Supporting Information

Zhang et al. 10.1073/pnas.1219690110

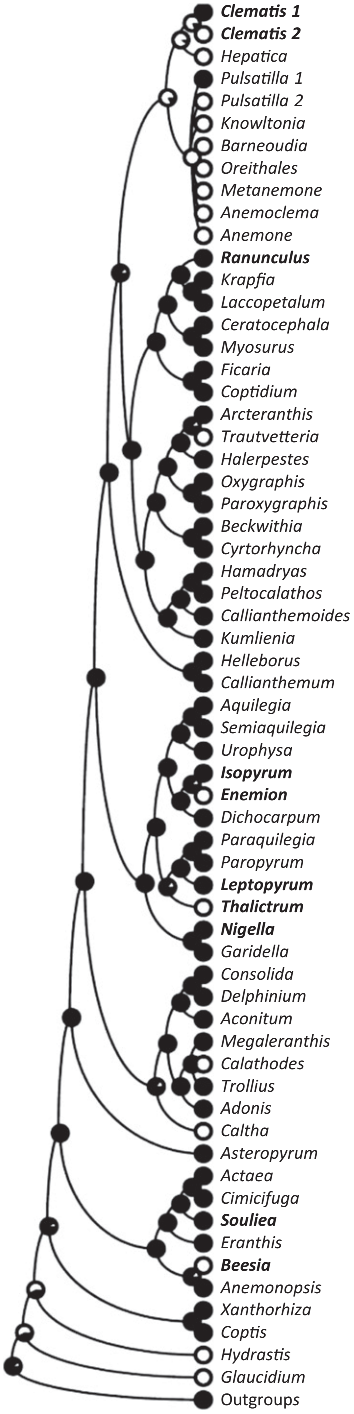
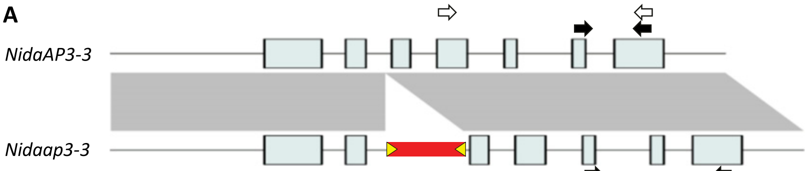


Fig. S1. Parallel petal losses within the Ranunculaceae. Filled and open circles indicate the character states of being petalous and apetalous, respectively. The probabilities of being petalous, which were inferred using the maximum likelihood method in Mesquite version 2.72, are indicated for each interior node. Note that in at least seven different lineages (excluding the two basal-most genera, *Glaucidium* and *Hydrastis*), apetalous genera all have petalous ancestors.



B

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acaaaatcagctcctttttttgctgtttcaaaacgactggaaacttttgcttttggctgcaattttt
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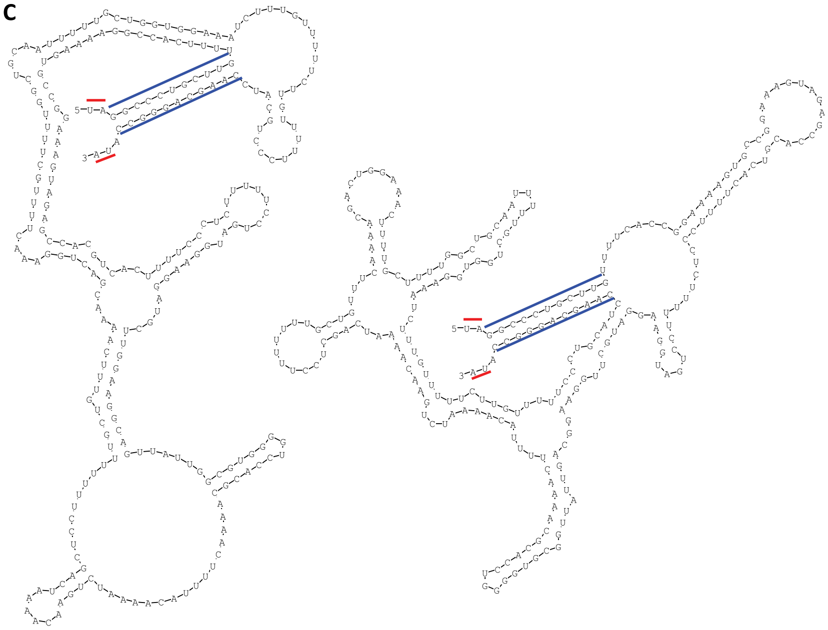


Fig. S2. Comparison of the functional and nonfunctional *AP3-3* alleles in *Nigella*. (*A*) Exon–intron structures of *NidaAP3-3* (*Upper*) and *Nidaap3-3* (*Lower*). Open and closed arrows indicate the positions from which primers used for in situ hybridization and qRT-PCR analyses, respectively, were derived (details given in Tables S1 and S3). The red block with two yellow triangles at both sides indicates the predicated *Gypsy/Ty3*-like miniature inverted-repeat transposable element (MITE) in *Nidaap3-3*. (*B*) Sequence of the predicted MITE, with the reverse complementary sequences and the “TA” repeats highlighted by blue and red bars, respectively. (*C*) Secondary structures of the MITE, predicted in DNAMAN 7.0 according to its minimum free energy.

