

# Genome-Wide Association and Genomic Prediction for Biomass Yield in a Genetically Diverse *Miscanthus sinensis* Germplasm Panel Phenotyped at Five Locations in Asia and North America

## Background/objective

Twenty years of research, pioneered in the U.S. by the University of Illinois, has demonstrated *Miscanthus* as an exceptionally productive and sustainable potential source of lignocellulosic bioenergy and bioproducts. However, there is a need to develop genomics-assisted selection by relating genotype to phenotype and breeding value across a broad range of environments. This study presents the first genome-wide association (GWA) and genomic prediction study of *Miscanthus* that uses multi-location phenotypic data.

## Approach

- ❖ A panel of 568 *M. sinensis* accessions was genotyped with 46,177 SNPs and evaluated at one subtropical and five temperate locations over three years for biomass yield and 14 yield-component traits.
- ❖ GWA and genomic prediction were performed separately for different years of data in order to assess reproducibility.

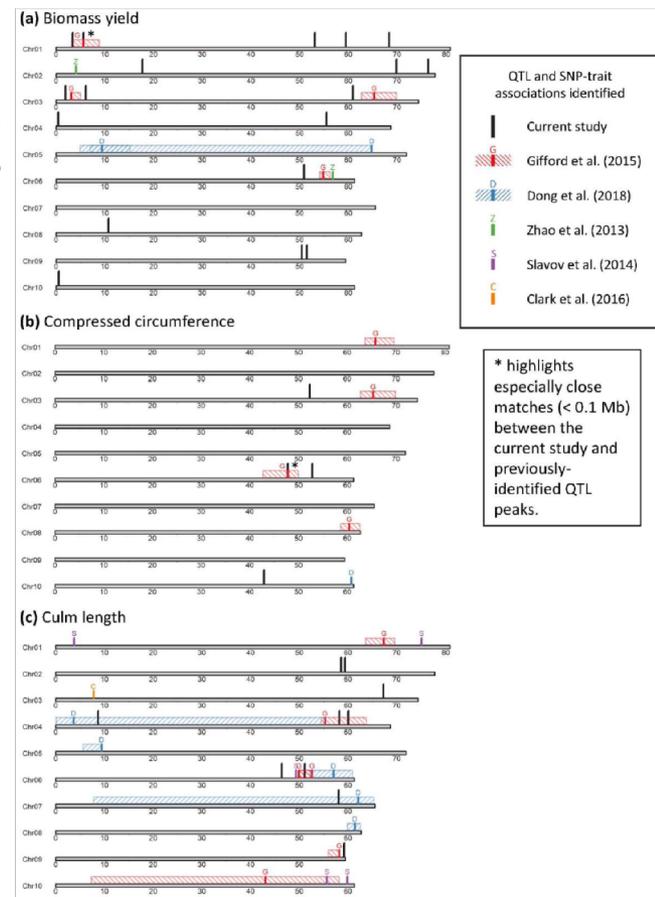
## Results

- ❖ GWA analyses identified 27 significant SNPs for yield, and a total of 504 associations across 298 unique SNPs over all traits, sites, and years.
- ❖ Genomic prediction accuracies of all traits were similar.

## Significance

- ❖ By facilitating genomic selection and prediction in *M. sinensis* and *M. xgiganteus*, these results will accelerate the breeding of *Miscanthus* for biomass yield by increasing genetic gain per year relative to phenotypic selection, which is critically important for the development of this long-lived perennial crop.

Clark, L., et al. 2019. "Genome-wide association and genomic prediction for biomass yield in a genetically diverse *Miscanthus sinensis* germplasm panel phenotyped at five locations in Asia and North America." *GCB Bioenergy*. DOI: <http://10.1111/gcbb.12620>



Locations of significantly associated SNPs and QTL from this study and others for biomass yield, compressed circumference, and culm length in *Miscanthus* with respect to the *Sorghum bicolor* reference genome.