Supplemental Table I: Degenerate primers used to isolate pea flowering gene homologues

Gene	**Primer**	**Primer sequence (5’ to 3’)**	**aa sequence**
CCA1	**MYB.4**	ACATCTTTTGTAAGGYTTRAANCC	TGFKPYKR
	MYB.6	CTTACTGATYCKTGGAARGARGT	TTDSWKEV
COLa	**CO.1**	GACTCTTGCTTCNCKRTCCAT	MDREARV
	CO.4	AAGCCGGCAYCAACGVGTNCC	ARRHQRVP
COLb	**CO.FX**	TGTGATTCAGAGGTTCATTCTGCNAAYCCWYTNGC	CDSEIHSANPLA
	CO.RX	TAAGCCTTTCTCGAAGCATACCTTATNGTYTTYTCRAA	FEKTIRYASRKA
ELF3	**DELF3.1**	TCTTCACCTAGTAGCAAACGCACCAGAGAYCCNGARGA	SSPSSKRTRDPEE
	DELF3.4	ATGCAGAGCCAGGAGGATGTGTNCKCATYTG	QMRTQPCGPAS
ELF4	**DELF4.1**	CAGTCGGTGCTTGACAGGAACAGAGCAATAATHCARCARGT	QSVLDRNRAIIQQV
	DELF4.2	GAGATCAGAATAAAGAGAAGCAACCTTTGAAATRTTNCCRTT	NGNISKVVSMYSDL
EMF1	**EMF.2**	ATGGCAAARAAYCARTAYGA	MAKNQYE
	EMF.3	GGAATGGTGAAATCNGCNGG	PADFTIP
FCA	**FCA.F2**	TGTTGGATCTGTTCCTAGACTCGCNGCNCANGARGA	FVGSVPRTATEE
	FCA.R9	GTTCAGCAAATCTAACAATCAGAGGYTGRTTRCA	CNQPLIVRFAEP
FLD	**DFLD.1**	TGGCAYCTTGCAAATTTGGAATATGCAAA	WHLANLEYAN
	DFLD.2	CYCCCACMMTTTCDGCTAAAATATCRTAATC	DYDILAESVGD
FPA	**DFPA.3**	GGGAAAGGGATCGGGACAGAGCTTCCNGARGTNGT	GKGIGTELPEVV
	DFPA.4	GTATTTGGAGAAGAAGATTGGCNGCRAAYTG	QFAANLLLQIQ
FT	**DFT.1**	TCTATACACTGGTGATGACAGACCCNGAYGYNCC	FYTLVMVDPDVP
	DFT.4	TCTTCCACCASAGCCAGATTCYCKCTGAMWRTT	NCQRESGCGGR
FVE	**DFVE.1**	GGAAATCTCTTGTTCCTGTTCTTTAYGAYTGGYT	KSLVPVLYDWL
	DFVE.4	AATGTTCCCCCTCCACCAGTACTTKCRCARTCRTC	DDCESTGGGGTL
GI	**GI.3**	CTCATAWGARCTRTAACTCC	WSYSSNE
	GI.5	TTCCTCAGCVGTTGATYTKC	NSSAVDLP
LD	**LD.5**	CTTGCCCTGYTYGADATRTC	DISNRAK
	LD.9	AATCCTCTCGCNCARGARATG	NPLAQEM
LHY	**MYB.1**	ACAAAGCAGMGAGARARDTGG	TKQRERW
	MYB.3	TTCTTTTAGGTCKKGGMGGNGG	PPPRPKR
PFT1	**DPFT.4**	TGTGAACATTTTGAAKAATCTCTCWCAAGCACGNCAGGTNATG	VNILNNLSQARQVM
	DPFT.7	CATGTGRTCCTGAGATATAAGCCGAACTATTTGCAT	MHDQSILRVIQM
SOC1a	**MADS.1**	ATGGTGAGAGGAAARACNCARATG	MVRGKTQM
	MADS.3	GACCTTTCTGTTYTNTGYGAYG	ELSVLCDA
SOC1b	**AGL.3**	TCAAGGAGKTCDATYTTYTTCAT	MKKIEQUE
	FLF.7	CTGGCCARTACYTKRTTYTC	ENQVLAS
SVP	**DSVP.1**	ATGGCTMGWGARAAGATTCAAATWAARAAGATTGAAAA	MAREKIQIKKIEN
	DSVP.4	AGCTYTCATAGTCYTGGGGRRGWCCAGTRGARTT	NSTGPPQDYESS
TOC1	**DTOC1.3**	AGTTGATAGGAGAGAAGCAGCATTGHTNAARTTYMG	VDRREAALMKFR
	DTOC1.4	GATCCACATTAATACCATTCAACTTHCTGACRAAYTGNCC	GQFVRKMNGINVDL
VRN1	**DVRN1.3**	TRCGRCCCTCMTATTTRTAYAGGGGRTGYATAATGTATYT	RPSYLYRGCIMYL
	DVRN1.4	GGCTTAACTTDGCYCKRCCWCCYYTATADAGGCAGCGAAC	VRCLYRGGRAKLSQ
VRN2	**DVRN2.1**	CACTCACACAGAGTYCAGCCYATGGCACTRGAACAAGT	HSHRVQPMALEQV
	DVRN2.2	TCAAGAAGVCCAKGATTCCAAAGTTT	KLWNHGLLD

