

Mt	ATGGGAAGAGGTAAGATTGAGATCAAGAGG	GATTGAAAACCTCAAGCAACAGGCAAGTTACT	60
Cb	ATGGGTAGAGGCAAGATTGAGATCAAGAGA	AATCGAGAACTCAAGCAACAGACAGGTTACT	60
Ca	ATGGGGAGAGGTAAGATTGAGATCAAGAGG	GATTGAGAACACAAACACAGGCATGTGACT	60
Pl	ATGGGAAGAGGTAAGATTGAGATCAAGAGG	GATTGAGAACTCAAATAACAGGCAGGTGACC	60
Pd	ATGGGGAGAGGTAAGATTGAGATCAAGAGG	GATTGAGAACGCAAGCAACAGGCAGGTGACC	60
Ck	ATGGGGAGAGGAAAGATAGAGATAAAGAGG	GATAGAGAACTCAAGCAACAGGCAGGTCACA	60
Vv	ATGGGGAGAGGGAAGATTGAGATCAAGAGG	GATCGAGAACTCAAGCAACAGGCAGGTGACC	60
	*****	*****	
Mt	TATTCAAAGAGAAAGAATGGAATCCTTAAGAAAGCAAAGGAAATAAGTGTCTTTGTGAT		120
Cb	TACTCAAAAAGAGAAATGGGATCATGAAAAAGCTAAGGAAATCAGTGTCTTTGCGAG		120
Ca	TACTCAAAGAGAAAACTGGGATCATGAAGAAGGCTAAGGAGATCACAGTTCTTTGTGAT		120
Pl	TACTCAAAGAGAGGACTGGGATCTTGAAGAAGGCCAGGAGATAACTGTTCTCTGCGAT		120
Pd	TACTCTAAGAGGAAAAATGGGATTATAAAAAAGCTAAGGAGATCACAGTTTATGCGAT		120
Ck	TACTCAAAGAGAAAGAATGGGATCATGAAGAAGGCAAGGAGATCACAGTTCTGTGTGAT		120
Vv	TACTCAAAGAGAGAAATGGGATCATGAAGAAGGCCAAGGAGATCACTGTTCTCTGCGAT		120
	***	***	
Mt	GCTCAAGTTTCCCTTATCTCTTTGGTGCTTCTGGAAAGATGCATGAATACATCAGCCCT		180
Cb	GCTCAGCTTTCTGTAGTCATCTTCGCTAGTTCTGGGAAGATGCATGAATTTTGAGCCCA		180
Ca	GCTAAGGTTTCCCTCATCATCTTCGGTACTTCTGGAAAGATGCATGAATATATAAGTCTT		180
Pl	GCTCATGTTTCTCTTGTATCTTTGCTACTTCAGGGAAAATGCACGAATACTGTAGCCCT		180
Pd	GCTCAAGTTTCTCTTGTATCTTTGCTAGTTCTGGAAGGATGCATGAGTACTGCAGCCCT		180
Ck	GCTCATGCTCTCTTGTATCTTTGCTAGTTCTGGCAAGATGCATGAGTACTGCAGCCCT		180
Vv	GCTCATGCTCTCTTGTATCTTTGCTAGCTCTGGAAAGATGCACGAGTACTGTAGCCCT		180
	***	***	
Mt	TCTACCACGTTGATTGATATTCTGGACAGATACCAGAGGCCTCTGGGAAAACCTATGG		240
Cb	AATACTACGTTAGTTGATATGTTGGATCAGTACCACAAGTTGTCTGGGAAGAGGCTCTGG		240
Ca	TCAACAAATTTGGTTGAAATGTTGGATGCTTACCAGAGGCTCTACTGGAAAGAAGCTGTGG		240
Pl	TCCACTACGGTGATTGATATTTTGGATAGATATCACAAAGCAGTCTACAAAGAAGCTGTGG		240
Pd	TCCACTACGGTGGTCGATCTGTTGGACAAGTTCACAAAGCAGTCTGGTAAGAGGCTATGG		240
Ck	TCAACTAAGTTGGTTGATATCTTGGATCGATATCACACACAGTCTGGGAAGAGGTTGTGG		240
Vv	TCTACACGTTGATTGATATCTTGGATAGGTATCACAAAGCAGTCTGGGAAGAGGCTCTGG		240
	***	***	
Mt	GATGCTAAGCATGAGAACCCTTAGCAATGAAATTGATAGAATCAAAAAGGAGAATGATAGC		300
Cb	GATGCAAAGCATGAGCATTTTGACAATGAAATCAACAGAATCAAGAAAGAGAATGACAGC		300
Ca	GATGCTAAGCATGAGAATTTAAGCAATGAAATTGATAGAGTTAAGAAAGAGAACGACAGC		300
Pl	GATCCTAAGCATGAAAATCTCAGCAATGAAGTGGATCGAGTCAAAAAAGAAAACGATAAC		300
Pd	GACGCTAAACATGAGAACCCTCAGCAAAGAGATTGACAGAATCAAGAAAGAGAATGACAGC		300
Ck	GATGCAAAGCATGAGAATTTGAGCAATGAAATTGATAGAATCAAGAAAGGAGAATGACAGC		300
Vv	GATGCAAAACATGAAAATCTCAGCAATGAATTGGATAGGATCAAAAAGGAGAATGATAGC		300
	***	***	
Mt	ATGCAAAATTGATCTCAGGCAC	TTGAAGGGAGAGGATATTACCTCACTGAATTACAAAGAG	360
Cb	ATGCAGATTGAGCTCAGGCAC	CTCAAGGGAGAAGATATCTCAACTTTGAAGTACAAAGAG	360
Ca	ATGCAGATTGAGCTCAGGCAC	CTAAAGGGGGAAGACATCACATCTTTGAATTACAAAGAG	360
Pl	ATGCAGATCGAGCTCAGGCAC	CTCAAGGGAGAGGATGTTACTTCTCTGAGTATCAAAGAG	360
Pd	ATGCAGATTGAGCTCAGGCAC	CTGAAAGGGGAAGATATCTCATCATTGCACCACACAGAG	360
Ck	ATGCAGATTGAGCTCAGGCAC	CTGAAGGGGGAAGATATCACATCTTTGCACTACAAAGAG	360
Vv	ATGCAGATTGAAGCTCAGGCAC	CTGAAGGGGGAGATATCTCATCTCTGCACCACAAAGAA	360
	*****	*****	

