

SUPPLEMENTARY DATA

TABLE S1. Tissue samples of *Clianthus maximus* 'Kaka King'[®] for RNA isolation

Sample types	Sample description	Sampling date
Vegetative tissue +/- reproductive structures	Shoot tips with/without inflorescence primordia	8/11/2002
	Shoot tips with/without inflorescence primordia	8/01/2003
	Shoot tips with/without inflorescence primordia	24/02/2003
	Shoot tips with/without inflorescence primordia	4/04/2003
	Shoot tips without inflorescence primordia	1/05/2003
	Shoot tips with inflorescence primordia	1/05/2003
	Fully expanded leaves	16/05/2003
	Shoot tips with/without inflorescence primordia	4/07/2003
	Shoot tips with/without inflorescence primordia	17/09/2003
Reproductive structures	Inflorescences (1–2 mm)	1/05/2003
	Inflorescences (15–20 mm)	28/01/2003
	Inflorescences (15–20 mm)	24/02/2003
	Inflorescences (15–20 mm)	4/04/2003
	Inflorescences (15–20 mm)	30/04/2003
	Inflorescences (15–20 mm)	11/06/2003
	Inflorescences (25–35 mm) with flower buds around 1 mm	11/06/2003
	Flower buds (2–3 mm)	11/06/2003
	Flower buds (2–3 mm)	24/07/2003
	Flower buds (5–7 mm)	11/06/2003
	Flower buds (10–12 mm) showing petal tip	15/08/2003
	Flower buds (10–12 mm) showing petal tip	26/09/2003
	Sepals from flower buds showing petal tip	26/09/2003
	Petals from flower buds showing petal tip	26/09/2003
	Stamens from flower buds showing petal tip	26/09/2003
	Carpels from flower buds showing petal tip	26/09/2003
	Mature flower buds before open	18/09/2003
	Mature flower buds before open	26/09/2003
	Fully opened flowers before senescence	26/09/2003
	Young seed pods 2 weeks after flower senescence	7/10/2003

TABLE S2. Floral identity gene homologues used for multiple alignment and phylogenetic analysis

Homologues	Gene names	Species	Accession No.
<i>LFY/FLO</i>	<i>CmLFY</i>	<i>Clianthus maximus</i>	DQ418756
	<i>LEAFY</i>	<i>Arabidopsis thaliana</i>	NM125579
	<i>FLO</i>	<i>Antirrhinum majus</i>	AAA62574
	<i>UNIFOLIATA (UNI)</i>	<i>Pisum sativum</i>	AAB88139
	<i>LcLFY</i>	<i>Lotus corniculatus var. japonicus</i>	AAX13294
	<i>MtUNI</i>	<i>Medicago truncatula</i>	AY928184
	<i>StLFY</i>	<i>Sophora tetraptera</i>	DQ418760
	<i>BoLFY</i>	<i>Brassica oleracea</i>	Q05536
	<i>NFL2</i>	<i>Nicotiana tabacum</i>	AAC48986
	<i>PtLF</i>	<i>Populus trichocarpa</i>	AAB51533
	<i>VvLFY</i>	<i>Vitis vinifera</i>	AAM46141
	<i>ZFL1</i>	<i>Zea mays</i>	AAO43175
	<i>NEEDLY</i>	<i>Pinus radiata</i>	AAB68601
	A class MADS-box genes (<i>API/SQUA</i> , <i>CAL</i> , <i>euFUL</i>)	<i>CmAPI</i>	<i>Clianthus maximus</i>
<i>API</i>		<i>Arabidopsis thaliana</i>	Z16421
<i>CAL</i>		<i>Arabidopsis thaliana</i>	NM102395
<i>SQUA</i>		<i>Antirrhinum majus</i>	CAA45228
<i>PEAM4</i>		<i>Pisum sativum</i>	AJ291298
<i>MtPIM</i>		<i>Medicago truncatula</i>	DQ139345
<i>StAPI</i>		<i>Sophora tetraptera</i>	DQ418761
<i>LcAPIa</i>		<i>Lotus corniculatus var. japonicus</i>	AY770395
<i>LcAPIb</i>		<i>Lotus corniculatus var. japonicus</i>	AY770396
<i>MdAPI</i>		<i>Malus x domestica</i>	AY071921
<i>MdCAL</i>		<i>Malus x domestica</i>	GU983665
<i>PtAPI-1</i>		<i>Populus trichocarpa</i>	AAT39554
<i>FRUITFULL</i>		<i>Antirrhinum majus</i>	AY306139
<i>NAPI</i>		<i>Nicotiana tabacum</i>	AAD01421
<i>EAPI</i>		<i>Eucalyptus globulus</i>	AAG24909
<i>MdMADS2</i>		<i>Malus x domestica</i>	U78948
<i>PsFUL</i>		<i>Pisum sativum</i>	AY884287
<i>AGL8</i>		<i>Arabidopsis thaliana</i>	NM125484
<i>LpMADS1</i>	<i>Lolium perenne</i>	AY198326	
<i>PrMADS2</i>	<i>Pinus radiata</i>	AAD09207	
B class MADS-box genes (<i>PI/GLO</i> , <i>AP3/DEF</i>)	<i>CmPI</i>	<i>Clianthus maximus</i>	DQ418758
	<i>PI</i>	<i>Arabidopsis thaliana</i>	D30807
	<i>GLO</i>	<i>Antirrhinum majus</i>	X68831
	<i>PEAM1</i>	<i>Pisum sativum</i>	AAW29099
	<i>MtPI</i>	<i>Medicago truncatula</i>	FJ403468
	<i>StPI</i>	<i>Sophora tetraptera</i>	DQ418762
	<i>LcPIa</i>	<i>Lotus corniculatus var. japonicus</i>	AY770398
	<i>LcPIb</i>	<i>Lotus corniculatus var. japonicus</i>	AY770399
	<i>VvPI</i>	<i>Vitis vinifera</i>	DQ059750
	<i>FBPI</i>	<i>Petunia hybrida</i>	Q03488
	<i>OsPI</i>	<i>Oryza sativa</i>	L37527
	<i>GmNMH7</i>	<i>Glycine max</i>	AY310303
	<i>LcAP3</i>	<i>Lotus corniculatus var. japonicus</i>	AY770400
	<i>DEF</i>	<i>Antirrhinum majus</i>	X62810
	<i>VvAP3</i>	<i>Vitis vinifera</i>	EF418603
	<i>AP3</i>	<i>Arabidopsis thaliana</i>	NM115294
	<i>PrDGL</i>	<i>Pinus radiata</i>	AF120097

