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RESEARCH PAPER

Contrasting allelic distribution of CO/Hd1 homologues in Miscanthus sinensis from the East Asian mainland and the Japanese archipelago

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Abstract

The genus Miscanthus is a perennial C₄ grass native to eastern Asia and is a promising candidate bioenergy crop for cool temperate areas. Flowering time is a crucial factor governing regional and seasonal adaptation; in addition, it is also a key target trait for extending the vegetative phase to improve biomass potential. Homologues of CONSTANS (CO)/Heading date 1(Hd1) were cloned from Miscanthus sinensis and named MsiHd1. Sequences of MsiHd1 homologues were compared among 24 wild M. sinensis accessions from Japan, 14 from China, and three from South Korea. Two to five MsiHd1 alleles in each accession were identified, suggesting that MsiHd1 consists of at least three loci in the Miscanthus genome. Verifying the open reading frame in MsiHd1, they were classified as putative functional alleles without mutations or non-functional alleles caused by indels. The Neighbor–Joining tree indicated that one of the multiple MsiHd1 loci is a pseudogene locus without any functional alleles. The pseudogene locus was named MsiHd1b, and the other loci were considered to be part of the MsiHd1a multi-locus family. Interestingly, in most Japanese accessions 50% or more of the MsiHd1a alleles were non-functional, whereas accessions from the East Asian mainland harboured only functional alleles. Five novel miniature inverted transposable elements (MITEs) (MsiMITE1–MsiMITE5) were observed in MsiHd1a/b. MsiMITE1, detected in exon 1 of MsiHd1a, was only observed in Japanese accessions and its revertant alleles derived from retransposition were predominantly in Chinese accessions. These differences in MsiHd1a show that the dependency on functional MsiHd1a alleles is different between accessions from the East Asian mainland and Japan.

Key words: Bioenergy, flowering time gene, gene duplication, geographical allelic differentiation, Miscanthus sinensis, MITEs.

Introduction

The genus Miscanthus is a rhizomatous perennial C₄ grass that grows naturally in East Asia and Oceania (Hodkinson et al., 2002). Miscanthus spp. are now a leading choice for bioenergy crops in cool temperate regions. Taxonomically, Miscanthus
belongs to the Andropogoneae tribe along with maize (Zea mays L.), sorghum (Sorghum bicolor (L.) Moench), and sugarcane (Saccharum hybrids) (Hodkinson et al., 2002). Among Miscanthus spp., Miscanthus sinensis Anderss., Miscanthus sacchariflorus (Maxim.) Franch. and Miscanthus giganteus Greef & Deuter ex Hodkinson & Renvoize have gained attention as bioenergy crop candidates. M. sinensis is naturally distributed in East and South-East Asia and it is typically diploid (Lafferty and Lelly, 1994; Sacks et al., 2013). M. sacchariflorus is also native to East Asia, and includes diploid and tetraploid ecotypes. Most M. sacchariflorus in China are diploid, whereas M. sacchariflorus in Japan is predominantly tetraploid. To date, commercial biomass production using Miscanthus is limited to M. sacchariflorus ecotypes. Most accessions from the Asian mainland. The factors involved support forest (Numata and Mitsudera, 1969; Stewart et al., 2009; Hodgson et al., 2010; Anzoua et al., 2015). M. sinensis is adapted primarily to environments that have an average annual minimum temperature of ~28.9 °C or greater (USDA hardness zone 5 or warmer) and receive ≥750 mm of precipitation annually (Clifton-Brown et al., 2008; Sacks et al., 2013). M. sinensis is an early colonizer after ecological disturbance in environments that would otherwise support forest (Numata and Mitsudera, 1969; Stewart et al., 2009). Its wide geographical range suggests opportunities for isolation and differentiation of populations. However, M. sinensis is self-incompatible and has wind-dispersed pollen and seed which are traits that would be expected to limit the differentiation of populations. Early population genetic studies with molecular markers evaluated accessions of M. sinensis over some of its native range, for example, in Japan (Shimono et al., 2013), the Izu Islands of Japan (Iwata et al., 2005, 2006), Taiwan and the Ryukyu Islands (Chou et al., 2000), South Korea (Qin et al., 2013), and China (Xu et al., 2013; Zhang et al., 2013; Zhao et al., 2013), and between South Korea and Japan (Slavov et al., 2013). More recently, many accessions of M. sinensis from most of its native range in Japan, China, and South Korea were evaluated with restriction site-associated DNA sequencing (RAD-Seq) single nucleotide polymorphism (SNP) markers, GoldenGate SNPs, and ten plastid microsatellite markers (Clark et al., 2014).