Supplementary Figure S1. Alignment of partial cDNA sequences (360 nucleotides) of *PISTILLATA* genes from selected woody species and from the mode legume *Medicago truncatula*. The regions highlighted with red rectangles presented four mismatches among the sequences and these regions were selected for the design of degenerated oligos. Mt, *Medicago truncatula*; Cb, *Catalpa bungei*; Ca, *Coffea arabica*; Pl, *Paeonia lactiflora*; Pd, *Populus deltoides*; Ck, *Cornus kousa*; Vv, *Vitis vinifera*.

a

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ATGGGTAGAGGCAAGATAGAGATCAAGAGAATAGAGAACTCGAGCAATAGGCAAGTGACA
M G R G K I E I K R I E N S S N R Q V T
TACTCCAAGAGGAGGAATGGGATCATGAAGAAGGCTAAGGAGATCACTGTACTTTGTGAT
Y S K R R N G I M K K A K E I T V L C D
GTCAGGTCTCTCTTGTATCTTTGGGAGTTCAGGCAAGATGCATGAGTACTGTAGCCCT
A Q V S L V I F G S S G K M H E Y C S P
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S T T L T D I L D K Y H K K S G K R L W
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D A K H E N L S N E L D R I K K E N D H
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M Q I E L R H L K G E E I T S L N H K E
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L M T I E E A L E N G L A C V R H K Q M
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E F T M M Q K N D K M L E D E N K Q L
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N F E L H Q Q E I I M G S R E M E N G Y
CATCAGCGAGTGAGAGAGTATCCGCCCCAGATGCCCTTTGCCTTCCGCGTGCAGCCAATC
H Q R V R E Y P P Q M P F A F R V Q P I
CAGCCCAATCTGCAGGAGAGAATTTAG
Q P N L Q E R I -
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b

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Seq569 CAGGAGAGAATTTAGAATAATAACATATAATTTTCTGGTATTAATTTGAACTCTAAACTA
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Seq570 CAGGAGAGAATTTAGAATAATAACATATAATTTTCTGGTATTAATTTGAACTCTAAACTA
Seq571 CAGGAGAGAATTTAGAATAATAACATATAATTTTCTGGTATTAATTTGAACTCTAAACTA
*****