	<i>CmAG</i>	<i>Clanthus maximus</i>	DQ418759
C class	<i>AG</i>	<i>Arabidopsis thaliana</i>	X53579
MADS-box	<i>StAG</i>	<i>Sophora tetraptera</i>	DQ418763
genes	<i>PsM7</i>	<i>Pisum sativum</i>	AY884291
(AG/FAR, PLE/SHP)	<i>LcAGa</i>	<i>Lotus corniculatus</i> var. <i>japonicus</i>	AY770402
	<i>LcAGb</i>	<i>Lotus corniculatus</i> var. <i>japonicus</i>	AY770403
	<i>NAG1</i>	<i>Nicotiana tabacum</i>	Q43585
	<i>VvAG</i>	<i>Vitis vinifera</i>	GU133631
	<i>PtAG1</i>	<i>Populus trichocarpa</i>	AF052570
	<i>PtAG2</i>	<i>Populus trichocarpa</i>	AF052571
	<i>BnAG</i>	<i>Brassica napus</i>	Q01540
	<i>FARINELLI (FAR)</i>	<i>Antirrhinum majus</i>	AB516405
	<i>PLENA (PLE)</i>	<i>Antirrhinum majus</i>	S53900
	<i>PsM8</i>	<i>Pisum sativum</i>	AY884292
	<i>LcAGL1</i>	<i>Lotus corniculatus</i> var. <i>japonicus</i>	AY770404
	<i>SHP1</i>	<i>Arabidopsis thaliana</i>	AY727644
	<i>SHP2</i>	<i>Arabidopsis thaliana</i>	AY727669
	<i>OsMADS3</i>	<i>Oryza sativa</i>	FJ750940
	<i>ZAG1</i>	<i>Zea mays</i>	NM001111851
	<i>ZAG2</i>	<i>Zea mays</i>	NM001111908
		<i>PrMADS9</i>	<i>Pinus radiata</i>

TABLE S3. Real-time PCR primers for expression analysis of floral identity genes and housekeeping genes in *Clianthus*

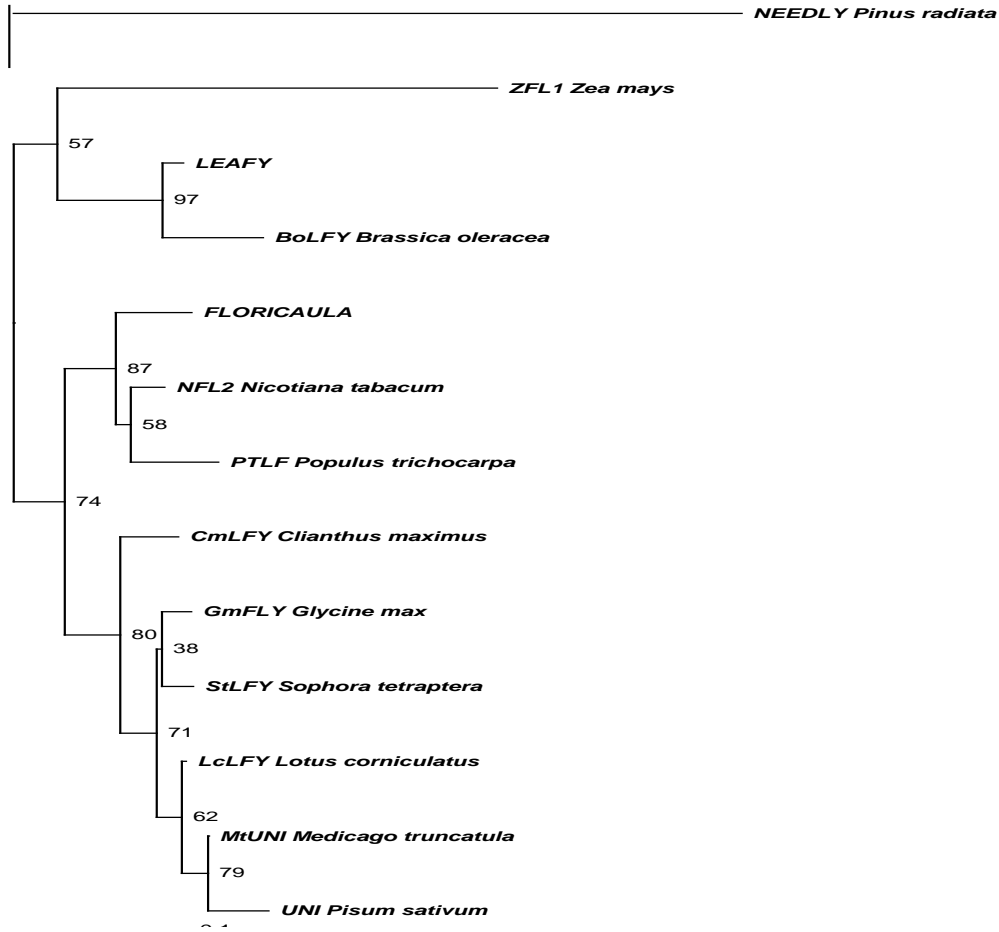
Genes	Primer sequences (5' to 3')	
<i>LEAFY</i>	Forward	ACG ATC AAT GCC GTG AGT TC
	Reverse	TCT AAC TGC TGC TCC AGA CTT TG
<i>APETALA1</i>	Forward	ATG CTG AGG TTG CTT TGA TTG
	Reverse	TCT AAC TGC TGT TCC AGA CTT TG
<i>PISTALLATA</i>	Forward	AGA ACA CAA GCA ACA GGC AAG T
	Reverse	GTG CCT GAG CTC AAT TTG CAT
<i>AGAMOUS</i>	Forward	TGG TCG CCT CTA TGA ATA TGC TA
	Reverse	GTT TGT CTG CTT CTT GCT GGT AA
<i>β-Actin</i>	Forward	GAG CTA TGA GCT GCC TGA TGG ACA
	Reverse	GTA ATC TCC TTG CTC ATC CTA TCA
<i>GAPDH</i>	Forward	ATG ACA GRT TTG GMA TTG TTG A
	Reverse	TGC CCT CAG AYT CYT CCT TGA
<i>18S rRNA</i>	Forward	TAC CGT CCT AGT CTC AAC CAT AA
	Reverse	AGA ACA TCT AAG GGC ATC ACA

