

# Genome-Wide Association and Genomic Prediction for Yield and Component Traits of *Miscanthus sacchariflorus*

## Background/Objective

Accelerating biomass improvement is a major goal of breeding miscanthus, a high-yielding C<sub>4</sub> perennial grass that can be used as feedstocks for bioenergy and bioproducts. The development and implementation of genomic-enabled breeding tools, like marker-assisted selection (MAS) and genomic selection, has the potential to improve the efficiency of miscanthus breeding. The objectives of this study were to: (1) identify SNP-trait association and candidate genes for yield and yield-component traits of *Miscanthus sacchariflorus*; and (2) determine the potential for employing genomic prediction to improve *M. sacchariflorus* by assessing prediction accuracies for yield and yield-component traits.

## Approach

We conducted GWAS and genomic prediction for 16 biomass yield-related traits on the diversity panel of 590 accessions of *M. sacchariflorus* grown across 4 years in one subtropical and three temperate locations. We then genotyped with 268,109 single-nucleotide polymorphisms (SNPs).

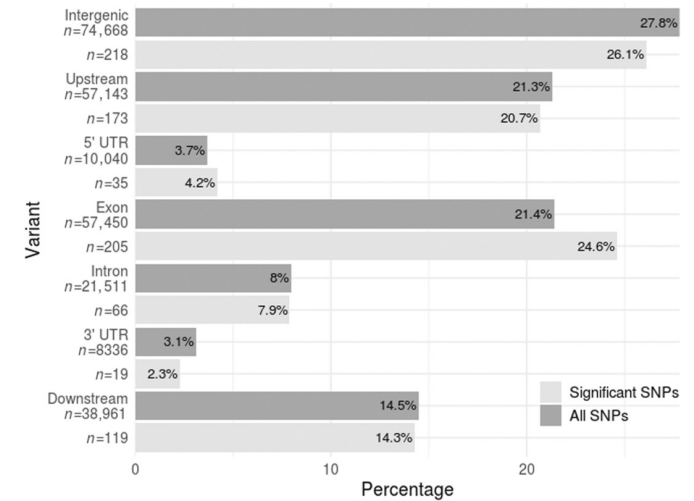
## Results

The GWA study identified a total of 835 significant SNPs and 674 candidate genes across all traits and locations. The Korea/NE China/Russia (N = 237) genetic group had the highest prediction accuracy of all genetic groups (ranging 0.26–0.71), suggesting that with adequate sample sizes, there is strong potential for genomic selection within the genetic groupings of *M. sacchariflorus*.

## Significance/Impacts

This study indicated that MAS and genomic prediction will likely be beneficial for conducting population-improvement of *M. sacchariflorus*. Development of broad-based, intermated breeding populations derived from multiple genetic groups of *M. sacchariflorus* that recombine genes for a range of geographic and climatic adaptations, as well as developing breeding populations within single genetic groups, is an important next step for breeding improved parents of *M. × giganteus*.

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**Bar plot showing the gene regions of the 835 significant single-nucleotide polymorphisms (SNPs) (light grey) that were identified.**