Flowering time is a crucial factor governing regional and seasonal adaptation; in addition, it is also a key target trait for extending the vegetative phase of Miscanthus to improve biomass potential. M. sinensis from high latitudes and high altitudes flower earlier than those from low-altitude and low-latitude regions in Japan, with the earliest M. sinensis flowering two months before the latest M. sinensis (Adati, 1958; Anzoua et al., 2015). The genetic mechanisms for the regulation of flowering time have been characterized in many plants. CONSTANS (CO) and Heading Date 1 (Hd1) are central regulators for the flowering pathway in Arabidopsis and rice, respectively (Valverde, 2011). CO and Hd1 are orthologues that have diverged from a common ancestral gene and encode a nuclear protein that contains a CCT (CONSTANS, CO-like, and TOC1) motif and two B-box-type zinc-finger domains. The CCT motif includes a nuclear import signal (Robson et al., 2001), and B-boxes are considered to be involved in protein–protein interaction rather than in DNA-binding functions (Khanna et al., 2009). CO promotes flowering only under long photoperiods, whereas Hd1 suppresses flowering under long-day conditions and promotes it under short-day conditions, showing bi-functionality to the photoperiodic response (Yano et al., 2000; Shrestha et al., 2014). In addition, in sorghum, which is closely related to Miscanthus, two floral activators, ShCO and ShEhd1 function in photoperiod-sensitive flowering (Yang et al., 2014). ShPRR37 and ShGhd7 repress the activity of ShCO and ShEhd1, respectively, and delay flowering in long-days (Murphy et al., 2011, 2014; Yang et al., 2014).

This is the first report to characterize flowering genes in the genus Miscanthus. Sequences of CO/Hd1 homologues were compared using a broad geographical sampling from Japan, South Korea, and China. In this study, it is shown that multiple homologous copies of CO/Hd1 are a common feature in Miscanthus. Furthermore, it was also shown that many non-functional alleles were detected in accessions from the Japanese archipelago, whereas non-functional alleles were not observed in most accessions from the Asian mainland. The factors involved with such a striking geographical difference are discussed.

Materials and methods

Plants

The accessions studied and their provenances are shown in Table 1. Genetic data were obtained from 44 Miscanthus genotypes, including 24 wild M. sinensis accessions collected from throughout Japan, 14 M. sinensis from throughout China, three M. sinensis from Korea, one M. sinensis ssp. condensatus from Japan, one M. floridulus from Japan, and one diploid M. sacchariflorus ‘Robustus’, and one tetraploid M. sacchariflorus from Japan. Subsets of accessions were phenotypically evaluated in two randomized complete block design field trials conducted at the Experiment Farm of the Field Science Center for Northern Biosphere, Hokkaido University (43°04’ N, 141°20’ E), in Sapporo, Japan. The first field trial had two replications and the second field trial had four replications. Seeds of Miscanthus were sown in March of 2007 in a greenhouse and seedlings of 14 Japanese M. sinensis accessions were transplanted in the field in June to establish the first field trial (Table 1). A second field trial was established at Hokkaido University from clonal divisions in June 2012 with nine of the Japanese accessions in the first field trial plus two additional Japanese accessions, one from Korea, and seven from China (Table 1). Accessions not included in the field trial were grown in a greenhouse.

