Supporting Information

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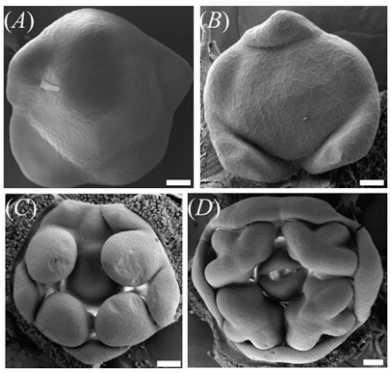

Fig. S1. Scanning electron micrographs showing flower development in insect-pollinated *Digitalis purpurea*. Floral organ differentiation proceeds from the ventral to dorsal domain (bottom to top in all images), starting with initiation of the ventral, followed by lateral, sepals (*A* and *B*). Although the dorsal sepal emerges last, it appears larger than the lateral sepals early in development due to repression of the latter by the lateral prophylls (*B*; prophylls removed). Stamens and petals develop around the same time in a ventral-to-dorsal sequence; the dorsal stamen fails to initiate, resulting in four stamens (*C*). During stamen differentiation, the gynoecium is initiated in the center of the flower and the two dorsal petals become almost completely fused (*D*). (Scale bars: 20 μm.)

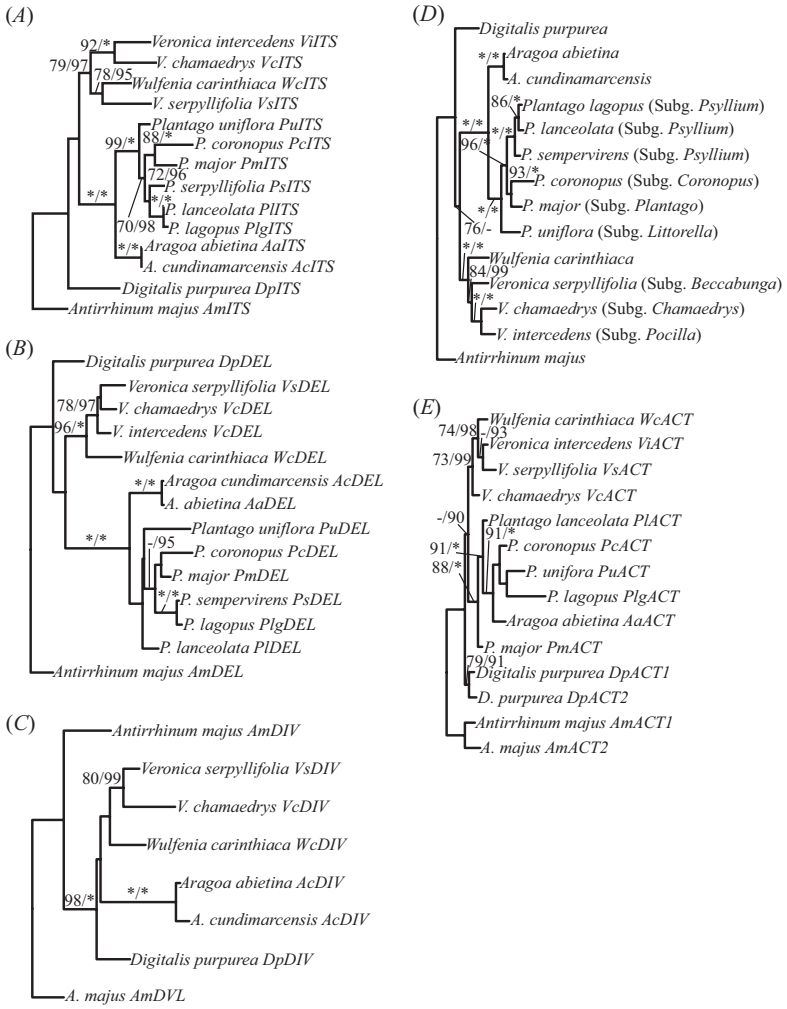

Fig. S2. Maximum-likelihood phylograms showing generic relationships between *Digitalis*, *Wulfenia*, *Veronica*, *Aragoa*, and *Plantago* inferred from the nuclear genes internal transcribed spacer (ITS) (*A*), *DELILA* (*DEL*) (*B*), the *DIVARICATA* (*DIV*) intron (*C*), *DEL*, ITS, and the *DIV* intron combined (*D*), and *ACTIN* (*ACT*) (*E*). The ITS dataset was assembled from GenBank-deposited sequences generated in previous studies (1–4). For all datasets, the closest homolog from *Antirrhinum majus* was selected as an outgroup to root the tree. Maximum-likelihood bootstrap values >70% (*Left*) and Bayesian posterior probabilities >90% (*Right*) are indicated. Asterisks represent support values of 100%. The subgenus (Subg.) is shown where applicable (*D*).

