

Supplementary Materials

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

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SUPPLEMENTARY DATA

Supplementary Figure S1 &S2; Supplementary Tables S1 &S2

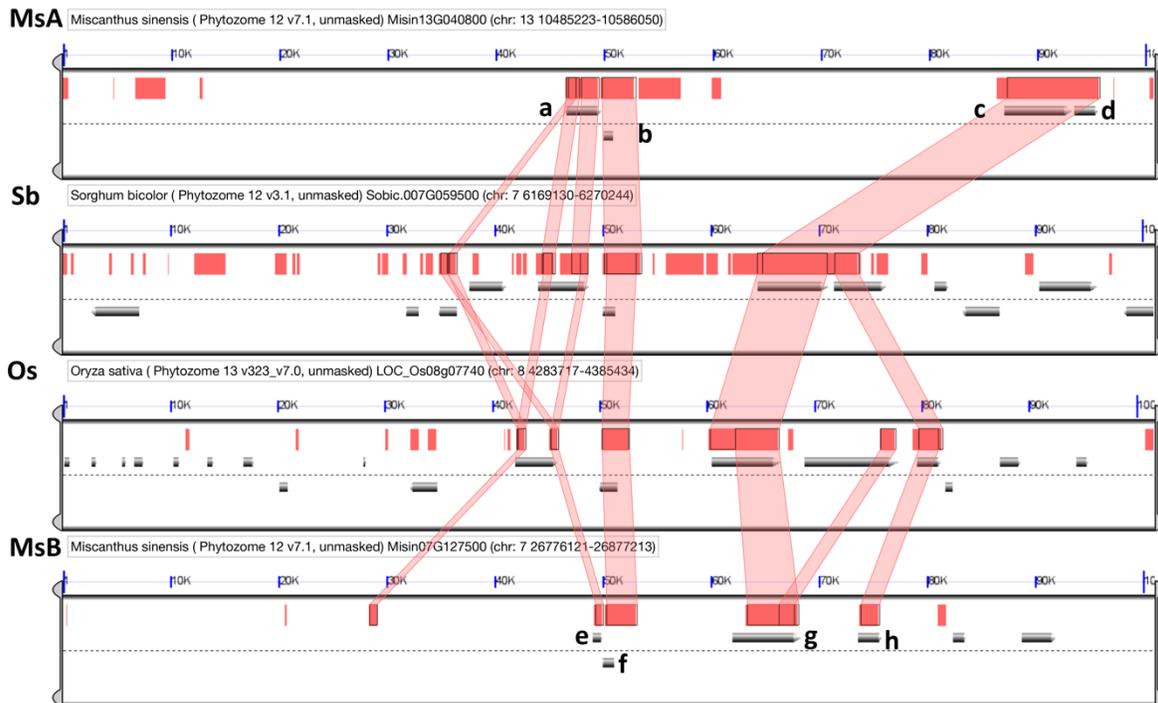


Figure S1. Chromosome organization of *Ghd8* gene orthologous regions (100 kbp) from *Oryza sativa*, *Sorghum bicolor*, *Miscanthus sinensis*. Only high-scoring sequence pairs (HSPs) between adjacent regions are drawn in the red boxes. The dashed line in the middle of each region represents the division between the top (5' on left) and the bottom (5' on right) strand. The full gene models are drawn as gray arrows directly above or below this line. Colinear genes within the aligned region are connected by red lines. a-h represent colinear genes among *Oryza sativa*, *Sorghum bicolor*, *Miscanthus sinensis* (Misin13G040700- Misin13G041000, MsA; Misin07G127400- Misin07G127700, MsB) including *MsiGhd8A* (Misin13G040800, b) and *MsiGhd8B* (Misin07G127500, f), corresponding to Table S2.

