

# Inter-Ecotypic Switchgrass Populations Provide QTLs Explaining Most Phenotypic Variation

## Background

- There are three switchgrass ecotypes: coastal, lowland and upland.
- Segregation distortion, which is a genetic deviation from expected Mendelian ratios, is a driving force of evolution that impacts the genetic compatibility between ecotypes (i.e., ability to inter-breed).
- Wide crosses between ecotypes can benefit switchgrass breeding efforts to improve growth and yield in unfavorable environmental conditions by selecting for desired genes and traits.

## Approach

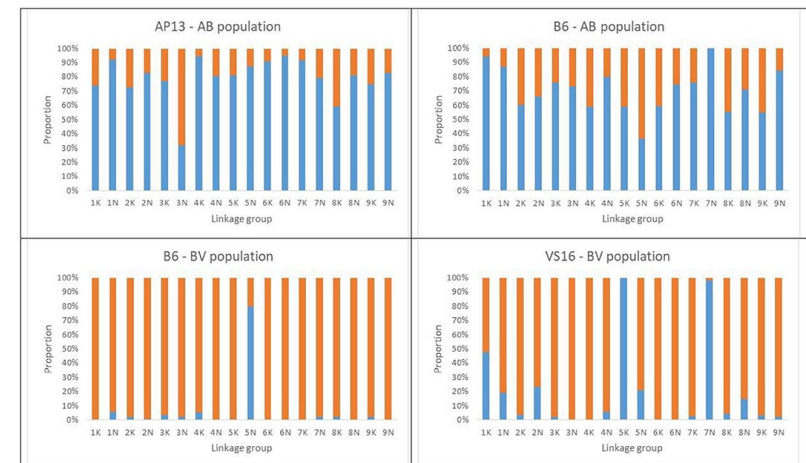
- Two inter-specific ecotypic switchgrass populations were generated: Lowland (AP13) x Coastal (B6) and Coastal (B6) x Upland (VS16) as AB and BV, respectively.
- The extent of genetic variance and patterns of segregation distortion were mapped for the two populations, AB (285 progeny) and BV (227 progeny) derived from these crosses.
- Biomass yield was analyzed across two years, and quantitative trait loci (QTL) mapping was performed to link genotypic and phenotypic information

## Results

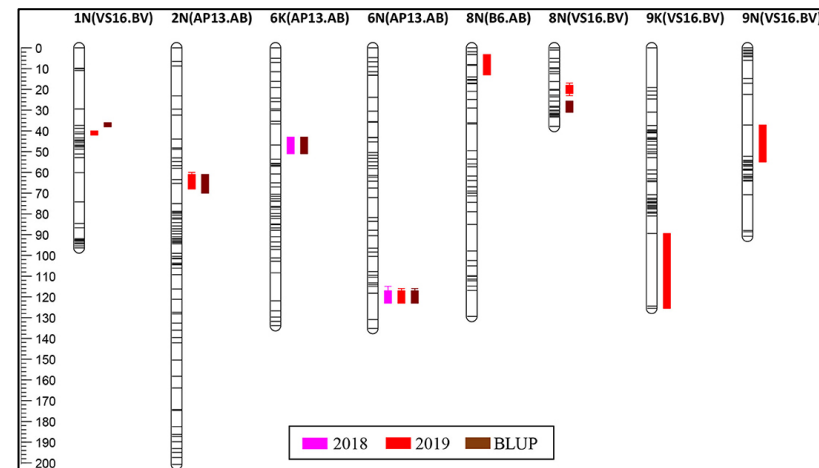
- More segregation distortion of alleles was seen in the AB population, and likely a result from zygotic or post-zygotic selection for increased levels of heterozygosity.
- The results suggest lower genetic compatibility between the lowland AP13 and the coastal B6 ecotypes was lower than B6 and the upland ecotype VS16.
- Four biomass yield QTLs were mapped in the AB population and six QTLs in the BV population

## Significance

- Strong evidence for biomass yield QTLs indicate that breeding can improve switchgrass, especially across compatible inter-ecotypes. A challenge to improved traits is segregation distortion leading to unexpected biases in what traits become inherited.



Proportion of distorted (blue bars) and Mendelian markers (orange bars) across LGs assessed by the Chi-square ( $\chi^2$ ) values for the goodness-of-fit test to 1:1 expected segregation ratios ( $p < 0.05$ ).



QTL positions on the genetic map. QTL are positioned at the right side of each LG; solid bars and whiskers on one or both ends represent coverage at LOD drop intervals of 1.0 and 2.0, respectively. QTL were mapped using LS means for each year and the BLUP value.

Razar, RM et al. (2022) *Frontiers in Plant Science* 13:739133, <https://doi.org/10.3389/fpls.2022.739133>