Genetics of Climate Adaptation Using Genome-Wide Association in Switchgrass

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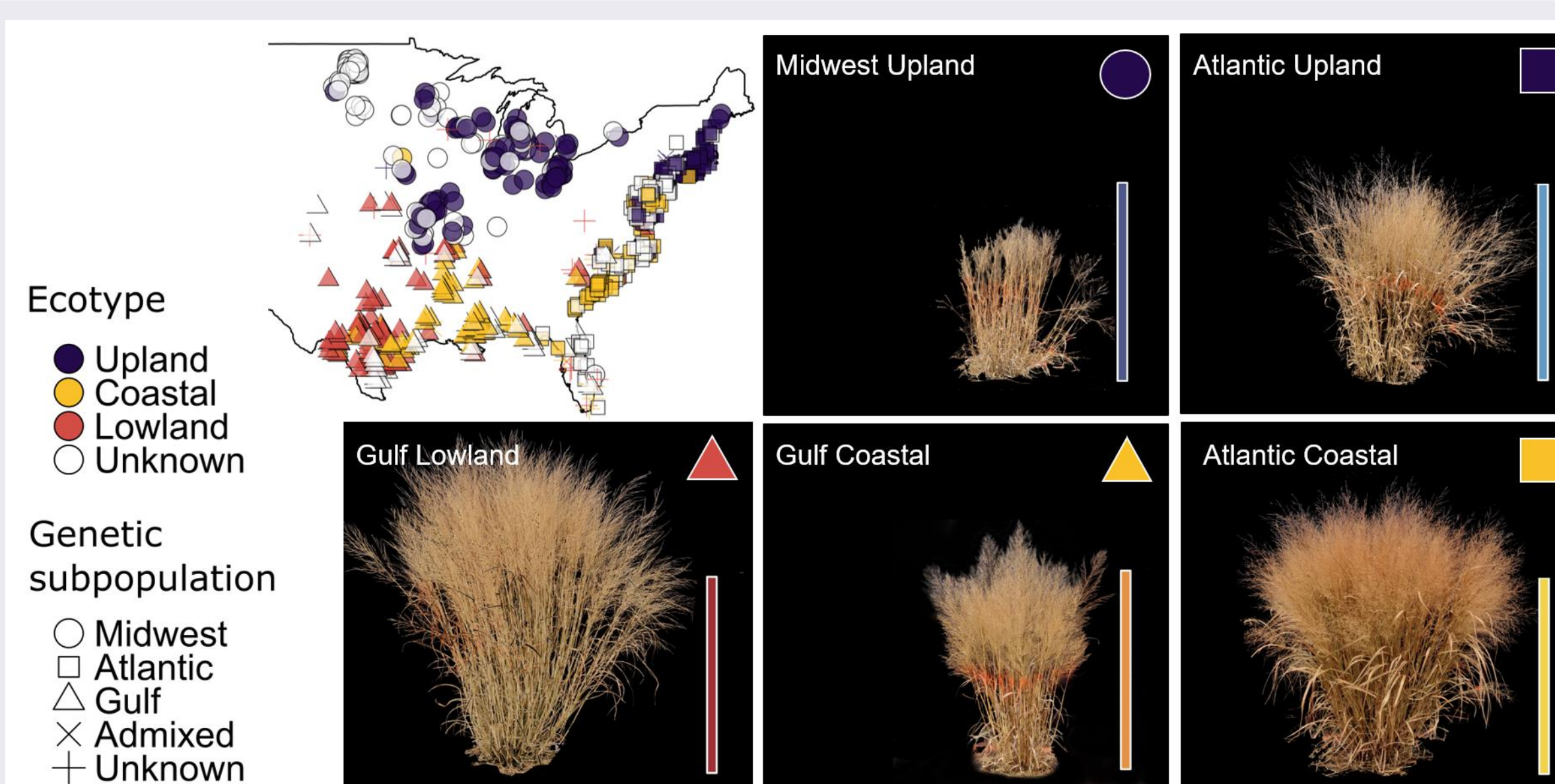
Why Switchgrass?

BIOFUELS: Switchgrass (Panicum virgatum) biomass can be effectively converted into ethanol and other bioproducts; ethanol yield can exceed that of maize on a per acre basis.

CLIMATE ADAPTATION: Natural switchgrass populations span >3,000 km of latitude. Natural selection to climate has shaped the genetics of these populations and shaped phenotypic groupings into *upland* (mostly northern) and *lowland* (mostly southern) ecotypes. These ecotypes likely have different adaptations to climate.