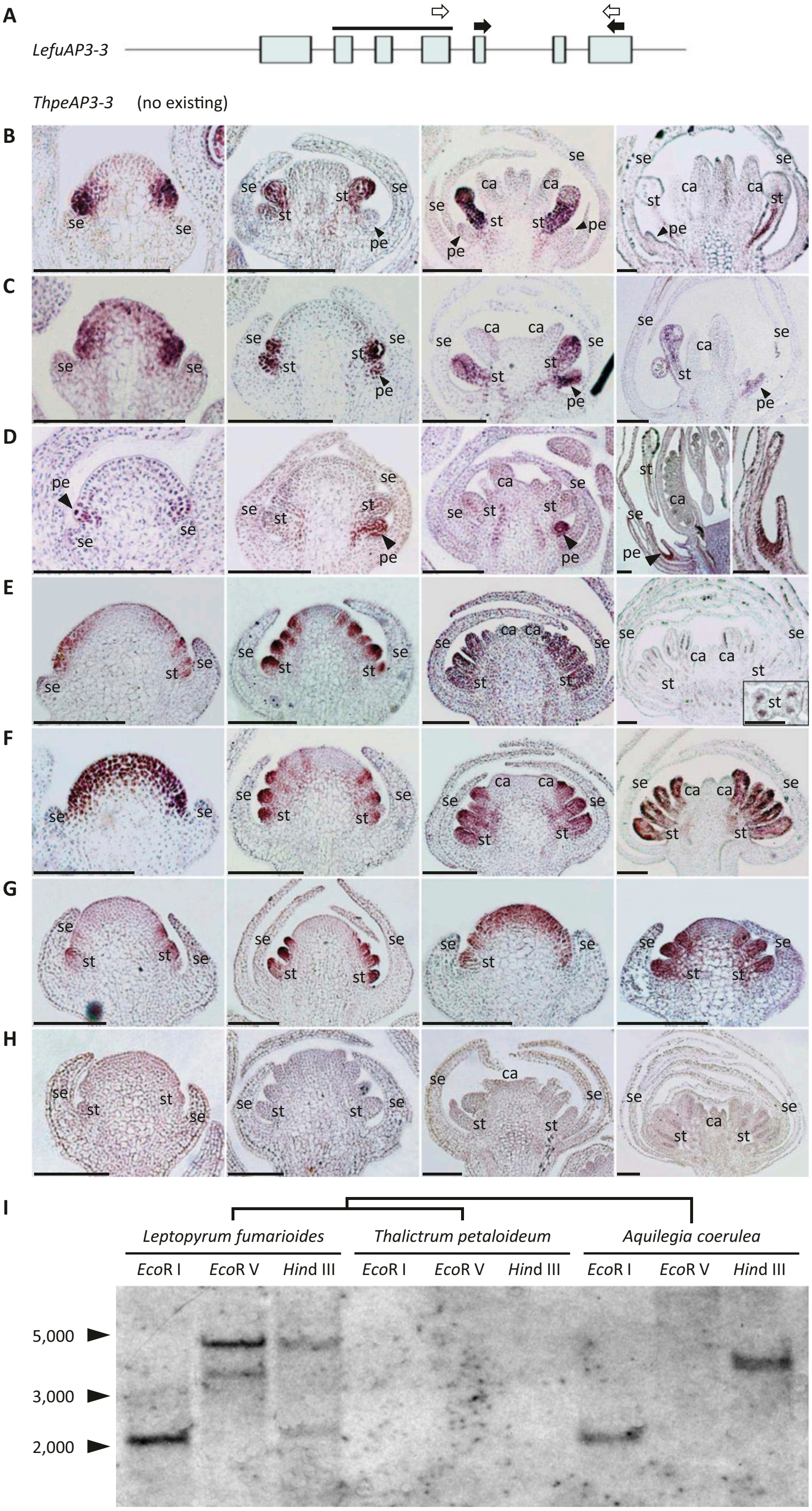


Fig. S3. The *AP3-3* genes from *Leptopyrum* and *Thalictrum*. (*A*) Exon–intron structure of *LefuAP3-3*. Open and closed arrows indicate the positions from which primers used for in situ hybridization and qRT-PCR analyses, respectively, were derived (Tables S1 and S3 give details). The black line indicates the region used as probe in Southern hybridization. (*B*–*H*) In situ hybridization of *LefuAP3-1* (*B*), *LefuAP3-2* (*C*), and *LefuAP3-3* (*D*) in *Leptopyrum*, *ThpeAP3-1* (*E*) and *ThpeAP3-2b* (*F*) in *Thalictrum*, and *LefuAP3-1* (*G*, left two pictures), *LefuAP3-2* (*G*, right two pictures), and *LefuAP3-3* (*H*) in *Thalictrum*. Arrowheads indicate petals; se, st, and ca refer to sepals, stamens, and carpels, respectively. (Scale bar, 50 μm.) (*I*) Southern hybridization of the *LefuAP3-3* probe in three species. For Southern hybridization, genomic DNA was extracted from fresh leaves of each species and digested with restriction enzymes *Eco*R I, *Eco*R V, and *Hin*d III. A 458-bp genomic DNA fragment covering the second to fourth exons of *Leptopyrum AP3-3* was labeled with a thermostable alkaline phosphatase enzyme (GE Healthcare) and used as a probe. The whole process was performed according to the instruction of Amersham Gene Images Alkphos Direct Labeling and Detection System (GE Healthcare).