FIG. S1. Comparison of amino acid sequences of CmLFY with representative FLO/LFY-like proteins

		301		360
CmLFY	(1)	-----PGEVARGKKNGLDYLFHLYDQCREFLIQVQTIAKDRGEKCP	TKVTNQVFR	
LcLFY	(233)	QREHPFIVTEPGEVARGKKNGLDYLFHLYEQCREFLIQVQAI	TAKDRGEKCP	TKVTNQVFR
UNI	(223)	QREHPFIVTEPAEVARGKKNGLDYLFHLYEQCREFLIQVQAI	TAKERGEKCP	TKVTNQVFR
MtUNI	(220)	QREHPFIVTEPGEVARGKKNGLDYLFHLYEQCREFLIQVQAI	TAKERGEKCP	TKVTNQVFR
GmFLY	(235)	QREHPFIVTEPGEVARGKKNGLDYLFHLYEQCREFLIQVQAI	TAKDRGEKCP	TKVTNQVFR
PTLF	(205)	QREHPFIVTEPGEVARGKKNGLDYLFHLYEQCRD	FLIQVQSI	TAKERGEKCP
NFL2	(237)	QREHPFIVTEPGEVARGKKNGLDYLFHLYEQCRD	FLIQVQNI	TAKERGEKCP
FLO	(220)	QREHPFIVTEPGEVARGKKNGLDYLFHLYEQCRD	FLIQVQTI	TAKERGEKCP
LFY	(232)	QREHPFIVTEPGEVARGKKNGLDYLFHLYEQCREFLIQVQTI	TAKDRGEKCP	TKVTNQVFR
BoLFY	(233)	QREHPFIVTEPGEVARGKKNGLDYLFHLYEQCREFLIQVQTI	TAKDRGEKCP	TKVTNQVFR
ZFL1	(220)	QREHPFVTEPGEVARAKKNGLDYLFHLYEQCRV	FLIQVQSI	TAKLGGHKS
NEEDLY	(245)	PREHPFIVTEPGELARGKKNGLDYLFHLYEQCGK	FLLEVQRI	TAKERGEKCP
		361		420
CmLFY	(51)	YAKKAGASYINKPKMRHYVHCYALHCLDEEASNE	LRAFKERGENV	GAWRQACYKPLVAI
LcLFY	(293)	YAKKAGASYINKPKMRHYVHCYALHCLDEEVSNE	LRRGFKERGENV	GAWRQACYKPLVAI
UNI	(283)	YAKKAGASYINKPKMRHYVHCYALHCLDEEVSNE	LRRGFKERGENV	GAWRQACYKPLVAI
MtUNI	(280)	YAKKAGASYINKPKMRHYVHCYALHCLDEEVSNE	LRRGFKERGENV	GAWRQACYKPLVAI
GmFLY	(295)	YAKKAGASYINKPKMRHYVHCYALHCLDEEVSNE	LRAFKERGENV	GAWRQACYKPLVAI
PTLF	(265)	YAKKAGASYINKPKMRHYVHCYALHCLDEEDASNA	LRAFKERGENV	GAWRQACYKPLVAI
NFL2	(297)	YAKKAGASYINKPKMRHYVHCYALHCLDEEASNA	LRAFKERGENV	GAWRQACYKPLVAI
FLO	(280)	YAKKAGANYINKPKMRHYVHCYALHCLDEEASNA	LRAFKERGENV	GAWRQACYKPLVAI
LFY	(292)	YAKKSASYINKPKMRHYVHCYALHCLDEEASNA	LRAFKERGENV	GSWRQACYKPLVNI
BoLFY	(293)	YAKKSAGANYINKPKMRHYVHCYALHCLDEEASNA	LRSFKVRGENV	GSWRQACYKPLVDI
ZFL1	(280)	YANKCASYINKPKMRHYVHCYALHCLDEEASNA	LRRAYKSRGENV	GAWRQACYAPLVEI
NEEDLY	(305)	HAKHNNAVYINKPKMRHYVHCYALHCLDSEQSNH	LRLRYKERGENV	GAWRQACYYPLVAI
		421		480
CmLFY	(111)	AARQGWDI	DAIFNAHPRLSIWY	-----
LcLFY	(353)	AARQGWDI	DAIFNAHPRLSIWY	VPTKLRQLCHAERN
UNI	(343)	AARQGWDI	DAIFNAHPRLSIWY	GPTKLRQLCHAERN
MtUNI	(340)	AARQGWDI	DAIFNAHPRLSIWY	VPTKLRQLCHAERN
GmFLY	(355)	AARQGWDI	DAIFNAHPRLSIWY	VPTKLRQLCHAERN
PTLF	(325)	ASRQGWDI	DSIFNAHPRLAIWY	VPTKLRQLCYAERN
NFL2	(357)	AARQGWDI	DTIFNAHPRLAIWY	VPTKLRQLCHSERS
FLO	(340)	AARQGWDI	DTIFNAHPRLSIWY	VPTKLRQLCHAERS
LFY	(352)	ACRHGWDI	DAVFNHPRLSIWY	VPTKLRQLCHLER
BoLFY	(353)	ACRHGWDI	DAVFNHPRLSIWY	VPTKLRQLCHLER
ZFL1	(340)	AARHGF	DI	DAVFAAHPRLAVWY
NEEDLY	(365)	ARENW	DI	EGIFNRNEKLIWY