Diversity Panel

Major phenotypic and genetic groups in the tetraploid switchgrass diversity panel. Plant specimens for the five major types are shown.
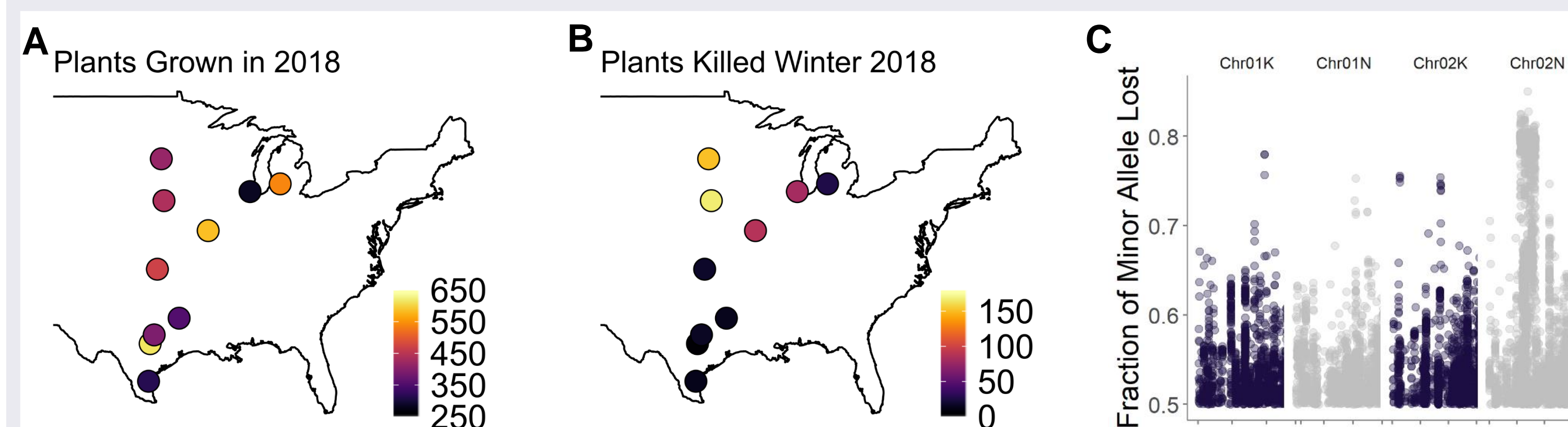
Ecotype
- Upland
- Coastal
- Lowland
- Unknown

Genetic subpopulation
- Midwest
- Atlantic
- Gulf
- Admixed
- Unknown

Midwest Upland / Atlantic Upland / Gulf Lowland / Gulf Coastal / Atlantic Coastal

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JGI JOINT GENOME INSTITUTE
A DOE Office of Science User Facility

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Jerry Jenkins, Chris Plott, Shengqiang Shu, Avinash Sreedasyam, Adam Healey, Li Zhang, Taslima Haque, Joe Napier, Adam Session, Michael Udvardi, Malay Saha, Yuhong Tang, Laura Bartley, Katrien Devos, Michael Casler, Jiming Jiang, David Lowry, Guohong Wu, David Kudma, Kerrie Barry, Jane Grimwood, Dan Rohksar

Continent-Scale Adaptation Using Common Gardens

A Plants Grown in 2018
B Plants Killed Winter 2018
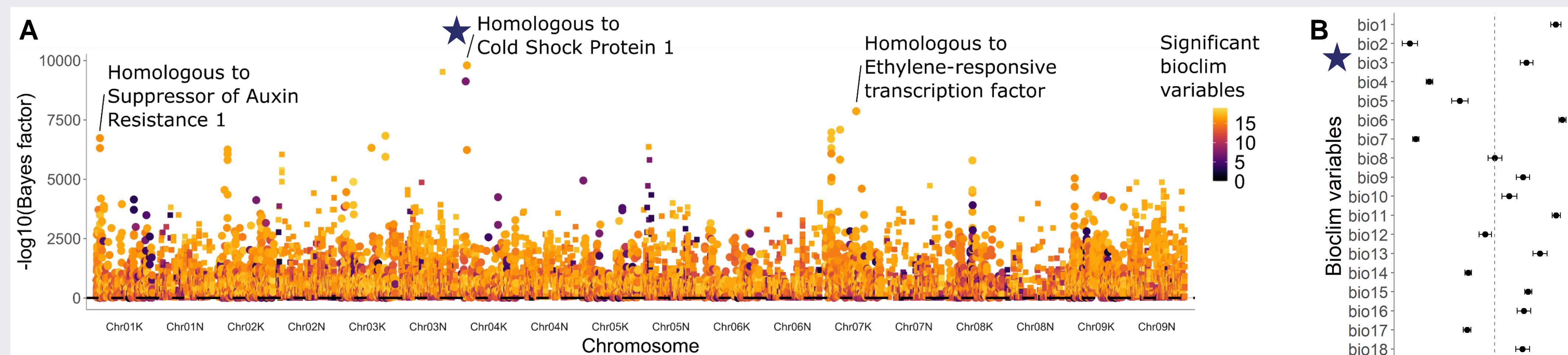**C** Chr01K Chr01N Chr02K Chr02N — Fraction of Minor Allele Lost