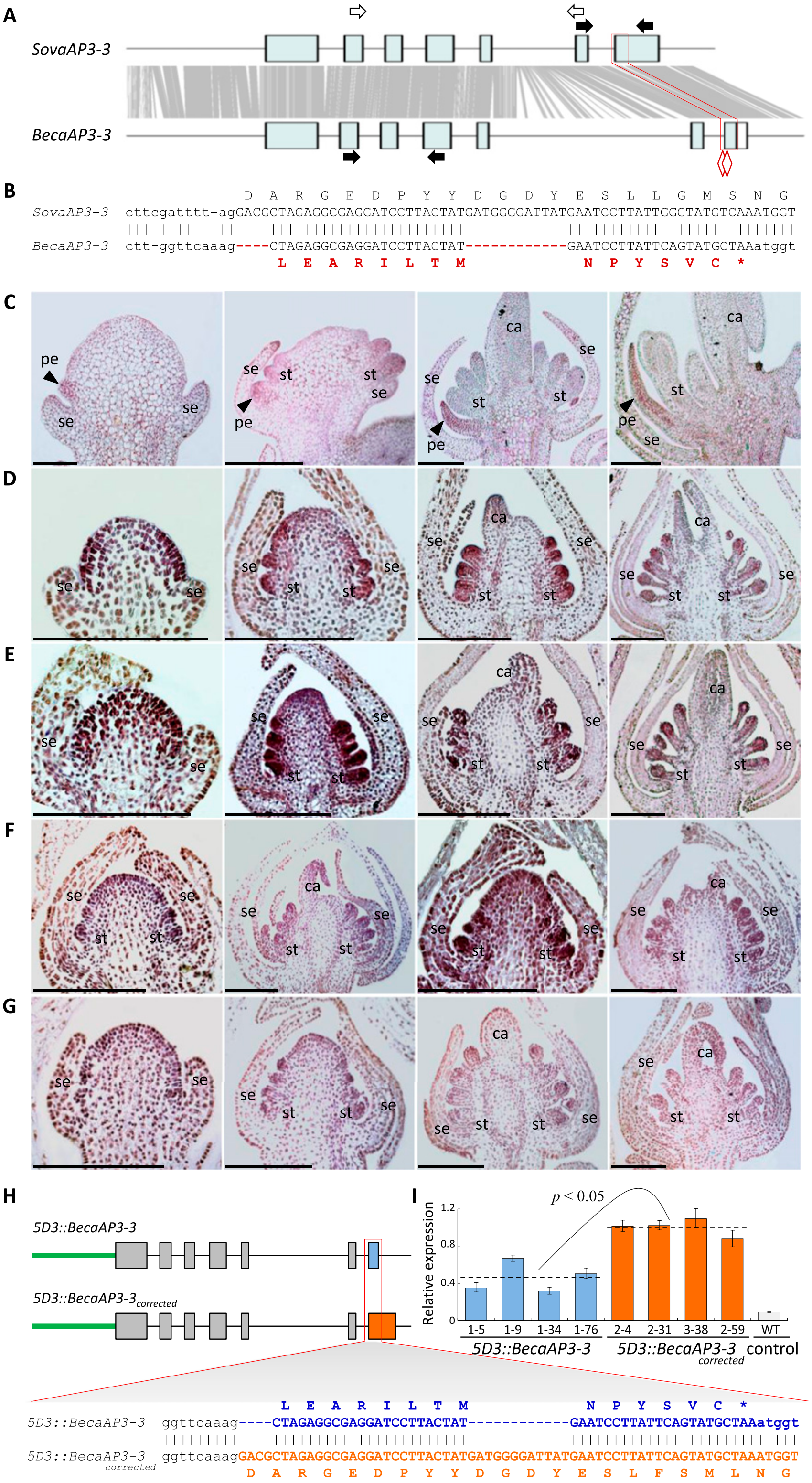


Fig. S4. The *AP3-3* genes from *Souliea* and *Beesia*. (*A*) Exon–intron structures of *SovaAP3-3* and *BecaAP3-3*. Open and closed arrows indicate the positions from which primers used for in situ hybridization and qRT-PCR analyses, respectively, were derived (Tables S1 and S3 give details). (*B*) Alignment of the regions included in the red polygon. Uppercase letters denote exonic sequences; lowercase letters denote intronic or 3′ UTR sequences. Corresponding amino acids are shown above and below the exons. (*C–G*) In situ hybridization of *SovaAP3-3* (*C*) in *Souliea*, *BecaAP3-1* (*D*), and *BecaAP3-2* (*E*) in *Beesia* and *SovaAP3-1* (*F*, left two pictures), *SovaAP3-2* (*F*, right two pictures), and *SovaAP3-3* (*G*) in *Beesia*. Arrowheads indicate petals; se, st, and ca refer to sepals, stamens, and carpels, respectively. (Scale bars, 50 μm.) (*H*) Schematics of the constructs *5D3::BecaAP3-3* and *5D3::BecaAP3-3*$_{corrected}$, with their actual sequences shown underneath. The green line denotes the promoter of the *Arabidopsis AP3* gene, *5D3*, and the blue and orange boxes indicate the differentiated exons between the two genes, respectively. (*I*) Expression levels of the two constructs in different transgenic lines of *Arabidopsis* as revealed by qRT-PCR analyses. Dashed lines show the average expression level of the two constructs. The expression of *BecaAP3-3* in the untreated *Arabidopsis* plants was used as a negative control.