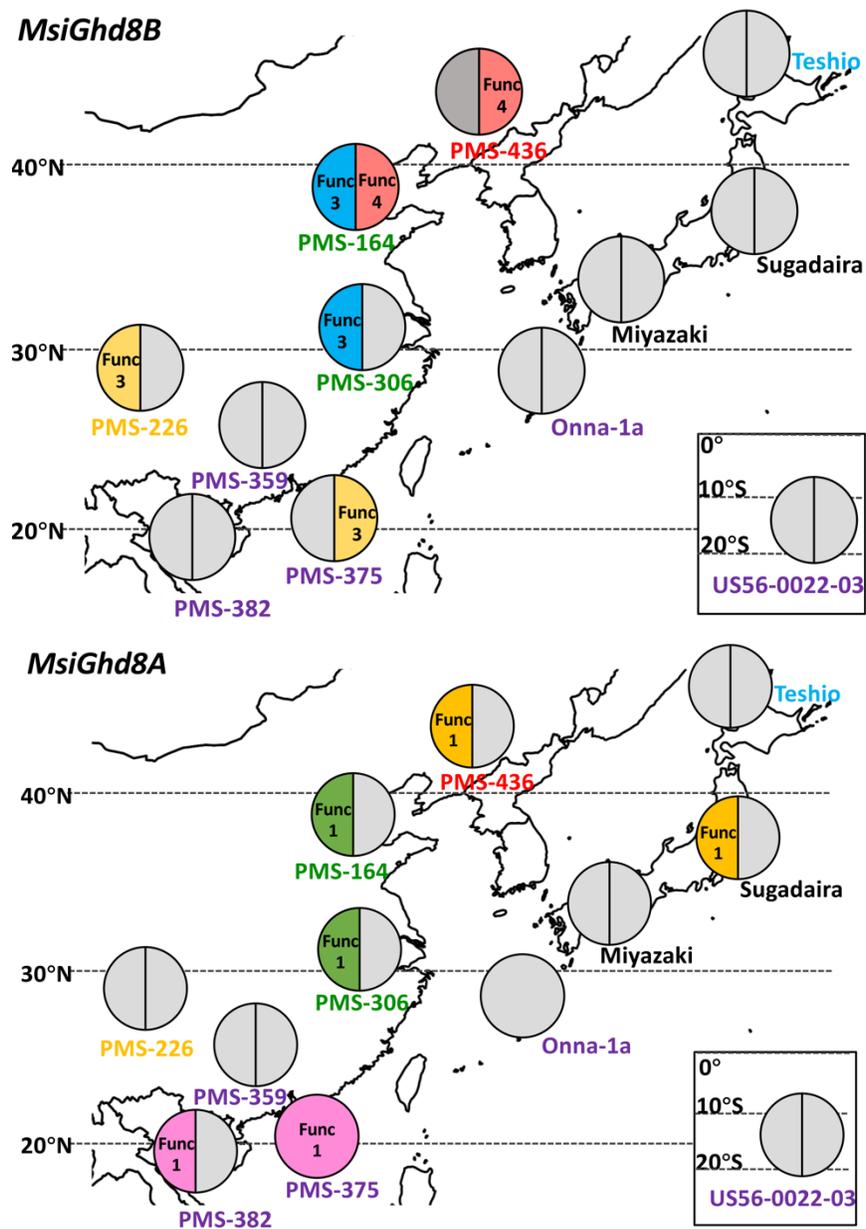


Figure S2. Geographical distribution of *MsiGhd8A* and *MsiGhd8B* alleles in *Miscanthus sinensis*. Pie charts with one to two sections represent the number of detected alleles. Func: putatively functional alleles, corresponding to the names in Figure 2. Pie charts with both the same color and Func number represent the same allele; alleles that were observed only once have a light gray background. Accessions' names were colored to represent *M. sinensis* genetic groups previously described by Clark et al. [49,50]; Sugadaira and Miyazaki were changed from yellow to black for making the map clear.

Table S1 (Excel): A summary of polymorphic sites in *MsiGhd8* open reading frames (ORFs) from 12 *Miscanthus sinensis* accessions. Cells with light blue represent single nucleotide variants (SNVs)/insertions relative to *MsiGhd8* (Misin13G040800 and Misin07G127500) in the *Miscanthus sinensis* v7.1 genome [41]. SNVs located in the domain were highlighted in the red. The A or B prefix with numbers in the right column were the protein types. Cells with different colors in the right column represent different variant types that occurred in more than one accession; variant types that were observed only once have a gray background, corresponding to Figures 2 and 3.

Table S2. Colinear genes near orthologs of *Ghd8* in *Miscanthus sinensis*, *Sorghum bicolor*, *Oryza sativa*

Colinear genes	Locus ID in <i>Miscanthus sinensis</i> *	Locus ID in <i>Sorghum bicolor</i>	Locus ID in <i>Oryza sativa</i>	Putative function
a, e	Misin13G040700 Misin07G127400	Sobic.007G059400	LOC_Os08g07730	Transferase family protein
b, f	Misin13G040800 Misin07G127500	Sobic.007G059500	LOC_Os08g07740	CCAAT-box-binding transcription factor
c, g	Misin13G040900 Misin07G127600	Sobic.007G059600	LOC_Os08g07760	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor
d, h	Misin13G041000 Misin07G127700	Sobic.007G059700	LOC_Os08g07790	CRS2-associated factor 2, mitochondrial precursor

* Gene Locus IDs in *Miscanthus sinensis*, *Sorghum bicolor*, *Oryza sativa* are from Phytozome v13 (<https://phytozome-next.jgi.doe.gov>).