE), Office of Science, Office of Biological and Environmental Research under Award Number DE-SC0018409. Additional funding was provided by a DOE Sustainability grant under Award Number DE-SC0014156.