1. Bello MA, Chase MW, Olmstead RG, Ronsted N, Albach D (2002) The páramo endemic *Aragoa* is the sister genus of *Plantago* (Plantaginaceae; Lamiales): Evidence from plastid *rbcL* and nuclear ribosomal ITS sequence data. *Kew Bull* 57:585–597.
2. Ronsted N, Chase MW, Albach DC, Bello MA (2002) Phylogenetic relationships within *Plantago* (Plantaginaceae): Evidence from nuclear ribosomal ITS and plastid *trnL-F* sequence data. *Bot J Linn Soc* 139:323–338.
3. Albach DC, Meudt HM, Oxelman B (2005) Piecing together the "new" Plantaginaceae. *Am J Bot* 92:297–315.
4. Reeves PA, Olmstead RG (2003) Evolution of the TCP gene family in Asteridae: Cladistic and network approaches to understanding regulatory gene family diversification and its impact on morphological evolution. *Mol Biol Evol* 20:1997–2009.

Table S1. Codon model parameter estimates for symmetry genes

Model*	Parameter estimates	ln*L*	2Δln*L*[†]
CYCLOIDEA			
One-ratio	$\varpi = 0.0868$	−1677.96	
Two-ratio: *CYC1*	$\varpi_0 = 0.0834$, $\varpi_1 = 0.4000$	−1677.00	(One- vs. two-ratio) $P < 1$
Two-ratio: *CYC2*a[‡]	$\varpi_0 = 0.0866$, $\varpi_1 = 0.0900$	−1677.96	(One- vs. two-ratio) $P < 1$
Two-ratio: *CYC2*b[§]	$\varpi_0 = 0.0906$, $\varpi_1 = 0.0001$	−1675.91	**(One- vs. two-ratio) $P < 0.05$**
Model 1a	$p_0 = 0.8632$, $p_1 = 0.1368$ ($p_{2a} + p_{2b} = 0.00$), $\varpi_0 = 0.0393$, $\varpi_{2a} = 1.00000$	−1630.11	
Null model A: *CYC1*	$p_0 = 0.00$, $p_1 = 0.00$, $p_{2a} = 0.8583$, $p_{2b} = 0.1417$, $\varpi_0 = 0.0334$, $\varpi_1 = 1.00$, $\varpi_{2aback} = 0.0334$, $\varpi_{2afore} = 1.00$, $\varpi_{2bback} = 1.00$, $\varpi_{2bfore} = 1.00$	−1625.19	
Model A: *CYC1*	$p_0 = 0.00$, $p_1 = 0.00$, $p_{2a} = 0.8583$, $p_{2b} = 0.1417$, $\varpi_0 = 0.0334$, $\varpi_1 = 1.00$, $\varpi_{2aback} = 0.0334$, $\varpi_{2afore} = 1.00$, $\varpi_{2bback} = 1.00$, $\varpi_{2bfore} = 1.00$	−1625.19	**(M1a vs. MA) $P < 0.01$** (null vs. MA) $P < 1$
Model A: *CYC2*a[‡]	$p_0 = 0.8166$, $p_1 = 0.1320$, $p_{2a} = 0.0443$, $p_{2b} = 0.0072$, $\varpi_0 = 0.0369$, $\varpi_1 = 1.00$, $\varpi_{2aback} = 0.0369$, $\varpi_{2afore} = 1.00$, $\varpi_{2bback} = 1.00$, $\varpi_{2bfore} = 1.00$	−1629.87	(M1a vs. MA) $P < 0.8$
Model A: *CYC2*b[§]	$p_0 = 0.8632$, $p_1 = 0.1368$, $p_{2a} = 0.0000$, $p_{2b} = 0.0000$, $\varpi_0 = 0.0393$, $\varpi_1 = 1.00$, $\varpi_{2aback} = 0.0393$, $\varpi_{2afore} = 1.00$, $\varpi_{2bback} = 1.00$, $\varpi_{2bfore} = 1.00$	−1630.11	(M1a vs. MA) $P < 1$
RADIALIS			
One-ratio	$\varpi = 0.0663$	−322.64	
Two-ratio	$\varpi_0 = 0.0564$, $\varpi_1 = 0.1024$	−322.54	(One- vs. two-ratio) $P < 0.75$
Model 1a	$p_0 = 0.9616$, $p_1 = 0.0384$ ($p_{2a} + p_{2b} = 0.00$), $\varpi_0 = 0.0468$, $\varpi_{2a} = 1.00000$	−319.10	
Model A	$p_0 = 0.00$, $p_1 = 0.00$, $p_{2a} = 0.9548$, $p_{2b} = 0.0452$, $\varpi_0 = 0.0233$, $\varpi_1 = 1.00$, $\varpi_{2aback} = 0.0233$, $\varpi_{2afore} = 1.00$, $\varpi_{2bback} = 1.00$, $\varpi_{2bfore} = 1.00$	−318.50	(M1a vs. MA) $P < 0.50$
DIVARICATA			
One-ratio	$\varpi = 0.0585$	−2151.50	(One- vs. two-ratio) $P < 1$
Two-ratio	$\varpi_0 = 0.0576$, $\varpi_1 = 0.0649$	−2151.50	
Model 1a	$p_0 = 0.9391$, $p_1 = 0.0609$ ($p_{2a} + p_{2b} = 0.00$), $\varpi_0 = 0.0425$, $\varpi_{2a} = 1.00000$	−2118.37	
Model A	$p_0 = 0.9391$, $p_1 = 0.0609$, $p_{2a} = 0.0000$, $p_{2b} = 0.0000$, $\varpi_0 = 0.0423$, $\varpi_1 = 1.00$, $\varpi_{2aback} = 0.0425$, $\varpi_{2afore} = 1.00$, $\varpi_{2bback} = 1.00$, $\varpi_{2bfore} = 1.00$	−2118.37	(M1a vs. MA) $P < 1$

