Table 1 Suppl. Sequences of primers. Underlined letters indicate restriction sites.

Function	Primer	Sequence (5′–3′)
Gene and genome gene clone	*MpWRKY6a*-S	ATGGACAAAGGATGGGGGCT
	MpWRKY6a-A	TTAATTTCCCGGGAAGCTGCCTG
Gene and genome gene clone	*MpWRKY6b*-S	ATGGACAAAGGATGGGGGCT
	MpWRKY6b-A	TTAATTTCCCGGGAAACCA
MpWRKY6a promoter clone	P- *MpWRKY6a*-S	TGGAGTCGTAATTACAGTCGAT
	P- *MpWRKY6a*-A	GAGCCCCCATCCTTTGTC
MpWRKY6b promoter clone	P- *MpWRKY6b*-S	GAGACTAAGCCACTGCTTCTC
	P- *MpWRKY6b*-A	GGTGAGCCCCCATCCTTTG
MpPHO1 promoter clone	P-*MpPHO1*-S	TCTCTTGTGTCTCCGACCAT
	P- *MpPHO1*-A	CAAGGGCAGCAACCTATGAAG
Vector construction	pET32a-*MpWRKY6a*-S	CCCAAGCTTGCATGGACAAAGGATGGGGGC
	pET32a-*MpWRKY6a*-A	CCGCTCGAGATTTCCCGGGAAGCTGCTAA
Vector construction	pET32a-*MpWRKY6b*-S	CCCAAGCTTGCATGGACAAAGGATGGGGGC
	pET32a-*MpWRKY6b*-A	CCGCTCGAGATTTCCCGGGAAACCACTAATC
Vector construction	GFP- *MpWRKY6a*-S	CCCAAGCTTATGGACAAAGGATGGG
	GFP- *MpWRKY6a*-A	ACGCGTCGACATTTCCCGGGAAG
Vector construction	GFP- *MpWRKY6b*-S	CCCAAGCTTATGGACAAAGGATGGG
	GFP- *MpWRKY6b*-A	ACGCGTCGACATTTCCCGGGAAACCACTAATC
Vector construction	pAbAi-p*MpPHO1*-S	CGGGGTACCTCTCTTGTGTCTCCGACCAT
	pAbAi-p*MpPHO1*-A	CCGCTCGAGCAAGGGCAGCAACCTATGAAG
Mutation of *MpPHO1* promoter	M-1-S	TATAAACCAAATGTGTTGATAAGACTTGCTCGCTACTCCTTCG
	M-1-A	CGAAGGAGTAGCGAGCAAGTCTTTTCAACACATTTGGTTTATA
Mutation of *MpPHO1* promoter	M-2-S	GAAATTCGTTCAAAGTTGATTGCATGTTTTCCTGGGC
	M-2-A	GCCCAGGAAAACATGCAATCAACTTTGAACGAATTTC
Vector construction	pGADT7-*MpWRKY6a*-S	CCCATCGATACATGGACAAAGGATGGGGGC
	pGADT7-*MpWRKY6a*-A	CCGCTCGAGTTAATTTCCCGGGAAGCTGC
Vector construction	pGBDT7-*MpWRKY6a*-S	CCGGCCATGGAGGGCCATGGACAAAGGATGGGGGC
	pGBDT7-*MpWRKY6a*-A	ACGCGTCGACTTAATTTCCCGGGAAGCTGC
Vector construction	pDEST32-*MpWRKY6b*-S	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGGACAAAGG--ATGGGGGC
	pDEST32-*MpWRKY6b*-A	GGGGACCACTTTGTACAAGAAAGCGGGTCTTAATTTCCCGGGA--AGCTGC
Vector construction	pWR306- *MpWRKY6b*-S	ACGCGTCGACATGGACAAAGGATGGGG
	pWR306- *MpWRKY6b*-A	CGGGGTACCTTAATTTCCCGGGAAGCTG
RT-qPCR	RT-*MpWRKY6a*-S	CAGACGGGGATGCTACGG
	RT-*MpWRKY6a*-S	GGCGAGGCTAATGG-TGGTG
RT-qPCR	RT-*MpWRKY6b*-S	CACCGCTGCTGTTGGACAT
	RT-*MpWRKY6b*-A	TGTGCAAGACGATGGTTTGATG
RT-qPCR	EF-S	ATTCAAGTATGCCTGGGTGC
	EF-A	CAGTCAGCCTGTGATGTTCC
RT-qPCR	*tublin8*-S	ATAACCGTTTCAAATTCTCTCTCTC
	tublin8-A	TGCAAATCGTTCTCTCCTTG

Table 2 Suppl. Predicted *cis*-acting elements in *MpWRKY6a* promoter. Location of first nucleotide 5' upstream of start codon is designated as -1 position.