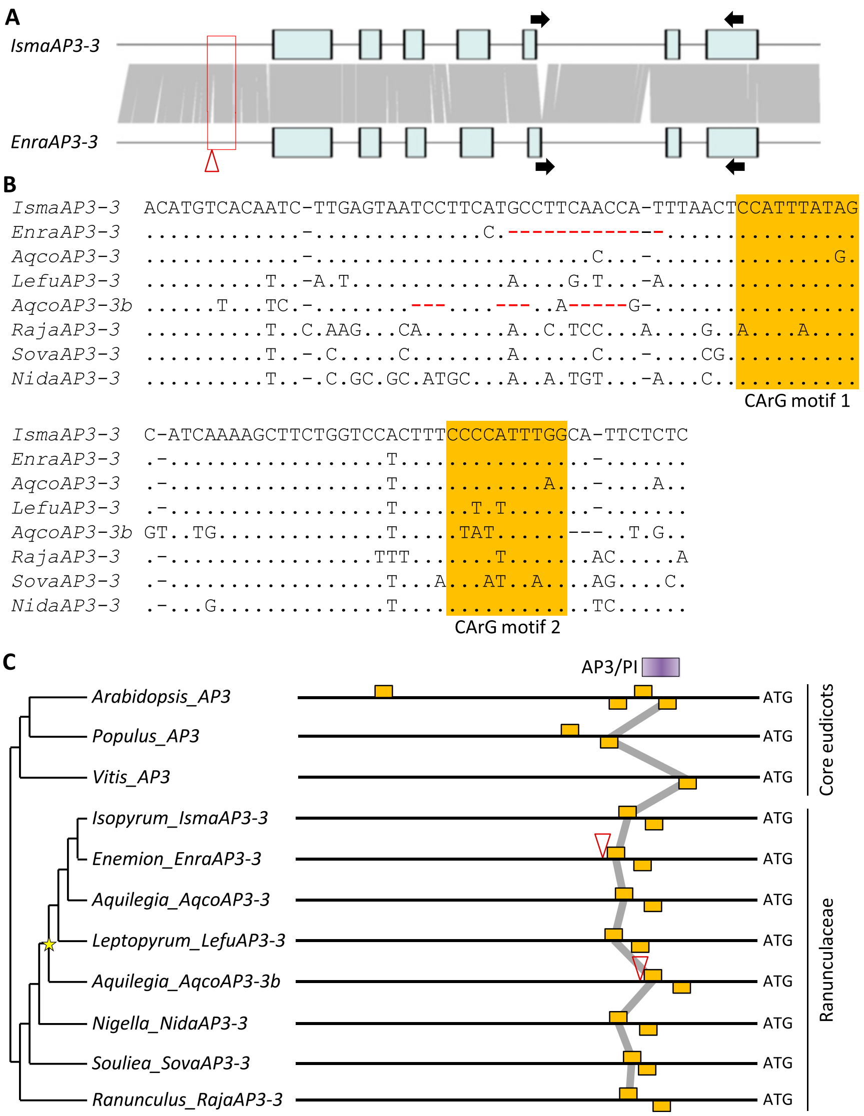
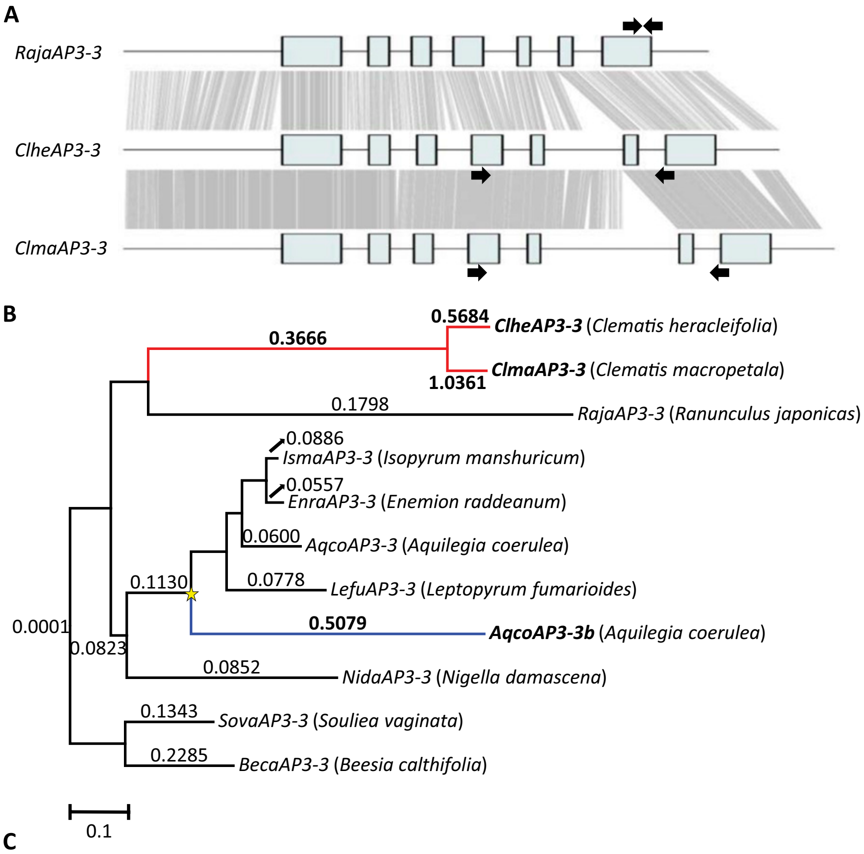


Fig. S5. The *AP3-3* genes from *Isopyrum* and *Enemion*. (*A*) Exon–intron structures of *IsmaAP3-3* and *EnraAP3-3*. Arrows indicate the positions from which primers used for qRT-PCR analyses were derived (Tables S1 and S3 give details). (*B*) Alignment of the promoter region of *AP3* orthologs covered with the red rectangle in *A*. The two yellow boxes show the highly conserved CArG-box motifs, named CArG motif1 and CArG motif2, respectively. (*C*) Conservativeness of the CArG motif1 across eudicots. The homolog of the CArG motif1 in *Arabidopsis*, CArG3, has been demonstrated to be the binding sites of the AP3/PI heterodimer and is indicated by a purple rectangle. The yellow star on the phylogenetic tree stands for inferred gene duplication event.



C

d_N/d_S	*Clhe AP3-3*	*Clma AP3-3*	*Raja AP3-3*	*Aqco AP3-3*	*Isma AP3-3*	*Enra AP3-3*	*Lefu AP3-3*	*Nida AP3-3*	*Sova AP3-3*	*Beca AP3-3*	*Aqco AP3-3b*
ClheAP3-3		**0.953**	**0.535**	**0.508**	**0.520**	**0.496**	**0.485**	**0.413**	**0.437**	**0.584**	**0.646**
ClmaAP3-3	**0.886**		**0.553**	**0.516**	**0.559**	**0.522**	**0.485**	**0.437**	**0.443**	**0.545**	**0.624**
RajaAP3-3	**0.380**	**0.381**		0.378	0.400	0.418	0.371	0.412	0.395	0.412	**0.507**
AqcoAP3-3	**0.385**	**0.384**	0.269		0.144	0.133	0.158	0.236	0.248	0.276	**0.687**
IsmaAP3-3	**0.394**	**0.409**	0.268	0.119		0.097	0.198	0.242	0.229	0.272	**0.655**
EnraAP3-3	**0.363**	**0.370**	0.281	0.107	0.088		0.205	0.239	0.251	0.277	**0.678**
LefuAP3-3	**0.390**	**0.389**	0.255	0.132	0.173	0.171		0.194	0.249	0.251	**0.584**
NidaAP3-3	**0.286**	**0.295**	0.283	0.164	0.162	0.166	0.127		0.167	0.235	**0.431**
SovaAP3-3	**0.322**	**0.322**	0.254	0.168	0.149	0.169	0.173	0.110		0.279	**0.428**
BecaAP3-3	**0.468**	**0.422**	0.275	0.190	0.188	0.194	0.179	0.163	0.247		**0.444**
AqcoAP3-3b	**0.482**	**0.462**	**0.334**	**0.515**	**0.505**	**0.498**	**0.478**	**0.300**	**0.291**	**0.316**	