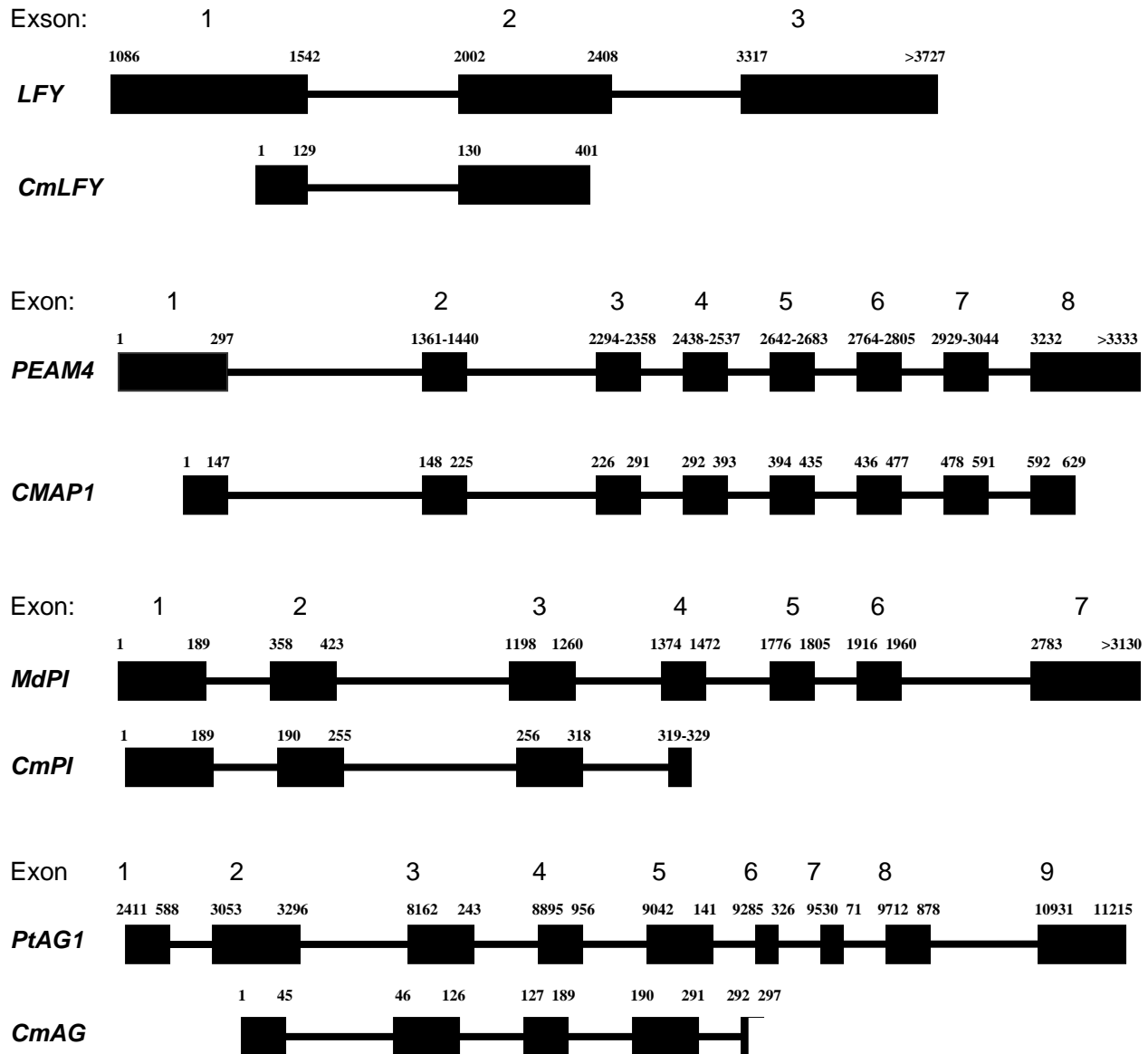
Identical and conserved amino acids are shaded. Sequence segments not covered by the CmLFY fragments were not included. ▼ intron/exon split site. E2 and E3: exon 2 and exon 3. Corresponding species names are listed in Table S2.

