

# Characterization of the *Ghd8* Flowering Time Gene in a Mini-Core Collection of *Miscanthus sinensis*

## Background/objective

The gene *Miscanthus* is a high-yielding C4 perennial grass often used as forage for livestock feed, an ornamental for landscapes, and also as a bioenergy crop. To obtain high biomass yield under differing environments, optimization of flowering time is essential. However, little is known about how genes that control flowering in other grasses contribute to regulation of flowering in miscanthus. In this study, scientists aimed to characterize *Ghd8* allelic and deduced amino acid sequence diversity and geographic distribution, and to determine expression patterns based on photoperiod response.

## Approach

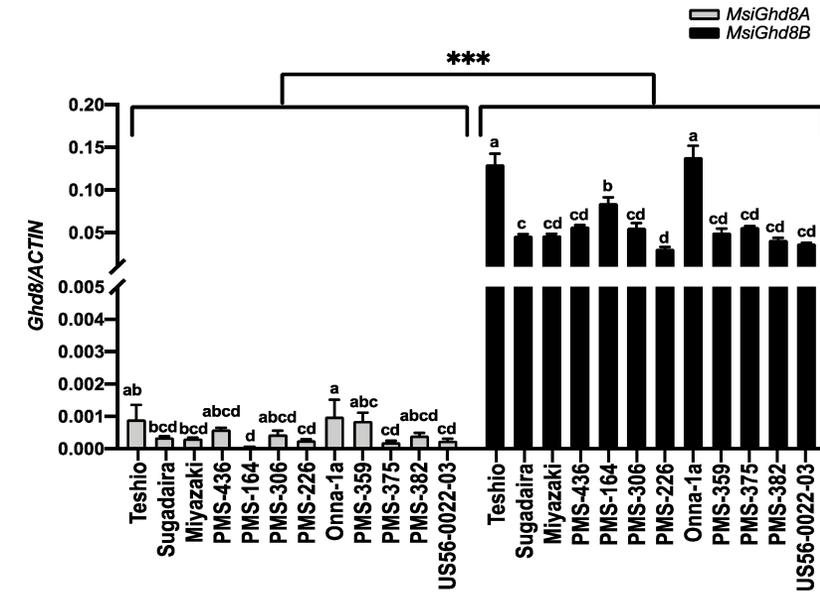
- ❖ Twelve *Miscanthus sinensis* accessions, from varying latitudes, were studied for gene sequence variation and expression over time in response to two photoperiod treatments (12.5 and 15 hours).
- ❖ Genomic DNA was isolated from young, healthy leaves, and gene-specific primers were designed for *Ghd8*. Transcript levels for candidate genes were determined by quantitative real-time PCR (qRT-PCR) to reveal expression of *MsiGhd8*.

## Results

- ❖ Two homeologous *Ghd8* loci, *MsiGhd8A* and *MsiGhd8B*, were identified. Sequence blasting and gene collinearity revealed similarity to those in other plants, such as sorghum, rice, and Arabidopsis.
- ❖ Allele comparison revealed that several protein variants showed geographic and latitudinal distribution.
- ❖ *MsiGhd8* expressed under both long and short days. Results indicated that *MsiGhd8B* affected flowering time in response to day length for some accessions.

## Significance

Insight was gained into the conserved function of *Ghd8* in the Poaceae, and is an important first step in elucidating the flowering regulatory network of miscanthus. In other species, *Ghd8* has also been found to regulate multiple developmental and physiological processes, such as stress tolerance, photosynthesis, tillering, and cold tolerance. Further studies into the molecular mechanism of regulatory networks of flowering-related genes in miscanthus might help to improve biomass yield and quality.



Expression of *MsiGhd8* at Zeitgeber time 9 for 12 *Miscanthus sinensis* accessions under long days (15 hours). Grey and black represent *MsiGhd8A* and *MsiGhd8B*, respectively.