Fig. S6. The *AP3-3* genes in *Ranunculus* and *Clematis*. (*A*) Exon–intron structures of *RajaAP3-3*, *ClheAP3-3*, and *ClmaAP3-3*. Arrows indicate the positions from which primers used for qRT-PCR analyses were derived (Tables S1 and S3 give details). (*B*) Phylogenetic relationships among *AP3-3*–like genes, with ω values, which represent the ratios of nonsynonymous substitution rate (d_N) versus synonymous substitution rate (d_S) and were estimated in PAML using the branch model, being indicated for each branch. Branches leading to the *Clematis AP3-3* genes are in red, whereas that to *AqcoAP3-3b*, which is no longer functional, is in blue. The yellow star stands for the inferred gene duplication event. (*C*) Pairwise comparisons of *AP3-3*–like genes in terms of their ω values, which were calculated in MEGA 5 with the Kumar (Kimura 2-para; *Lower*) and modified Nei–Gojobori (proportion; *Upper*) models.

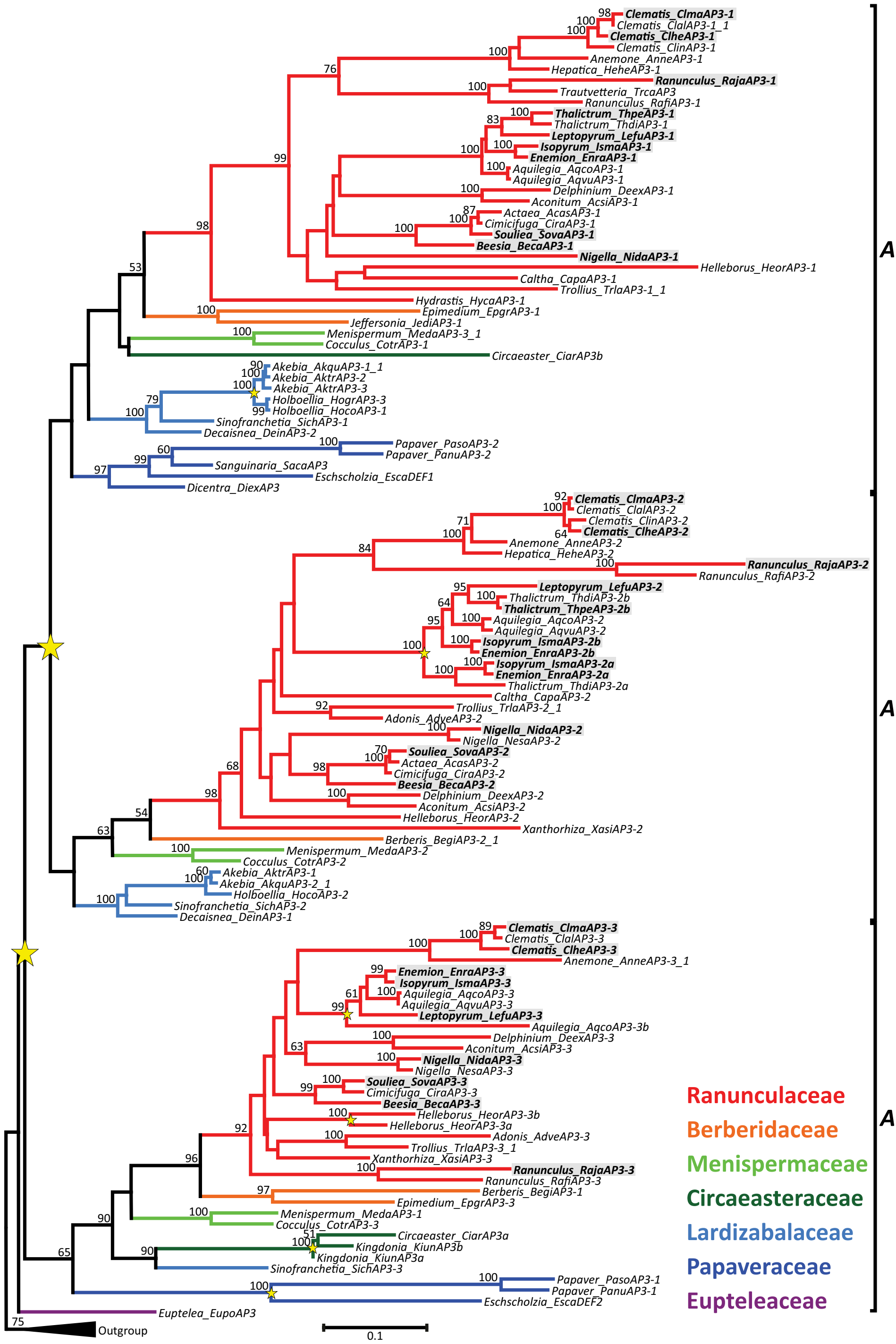


Fig. S7. Phylogenetic relationships of *AP3*-like genes from the Ranunculales. The tree was reconstructed in PhyML by using the maximum likelihood method, with higher-than-50% bootstrap supports indicated for each node. Yellow stars stand for the inferred gene duplication events. Sequences isolated in this study are highlighted in bold with gray shadow. Information on sequences is given in Table S4.

