

'Testing predictions of plant-microbe-environment interactions to optimize climate adaptation and improve sustainability in switchgrass feedstocks gradients'

# Community Resources to Study Switchgrass Adaptation Using Genome-Wide Association

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### Why Switchgrass?

**BIOFUELS:** Switchgrass (*Panicum virgatum*) is the model herbaceous bioenergy crop; it has high biomass yields and is productive on marginal lands; its ethanol yield can exceed that of maize on a per acre basis.

GENETIC DIVERSITY: Natural switchgrass populations are found across North America east of the Rocky Mountains. These populations are morphologically and genetically divergent and have distinct environmental adaptations. Genetic differences in flowering date and photoperiod response will be an early point of exploitation in biomass crop breeding.

# 2. switchgrassGWAS R Package

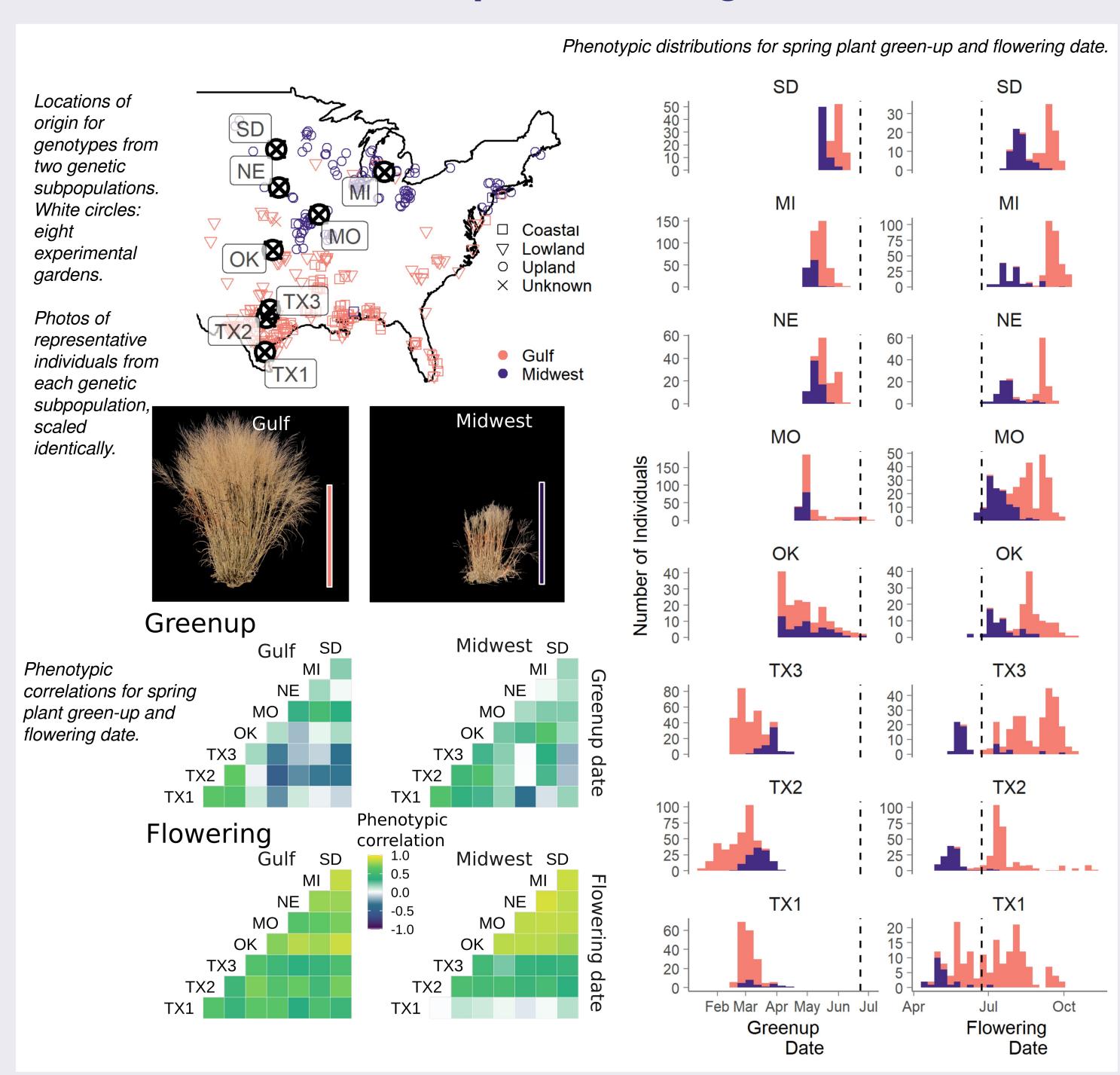
https://alice-macqueen.github.io/switchgrassGWAS/

- 1. Run Genome-Wide Association with `pvdiv standard gwas'
- 2. Conduct multivariate analysis using mash with `pvdiv\_bigsnp2mashr`, `mash\_standard\_run`, `mash\_plot\_effects`.

