

Supplementary Materials

>MDP0000215587

MGDTYECDHYK NATC SSSPPA APPHSA ADDMSLFLQQILVRSSTSLASGKAPQSLFSSSSPSVGALLPGNL
DRPCHSGFLGDGIPAVDSFAAFVSGHPNEASENEADEDCESEEGLEAFVEARPGGGRSSSKRSRAAEVHN
LSEKRRRSRINEKMKALQNLIPNSNKTDKASMLDEAIEY LKQLQLQVQMLSMRNGMSLHPLYLPGTLQP
VQLSQMRMELGEENRPLHLDMTGTLHMNLESSTQNLFNLSNQCTAANESYVPDMSNVVNSETSFVLEPSI
QSHLGPFQLPASSQEICRDDLLQH QKIDVNHSEMNL SVTATVSLPFAQVSDPKSTFDTCIIGRDRQEVGLLR
SIEQNFHIDRCLGIFELS



Figure S1. Amino acid sequence of candidate MdPIF6.

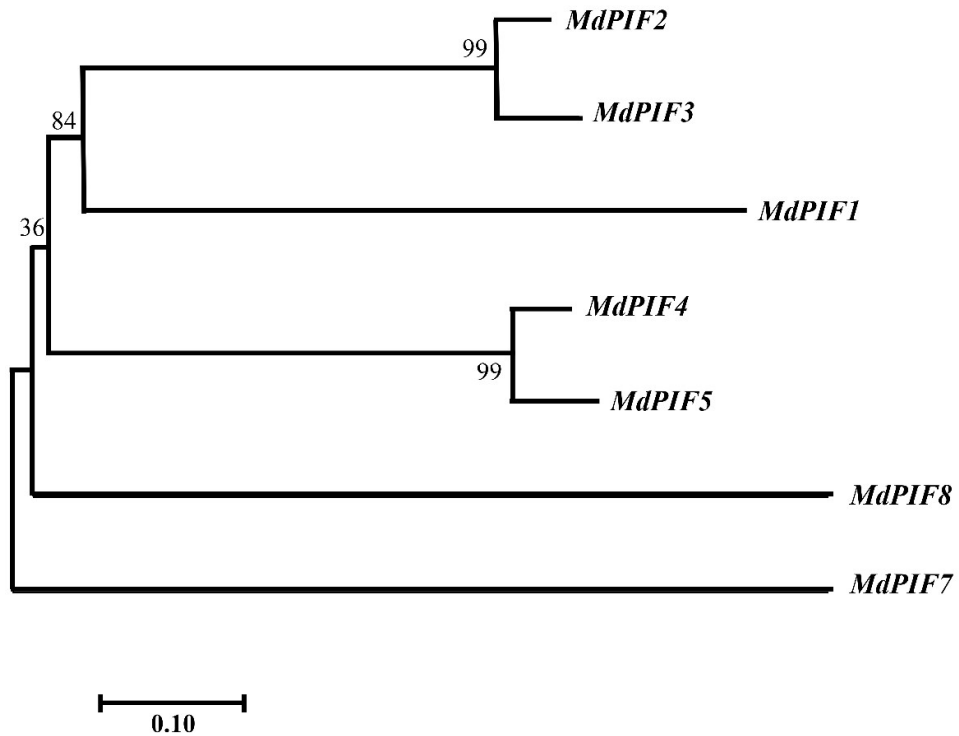


Figure S2. Phylogenetic tree analysis of the *MdPIF* cDNA sequences.

