

'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

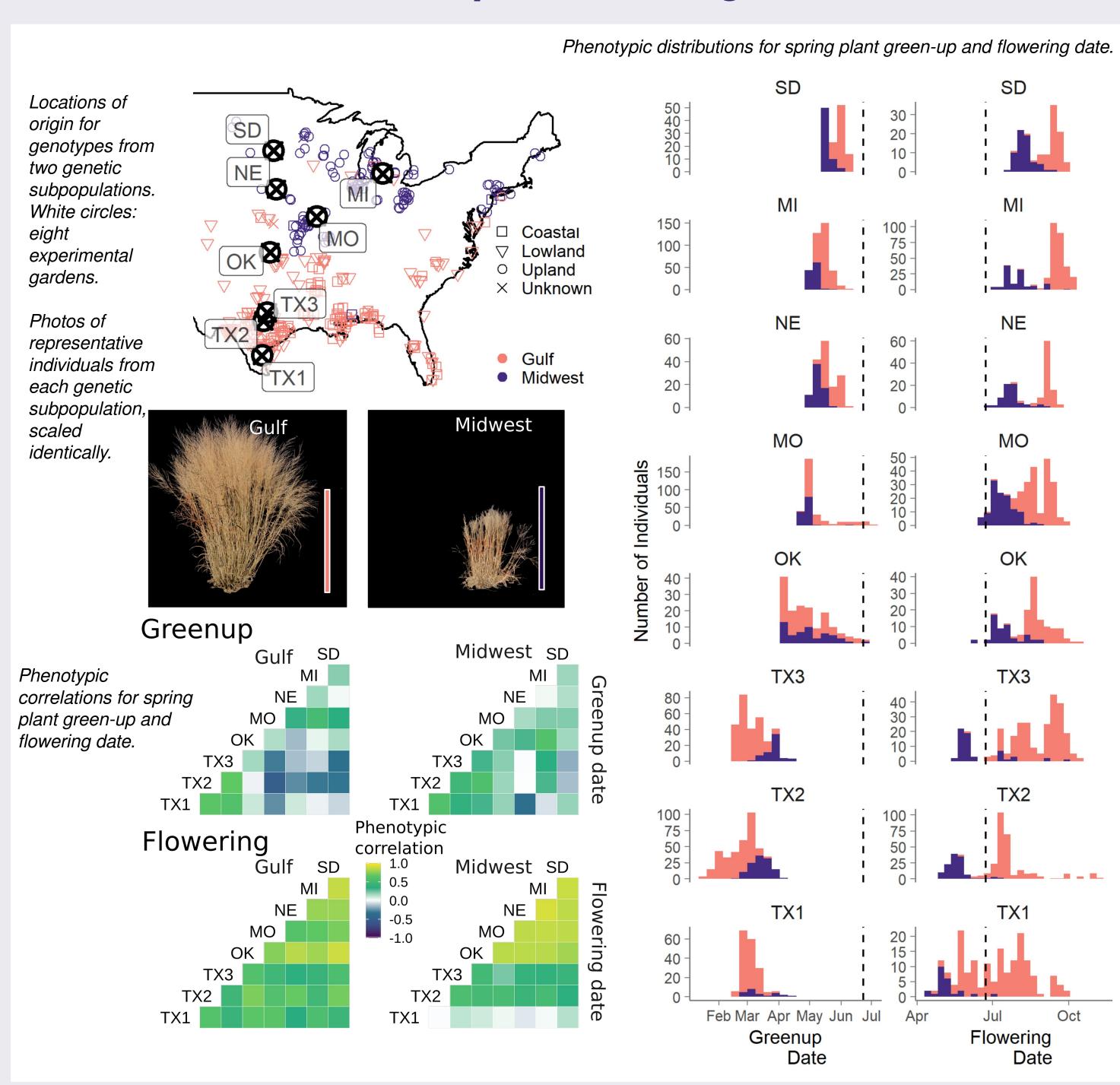
https://alice-macqueen.github.io/switchgrassGWAS/

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

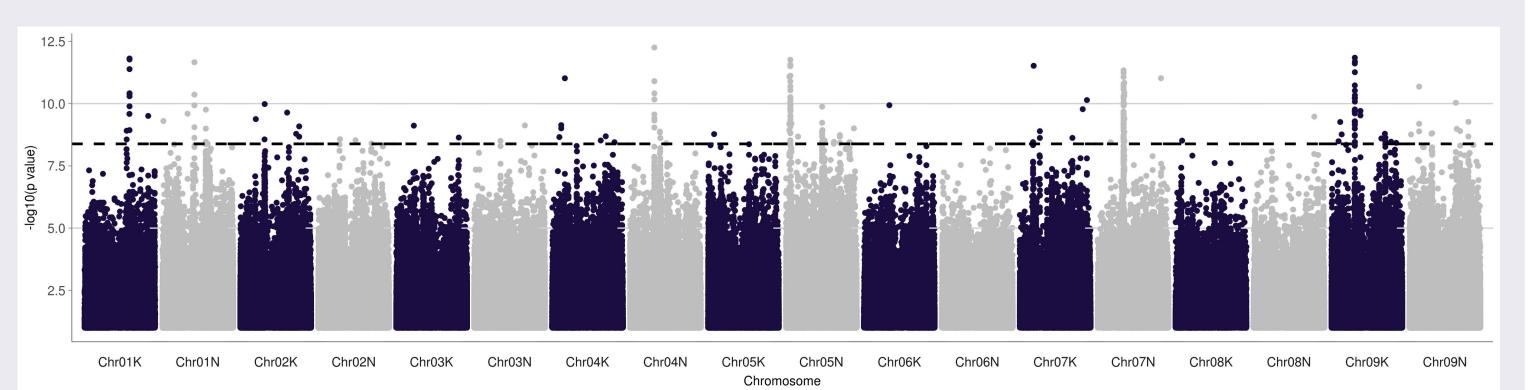
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### 1. Continent-Scale Adaptation Using Common Gardens



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

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

equal effects

Effect covariance cumulative GDD daylength at flowering

Covariance matrices created by correlating environmental variables at each genotype's

Both

2. Assign SNPs posterior weights on each covariance matrix using maximum likelihood.

Midwest Gulf genotype effects have high posterior weights on flowering daylength at flowering (Both) daylength covariance matrices; daylength at flowering (Gulf) Midwest genotype effects have high daylength change at flowering (Midwest) posterior weights on cumulative cumulative GDD (Midwest) GDD covariance matrices. cumulative GDD (Both) cumulative GDD (Gulf) Posterior weight

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 pseudo-F2 cross grown at the same eight common gardens.

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

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

Magnitude changes (DS) Sign changes (AP) Number of SNPs with sign changes (antagonistic MO 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 TX2 Effect Size (% total variation)

# The University of Texas at Austin

# 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.