FIG. S2.. Neighbor-joining phylogenetic tree of representative FLO/LFY orthologues generated with 1000 bootstrap replicates



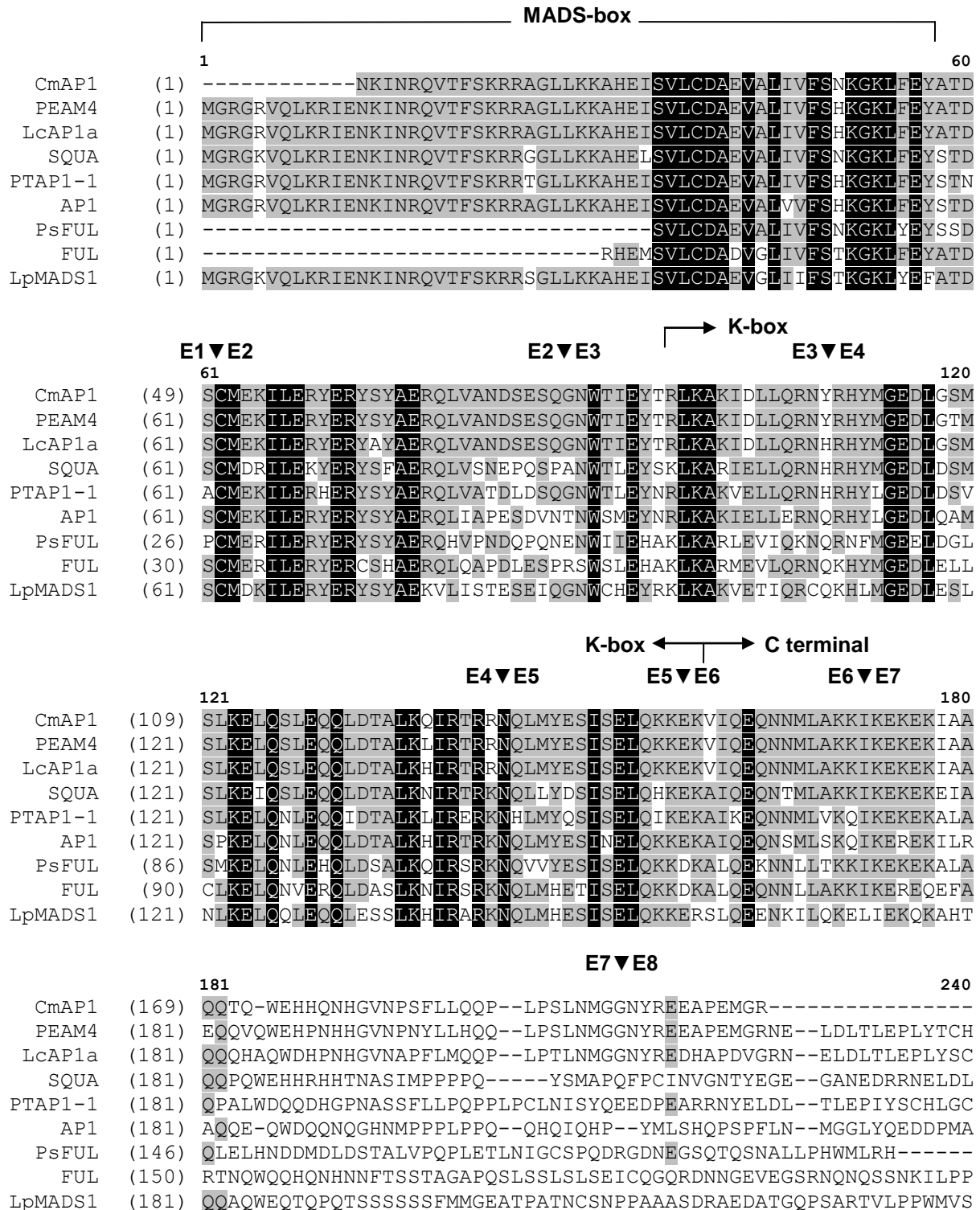
Species names and NCBI accession numbers are listed in Table S2.

FIG. S3. Deduced gene structure of *CmLFY*, *CmAPI*, *CmPI* and *CmAG* fragments in *C. maximus*



LFY: *Arabidopsis thaliana* *LEAFY* gene (AF466791); *PEAM4*: *Pisum sativum* *API* homologue (AJ291298); *MdPI*: *Malus domestica* *PI* homologue (AJ291491); *PTAG1*: *Populus trichocarpa* *AG* homologue (AF052570).