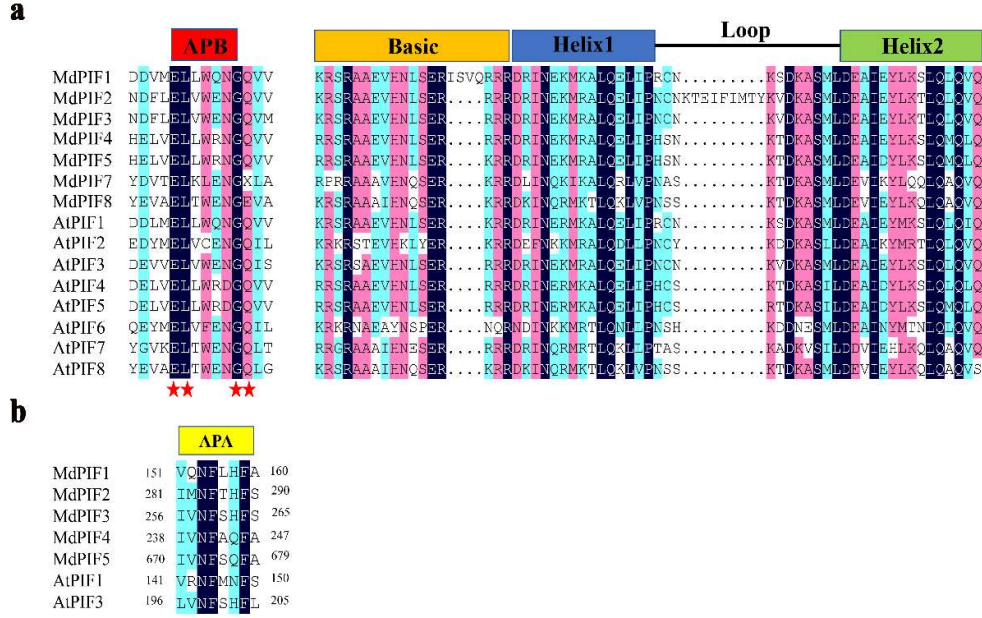


Figure S3. (a) Multiple sequence alignment of the bHLH and APB domains of the PIF proteins. Asterisks represent conserved amino acid residues. **(b)** Multiple sequence alignment of the APA domain in the PIF proteins.

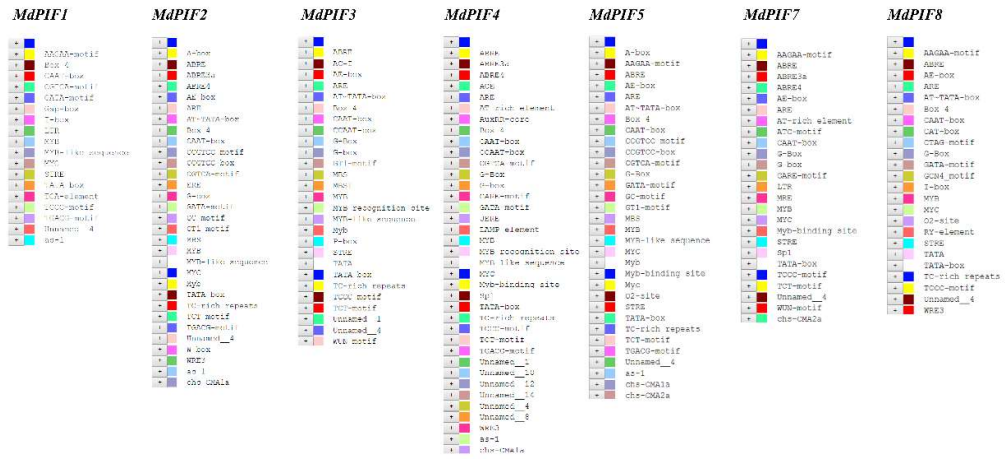


Figure S4. Cis-acting element analysis in the *MdPIF* genes promoter regions.

Table S1. Primers used for the gene expression analysis and vector construction in this study.

Primer name	Sequence (5'→3')
18S-F	ACACGGGGAGGTAGTGACAA
18S-R	CCTCCAATGGATCCTCGTTA
MdPIF1(qRT)-F	ATGAATGGGTGCGTCCCCGATTTTCGAA
MdPIF1(qRT)-R	TAGAGGAGGTCCGCGGAGAAGGGGT
MdPIF2(qRT)-F	CAGGAACAATCTGCCCCGAGT
MdPIF2(qRT)-R	CTAAGGGCGCACATTGCATC
MdPIF3(qRT)-F	GTCAAGGAGTTCAGTGCCGATG
MdPIF3(qRT)-R	TCCGCTTGGTGAGTTCATGTTCTG
MdPIF4(qRT)-F	TGGATGGGAAGCGGGATGGC
MdPIF4(qRT)-R	CGAGCGGGTGCCTAGGTAGAC
MdPIF5(qRT)-F	CTAGGCATCCGCTCGTTGAT
MdPIF5(qRT)-R	CAGCTCTTCCACCGAAAGGT
MdPIF7(qRT)-F	TAGTGGATCGGGGGACCATT
MdPIF7(qRT)-R	CATCTCGTTTTTCCAGCCCT
MdPIF8(qRT)-F	TTCTCGCTCCCCTCCCTTCAC
MdPIF8(qRT)-R	GCTACCTCGCCGTTTTCCCATG
MdAREB3.1(qRT)-F	GGTGCTTGCTGGGTATTAATCTC
MdAREB3.1(qRT)-R	TCTCCTCTCTCTCTCTAGC
MdEM1(qRT)-F	AATGGGGGAGCTGGATAATTCT
MdEM1(qRT)-R	CTAGAGCAATGAGACCTATCGGGC
MdEM6(qRT)-F	AATGGGGGAGCTGGATAATTCT
MdEM6(qRT)-R	CTAGTGCTTCAACTTCGGTTTCAAT
MdRAB18(qRT)-F	ATGGAAACCTCTACCAAGTCTG
MdRAB18(qRT)-R	TTACCGGACCTCGGGCCGAAA
MdRD29A(qRT)-F	ATGGAGAGTGGAGGTTCTGCAAGT
MdRD29A(qRT)-R	CTAGATTGGCTTACATCTTTTGCCT
MdPIF1-F	ATGAATGGGTGCGTCCCCGATTTTCG
MdPIF1-R	TCACGTGGTGAGTGCTATATGACGTA
MdPIF3-F	ATGCCTTTGTCCGAGCTTTATCGGATG
MdPIF3-R	TTATCCGTTAGCTCTGRTGTTGTT
MdPIF4-F	ATGGATACCAAGTCTAATGCTTGTA
MdPIF4-R	TCAATTGTCCGGCGTGAGATTCTT
MdPIF8-F	ATGAGCCAGCGGTTCTAGCTGGG
MdPIF8-R	TTAGCCCTTAGAGCTAGATGCTGGA
MdPIF1(GFP)-F	AAGGAGCCCTTCACC ATGAATGGGTGCGTCCCCGATTTTCG
MdPIF1(GFP)-R	GGCGCGCCCACCCTTTACAGTGGTGAGTGCTATATGACGTA
MdPIF3(GFP)-F	AAGGAGCCCTTCACCATGCCTTTGTCCGAGCTTTATCGGATG
MdPIF3(GFP)-R	GGCGCGCCCACCCTTTTATCCGTTAGCTCTGRTGTTGTT
MdPIF4(GFP)-F	AAGGAGCCCTTCACCATGGATACCAAGTCTAATGCTTGTA
MdPIF4(GFP)-R	GGCGCGCCCACCCTT TCAATTGTCCGGCGTGAGATTCTT
MdPIF8(GFP)-F	AAGGAGCCCTTCACCATGAGCCAGCGGTTCTAGCTGGG
MdPIF8(GFP)-R	GGCGCGCCCACCCTT TTAGCCCTTAGAGCTAGATGCTGGA