Table S1. Primers used in this study

Taxon/species and purpose	Gene name	Primer name
Ranunculaceae		
cDNA synthesis		polyT
cDNA amplification*	*AP3*-like	B1
		R_AP3-1
		R_AP3-2
		R_AP3-3
		Adaptor
qRT-PCR	*ACTIN*	*R_ACTIN*
Nigella damascena		
qRT-PCR	*NidaAP3-1*	*NidaAP3-1*_RT
	NidaAP3-2	*NidaAP3-2*_RT
	NidaAP3-3	*NidaAP3-3*_RT
In situ hybridization	*NidaAP3-3*	*NidaAP3-3*_In
Leptopyrum fumarioides		
qRT-PCR	*LefuAP3-1*	*LefuAP3-1*_RT
	LefuAP3-2	*LefuAP3-2*_RT
	LefuAP3-3	*LefuAP3-3*_RT
In situ hybridization	*LefuAP3-1*	*LefuAP3-1*_In
	LefuAP3-2	*LefuAP3-2*_In
	LefuAP3-3	*LefuAP3-3*_In
Southern hybridization	*LefuAP3-3*	*LefuAP3-3*_S
Thalictrum petaloideum		
qRT-PCR	*ThpeAP3-1*	*ThpeAP3-1*_RT
	ThpeAP3-2b	*ThpeAP3-2b*_RT
In situ hybridization	*ThpeAP3-1*	*ThpeAP3-1*_In
	ThpeAP3-2b	*ThpeAP3-2b*_In
Souliea vaginata		
qRT-PCR	*SovaAP3-1*	*SovaAP3-1*_RT
	SovaAP3-2	*SovaAP3-2*_RT
	SovaAP3-3	*SovaAP3-3*_RT
In situ hybridization	*SovaAP3-1*	*SovaAP3-1*_In
	SovaAP3-2	*SovaAP3-2*_In
	SovaAP3-3	*SovaAP3-3*_In
Beesia calthifolia		
In situ hybridization	*BecaAP3-1*	*BecaAP3-1*_In
	BecaAP3-2	*BecaAP3-2*_In
qRT-PCR	*BecaAP3-1*	*BecaAP3-1*_RT
	BecaAP3-2	*BecaAP3-2*_RT
	BecaAP3-3	*BecaAP3-3*_RT
Isopyrum manshuricum		
qRT-PCR	*IsmaAP3-1*	*IsEnAP3-1*_RT
	IsmaAP3-2b	*IsEnAP3-2*_RT
	IsmaAP3-3	*IsEnAP3-3*_RT
Enemion raddeanum		
qRT-PCR	*EnraAP3-1*	*IsEnAP3-1*_RT
	EnraAP3-2b	*IsEnAP3-2*_RT
	EnraAP3-3	*IsEnAP3-3*_RT
Ranunculus japonicus		
qRT-PCR	*RajaAP3-1*	*RajaAP3-1*_RT
	RajaAP3-2	*RajaAP3-2*_RT
	RajaAP3-3	*RajaAP3-3*_RT
Clematis heracleifolia		
qRT-PCR	*ClheAP3-1*	*ClAP3-1*_RT
	ClheAP3-2	*ClAP3-2*_RT
	ClheAP3-3	*ClAP3-3*_RT
C. macropetala		
qRT-PCR	*ClmaAP3-1*	*ClAP3-1*_RT
	ClmaAP3-2	*ClAP3-2*_RT
	ClmaAP3-3	*ClAP3-3*_RT
Arabidopsis		
Genotyping	*BecaAP3-3*	Bc33_GT
	BecaAP3-3	Bc33$_{corrected}$_GT
	BecaAP3-3	5D3::Bc33_GT
qRT-PCR	*ACTIN*	*At_ACTIN*_RT

*For amplification of *AP3*-like cDNA, B1 was used for the first round of PCR and *R_AP3-1*, *R_AP3-2*, and *R_AP3-3* were used for the second round of PCR.

Table S2. Information on the species sampled in this study

Species	Location	Voucher
Beesia calthifolia	33°38′ N, 106°52′ E, Hanzhong, Shaanxi, China	Chunce Guo 0804-103
Clematis heracleifolia	39°59′ N, 116°12′ E, Institute of Botany, Chinese Academy of Sciences (CAS), Beijing, China	Chunce Guo 0807-16
Clematis macropetala	40°02′ N, 115°29′ E, Dongling Mountain, Beijing, China	Chunce Guo 0806-75
Enemion raddeanum	40°42′ N, 126°05′ E, Tonghua, Jilin, China	Rui Zhang 1004-33
Isopyrum manshuricum	40°43′ N, 126°01′ E, Tonghua, Jilin, China	Rui Zhang 1004-27
Leptopyrum fumarioides	45°43′ N, 126°37′ E, Harbin, Heilongjiang, China	Chunce Guo 0805-56
Nigella damascena	Cultivated in Institute of Botany, CAS, Beijing, China	Wengen Zhang 1012-06
N. damascena "Double Sepal"	Cultivated in Institute of Botany, CAS, Beijing, China	Wengen Zhang 1012-07
Ranunculus japonicus	39°59′ N, 116°12′ E, Institute of Botany, CAS, Beijing, China	Rui Zhang 1205-07
Souliea vaginata	33°58′ N, 107°45′ E, Taibai Mountain, Shaanxi, China	Chunce Guo 0804-114
Thalictrum petaloideum	40°02′ N, 115°29′ E, Dongling Mountain, Beijing, China	Rui Zhang 1006-05