Cis-acting elements	Sequence	Position	Function
ABRE	CACGTG	+769, +714	abscisic acid response
ARE	TGGTTT	-36, -208	anaerobic induction
ATCT Motif	AATCTAATCT	+944, -966	light response
Box 4	ATTAAT	+495, +665, +1141	light response
Box W1	TTGACC	-135	fungal elicitor response
CGTCA -Motif	CGTCA	+203, +1132, -837, -382, -849	MeJA response
G Box	CACGTT	-106, +713, +441	light response
MBS	CGGTCA	+165	MYB binding site
MBS	CAACTG	+408, -231	MYB binding site; drought-inducibility
P Box	CCTTTTG	+419	gibberellin response
circadian	CAANNNNATC	-997	circadian control
W Box	TGAC	+56, -155, +216, +383, -409, +659, +823, -836	WRKY binding site

Table 3 Suppl. Predicted *cis*-acting elements in *MpWRKY6b* promoter. Location of first nucleotide 5' upstream of start codon is designated as -1 position.

Cis-acting elements	Sequence	Position	Function
ABRE	CACGTG	+123, +325	abscisic response
ACE	AAAACGTTTA	-349	light response
ARE	TGGTTT	+77	anaerobic induction
ATCT Motif	AATCTAATCT	+944, -966	light response
Box 4	ATTAAT	+336, +713, +1148	light response
Box II	TGGTAATAA	-547	light response
CGTCA -Motif	CGTCA	+60, +120, +826, -872, -884	MeJA response
LTR	CCGAAA	-310	low temperature response
MBS	CGGTCA	+22, -768	MYB binding site
TC-rich repeats	ATTTTCTTCA	+1100	defense and stress response
TGA element	AACGAC	-435	auxin response
WUN motif	TCATTACGAA	+232	wound response
circadian	CAANNNNATC	-997	circadian control
W Box	TGAC	+12, +73, +804, +858, +873, +885	WRKY binding site

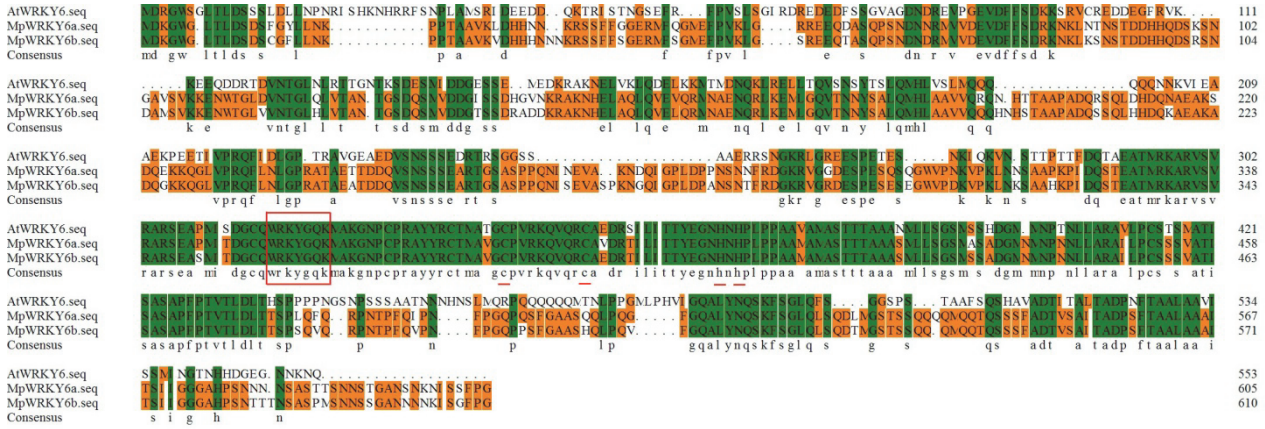

Fig. 1 Suppl. Amino acid sequence alignment of MpWRKY6a, MpWRKY6b, and AtWRKY6, showing WRKY domain (*red boxes*) and novel zinc finger structure, $CX_5CX_{23}HXH$ (*red lines*).