Seq569 AACTCAGACTCGGATTGTTTAATGTTAAGCCTTTTAGCTGTGATTGTTTGTCAAAAAAAAA
Seq568 AACTCAGACTCGGATTGTTTAATGTTAAGCCTTTTAGCTGTGATTGTTTGTCATGGGGAC
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*****

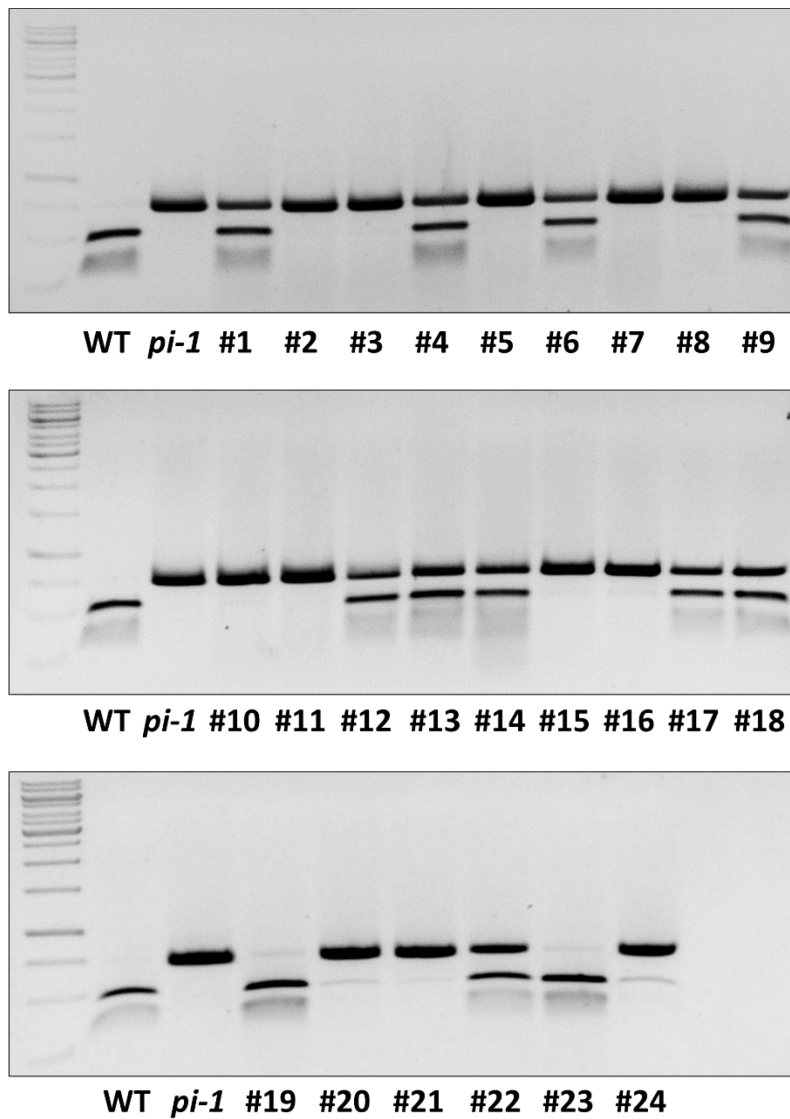
Seq569 AAAAAAAAAAAA
Seq568 GTCTTAGTTAAGCTTCTTCTAATAAGGTAAACTTGCTTTGTGAAACATTTATCGTGTGAT
Seq570 GTCTTAGTTAAGCTTCTTCTAATAAGGTAAACTTGCTTTGTGAAAAAAAAAAAAAAAA
Seq571 GTCTTAGTTAAGCTTCTTCTAATAAGGTAAACTTGCTTTGTGAAAAAAAAAAAAAAAA

Seq569
Seq568 TAATGCTTGTCTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Seq570
Seq571 AAAA
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Supplementary Figure S2. *PISTILLATA* gene sequence. (a) Coding sequence and protein from *PISTILLATA* gene from *Argania spinosa*. Conserved amino acid domains are highlighted in red (MADS domain), green (K-domain) and purple (PI-motif). Potential NLS sequences are underlined; (b) Sequences obtained by 3'RACE of the 3' untranslated region of the gene showing different lengths and polyadenylation position. The stop codon is marked in red.