Heading date

The date of first heading in the field trials was recorded weekly during the growing season; heading date was recorded and analysed instead of flowering time because the former was more consistent than the latter in our short-season location (data not shown). Heading was defined as the flower stalk emerging from the leaf sheath by ≥1 cm. The 2012 heading date data was from the first field trial established in 2007, and the 2014 data was from the second field trial established in 2012 (Table 1).
Table 1. Plant materials and their characteristics

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<th>No. of sequenced plasmid clones</th>
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<th>Country</th>
<th>Latitude</th>
<th>Longitude</th>
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Genomic DNA of 28 Miscanthus accessions (nos. 1–21, 25, 27, 29, and 41–44 in Table 1) was extracted from 200 mg of adult leaves using the DNeasy plant DNA extraction kit (Qiagen, Tokyo, Japan) according to the manufacturer’s instructions. The remaining genomic DNA of 16 accessions was provided by the University of Illinois. Total RNA (JM0079-2 and JM0125-1) was prepared from 200 mg of adult leaves using the TRIZol reagent (Life Technologies Japan Ltd., Tokyo, Japan). One microgram of total RNA was used to synthesize oligo dT primed cDNA at 50 °C for 30 min using the TaKaRa AMV kit (TaKaRa Bio Inc., Shiga, Japan). This cDNA was amplified by PCR with a forward primer (5’-GATCAGGAGAAGACATATACACCC-3’) for determining the sites of splicing and terminal end in the transcript.

DNA amplification and sequencing
Primers used in gene cloning were designed based on CO1Hd1 homologues in sorghum, the closest relative of Miscanthus with an annotated genome. Version 1.4 of the Sorghum bicolor genome was queried using a BLAST search at Phytozome (http://www.phytozome.net/) and the nucleotide region detected with about 2 kb on chromosome 10 was used for primer design. For 5’ and 3’ untranslated regions, the TaKaRa LA PCR in vitro Cloning Kit (TaKaRa) was used to obtain DNA fragments. Finally, DNA fragments (2–2.5 kb) containing the 5’ flanking region to 3’ flanking region were amplified using specific primers (F14: 5’- GATCAGGAGAAGACATATACACCC-3’ and R17: 5’- GATCACTGACCACTCATGGTATAAC-3’) and Taq polymerase (TaKaRa). PCR conditions were as follows: 30 s at 96 °C, 30 s at 50 °C, and 3 min at 72 °C (30 cycles). The buffer and Mg2+ concentration were prepared according to the user’s manual. PCR products containing the coding region were cloned into a pGEM vector (Promega KK., Tokyo, Japan). In total, seven to 25 plasmid clones of each accession were sequenced (Table 1). The nucleotide sequence was determined in both directions using an ABI 3130 genetic analyser (Life Technologies, Carlsbad, USA) with a BigDye Terminator Cycle Sequencing Kit v3.1 and then aligned with ATGC software (GENETYX Co., Tokyo, Japan). The DNA sequences obtained are available from DDBJ (http://www.ddbj.nig.ac.jp/index-e.html) with the accession numbers AB973600 to AB973675 and LC010137 to LC010211.

Phylogenetic analysis
Phylogenetic trees were constructed using GENETYX software, version 10.1.4 (GENETYX Co, Tokyo, Japan). The Neighbor–Joining (NJ) method (Saitou and Nei, 1987) was conducted with Kimura’s (1980) two-parameter distances, ignoring indels. The corresponding sequences of sorghum were used as an out-group.