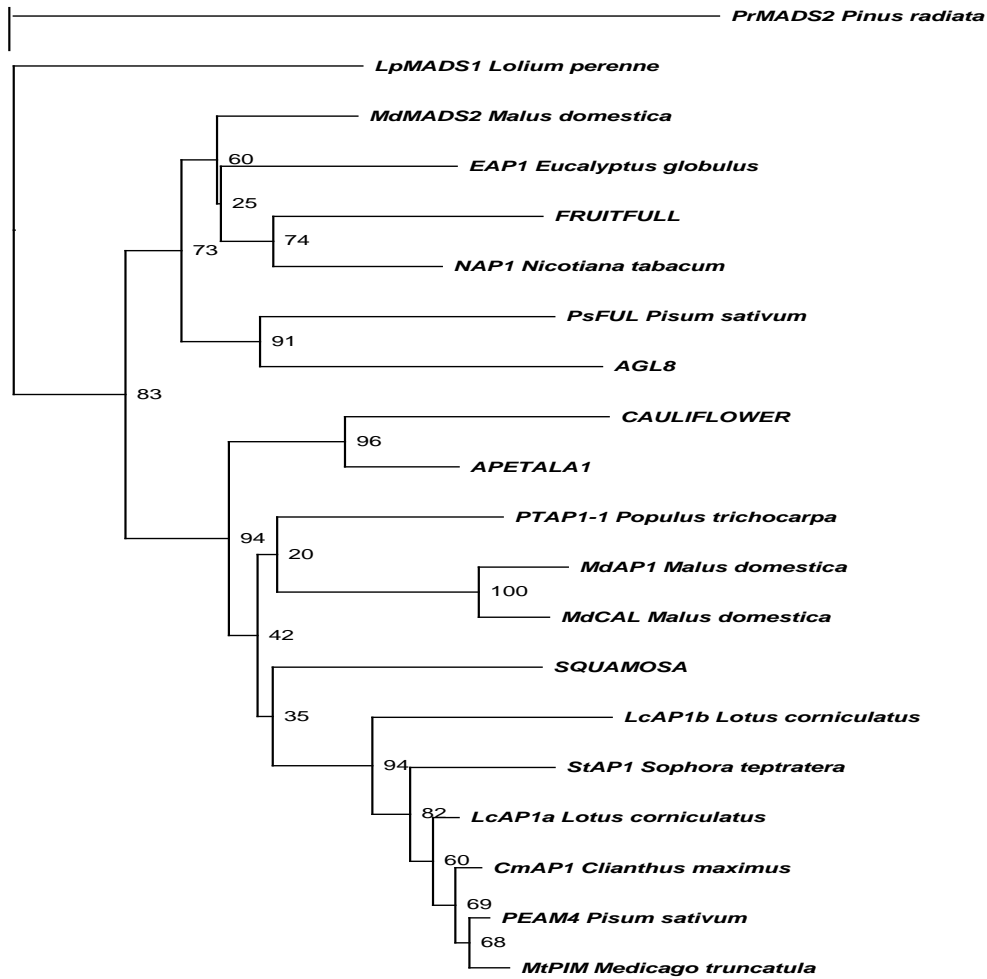
FIG. S4. Comparison of amino acid sequences of CmAP1 with representative class A MADS-box gene proteins



Identical and conserved amino acids were shaded. Sequence segments not covered by CmAP1 were not included.

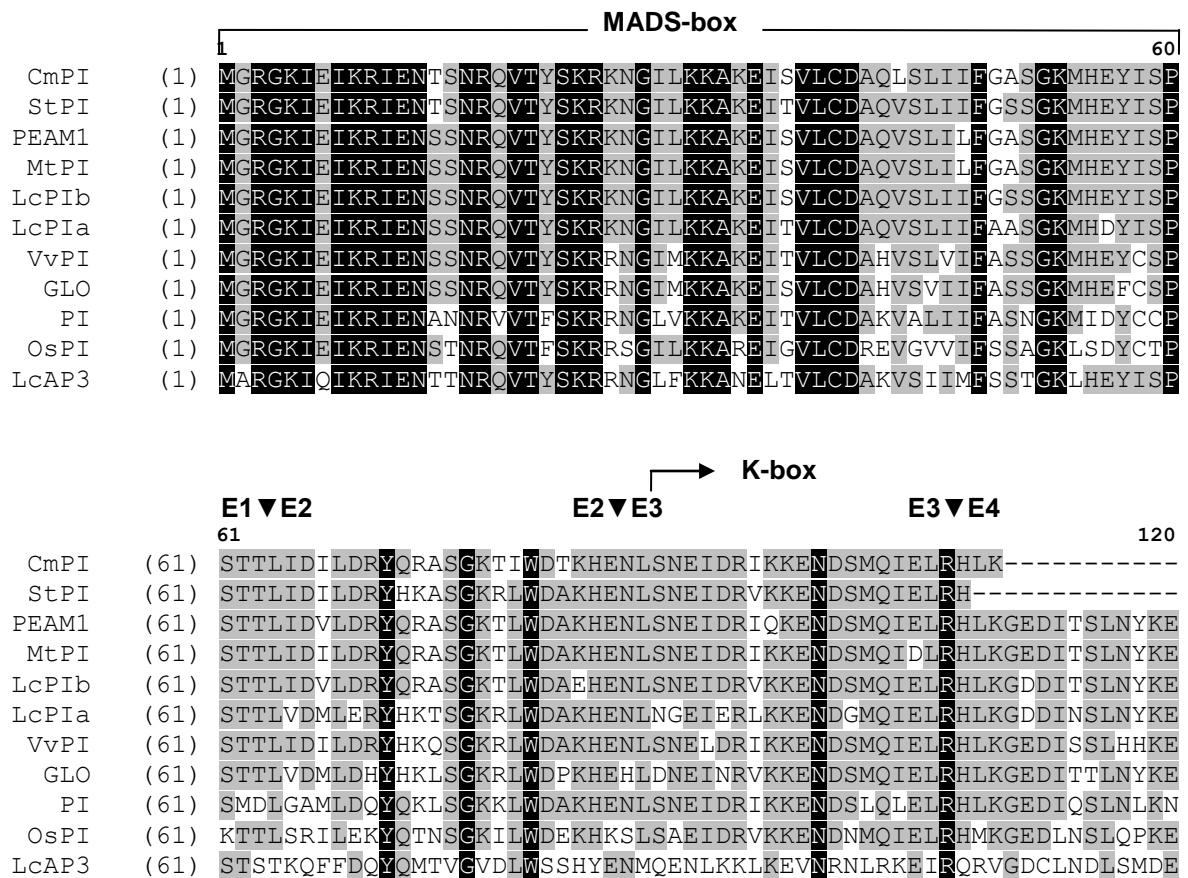
▼ split sites of intron/exon. E1-E8: exon 1- 8. Corresponding species names are listed in Table S2.