Supplemental Table II: MADS-box genes

Name	Arabidopsis	Pea			Medicago		Soybean	Lotus
	Gene	Gene	%[a]	Ref.	Genomic	EST	EST	EST
AP1 ***APETALA 1***	AT1G69120	*PsPIM*[b] (AJ291298)	71% (FL)	2,6	AC144726[b]	-	TC202688	-
FUL ***FRUITFULL***	AT5G60910	*PsFUL* (AY884287)	64% (FL)	1,5	 AC146650b[b,d,e]	TC84496[d] TC82227[d] AL387855[b,d,e]	TC196829	-
AGL6 ***AGAMOUS-LIKE 6***	AT2G45650	*PsMADS3*[b,d] (AY884288)	38% (FL)	1	-	AW688164[d]	TC220575[d]	-
AGL13 ***AGAMOUS-LIKE 13***	AT3G61120	*PsMADS5*[b,d] (AY884289)	56% (FL)	1	-	-	-	-
SEP1 ***SEP2*** ***SEPALLATA 1, 2***	AT5G15800 AT3G02310	*PsSEP1-2*[b] (AY884290)	72% (FL)	1	AC146650a[b,d,e]	BQ123807[b,d,e]	TC173284[d] TC195391[d]	-
SEP3 ***SEPALLATA 3***	AT1G24260	*PsMTF1* (AJ223318)	71% (FL)	4	AC144644	-	TC194024[d] TC199866[d]	BP037461
SEP4 ***SEPALLATA 4***	AT2G03710	-			-	-	-	TC17725[d]
SOC1 ***SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1***	AT2G45660	*PsSOC1a*[b,c,f] (AY830920)	64% (FL)	1	-	TC78994	TC184543	-
		PsSOC1b[b,c] (AY826729)	63% (P:86%)	1				
AGL14 ***AGL19*** ***AGAMOUS-LIKE 14, 19***	AT4G11880 AT4G22950	-			-	TC78724[d] BE124909[d]	-	-
SVP ***SHORT VEGETATIVE PHASE***	AT2G22540	*PsSVP* (AY830919)	71% (P:90%)	1	AC135848[b,e]	TC87621[b,e]	TC183173	-
AGL24 ***AGAMOUS-LIKE 24***	AT4G24540	-			-	TC90799[d]	-	-
AP3 ***APETALA 3***	AT3G54340	-			AC136451[b,e]	TC90653[b,e]	TC194043	TC8956
PI ***PISTILLATA***	AT5G20240	*PsPI* (AY842491)	52% (FL)	3	-	TC92737	TC179294	TC17763
AG ***AGAMOUS***	AT4G18960	*PsAG*[b] (AY884291)	70% (FL)	1	AC137837[b]	-	-	TC9670
SHP1 ***SHP2*** ***SHATTERPROOF***	AT3G58780 AT2G42830	*PsSHP*[d] (AY884292)	66% (FL)	1	-	TC86876[d]	TC194475[d]	-
STK ***SEEDSTICK***	AT4G09960	-			-	TC93057	TC177507	-
ANR1 ***AGL16*** ***AGL17*** ***AGL21*** ***AGAMOUS-LIKE***	AT2G14210 AT3G57230 AT2G22630 AT4G37940	-			AC123898[b,c] AC144564[c] AC126010[b,c,e]	 TC82622[b,c,e] TC81292[c,d]	AW706936[c]	-

(1) This study; (2) Berbel et al., 2001; (3) Berbel et al., 2005; (4) Buchner and Boutin, 1998; (5) Litt and Irish, 2003; (6) Taylor et al., 2002. (a) identity percentage at the amino-acid level, (FL) full length cDNA, (P) partial cDNA: percentage of Arabidopsis cDNA; (b) map position available; (c) multiple distinct sequences corresponding to a single Arabidopsis gene; (d) exact relationship to Arabidopsis gene unclear; (e) Medicago genomic and EST sequences correspond to the same gene; (f) Several EST sequences available corresponding to the same gene, see supplementary Table 8 for other accession numbers; (-) Sequence not identified.