Results
Heading date
For the subset of Japanese accessions that were evaluated for heading date in both years, the correlation between years was $r=0.889$ indicating that heading date is quite stable from year to year. A significant correlation ($r=-0.853$) was observed between latitude and heading date (Fig. 1). As expected from previous studies, there was a latitudinal gradient of heading date for both the accessions from mainland Asia and for those from Japan, with northern accessions heading earlier in the growing season than southern ones when grown in a common garden in Sapporo (Table 1). There was no latitudinal difference in flowering time between Asian mainland and Japanese accessions (Table 1; Fig. 1).
Isolation of MsiHd1 homologues

To isolate CO/Hd1 homologues of *M. sinensis*, PCR amplification was carried out for 23 accessions derived from the Japanese archipelago, three accessions from South Korea, and 14 from China. Specific 2–2.5 kb PCR products were amplified from all accessions. Based on the results of RT-PCR, the *M. sinensis* CO/Hd1 sequence consisting of two exons and one intron in the PCR fragment was identified and named as *MsiHd1* (Fig. 2). The *MsiHd1* encoded approximately 400 amino acids with two conserved B-box zinc finger domains, which may be responsible for protein–protein interactions (Ben-Naim et al., 2006; Wenkel et al., 2006), and a CCT domain, which is involved with nuclear localization signal (Robson et al., 2001) (see Supplementary Fig. S1 at JXB online). Both domains are features of CO/Hd1. Splicing sites of *MsiHd1* matched to those of sorghum and rice. PolyA addition sites were 159 bp downstream of the stop codon (Fig. 2).

Identification of alleles and analysis of gene phylogenetic tree

Two to five different alleles of *MsiHd1* were found in each accession, indicating that *MsiHd1* consists of at least three loci in the *Miscanthus* genome (Table 1). Based on nucleotide sequences, alleles could be assigned to two broad groups: putative functional alleles with an open reading frame and putative loss-of-function alleles caused by the same deleterious, 1 bp insertion that resulted in a premature stop codon in exon 1 (Figs 2, 3).

An NJ tree indicated that at least one of the multiple *MsiHd1* loci was a pseudogene locus with deleterious mutations, forming a distinctive monophyletic clade (Fig. 3; see Supplementary Fig. S2 at JXB online). The pseudogene locus was named as *MsiHd1b* and the others were considered alleles of the *MsiHd1a* multi-locus family. All 46 alleles of *MsiHd1a* detected in accessions from China and South Korea appeared to be functional based on their sequence, whereas about half of the alleles of *MsiHd1a* from Japanese accessions had putative loss-of-function mutations (35 functional alleles/68 total alleles=51.5%). Thus, a strikingly large difference was observed in the number of putative functional alleles between accessions from the Asian mainland and the Japanese archipelago (Fig. 4), although no clear difference for *Hd1a* alleles was observed among northern, middle, and southern latitudinal regions.

Identification of MITE transposon and revertant alleles

Five novel types of miniature inverted transposable elements (MITEs) with distinctive terminal structures (TIRs: terminal inverted repeats, TSDs: target site duplications) were identified in *MsiHd1* alleles and named as *MsiMITE1*–*MsiMITE5* (Fig. 5; see Supplementary Fig. S3 at JXB online). *MsiMITE1* and *MsiMITE5* were found in *MsiHd1a*, whereas the other three MITEs were found in *MsiHd1b* (Table 1; Figs 2, 3). MITEs are known to be preferentially located in the vicinity of genes (Bureau and Wessler, 1994; Feschotte et al., 2002). During the alignment work, if a relatively large insertion gap (<500 bp) was found and both ends of the gap had TIRs and TSDs, the insertion sequence was identified as a MITE. *MsiMITE1*, which was only detected in Japanese accessions, was found to cause loss-of-function of *MsiHd1a* at the insertion site by forming a stop codon. On the other hand, many accessions from the Asian mainland had revertant alleles derived from retransposition, leaving a footprint of 6 bp instead of a full *MsiMITE1* sequence (Fig. 5). Revertant alleles were found in most accessions from the Asian mainland but in only one Japanese accession (JM0119-5; although another Japanese accession, JM0058-1, also had a footprint of 6 bp, that allele was considered not to be a revertant allele because it had an additional putative loss-of-function mutation; Table 1). Two MITE subfamilies
(MsiMITE2 and MsiMITE3) were observed in tandem in the 5’ untranslated region of the MsiHd1b locus (Fig. 2). MsiMITE3, MsiMITE4, and MsiMITE5 were only detected in JM0125-1, JM0058-1, and PMS007, respectively. These three MITEs were also detected in other Poaceae species (see Supplementary Fig. S4 at JXB online), but MsiMITE1 and MsiMITE2 were not (see Supplementary Fig. S3 at JXB online).

