**Genetics of Genotype-By-Environment Interactions in the Switchgrass Diversity Panel**

As sessile organisms, plants cannot move to escape unpredictable and changing environments. Which environments impact plants the most? How do plant genetic responses to the environment vary, and how do these responses evolve? One common hypothesis is that adaptation to specific environments, or local adaptation, occurs via tradeoffs involved in specialization: alleles with antagonistic pleiotropy increase fitness in specific environments, but have negative, pleiotropic effects in alternate environments. A contrasting hypothesis at the level of the allele is conditional neutrality, where alleles can increase fitness in specific environments without costs in alternative environments. As climates shift and climate variability increases, access to conditionally neutral alleles that improve fitness in specific stressful environments will be essential for improving crop species. Genomics-enabled research is now providing the statistical power to discover and characterize allelic variation in genes involved in adaptation.

Switchgrass (*Panicum virgatum*) is an outcrossing, polyploid C4 perennial grass that has been championed as a promising biofuel feedstock. It is a common member of most native North American prairie communities and exhibits extensive phenotypic variability and adaptation across its range, particularly in response to latitude and precipitation gradients. Here, I report on the development of a diversity panel for switchgrass. This diversity panel includes over 700 sequenced genotypes sampled from the majority of the range of switchgrass across the eastern United States. Clones of the sequenced individuals were planted at ten field sites covering 17° of latitude (1800 km) in the central United States. This allowed us to evaluate the contributions of individual loci to traits and fitness over a wide range of climatic conditions. Here, I present genetic analyses of phenology data from the 2019 growing season. In particular, I present preliminary results from genome-wide association studies aimed at detecting gene-by-environment interactions for phenology traits across the species’ latitudinal range.

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The grandparents of the mapping population were derived from highly divergent southern lowland and northern upland ecotypes (25). The southern lowland ecotype of switchgrass is typically found in riparian areas of the southern United States, produces large amounts of biomass, and is more nutrient-use-efficient, heat-tolerant, pathogen-resistant, and flooding-tolerant than the northern upland ecotype (26–30). However, the northern upland ecotype is typically more freezing-tolerant than the southern lowland ecotype (31–35). Flowering time in switchgrass, a trait correlated with biomass production, follows a strong latitudinal pattern, where flowering time becomes progressively later in more southern populations (29, 36–38). (Lowry et al., 2019)

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Plants live in an ever-changing and unpredictable environment. As sessile organisms, they must cope with perturbations to their particular microhabitat in space and time. Which environments matter most? How are environmental responses encoded in genomes and how do they evolve? Genome-enabled research has characterized the myriad expression and metabolite responses of many species to common stresses including drought, temperature extremes, light stress and salinity. The challenge now is to disentangle evolved and adaptive responses of plants to stress from the deleterious results of stress. A promising avenue is the use of locally adapted natural variation to winnow the beneficial responses from the maladaptive consequences of stress. Switchgrass (*Panicum virgatum*) is a polyploid C4 perennial grass that is native to North America and has been championed as a promising biofuel feedstock. It is a common member of most native prairie communities and exhibits extensive phenotypic variability and adaptation across its range, especially related to latitude and precipitation gradients. Much of this variability is associated with evolved lowland and upland ecotypes. Here, I report on the development of genetic and genomic resources for switchgrass, as well as present results from field experiments aimed at understanding upland/lowland ecotype divergence and local adaptation. In particular, I present preliminary results from QTL studies aimed at detecting gene-by-environment interactions for a variety of traits utilizing collaborative common garden experiments across the species latitudinal/climatic range.