MdPIF4(OE)-F	GTCGACATGGATAACCAAGTCTAATGCTTGTA
MdPIF4(OE)-R	GGATCCATTGTCCGGCGTGAGATTCTTACATT
MdPIF1(GAL4BD)-F	ATGGCCATGGAGGCCGAATTCATGAATGGGTGCGTCCCC
MdPIF1(GAL4BD)-R	ATGCGGCCGCTGCAGGTCCGACTCACGTGGTGAGTGCTATATGACG
MdPIF3(GAL4BD)-F	ATGGCCATGGAGGCCGAATTCATGCCTTTGTCCGAGCTTTATC
MdPIF3(GAL4BD)-R	ATGCGGCCGCTGCAGGTCCGACTCCGTTAGCTCTGTGTTGTTAACAT
MdPIF4(GAL4BD)-F	ATGGCCATGGAGGCCGAATTCATGGATAACCAAGTCTAATGCTTGATA
MdPIF4(GAL4BD)-R	GA
MdPIF8(GAL4BD)-F	ATGCGGCCGCTGCAGGTCCGACTTGTCCGGCGTGAGATTCTT
MdPIF8(GAL4BD)-R	ATGGCCATGGAGGCCGAATTCATGAGCCAGCGCGTTCCT
	ATGGCCATGGAGGCCGAATTCATGAGCCAGCGCGTTCCT

Table S2. *Cis*-acting element analysis in the *MdPIF* genes promoter regions. The numbers in the table represent the number of *cis*-acting elements on the positive and negative chains.

Cis-acting element Name	Signal Sequence	<i>MdPI</i> F1	<i>MdPI</i> F2	<i>MdPI</i> F3	<i>MdPI</i> F4	<i>MdPI</i> F5	<i>MdPI</i> F7	<i>MdPI</i> F8
ATC	AGTAATCT						1/0	
LAMP	CTTTATCA				1/0			
GATA	AAGGATAAG G	0/1	1/0		0/1	0/1		0/1
ACE	CTAACGTATT				1/0			
TCT-motif	TCTTAC		0/1	0/2	1/0		1/0	
TCCC-motif	TCTCCCT	0/1			0/1		1/0	1/0
AE-box	AGAAACAA		0/1	1/1		0/1	1/1	2/0
G-box	TACGTG		3/1	2/0	4/2	1/1	2/1	1/0
GT1-box	GGTTAA		1/0	1/1		0/2		
Box4	ATTAAT	0/1	3/1	2/0	1/0	3/1		3/1
chs-CMA1a	TACTTAA		0/1		0/1	1/0		
chs-CMA2a	TCACTTGA					1/0	0/1	
Gap-box	CAAATGAA(A /G)A	1/0						
I-box	AGATAAGG	0/1						
AUXBR-core	GGTCCAT				1/0			
ABRE	ACGTG		1/2	0/2	3/2	1/1	1/1	0/1
GARE	TCTGTTG			1/0	1/0		1/2	
CGTCA	CGTCA	1/0	1/0			2/0		
TGACG	TGACG	0/1	0/1		1/0			
TCA-element	CCATCTTTTT	1/0						
P-box	CCTTTTG			1/0				

MBS	CAACTG	0/1	1/1	1/0			
LTR	CCGAAA	0/1				0/1	
TC-rich	ATTCTCTAAC	1/0	0/1	1/0			1/0
WUN-motif	AAATTCCT		0/1			1/1	
ARE	AAACCA	1/0	2/1	0/1	1/3	2/1	1/1