Variation in the number of copies of MsiHd1 among Miscanthus species

Specific PCR products of CO/Hd1 homologues were also obtained from other Miscanthus species including M. sinensis

Fig. 3. Neighbor–Joining (NJ) tree showing the relationships among 54 CO/Hd1 alleles of 16 accessions of Miscanthus sinensis, six CO/Hd1 alleles from one of M. floridulus, five CO/Hd1 alleles from one of M. sinensis ssp. condensatus, three CO/Hd1 alleles from one of M. sacchariflorus (2x), and eight CO/Hd1 alleles from one of M. sacchariflorus (4x). To facilitate viewing this figure on a single page, only about half of the accessions analysed are shown here (see Supplementary Fig. S2 at JXB online for the complete tree). Sixteen accessions of M. sinensis that represent a range of MITE insertions and latitudes of origin were included in this figure. Sorghum bicolor was used as an out-group. The phylogenetic tree was split largely into two clades, which were classified as two loci, Hd1a and Hd1b. All detected alleles of Hd1b in M. sinensis were non-functional. Major mutations that caused loss-of-function are shown to the right of the red circles, which represent non-functional alleles. The double slash on the out-group branch indicates shortening of the branch length by approximately half. Bootstrap values for nodes supported in >50% of 1000 bootstrap replicates are shown. The unnumbered squares, circles, and triangles represent the geographic origin of accessions, putative gene function, and the existence of MsiMITE1, respectively. The numbered triangles show MsiMITE2 to MsiMITE5.
M. sacchariflorus (4x). M. floridulus had a revertant allele with a 6bp footprint, however, Ms IMTE1-like sequences could not be detected from the M. floridulus genome.

Discussion

Unexpectedly, among M. sinensis accessions from a broad latitudinal distribution, no correlation between days to heading and the polymorphisms of Ms IMTE1 was observed. However, a clear difference in the distribution of the putative functional genes in Ms IMTE1a was observed between accessions from the Asian mainland and those from the Japanese archipelago (Fig. 4; Table 1). This difference shows that dependency on the gene function of Ms IMTE1a is different between the two areas. In Miscanthus, the presence or absence of other flowering-time genes epistatic to Hd1 might have promoted the geographic allelic differentiation of Ms IMTE1a between populations from the Asian mainland and the Japanese archipelago. Similar patterns of differentiation of flowering-time genes have been observed in other plant species. For example, FRIGIDA (FRI) in Arabidopsis enhances the effect of FLOWERING LOCUS C (FLC), which is downstream of FRI in the floral pathway, and thus only accessions with functional alleles of FRI are subjected to the influence of FLC alleles for the number of days to flowering (Caicedo et al., 2004). In addition, in a field experiment with Arabidopsis, a correlation between the number of days to flowering and the latitude of origin was observed only among accessions with functional FRI alleles, and accessions from lower latitudes flowered earlier (Stinchcombe et al., 2004). Since no correlation was observed among accessions with non-functional FRI, it seems that geographic differentiation of FLC alleles in Arabidopsis depends on the epistasis (gene interaction) of FLC and FRI. In rice, much research on the epistasis of Hd1 to other flowering-time genes has been reported (Lin et al., 2000; Uwatoko et al., 2008; Takahashi et al., 2009; Ito and Izawa, 2013; Chen et al., 2014). Rice Hd6, which encodes a protein kinase CK2α, suppresses flowering only in the presence of functional Hd1 (Takahashi et al., 2001; Ogiso et al., 2010). In a population structure study using neutral genetic markers, Slavov et al. (2013) identified two subpopulations of M. sinensis, with one from mainland Asia around the Korean peninsula and the other from Japan, but they also observed a similar latitudinal cline for flowering time in both subpopulations; their results are consistent with our findings. It is expected that analyses of individual genes could best explain local adaptation and the evolutionary history of M. sinensis. Studies on other flowering-time genes of Miscanthus would further elucidate the population differentiation observed in Ms IMTE1a alleles in the present study.