AtPI	MGRGKIEIKRIENANNRVVTFSKRRNGLVKKAKEITVLCDAKVALIIFASNGKMIDYCCP	60
PhGLO2	MGRGKIEIKRIENSSNRQVTYSKRRNGIKKAKEITVLCDAKVSLIIFGNSGKMHEYCS	60
MtNGL9	MGRGKIEIKRIENSSNRQVTYSKRRSGILKKAKEINVLCDAQVSTIIIPSGKMHEYISP	60
AsPI	MGRGKIEIKRIENSSNRQVTYSKRRNGIMKKAKEITVLCDAQVSLVIFGSSGKMHEYCS	60
MtPI	MGRGKIEIKRIENSSNRQVTYSKRRNGILKKAKEISVLCDAQVSLILFGASGKMHEYISP	60
PhGLO1	MGRGKIEIKRIENSSNRQVTYSKRRNGILKKAKEISVLCDARVSVIIFASSGKMHEFSS-	59
AmGLO	MGRGKIEIKRIENSSNRQVTYSKRRNGIMKKAKEISVLCDAHVSIIIFASSGKMHEFCSP	60
	*****:.* **:*	
AtPI	SMDLGAMLDQYQKLSGKKLWDAKHENLSNEIDRIKKENDSLQLELRHLKGEDIQSLNLKN	120
PhGLO2	STTLPDMLDGYQKTSGRRLWDAKHENLSNEIDRIKKENDNMQVKLRHLKGEDINSLNHKE	120
MtNGL9	STTLIDMLERYHKASGKRLWDAKHENLKNEIEKLKKENEDMQIQLRHLKGKDINTLNYKK	120
AsPI	STTLTDILDYHKSGKRLWDAKHENLSNELDRICKENDHMQIELRHLKGEEITSLNHKE	120
MtPI	STTLIDILDYQASGKTLWDAKHENLSNEIDRIKKENDSMQIDLRHLKGEDITSLNYKE	120
PhGLO1	-TSLVDILDQYHKLGTGRRLWDAKHENLDNEINKVKDNDNMQIELRHLKGEDITSLNHRE	118
AmGLO	STTLVDMLDHYHKLSGKRLWDPKHEHLNEINRVKKENDSMQIELRHLKGEDITTLNYKE	120
	* :*: *: *: * * *:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*	
AtPI	LMAVEHAIEHGLDKVRDHQMEILISKRRNEKMMAEQRLTFQLQQQEMAIASNARGMM	180
PhGLO2	LMVLEEGTLNGLSSISAKQSEILRMVRKNDQILEEEHKQLQYALHQKEMAAMGGNMRMIE	180
MtNGL9	LMSLEDVLENGLLTVRHQKQMEVYKMKVRNDKILKEENRELNFIQQQQGYGSGRW---EI	177
AsPI	LMTIEEALENGLACVRHKQMEFFTMQKNDKMLEDENKQLNFELHQEIIIMGSRE---ME	177
MtPI	LMALEESLENGLTGVDRKKMEVHRMFKRNGKILEDENKELNFIQQHMALEGVGN---MH	177
PhGLO1	LMILEDALENGLTSIRNKQNEVLRMMRKKTSMEEEQDQLNCQLRQLEIATMNRNMGEIG	178
AmGLO	LMVLEDALENGTSALKNKQMEFVRMMRKHNEVEEENQSLQFKLRQMHLDPMNDNVMESQ	180
	** :*. : :* : : * . : : : : :*:.* *:*	
AtPI	R-----DHDGQFGYRVQPIQPNLQEKIMSLVID	208
PhGLO2	EVYHQ----RDRDYEYQMPFALRVQPMQPNLHERM-----	212
MtNGL9	NGL-----	180
AsPI	NGYHQ----RVREYP-QMPFAFRVQPIQPNLQERI-----	208
MtPI	GQWI-----	181
PhGLO1	EVFQQR---ENHDYQ-NHMPFAFRVQPMQPNLQERL-----	210
AmGLO	AVYDHHHHQNIADYE-AQMPFAFRVQPMQPNLQERF-----	215

Supplementary Figure S3. Protein alignment of AsPI and functional characterized PI/GLO-related proteins from different species. Amino acid residues identical to all the sequences are indicated by stars (*). To improve the alignment, dashes were introduced into the sequence. The region designated as the PI motif is boxed. At, *Arabidopsis thaliana*; Ph, *Petunia hybrida*; Mt, *Medicago truncatula*; As, *Argania spinosa*; Am, *Antirrhinum majus*.



