

**Title:** Modeling Environmental Influences on Biomass Composition of Diverse Switchgrass Genotypes

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**Project Goals:** This project aims to understand the environmental and genetic influences on switchgrass composition towards increasing sustainability of switchgrass production for biorefining by developing generalist and specialist plant ideotypes that maximize biomass yield and composition, stress tolerance, and carbon sequestration capacity.

**Abstract Text:** Biomass composition influences biorefining yield and conversion efficiency. Towards optimizing composition and related physiological traits of switchgrass, this project seeks to understand the genetic and environmental determinants of switchgrass biomass composition. Switchgrass consists of multiple ecotypes, akin to races, that possess distinctive phenotypes. Compared to the northern upland ecotype, the southern lowland ecotype is characterized by greater biomass production but reduced abiotic stress tolerance, and in some studies, compositional differences, including lower lignin, ash, and nitrogen content. Here we report results of ten near-infrared reflectance spectroscopy-predicted cell wall composition traits, including in vitro dry matter digestibility (IVDMD), lignin, glucan and xylan, for F<sub>2</sub> plants of a cross of lowland and upland genotypes grown in common gardens at 10 sites across central North America. For biomass harvested at the end of the season, all trait means varied significantly among genotypes and locations, though heritable variation was only 20-40% on average. Still, we found a total of 68 quantitative trait loci (QTL) across all traits, of which 47 QTL (70%) showed gene-by-environment (Gx E) interactions, meaning that the magnitude of the QTL effects varied with location. Several QTL were pleiotropic. Consistent with single loci controlling multiple traits, we found many strong negative and positive genetic correlations. In contrast to the phenotypic correlations, which except for those with xylan were fairly strong and consistent across sites, genetic correlations often varied, even showing different signs at different sites. For example, glucan was positively genetically correlated with IVDMD at most sites, but negatively correlated at two southern sites. This is consistent with the strong environmental influence on composition. To better understand the components of the environment that influence composition, we are

conducting a meta-regression analysis of weather on trait variation across sites using principal components (PCs) of seven weather statistics (e.g., coldest, warmest, driest, and wettest 14-day spans) in each of three intervals of the growing season. Across all modeled genotype groups, variation in xylan was highly influenced by weather PC1; but for most traits, models of the influence of weather on composition greatly varied with genotype. In one F<sub>0</sub> lowland genotype, WBC, 48% of the total weather variation (PC1 and PC4) explained lignin, which was mutually exclusive with the 25% of the variation (PC2 and PC6) that explained glucan. On the other hand, for the F<sub>0</sub> upland genotype VS16, lignin was not significantly influenced by PC1 (38% weather variation). WBC lignin was highly positively related to the mean daily minimum temperature and negatively related to the driest span; whereas, glucan was highly positively related to precipitation in the wettest spans. Understanding the interaction of climatic drivers with genetic covariance and QTL that are antagonistic across sites may help to minimize composition tradeoffs. Thus, this study provides insights and expands the foundation for optimal manipulation of cell wall chemistry to improve biorefining.

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