QTL x Environment Interactions in Switchgrass (*Panicum virgatum*)

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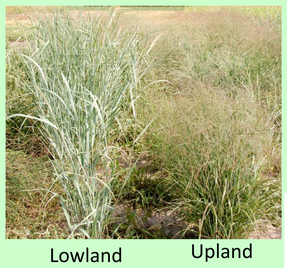
Genetics of Divergence in Upland and Lowland Switchgrass

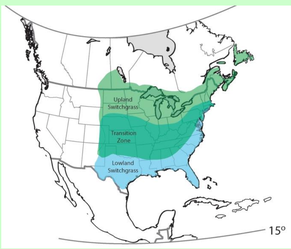
Understanding the genetic basis of local adaptation is a key goal in modern evolutionary biology and is important for plant breeding. Switchgrass (*P. virgatum)* is a C4 perennial grass, native to most of the US. It is also a USDA designated bioenergy feedstock. Variation observed between northern upland and southern lowland ecotypes of switchgrass has been shown to be adaptive.

We have developed a genetic mapping population that captures variation observed between upland and lowland ecotypes to study the underlying genetic architecture of locally adaptive traits. For example, upland and lowland switchgrass differ in a number of critical traits including flowering time, tillering architecture, leaf traits, rust susceptibility, and belowground rooting characteristics. The mapping population is derived from a balanced 4-way outbred cross between well known tetraploid accessions Alamo (lowland), Dacotah (upland), Summer (upland) and one lowland wild cultivar from Austin, TX.



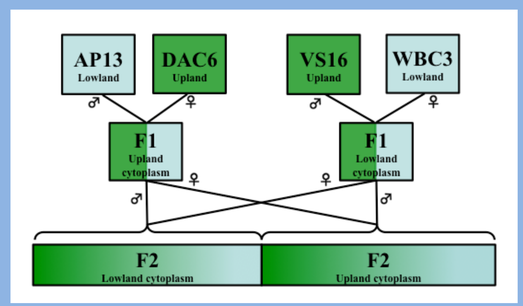
Lowland Ecotype | Upland Ecotype

Switchgrass genotypes and range distribution (from Casler et al 2011)



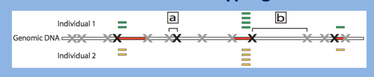
Outbred Genetic Mapping Resources

The mapping population is derived from a balanced 4-way outbred cross between well known tetraploid accessions Alamo (lowland), Dacotah (upland), Summer (upland) and one lowland wild cultivar from Austin, TX. The mapping population was reciprocally crossed to explore cytoplasmic and nuclear x cytoplasmic interactions. We used a double-digest RAD scheme to identify genetic markers and construct a genetic map.

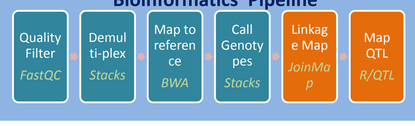


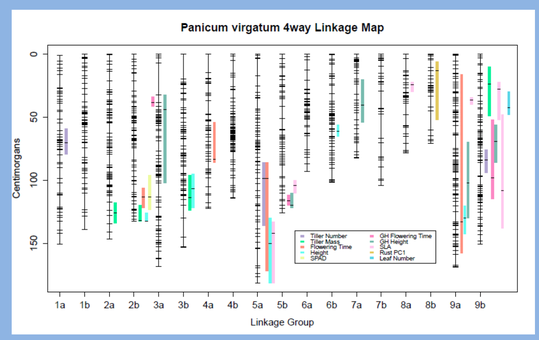
All 4 parental lines are tetraploids. F2 population totals 800 individuals, 400 from each genetic background.

ddRAD Genotyping



Bioinformatics Pipeline

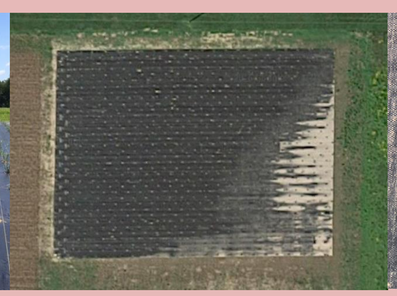




Initial QTL results from greenhouse grown material (Milano et al. 2016).

Field Trials Across the Latitudinal Gradient

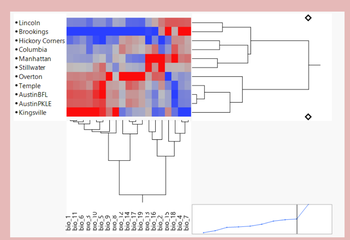
Planting



From Space

First Year Over Winter

Our collaborative group is interested in understanding broad scale local adaptation and GxE in switchgrass. As such, we have clonally propagated and planting the upland/lowland mapping population at 10 locations across the latitudinal gradient



Multivariate analyses of historic climate patterns reveal strong temperature and precipitation gradients associated with our planting locations

Field sites were established in 2015 and data collected during the 2016 growing season. Adjacent is a representative field planting in Stillwater, OK taken in early spring of 2016.