The NJ tree showed that 20 of the 44 Miscanthus accessions that were analysed had two diverged loci, Ms IMTE1a and Ms IMTE1b (Fig. 3; see Supplementary Fig. S2 at JXB online). Although their positions on the Miscanthus genome are unknown, the existence of duplicated Hd1 loci can be considered to be universal within the genus Miscanthus, in contrast to sorghum, maize, and rice which have only one Hd1 locus. The recent genome duplication of Miscanthus relative to sorghum (Kim et al., 2012; Ma et al., 2012; Swaminathan et al., 2012) can at least partially account for differences in the number of Hd1 loci. Large-scale genomic analyses of M. sinensis have revealed that M. sinensis (x=19) is a diploidized tetraploid species formed by the duplication of chromosomes after the divergence from an x=10 ancestor (Kim et al., 2012; Ma et al., 2012; Swaminathan et al., 2012). The three or more loci of Ms IMTE1 identified by this
study in *M. sinensis* might have been caused in part by the whole genome duplication (*MsiHd1a* and *MsiHd1b*) and also by local gene duplications (multiple *MsiHd1a*) via unequal crossing-over (Fig. 6). Although gene duplication can be an evolutionary process to gain new function (Ohno, 1970), a duplicated gene can alternatively be subjected to inactivation by mutations and genetic drift (Hughes, 1994; Force et al., 1999). Redundancy of gene functions among multiple *MsiHdl* loci through polyploidization might have allowed pseudogenization of *MsiHdlb*. The precise number of *MsiHd1a* loci in *Miscanthus* remains unknown. In two Japanese accessions, JM0190-5 and JM0091-2, five copies of *MsiHd1a* were detected, suggesting the possibility of additional duplications in *MsiHd1a*. The *M. floridulus* *Hdl* locus, having a revertant allele, showed the greatest sequence similarity to the *M. sinensis* *Hdl* locus (Fig. 3) of the species evaluated. *M. condensatus* and *M. sacchariflorus* (*4x*), respectively, each had three alleles, suggesting at least two loci, in contrast to the putative single locus in *M. sinensis*. The observation of five alleles of *Msa(4x)*-*Hdl1a* within one individual *M. sacchariflorus* (*4x*) indicates that there are at least three *Msa(4x)*-*Hdl1a* loci in this individual. As observed above, copy number of *Hdl1a/b* varies among species in the genus *Miscanthus*.

Differentiation of *M. sinensis* between mainland Asian populations and Japanese populations for number of functional *Hdl1* alleles is consistent with Clark et al.’s (2014) finding that migration after the last glacial maximum from a refugium in south-eastern China to Japan occurred prior to migrations northward in mainland Asia. Moreover, Clark et al. (2014) estimated that the nascent Japanese *M. sinensis* population survived the Younger Dryas as a distinct group, which probably included strong natural selection for adaptation to a short growing season, whereas *M. sinensis* in mainland Asia remained in longer-season lower latitude environments until more recently. However, the phylogenetic tree of *MsiHd1* in the present study identified no distinct clear clade that separates Japan from the Asian mainland (Fig. 3). Thus, our hypothesis is that the polymorphism seen within *MsiHdl* existed in the ancestral population of *M. sinensis*, as opposed to being a recent set of mutations originating from distinct geographic regions, which is consistent with the data of Clark et al. (2014) that suggested a recent (14 000 years before present and later) but differential expansion of the range of *M. sinensis* throughout East Asia that allowed for a different history of selection pressure on mainland and Japanese populations. Although *M. sinensis* populations from mainland Asia and Japan currently differ in the number of functional *MsiHdl* alleles, genotypes of both populations collected from similar latitudes head at similar times when grown in a common garden, suggesting that they may have differing genetic mechanisms to arrive at the same phenotypic result. This insight leads to the hypothesis that crosses between mainland *M. sinensis* genotypes and Japanese *M. sinensis* genotypes are more likely to exhibit transgressive segregation for heading date than crosses within either geographic group, assuming similar latitudes of origin of the parents for the comparisons.