Sequence of *MpPHO1* promoter region

TCTCTTGTGTCTCCGACCATTTAATTACAAAGGGTACTCGTCCCCCTTTTATAGGCCTT
CAAGAAGACCCAAAAGTCCTAGGCTCTCAAGTACCTCACCGCTGAGCATTAATATAAA
M-1-S 5'-TATAAACCAAATGTGTTGATAAGACTTGCTCGCTACTCCTTCG-3'
CCAAATGTGTTGACTAGACTTGCTCGCTACTCCTTCGTTCTTTGGTCGACACATGGA
M-1-A 5'-CGAAGGAGTAGCGAGCAAGTCTTTTCAACACATTTGGTTTATA-3'
M-2-S 5'-GAAATTCGTTCAAAGTTGATTGCATGTTTTCCTGGGC-3'
GATGAATTGAAATTCGTTCAAAGTTGACTGCATGTTTTCCTGGGCCAACACATACCGA
M-2-A 5'-GCCCAGGAAAACATGCAATCAACTTTGAACGAATTTC-3'
GCACCTTGTTCAAACATGGGTTTAAGGAAGCCCATGCCCAAGCGCTTAGTCTGACAA
CCTTTATGTCCCTTCATAGGTTGCTGCCCTTG

Sequence of mutant *MpPHO1* promoter region

TCTCTTGTGTCTCCGACCATTTAATTACAAAGGGTACTCGTCCCCCTTTTATAGGCCTT
CAAGAAGACCCAAAAGTCCTAGGCTCTCAAGTACCTCACCGCTGAGCATTAATATAAA
CCAAATGTGTTGATTAGACTTGCTCGCTACTCCTTCGTTCTTTGGTCGACACATGGAG
ATGAATTGAAATTCGTTCAAAGTTGATTGCATGTTTTCCTGGGCCAACACATACCGAG
CACCTTGTTCAAACATGGGTTTAAGGAAGCCCATGCCCAAGCGCTTAGTCTGACAAC
CTTTATGTCCCTTCATAGGTTGCTGCCCTTG

Fig. 2 Suppl. Sequences of *MpPHO1* promoter region and mutant *MpPHO1* promoter region used in yeast one-hybrid assays. Primers used in sequence mutation were listed. M-1-S and M-1-A is one primer pair used in the first W-box mutation. M-2-S and M-2-A is one primer pair used in the second W-box mutation.

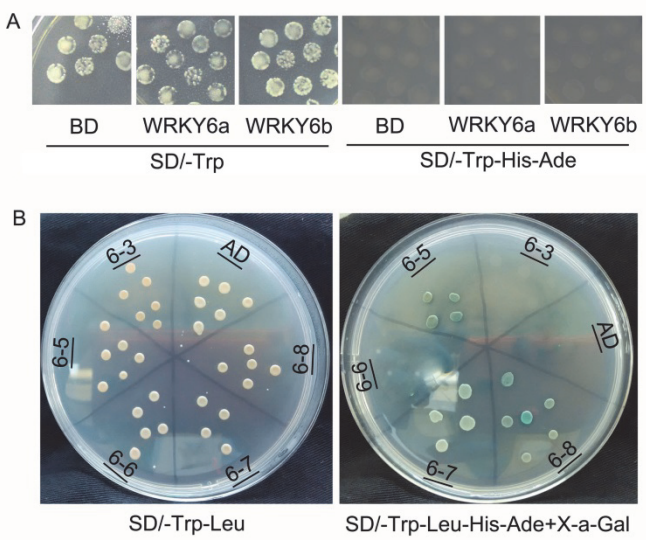

Fig. 3 Suppl. MpWRKY6a interaction proteins screened *via* yeast two-hybrid assays. *A* - All yeast cells, whether transferred with the pGBKT7, p-*MpWRKY6a*-GBKT7, or p-*MpWRKY6b*-GBKT7 vectors, were unable to survive on media that lacked Trp, His, and Ade. *B* - Only lines 6-5, 6-6, and 6-8 survived on SD/-Leu-Trp-His-Ade media with 5-bromo-4-chloro-3-indolyl α-D-galactopyranoside (X-α-gal). Among them, only 6-5 and 6-8 turned blue.

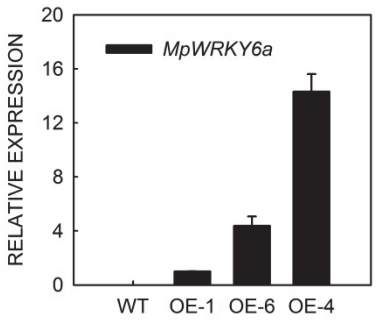

Fig. 4 Suppl. Expression of *MpWRKY6a* in different *Arabidopsis* over-expression lines. Expression levels were calculated relative to expression of *Attublin8* mRNA. Data represent means ± SD for 3 replicate samples.