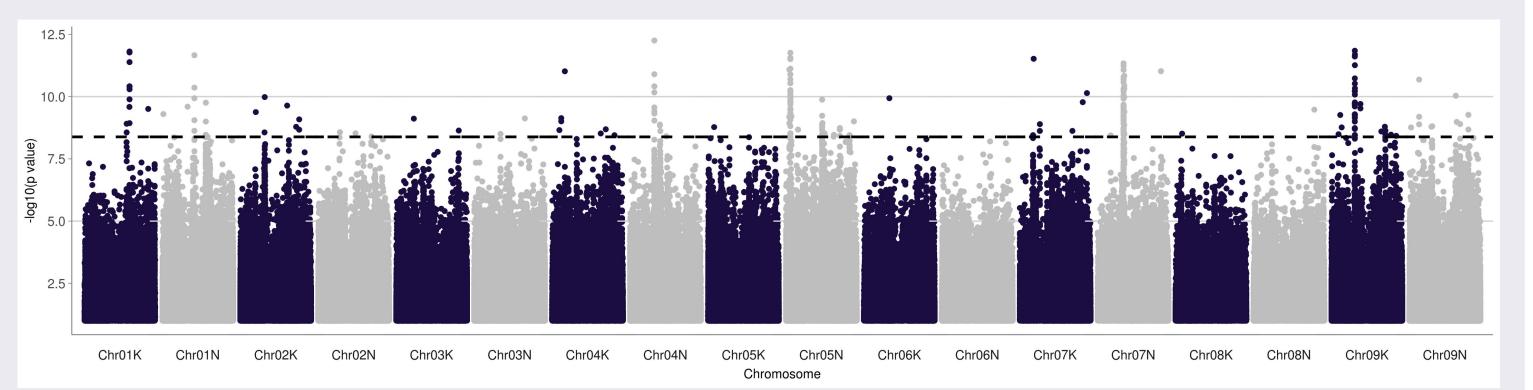
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Article  News & Views

#### 1. Continent-Scale Adaptation Using Common Gardens



#### 3. Genome-Wide Association Studies



Manhattan plot showing genome-wide association results for flowering date in MI for both the Gulf and Midwest genetic subpopulations. Effect size estimates for the most significant SNPs are used for multivariate analysis with mash (Urbut et al 2019 Nat. Gen.)

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Take-home message

The switchgrassGWAS R package allows genetic mapping of genetic and genotype-by-environment effects in the switchgrass diversity panel.

The Midwest and Gulf genetic subpopulations flower in response to distinct environmental cues: only Gulf genotypes are photoperiod responsive.

# 4. Multivariate analysis assigns environmental drivers to SNP effect patterns

equal effects

1. Make covariance matrices using environmental cues (shown here are matrices for flowering date).

2. Assign SNPs posterior weights on each covariance matrix Midwest

Posterior weight

Gulf genotype effects have high posterior weights on flowering daylength covariance matrices; Midwest genotype effects have high posterior weights on cumulative GDD covariance matrices.

Effect

covariance cumulative GDD daylength at flowering Covariance matrices created by correlating environmental variables at each genotype's

Both

Patterns of highly significant SNP effects across eight common gardens. These SNPs were also in significant quantitative trait loci for flowering date in an independent F2 cross grown at the same eight common gardens in 2019.

3. Find significant SNP effects that covary with particular environmental drivers using multivariate adaptive shrinkage (mash).

daylength at flowering (Both) -

daylength at flowering (Gulf)

cumulative GDD (Midwest)

cumulative GDD (Both)

cumulative GDD (Gulf)

4. Explore overall patterns of SNP effects, including those not affected by any hypothesized environmental driver.

using maximum likelihood.

daylength change at flowering (Midwest)

**Sign Changes (AP) Magnitude changes (DS)** Number of SNPs with sign changes (antagonistic pleiotropy) and magnitude changes (differential sensitivity) for flowering date between pairs of common gardens.

Chr05N 63.1 Mb Chr04K 12.9 Mb Chr05N 65 Mb **Both Both** Midwest TX3 Effect Size (% total variation)

