Genome Biology of the Paleotetraploid Perennial Biomass Crop Miscanthus

Background/objective

Miscanthus is a perennial wild grass that is of global importance and is an emerging highly productive temperate biomass crop. Despite C4 perennial crops having tremendous potential for maximizing agricultural yields and minimizing environmental impacts, genetic improvement is limited due to the complexity of their genomes. This study reports a chromosome-scale assembly of the paleotetraploid *M. sinensis* genome, providing a resource for *Miscanthus* that links its chromosomes to the related diploid Sorghum and complex polyploid sugarcanes.

Approach

❖ The *M. sinensis* genome was assembled into n = 19 chromosomes by combining short-read whole-genome shotgun (WGS) and fosmid-end data with *in vitro* and *in vivo* chromatin proximity libraries.

❖ Performed RNA-seq from the same tissue samples collected for profiling nitrogen cycling to characterize the seasonal dynamics of gene expression and regulatory programs associated with perenniality in *Miscanthus.*

Results

❖ The miscanthus and sorghum genomes show extensive 2:1 conserved collinear synteny, consistent with a whole-genome duplication in the *Miscanthus* lineage.

❖ Identified and characterized the transcriptional network regulating seasonal nutrient mobilization in miscanthus, which is central to the perennial lifecycle and efficient recycling of resources.

Significance

❖ The genome sequence and genomic analysis presented here provides a foundation for systematic improvement of *Miscanthus* to optimize its productivity and robustness.

❖ The seasonal gene expression data reveal a group of regulators and enzymes that may be key for promoting the nitrogen remobilization in spring.
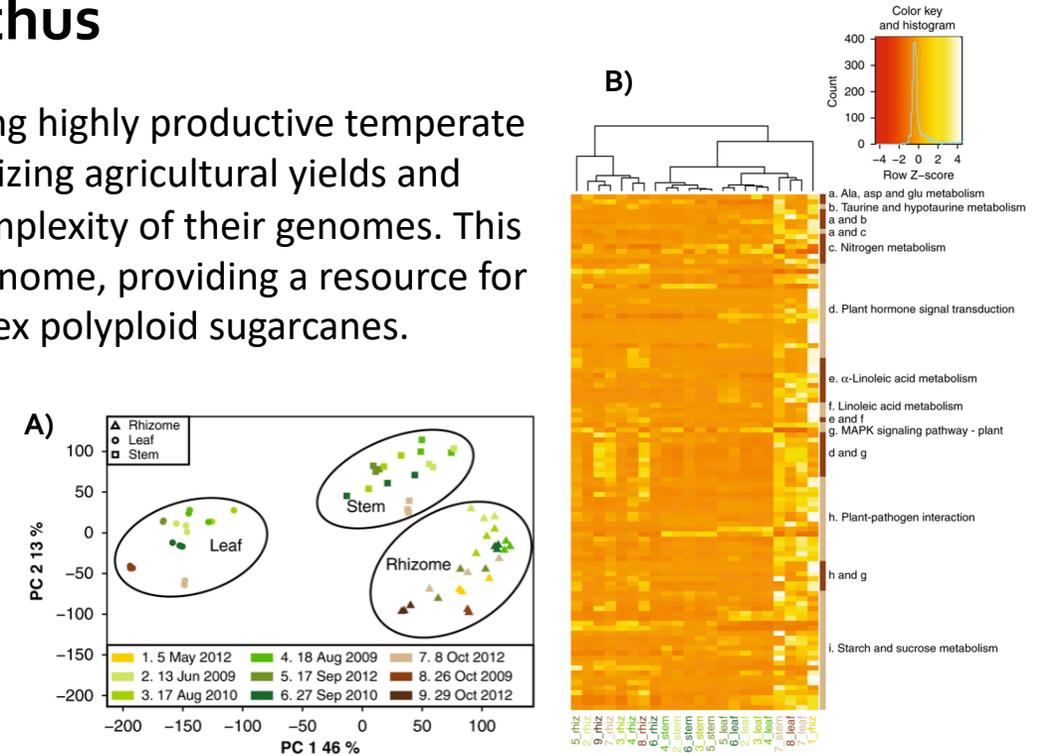
A) Principal component analysis of RNA-seq read counts normalized using the DESeq2 variance-stabilizing transformation method.

B) Heatmap across all tissues in the study comparing the expression of a subset of genes expressed in tissues that are actively remobilizing nutrients.