*Null model A was run only when the likelihood ratio test comparing model 1a (M1a) and model A (MA) was significant at the 0.05 level (bold).
[†]The likelihood ratio test was conducted using one (one-ratio vs. two-ratio; null vs. MA) and two (M1a vs. MA) degrees of freedom.
[‡]*Plantago TCP1* as the foreground branch.
[§]*Plantago* + *Aragoa TCP1* as the foreground branch.

Table S2. Primers used in this study

Name	Sequence (5′-3′)	Genes amplified
MYKF1	**CAATGGAGYTATRTYTTHIGGTC**	***DELILA* orthologs**
MYKR2	**AARGTRAGRTCTTGWGGDCATAATGC**	***DELILA* orthologs**
ACT1	**GATGGATCCTCCAATCCAGACACTGTA**	***ACTIN* orthologs**
ACT2	**GTATTGTGTTGGACTCTGGTGATGGTGT**	***ACTIN* orthologs**
Arag.CYC.A.F	**TCTTTGACCTWCAAGARATGCT**	***CYC* A orthologs**
Arag.CYC.A.R	**TGCYTTTGCTCTTGACTCCTT**	***CYC* A orthologs**
Arag.CYC.B.F	**GATCTYCARGAGCTTCTAGG**	***CYC* B orthologs**
Arag.CYC.B.R	**GCACATTTTCTCCTTAGT**	***CYC* B orthologs**
DIV.deg.F	**TGGSAIAGAGTKGCYGARATGGTCCCIGG**	***DIV* homologs**
DIV.deg(2).F	**GAGAACAAGGCCTTYGAGAATGC**	***DIV* homologs**
RAD-70-F	**GCATTGGCGGTTTACGAYMAAG**	***RAD* orthologs**
RAD-240-R	**ACYRGTGGTCCTRTAGTTRGG**	***RAD* orthologs**
DIV-55-F	**GTCCCTGGAAAGACTGTG**	***DIV* orthologs**
DIV-403-R	**ATGGCTCGCAACTTGAGTTGG**	***DIV* orthologs**
DpCYC1F	**GAAAGTGGTAATCAGAGTGATTCC**	***DpCYC1***
DpCYC1R	**CCAATGCAGCTGTATCTTTTCC**	***DpCYC1***
DpCYC2F	**CTAAGAATACTGCTAAGAGGAG**	***DpCYC2***
DpCYC2R	**TCTCCTTCACCAGATTCATCG**	***DpCYC2***
DpCYC3F	**GAGCTTGTTCAGTCCAAAACC**	***DpCYC3***
DpCYC3R	**CGCTTCGTTCAGCTGCTTGATGC**	***DpCYC3***
PmTCP1-F	**GCAAGTCAAGGGCAGGTAAC**	***PmTCP1***
PmTCP1-R	**TTCCGGAAGCATGTACACAA**	***PmTCP1***
DpCYC1qrtF*	**TATGGAGCATCAACGGATCA**	***DpCYC1***
DpCYC1qrtR*	**GGCACATAGCTGGTTGGATT**	***DpCYC1***
DpCYC2qrtF*	**AGCAGCTGAATGAGGCAACT**	***DpCYC2***
DpCYC2qrtR*	**CTCAAATCCCTCGCTCCATA**	***DpCYC2***
DpCYC3qrtF*	**AATTCGGTTGTTGGAACGAG**	***DpCYC3***
DpCYC3qrtR*	**TTTCTGCAAGCAAAAGCAGA**	***DpCYC3***
DpRADqrtF*	**ATTGGCGGTTTACGATCAAG**	***DpRAD***
DpRADqrtR*	**GTTGGGGAAGGGCAGCTT**	***DpRAD***
PmTCP1qrtF*	**GATCTCCAGGAGCTTCTAGG**	***PmTCP1***
PmTCP1qrtR*	**GCACATTTTCTCCTTAGT**	***PmTCP1***

***Primers used for quantitative RT-PCR. Optimal annealing temperatures range from 57 to 62 °C.