FIG. S5. Neighbor-joining phylogenetic tree of representative representative class A MADS-box gene proteins generated with 1000 bootstrap replicates



Species names and NCBI accession numbers are listed in Table S2.

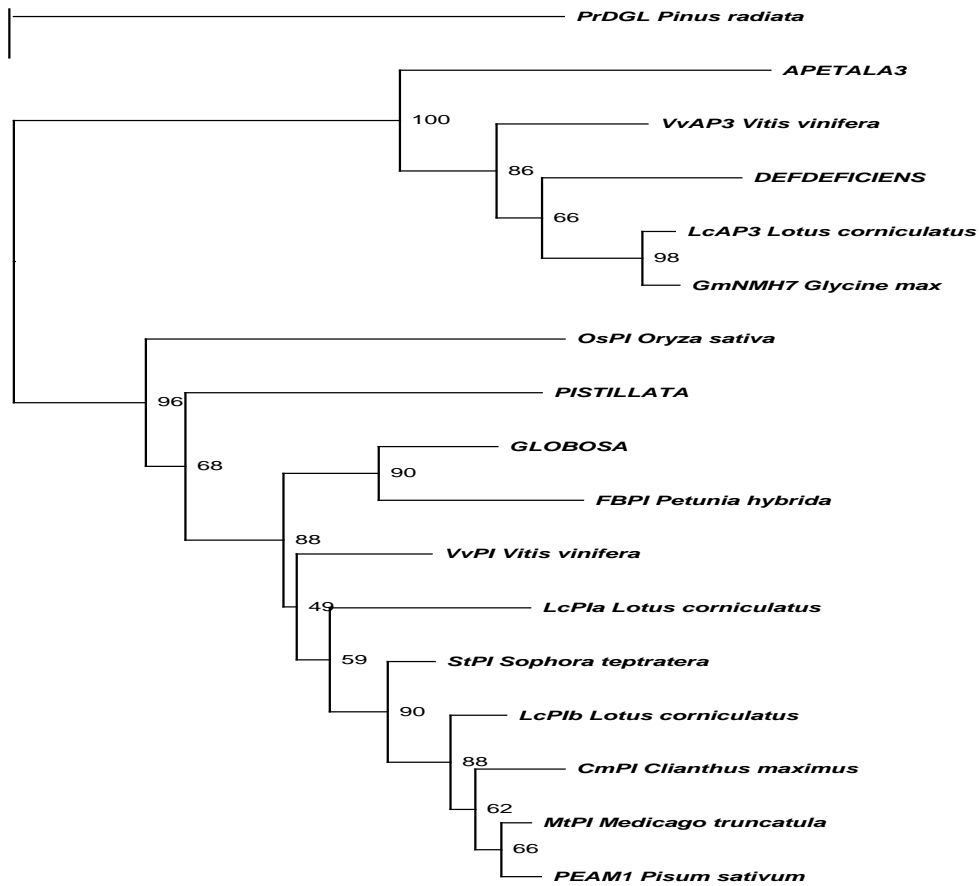
FIG. S6. Comparison of amino acid sequences of CmPI with representative class B MADS-box gene proteins



Identical and conserved amino acids were shaded. Sequence segments not covered by CmPI were not included.