Supplemental Table III: *CONSTANS*-like genes

Name	Arabidopsis	Pea		Medicago		Soybean	Lotus
	Gene	Gene	% [a]	Genomic	EST	EST	EST
CO CONSTANS	AT5G15840	*PsCOLa* [b,d,f]	72%	-	TC86982 [d]	-	-
COL1	AT5G15850	(AY830921)	(FL)				
COL2	AT3G02380						
CONSTANS-LIKE 1, 2							
COL3	AT2G24790	*PsCOLb* [b,d,f]	55%	AC127169 [b,d,e]	AW693899 [b,d,e,f]	TC204287 [c,d]	TC15164 [d]
COL4	AT5G24930	(AY830922)	(FL)		TC87753 [d]	TC204284 [c,d]	
COL5	AT5G57660				TC78669 [d]	TC203807 [c,d]	
CONSTANS-LIKE 3, 4, 5						TC203446 [c,d]	

(a) identity percentage at the amino-acid level, (FL) full length cDNA, (P) partial cDNA: percentage of Arabidopsis cDNA; (b) map position available; (c) multiple distinct sequences corresponding to a single Arabidopsis gene; (d) exact relationship to Arabidopsis gene unclear; (e) Medicago genomic and EST sequences correspond to the same gene; (f) Several EST sequences available corresponding to the same gene, see supplementary Table 10 for other accession numbers; (-) Sequence not identified.

Supplemental Table IV: *FLOWERING LOCUS T-TERMINAL FLOWER 1*-like genes

Name	**Arabidopsis**	**Pea (Garden)**			**Medicago**		**Soybean**	**Lotus**
	Gene	**Gene**	**%** [a]	**Ref.**	**Genomic**	**EST**	**EST**	**EST**
FT ***FLOWERING TIME***	AT1G65480	*PsFTL* [d] (AY830923)	61% (P:23%)	1	AC123593a [b,c,d] AC123593b [b,c,d] AC123593c [b,c,d]	-	TC219541 [c,d] BU548465 [c,d]	-
TSF ***TWIN SISTER OF FT***	AT4G20370							
BFT ***BROTHER OF FT***	AT5G62040	-			AC146807	-	AW707147	AU089275
MFT ***MOTHER OF FT***	AT1G18100	-			AC139526 [b,e]	TC81061 [b,e]	TC216444	-
TFL1 ***TERMINAL FLOWER 1***	AT5G03840	*PsTFL1a* [b,c] (DET) (AY340579)	72% (FL)	2	AC147007 [d,e]	TC78713 [d,e]	-	-
		PsTFL1b [b,c] (AY340580)	73 % (P:50%)	2	-	-	-	-
		PsTFL1c [b,c] (LF) (AY343326)	65% (FL)	2	-	-	-	CTL (AY423715)

(1) This study; (2) Foucher et al., 2003. (a) identity percentage at the amino-acid level, (FL) full length cDNA, (P) partial cDNA: percentage of Arabidopsis cDNA; (b) map position available; (c) multiple distinct sequences corresponding to a single Arabidopsis gene; (d) exact relationship to Arabidopsis gene unclear; (e) Medicago genomic and EST sequences correspond to the same gene; (f) Several EST sequences available corresponding to the same gene, see supplementary Table 10 for other accession numbers; (-) Sequence not identified.

Supplemental Table V: CAPS and dCAPS markers for mapping pea genes

Gene	**Primers**	**Sequence**	**Tm (ºC)**	**Restriction enzyme**	**Mapping population**
PsAG	pM7-FOR	GAAATTGAGTACATGCAGAAAAGGG	60	-	JI15 x JI399
	pM7-REV	TTCCAATGAGTACTAACCAACTAAC			
PsCOLa	COP.2F	GCTGGATTCAGTTACAATGG	60	*TaqI*	JI281 x JI399
	COP.2R	CTGGTACAACACCAACATCC			
PsCOLa	COMseI	CCATGATCATAATCAAGAAGGTAATATT	55	*MseI*	TOR x TER
	CO14	GATTCAAACTCCAACCCAAGT			
PsEMF1a	EMF4	GGATGGTTGTGGTGGATACGG	57	*BseNI*	TOR x TER
	EMF8	CTGGAAAGGGAAATCACTATG			
PsEMF1b	EMF4	GGATGGTTGTGGTGGATACGG	57	*DraI*	TOR x TER
	EMF8	CTGGAAAGGGAAATCACTATG			
PsFCA	FCA.1	TGAGAGGCTGATAGGGAAGAC	55	*BselI*	TOR x TER
	FCA.3	ATAAGCAAAGGCAAAAGAACG			
PsFPA	FPA1	AAACTTGAGAACGACNCCRTA	58	*MboII*	JI281 x JI399
	FPA3	GCGGACTTATTGCMAARGGNGG			
PsFVE	FVEP.11	TTTGAGGCTCATAAAGCTGC	55	*RsaI*	JI281 x JI399
	FVEP.14	GATCATAAGCATTCCAATGG			
PsGI	Gi3	CTCATAWGARCTRTAACTCC	55	*TaqI*	TOR x TER
	Gi5	TTCCTCAGCVGTTGATYTKC			
PsLD	LD11	ATCAGTGCTTTATTTGGCGTAA	60	*SspI*	TOR x TER
	LD12	AAGACGGAAAAGTTCTGTATTG			
PsMYB2	CCA4	CGTATCGTTCCCATTAGTGTC	60	*StyI*	JI281 x JI399
	CCA5	ATTCGAAGTCATGCTCAGAAG			
PsSOC1a	AGLR3	CAGTTGGAAAAGTGTGTAAGC	60	*HinfI*	TOR x TER
	AGLR6	GGTGGCGGTGGTGGTAGTTGC			
PsSOC1b	AGLR8	TGCTGTTCTATCTTTTGTAATTC	57	*SspI*	TOR x TER
	AGLR11	AGCCGGATTAATAATACTCAAACA			