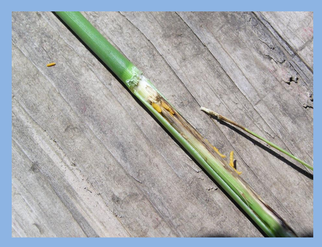
Phenotyping Across Ten Field Locations

Our project involves coordinated intensive season long field phenotyping across a broad geographical area involving multiple facilities conducted by a large group of primary investigators, technicians, and students. We have been especially interested in characterizing phenological, physiological, and anatomical differences in year 1 of our study.

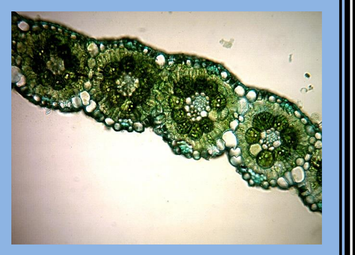
First full season growth up to 2.5 meters!

Columbia Missouri LICOR Campaign Team

Organization and planning ahead are key to successful field campaigns.



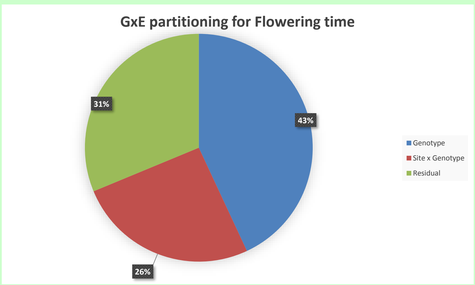
We've observed differential susceptibility to herbivores and fungal pathogens in our population.



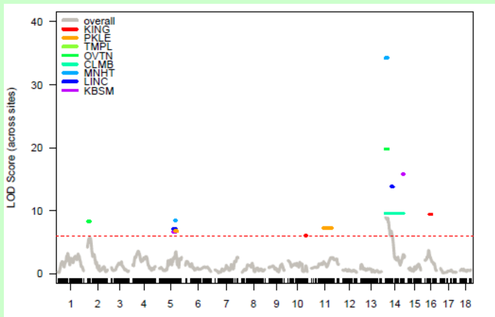
Leaf anatomical traits show interesting variation.

QTL x Environment Interactions for Flowering Phenology

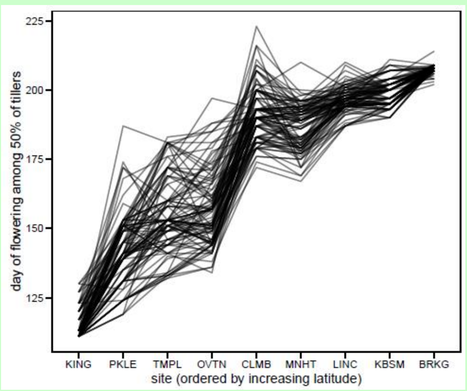
We've used linear mixed models to perform genetic partitioning of flowering time variation into Site, Genotype, and Site x Genotype interactions. We detect enormous fixed site effects associated with the latitudinal gradients and roughly equal Genotype and Genotype x Interaction effects.

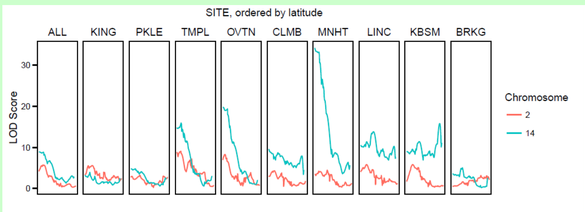


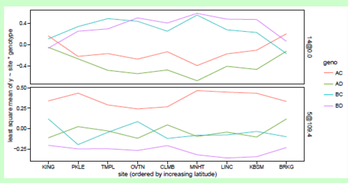
Preliminary genomewide QTL mapping scans identify constitutive and QTL x Site interactions across several linkage groups. In particular, we identify a gene of major effects localized to the top of chromosome 14



Reaction norm plots of flowering time depict strong latitudinal gradient and both ranking and variance changing G x E.







LOD and QTL effect plots exhibit interesting site specific effects and unexpected latitudinal patterns

This project was generously funded by NSF PGRP Grants IOS-0922457 and IOS-1444533