Table S3. Sequence information on primers listed in Table S2

Primer name	Forward primer (5′-3′)	Reverse primer (5′-3′)
5D3::Bc33_GT	CGTTAAGTTTGTCACCGTC	GATCAATCAACCTCGTAGTG
Adaptor		CCGGATCCTCTACAGCGGCCGC
*At_ACTIN*_RT	TCGTTTGTGGGAATGGAAGC	GATACCTGAGAACATAGTGGT
B1	AACAGGCAGGTSACCTAYTC	
Bc33_GT	ATACATACCAGCGTCTCACC	CAGAACCGTCCAGATCTTG
Bc33$_{\textit{corrected}_}$GT	GAGAAAGTGTCCCAGTTGC	GGATTCATAATCCCCATC
*BecaAP3-1*_In	GGAAGTTTGGTGTGTTAGG	TCACGAAGATTGGGTTGG
*BecaAP3-1*_RT	AGGAAGTTTGGTGTGTTAGG	AGATTGGGTTGGCTTGGTTG
*BecaAP3-2*_In	CACAGACCGATACATACAAG	ACCATACGAGGCATAACC
*BecaAP3-2*_RT	CATTTGAAGGGAGAGACGAG	AAACCATACGAGGCATAACC
*BecaAP3-3*_RT	ATACATACCAGCGTCTCACC	CAGAACCGTCCAGATCTTG
*ClAP3-1*_RT	CACTAGCCAACCATCAAGG	TCCATTTCCACTCAAGCCAG
*ClAP3-2*_RT	AAGAGGGAGATACGTCGTG	CCATAGGAGCAGTAGAGAG
*ClAP3-3*_RT	TGGGAAGGAAAGTCTTGATG	TCCGTAGTAAGCAACCTCAC
*IsEnAP3-1*_RT	ATTGTGTGGTCTTGAGCAAC	TCCTTCATGATCGGCTAGTG
*IsEnAP3-2*_RT	CCATAACAGTCTGATACGTG	CATCCTGAAGATCGGCTGAC
*IsEnAP3-3*_RT	CCTACAGGAAGAAACTAAGG	TGAATGTTGTGTTGGCTTGG
*LefuAP3-1*_In	AAGGGTTGGTGGTGATGA	AAGATTAGGCTGGCTTGG
*LefuAP3-1*_RT	ATCATGAAGGATTGTCTGCAC	CAACCTAGTCGGAGATTCTC
*LefuAP3-2*_In	CTGAAGGAGACTAACAACAAAC	CAAGTGATGGAAAGCGGA
*LefuAP3-2*_RT	ATGCAGACTTCCGCTTTCC	ATCCATATGGTTCTTCATCCT
*LefuAP3-3*_In	CAAGATTTGGATGAGTCAGT	CGATAAGAGACAAGGTGTG
*LefuAP3-3*_RT	CATGATTGCTACACAGACTG	CAAACGATAAGAGACAAGGTG
*LefuAP3-3*_ S	CAGAACAAAGAAAGTATATGATC	ATAACCTTTCGATCGCGAACCAG
*NidaAP3-1*_RT	CTCATTGAGGATTGTTAGCC	GGTGGTGTTGGGTTGGTTG
*NidaAP3-2*_RT	AGTGTTTGCTTTCAGGTTGC	CATAACTACTTAGTCCAGAGAG
*NidaAP3-3*_In	GATTGGAGAAAGTGTTGATGAC	TGAAGATTAGGTTGGCTTGG
*NidaAP3-3*_RT	GAACTTGCGAGAAACACATAC	AGATTAGGTTGGCTTGGTTG
polyT		CCGGATCCTCTAGAGCGGCCGC(T)$_{17}$
R_ACTIN	CCGTTCTGCTGTGGTTGTG	GTGTTGGACTCTGGTGATGG
R_AP3-1	GTTCTTTGTGATGCYGAGGTT	
R_AP3-2	CTYACTGTTCTYTGYGATGCT	
R_AP3-3	CTYACTGTTCTTTGTGATGC	
*RajaAP3-1*_RT	GTGGACTATCTGCACTTGAAC	ACCTCCCATTTCTACTGATTG
*RajaAP3-2*_RT	CCCAGTATTCATTTGTTCAGC	TAAGAGCCATAGTCTTGAGC
*RajaAP3-3*_RT	GTTTCCTATGGTCTTCAGCC	CATCACCTGTTAACGCCAATG
*SovaAP3-1*_In	TTGCTGAGTTGCGTGGTC	CGAAGATTGGGTTGGCTG
*SovaAP3-1*_RT	GGGATCTCTACAAATGAACTG	ATCTACTCAACCAAGTCGG
*SovaAP3-2*_In	CGTGATTGGTACTTCGACAG	CTCTATTCATTCAAGCAAGACG
*SovaAP3-2*_RT	ACTACGCACTCATTGATCAG	AAGCAAGACGTGAACCATAC
*SovaAP3-3*_In	CCAACAGGTCAATGGAGT	ATCAGATGTGTGTGCGTC
*SovaAP3-3*_RT	GCAAGAGACGCACACACATC	ATCGTAGGATCCATAGGTTTC
*ThpeAP3-1*_In	TTGAAGAATTGTGCGGTCTTGAGC	TCGAATCCATATCCTCCATCACCA
*ThpeAP3-1*_RT	TGAGGGAGAATATGCACTAG	GATTAGGCTGGCTTGGTTGC
*ThpeAP3-2b*_In	GTTGAGTGTGTTCGTAATC	GTCTAGATGTGGAACGATAAC
*ThpeAP3-2b*_RT	ACCAAAGCTGCAGTCCAATC	GGAACGATAACATGATATCCAG

