

Community Resources to Study Switchgrass Adaptation Using Genome-Wide Association

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<https://alice-macqueen.github.io/switchgrassGWAS/>

Project Goals:

- **Establish software and genomic resources supporting study of common gardens of clonally replicated switchgrass genotypes across broad environmental gradients (e.g., precipitation, temperature, and soils).**
- **Identify genomic regions underlying adaptation and sustainability in switchgrass using genomewide associations.**
- **Investigate key switchgrass traits (resource use efficiency, drought tolerance, growing season phenology, freezing tolerance, tissue characteristics, and root system attributes) in climate adaptation and sustainability of switchgrass feedstock production.**

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 genome-wide association resources for a diversity panel of 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. Phenotyping at these common garden sites allowed us to evaluate the contributions of individual loci to traits and fitness over a wide range of climatic conditions (Lovell et al. 2021). In this poster, I present genetic analyses of phenology data collected during the 2019 growing season. In particular, I

present results from multivariate analyses of genome-wide association studies aimed at detecting genomic regions that both affect greenup or flowering in ways consistent with specific environmental cues, such as temperature and daylength. I also present some of the resources I have developed to conduct genetic and genomic studies on the switchgrass diversity panel at these common gardens, including the R software package, switchgrassGWAS.

Publications

1. Lovell, John T., Alice H. MacQueen, Sujan Mamidi, Jason Bonnette, Jerry Jenkins, Joseph D. Napier, Avinash Sreedasyam, *et al.* 2021. “Genomic Mechanisms of Climate Adaptation in Polyploid Bioenergy Switchgrass.” *Nature*, January, 1–7. <https://doi.org/10.1038/s41586-020-03127-1>.
2. Alice H. MacQueen. “The switchgrassGWAS R package.” <https://alice-macqueen.github.io/switchgrassGWAS/>

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