

Environmental and Genetic Effects on Switchgrass (*Panicum virgatum*) Biomass Composition across Diverse Environments

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Project Goals:

- **The long-term objective of this project is to develop switchgrass with consistently high cell wall composition across diverse growing environments to promote efficient and sustainable biorefining.**
- **Here, we aim to:**
 - **Understand how growth environment effects switchgrass composition**
 - **Identify switchgrass genomic loci that influence composition and that are or are not dependent on the environment**

Abstract: Biorefining of lignocellulosic material can reduce dependence on fossil sources of fuels and chemicals, thereby mitigating global climate change. Because lignocellulosic compositional traits influence efficiency of biorefining the long-term goal of this research is to identify genes for optimizing switchgrass lignocellulosic composition across diverse growth environments. Here we present the composition and quantitative trait loci for a switchgrass mapping population grown at 10 sites spanning 14 degrees of latitude in the USA. The mapping population was constructed from a cross of four grandparents, two from the upland ecotype and two from the lowland ecotype. Lignocellulosic composition (e.g., lignin, ash, nitrogen, in vitro dry matter digestibility, etc.) was predicted from near-infrared reflectance spectroscopy for ~11K samples from mid- and end-of-season 2016 harvests. Growth location affected compositional traits significantly, but not with a simple latitudinal pattern. Heritability (h^2) of composition traits was <0.5 depending on the location, with higher heritability typically at the end-of season harvest. For a subset of traits, we identified 119 quantitative trait loci (QTL), 21 of which overlapped between the mid and end-of-season, and several of which controlled multiple traits. About 40% of QTL did not show genotype by environment interactions and thus are of major interest for genes that can improve composition across diverse environments. Lowland alleles increased lignin and ash per g dry matter more than upland alleles; whereas, upland alleles increased digestibility and nitrogen. Integration of these results with gene expression and other population genetic analyses will help to identify causative

alleles for improving biorefining and may reveal more about the agronomic consequences of variation in lignocellulose towards mitigating these effects.

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