Table S4. Information on the *AP3*-like genes used in this study

Taxon and species*	Gene name*	Accession no.[†]	Source
Ranunculaceae			
Aconitum sinomontanum	*AcsiAP3-1*	EU481818	1
	AcsiAP3-2	EU481817	1
	AcsiAP3-3	EU481816	1
Actaea asiatica	*AcasAP3-1*	HQ647375	2
	AcasAP3-2	HQ647376	2
Adonis vernalis	*AdveAP3-2*	HQ694800	2
	AdveAP3-3	HQ694799	2
Anemone nemorosa	*AnneAP3-1*	AY162841	3
	AnneAP3-2	AY162842	3
	AnneAP3-3_1	AY162843	3
Aquilegia coerulea	*AqcoAP3-1*	Aquca_006_00074[‡]	—
	AqcoAP3-2	Aquca_006_00072[‡]	—
	AqcoAP3-3	Aquca_007_00336[‡]	—
	AqcoAP3-3b	HQ694798	2
Aquilegia vulgaris	*AqvuAP3-1*	EF489478	4
	AqvuAP3-2	EF489477	4
	AqvuAP3-3	EF489476	4
Beesia calthifolia	***BecaAP3-1***		This study
	BecaAP3-2		This study
	BecaAP3-3		This study
Caltha palustris	*CapaAP3-1*	EU481813	1
	CapaAP3-2	EU481812	1
Cimicifuga racemosa	*CiraAP3-1*	AY162862	3
	CiraAP3-2	AY162863	3
	CiraAP3-3	AY162864	3
Clematis alpina	*ClalAP3-1_1*	EU481808	1
	ClalAP3-2	EU481807	1
	ClalAP3-3	EU481806	1
Clematis integrifolia	*ClinAP3-1*	AY162870	3
	ClinAP3-2	AY162871	3
Clematis heracleifolia	***ClheAP3-1***		This study
	ClheAP3-2		This study
	ClheAP3-3		This study
Clematis macropetala	***ClmaAP3-1***		This study
	ClmaAP3-2		This study
	ClmaAP3-3		This study
Delphinium exaltatum	*DeexAP3-1*	EU481804	1
	DeexAP3-2	EU481803	1
	DeexAP3-3	EU481802	1
Enemion raddeanum	***EnraAP3-1***		This study
	EnraAP3-2a		This study
	EnraAP3-2b		This study
	EnraAP3-3		This study
Helleborus orientalis	*HeorAP3-1*	AY162874	3
	HeorAP3-2	AY162875	3
	HeorAP3-3a	AY162876	3
	HeorAP3-3b	AY162877	3
Hepatica henryi	*HeheAP3-1*	HQ647378	2
	HeheAP3-2	HQ647379	2
Hydrastis canadensis	*HycaAP3-1*	EU481800	1
Isopyrum manshuricum	***IsmaAP3-1***		This study
	IsmaAP3-2a		This study
	IsmaAP3-2b		This study
	IsmaAP3-3		This study
Leptopyrum fumarioides	***LefuAP3-1***		This study
	LefuAP3-2		This study
	LefuAP3-3		This study
Nigella damascena	***NidaAP3-1***		This study
	NidaAP3-2		This study
	NidaAP3-3		This study
Nigella sativa	*NisaAP3-2*	HQ694795	2
	NisaAP3-3	HQ694794	2

Table S4. Cont.

Taxon and species*	Gene name*	Accession no.[†]	Source
Ranunculus ficaria	*RafiAP3-1*	AF052854	5
	RafiAP3-2	AF130870	6
	RafiAP3-3	AY162883	3
Ranunculus japonicus	***RajaAP3-1***		This study
	RajaAP3-2		This study
	RajaAP3-3		This study
Souliea vaginata	***SovaAP3-1***		This study
	SovaAP3-2		This study
	SovaAP3-3		This study
Thalictrum dioicum	*ThdiAP3-1*	AY867875	7
	ThdiAP3-2a	AY867876	7
	ThdiAP3-2b	AY867877	7
Thalictrum petaloideum	***ThpeAP3-1***		This study
	ThpeAP3-2b		This study
Trautvetteria caroliniensis	*TrcaAP3*	AY162904	3
Trollius laxus	*TrlaAP3-1_1*	AY162890	3
	TrlaAP3-2_1	AY162892	3
	TrlaAP3-3_1	AY162894	3
Xanthorhiza simplicissima	*XasiAP3-2*	EU481797	1
	XasiAP3-3	EU481796	1
Berberidaceae			
Berberis gilgiana	*BegiAP3-1*	AY162857	3
	BegiAP3-2_1	AY162858	3
Epimedium grandiflorum	*EpgrAP3-1*	EU481793	1
	EpgrAP3-3	EU481794	1
Jeffersonia diphylla	*JediAP3-1*	EU481791	1
Menispermaceae			
Cocculus trilobus	*CotrAP3-1*	HQ694788	2
	CotrAP3-2	HQ694789	2
	CotrAP3-3	HQ694790	2
Menispermum dauricum	*MedaAP3-1*	EU481786	1
	MedaAP3-2	EU481784	1
	MedaAP3-3_1	EU481783	1
Circaeasteraceae			
Circaeaster agrestis	*CiarAP3a*	HQ647369	2
	CiarAP3b	HQ647370	2
Kingdonia uniflora	*KiunAP3a*	HQ647371	2
	KiunAP3b	HQ647372	2
Lardizabalaceae			
Akebia quinata	*AkquAP3-1_1*	AY162835	3
	AkquAP3-2_1	AY162839	3
Akebia trifoliata	*AktrAP3-1*	AY627630	8
	AktrAP3-2	AY627631	8
	AktrAP3-3	DQ303124	8
Decaisnea insignis	*DeinAP3-1*	JQ806400	9
	DeinAP3-2	JQ806401	9
Holboellia coriacea	*HocoAP3-1*	EU481789	1
	HocoAP3-2	EU481788	1
Holboellia grandiflora	*HograAP3*	JQ806404	9
Sinofranchetia chinensis	*SichAP3-1*	JQ806394	9
	SichAP3-2	JQ806395	9
	SichAP3-3	JQ806396	9
Papaveraceae			
Eschscholzia californica	*EscaDEF1*	EF378697	10
	EscaDEF2	EF378698	10
Papaver nudicaule	*PanuAP3-1*	AF052873	5
	PanuAP3-2	AF052874	5
Papaver somniferum	*PasoAP3-1*	EF071993	—
	PasoAP3-2	EF071992	—
Sanguinaria canadensis	*SacaAP3*	AF130868	6
Dicentra eximia	*DiexAP3*	AF052875	5
Eupteleaceae			

Table S4. Cont.

Taxon and species*	Gene name*	Accession no.†	Source
Euptelea polyandra	*EupoAP3*	EU481781	1
Trochodendraceae			
Trochodendron aralioides	*TrarAP3*	DQ453774	11
Sabiaceae			
Meliosma dilleniifolia	*MediAP3-1*	AY436709	12
Buxaceae			
Pachysandra procumbens	*PaprAP3-1*	DQ479360	11
Magnoliaceae			
Magnolia praecocissima	*MpMADS7*	AB050649	—
Chloranthaceae			
Chloranthus spicatus	*ChspAP3*	AF230701	13
Aristolochiaceae			
Aristolochia eriantha	*ArerAP3*	AY436714	12

*Species sampled and genes cloned in this study are highlighted in bold.

†The sequences were retrieved from National Center for Biotechnology Information (NCBI).

‡The sequences were retrieved from the *Aquilegia* genome database (www.phytozome.net/).

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