In this study, in addition to the five novel MITE-like transposable elements (*MsiMITE1–5*) that were identified in the *CO/Hdl* homologues of *M. sinensis*, a putative revertant allele with evidence of retransposition of *MsiMITE1* was also found (Figs 3, 5; Table 1). It is possible to identify MITEs if their basic features, including TIRs and TSDs, are determined using sequence alignments (Nagano et al., 2002). Of the five detected *MsiMITEs*, three were found to have homologues with similar sequences in the genomes of sugarcane, sorghum, and switchgrass (see Supplementary Fig. S4 at *JXB* online). The TIRs and TSDs were also observed in the genomes of these other plant species, suggesting that at least these elements are shared among other plant species. Since the early 1990s, when MITEs were reported in the vicinity of the *waxy* gene of rice and maize, respectively (Umeda et al., 1991; Bureau and Wessler, 1992), many more
MITE families were identified in plants and animals including humans (Feschotte et al., 2002). MITEs are currently ordered and classified into six superfamilies (Tc1/mariner, PIF/Harbinger, hAT, Mutator, CACTA, and/or Micron; Lu et al., 2012; Han et al., 2013). In these definitions, MsiMITE1, MsiMITE3, and MsiMITE5 belong to the hAT superfamily (8 bp of TSD, >5 bp of TIR), and MsiMITE2 and MsiMITE4 belong to the PIF/Harbinger superfamily (3 bp of TSD, >4 bp of TIR) (see Supplementary Fig. S3 at JXB online). MsiMITE1 and MsiMITE2, which are specifically identified within MsiHd1a or in the 5’ UTR of MsiHd1b, respectively, do not have similar sequences in any genome database. However, our Southern blot analysis using a probe spanning the full length of MsiMITE1 (ca. 500 bp) detected multiple discrete signals in the M. sinensis genome (see Supplementary Fig. S5 at JXB online). This result suggests that many unidentified MsiMITE1 sequences exist in M. sinensis. It remains unclear whether the richness of MITEs observed in the region of MsiHd1alb is typical of most genes in M. sinensis. The future accumulation of genome information for M. sinensis will help to address these questions.

In conclusion, the comparison of MsiHd1 homologous sequences among accessions derived from East Asia revealed contrasting allelic distribution in M. sinensis from the Asian mainland and Japanese archipelago. Further studies on other flowering-time genes will be necessary to elucidate the genetic architecture of flowering time and its evolution in Miscanthus and to improve biomass potential by regulation of the reproductive phase.

**Supplementary data**

Supplementary data can be found at JXB online.

**Supplementary Fig. S1.** Alignment of the CO/Hd1 homologues from Miscanthus sinensis (a functional allele from JM0079-2), Sorghum bicolor and Oryza sativa.

**Supplementary Fig. S2.** Complete phylogenetic tree constructed using the Neighbor–Joining (NJ) method.

**Supplementary Fig. S3.** The structure of MsiMITE2-5.

**Supplementary Fig. S4.** Comparison of three miniature inverted transposable elements (MITEs) found in the genomes of M. sinensis, sugarcane, sorghum and switchgrass.

**Supplementary Fig. S5.** Comparison of Southern blotting patterns between MsiHd1 (left panel) and MsiMITE1 (right panel).

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