A The diversity panel was planted at ten common garden locations in 2018.
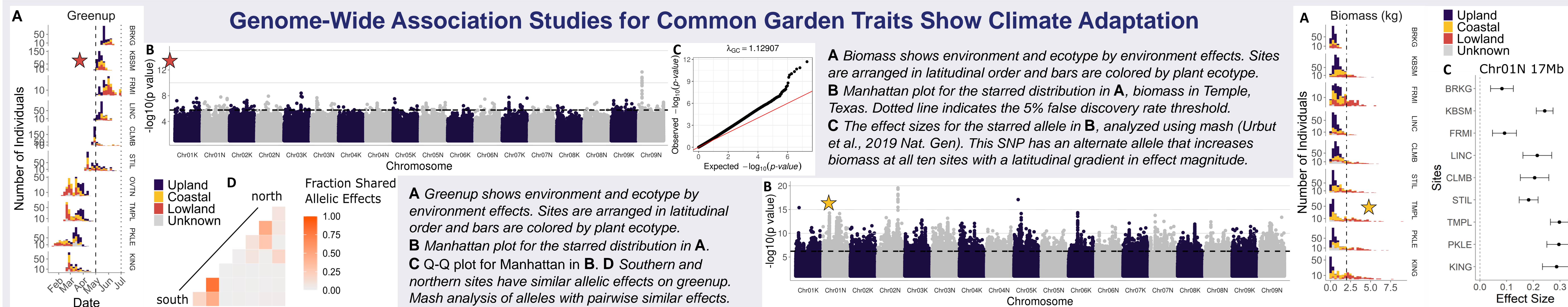**B** Four northern common garden locations had significant overwinter plant death in winter 2018-2019.
C Specific gulf alleles were lost at high frequency in the north in the winter of 2018/2019. The fraction of alleles lost varied across the genome (first four chromosomes are shown).

Genome-Wide Association Studies of Environments at Plant Locations of Origin

A Homologous to Suppressor of Auxin Resistance 1 / Homologous to Cold Shock Protein 1 / Homologous to Ethylene-responsive transcription factor / Significant bioclim variables
-log10(Bayes factor)

B Bioclim variables bio1–bio19 / Effect Size

SNPs with significant associations with one or more bioclim variable. **A** Significant SNPs were typically associated with 14-18 bioclim variables when analyzed with mash (Urbut et al., 2019 Nat. Gen.) Three nearby genes are noted.
B The starred allele in **A** has alternate alleles found in plants from consistent temperature, warmer climates.

Genome-Wide Association Studies for Common Garden Traits Show Climate Adaptation

A Greenup — Number of Individuals / Date (Feb, Mar, Apr, May, Jun, Jul)
Sites: BRKG, KBSM, FRMI, LINC, CLMB, STIL, OVTN, TMPL, PKLE, KING

Upland / Coastal / Lowland / Unknown

B -log10(p value) / Chromosome (Chr01K … Chr09N)
C $\lambda_{GC} = 1.12907$ — Observed -log10(p-value) vs Expected -log10(p-value)
D Fraction Shared Allelic Effects (north / south)

A Greenup shows environment and ecotype by environment effects. Sites are arranged in latitudinal order and bars are colored by plant ecotype.
B Manhattan plot for the starred distribution in **A**.
C Q-Q plot for Manhattan in **B**. **D** Southern and northern sites have similar allelic effects on greenup. Mash analysis of alleles with pairwise similar effects.

A Biomass (kg) — Number of Individuals
Sites: BRKG, KBSM, FRMI, LINC, CLMB, STIL, TMPL, PKLE, KING
Upland / Coastal / Lowland / Unknown

A Biomass shows environment and ecotype by environment effects. Sites are arranged in latitudinal order and bars are colored by plant ecotype.
B Manhattan plot for the starred distribution in **A**, biomass in Temple, Texas. Dotted line indicates the 5% false discovery rate threshold.
C The effect sizes for the starred allele in **B**, analyzed using mash (Urbut et al., 2019 Nat. Gen). This SNP has an alternate allele that increases biomass at all ten sites with a latitudinal gradient in effect magnitude.

B -log10(p value) / Chromosome (Chr01K … Chr09N)
C Chr01N 17Mb — Sites (BRKG, KBSM, FRMI, LINC, CLMB, STIL, TMPL, PKLE, KING) / Effect Size

Take-home message

Winter survival in the northern U.S. is a major selective agent in switchgrass.

Environmental GWAS show allelic effects that partition plants into "winter kill" and "non-winter kill" locations; e.g., warmer climates with more consistent temperatures (and more variable precipitation) versus cooler climates with more variable temperatures and more consistent precipitation.

Common garden phenotypes show genotype by environment interactions and strong signals of genetic association that vary by location.

switchgrassGWAS R Package

https://github.com/Alice-MacQueen/switchgrassGWAS

1. Run Genome-Wide Association with `pvdiv_gwas`
2. Find annotations with `pvdiv_table_topsnps`
3. Analyze data at multiple sites using mash, with:
   `pvdiv_bigsnp2mashr`
   `mash_standard_run`
   `mash_plot_manhattan_by_condition`
   `mash_plot_effects`

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