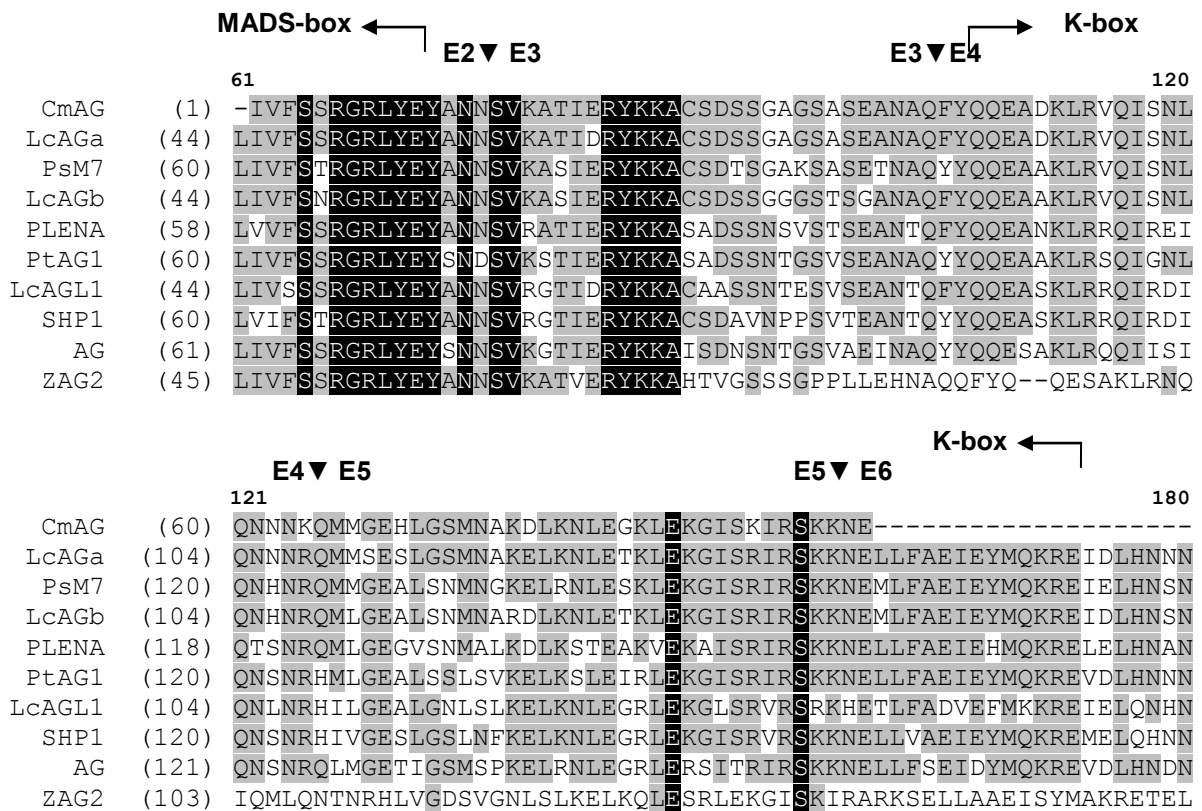
▼ split sites of intron/exon. E1-E4: exon 1- 4. Corresponding species names are listed in Table S2.

FIG. S7. Neighbor-joining phylogenetic tree of representative representative class B MADS-box gene proteins generated with 1000 bootstrap replicates.



Species names and NCBI accession numbers are listed in Table S2.

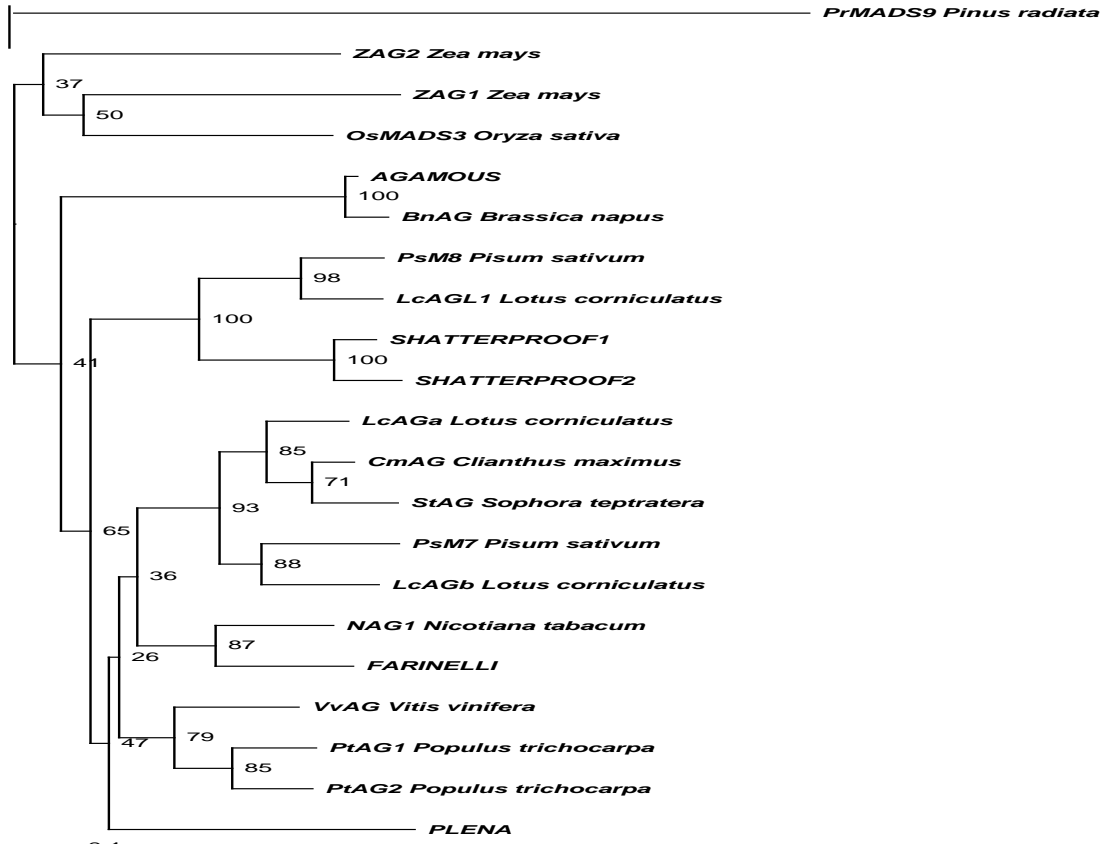
FIG. S8. Comparison of amino acid sequences of CmAG with representative class C MADS-box gene proteins



Identical and conserved amino acids were shaded. Sequence segments not covered by CmAG were not included.

▼ split sites of intron/exon. E2-E6: exon 2- 6. Corresponding species names are listed in Table S2.

FIG. S9. Neighbor-joining phylogenetic tree of representative representative class C MADS-box gene proteins generated with 1000 bootstrap replicates



Species names and NCBI accession numbers are listed in Table S2.