Supplementary Figure S4: Genotyping of transgenic plants transformed with 35S::*AsPI* for the presence of the *pi-1* mutation. A genomic PCR product (729 bp) was amplified and digested by *Bse*GI. Two fragments (451 and 278 bp) were obtained in the case of wild-type plants (lower bands are generally faint in the gels). *Bse*GI does not cut the 729 bp PCR fragment in *pi-1/pi-1* homozygous plants. Heterozygous *PI/pi-1* plants showed three bands. Twenty-four transformants were analysed.

Supplementary Table S1. Primers used in this work.

Primer name	Primer sequences (5' to 3')	
PI DEG FOR	ATG GGD AGA GGH AAG ATW GAG ATM AAG	Degenerated oligo
PI DEG REV	GTG CCT SAG HTC RAT YTG CAT	Degenerated oligo
AsPI GSP2	GAG AAC CTC AGC AAC GAA CT	3' RACE
AsPI GSP7	CCT CTT CCC AGA CTT CTT GTG AT	5' RACE
PI argan ATG For	ATG GGT AGA GGC AAG ATA GAG	AsPI cDNA amplification
PI argan -STOP Rev	AAT TCT CTC CTG CAG ATT GGG C	
Q-AsPI For3	GGG ATC ATG AAG AAG CTA AGG	qRT-PCR
Q-AsPI Rev3	GGC TAC AGT ACT CAT GCA TCT T	
Arg YCF2 For	CCC GAA CCA AGG AAT CCC T	qRT-PCR
Arg YCF2 Rev	TCC CCT TCT TCA AAC TCC GAT	
AtTIP41 For	GTG AAA ACT GTT GGA GAG AAG CAA	qRT-PCR
AtTIP41 Rev	TCA ACT GGA TAC CCT TTC GCA	

Supplementary Table S2. Accession numbers of the *AP3/DEF*- and *PI/GLO*-related MADS-box genes used for phylogenetic analysis.

Gene	Species	GenBank Id
<i>MtPI</i>	<i>Medicago truncatula (Mt)</i>	FJ403468
<i>PIPI</i>	<i>Paeonia lactiflora (Pl)</i>	KC354379
<i>CabuPI</i>	<i>Catalpa bulgaei (Cabu)</i>	KM112022.1
<i>CaPI</i>	<i>Coffea arabica (Ca)</i>	KJ483234
<i>CorPI</i>	<i>Cornus kousa (Cor)</i>	JQ753781
<i>PdPI</i>	<i>Populus deltoides (Pd)</i>	EU029172
<i>VvPI</i>	<i>Vitis vinifera (Vv)</i>	NM_001280946.1
<i>MASAKO BP</i>	<i>Rosa rugosa</i>	AB038462.1
<i>SITM6/FBP1</i>	<i>Solanum lycopersicum (Sl)</i>	XM_004245154.4
<i>PhGLO1</i>	<i>Petunia Hybrida (Ph)</i>	M91190.1
<i>PhGLO2</i>	<i>Petunia Hybrida (Ph)</i>	X69947.1
<i>AmGLO</i>	<i>Antirrhinum majus (Am)</i>	AB516403
<i>MtPI</i>	<i>Medicago truncatula (Mt)</i>	FJ403468
<i>MtNGL9</i>	<i>Medicago truncatula (Mt)</i>	FJ403469
<i>Paps PI-1</i>	<i>Papaver somniferum (Ps)</i>	EF071994.1
<i>Paps PI-2</i>	<i>Papaver somniferum (Ps)</i>	EF071995.1
<i>AtPI</i>	<i>Arabidopsis thaliana (At)</i>	NM_122031
<i>MtTM6</i>	<i>Medicago truncatula (Mt)</i>	JN412097.1
<i>MtNMH7</i>	<i>Medicago truncatula (Mt)</i>	JN412096.1
<i>AtAP3</i>	<i>Arabidopsis thaliana (At)</i>	AY142590
<i>PhTM6</i>	<i>Petunia Hybrida (Ph)</i>	AF230704
<i>PhDEF</i>	<i>Petunia Hybrida (Ph)</i>	DQ539416.1
<i>SITAP3/TDR6</i>	<i>Solanum lycopersicum (Sl)</i>	AY098734.2
<i>AmDEF</i>	<i>Antirrhinum majus (Am)</i>	HQ853386.1
<i>MdMADS13</i>	<i>Malus domestica (Md)</i>	NM_001328749.1
<i>MdTM6</i>	<i>Malus domestica (Md)</i>	AB081093.1