TOR x TER population (Laucou et al., 1998); JI281 x JI399 and JI15 x JI399 (Hall et al., 1997);

Supplemental Table VI: Additional EST sequences corresponding to genes listed in Tables 1 to 4 and Suplementary Tables 6 to 8

Name	Arabidopsis	Pea [a]	Medicago	Soybean [c]	Lotus [c]
AP2 ***APETALA 2***	AT4G36920			TC21901 BE65994	
CO CONSTANS	AT5G15840	AY830921			
COL1	AT5G15850	AY826727			
COL2 ***CONSTANS-LIKE 1, 2***	AT3G02380				
COL3	AT2G24790	AY830922	AW693899 [b]		
COL4	AT5G24930	AY805328	TC88293 [b]		
COL5 ***CONSTANS-LIKE 3, 4, 5***	AT5G57660				
CRY1 ***CRYPTOCHROME 1***	AT4G08920		TC89497 [c] TC79909 [c]		TC15430 AV424420
CRY2 ***CRYPTOCHROME 2***	AT1G04400		TC78737 [c] TC79042 [c]		AV417531 AV424018
ELF5 ***EARLY FLOWERING 5***	AT5G62640			TC192128 TC185647	BI417263 TC13271
EMF2 ***EMBRYONIC FLOWER 2***	AT5G51230			TC184854 TC182138	
FKF1 ***FLAVIN-BINDING, KELCH REPEAT, F-BOX 1***	AT1G68050			AI960991 TC182454	
FLD ***FLOWERING LOCUS D***	AT3G10390		AW586703 [c] TC83020 [c]		
FLK ***FLOWERING LOCUS K***	AT3G04610		TC89387 [c] BF636961 [c]		TC13879 TC17620
FPA	AT2G43410		TC84230 [c] TC82911 [c]		TC19296 TC16749
FPF1 ***FLOWERING PROMOTING FACTOR 1***	AT5G24860		TC87988 [c] TC90090 [c]		
FUL ***FRUITFULL***	AT5G60910	AY884287 AY306169			
FVE	AT2G19520		TC87417 [b] TC91602 [b]		BP058734 TC13946
GI ***GIGANTEA***	AT1G22770			TC17500 TC17499	TC7440 TC7235
LD ***LUMINIDEPENDENS***	AT4G02560			AW569075 BE824317	
LHY ***LATE ELONGATED HYPOCOTYL***	AT1G01060		TC89350 [b] CA917283 [b]	TC189020 TC196676	
PFT1 ***PHYTOCHROME AND FLOWERING TIME***	AT1G25540			TC182513 BG041259	
PHYB ***PHYTOCHROME B***	AT2G18790				TC13239 AV427846
PIF3 ***PHYTOCHROME INTERACTING FACTOR 3***	AT1G09530		CA919209 [c] AW775035 [c]		
REF6 ***RELATIVE TO ELF6***	AT3G48430			TC196271 TC219371	
SOC1 ***SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1***	AT2G45660	AY830920 AY826728			
TFL2 ***TERMINAL FLOWER 2***	AT5G17690			AW471580 TC197445	
VRN1 ***VERNALIZATION 1***	AT3G18990			TC229117 TC229118	
ZTL ***ZEITLUPE***	AT5G57360			TC198766 TC195494	

(a) Same pea genes sequenced from different cultivars; (b) Medicago ESTs verified against genomic sequences as same gene; (c) Not experimentally verified.