

Supporting Information

Guisinger et al. 10.1073/pnas.0806759105

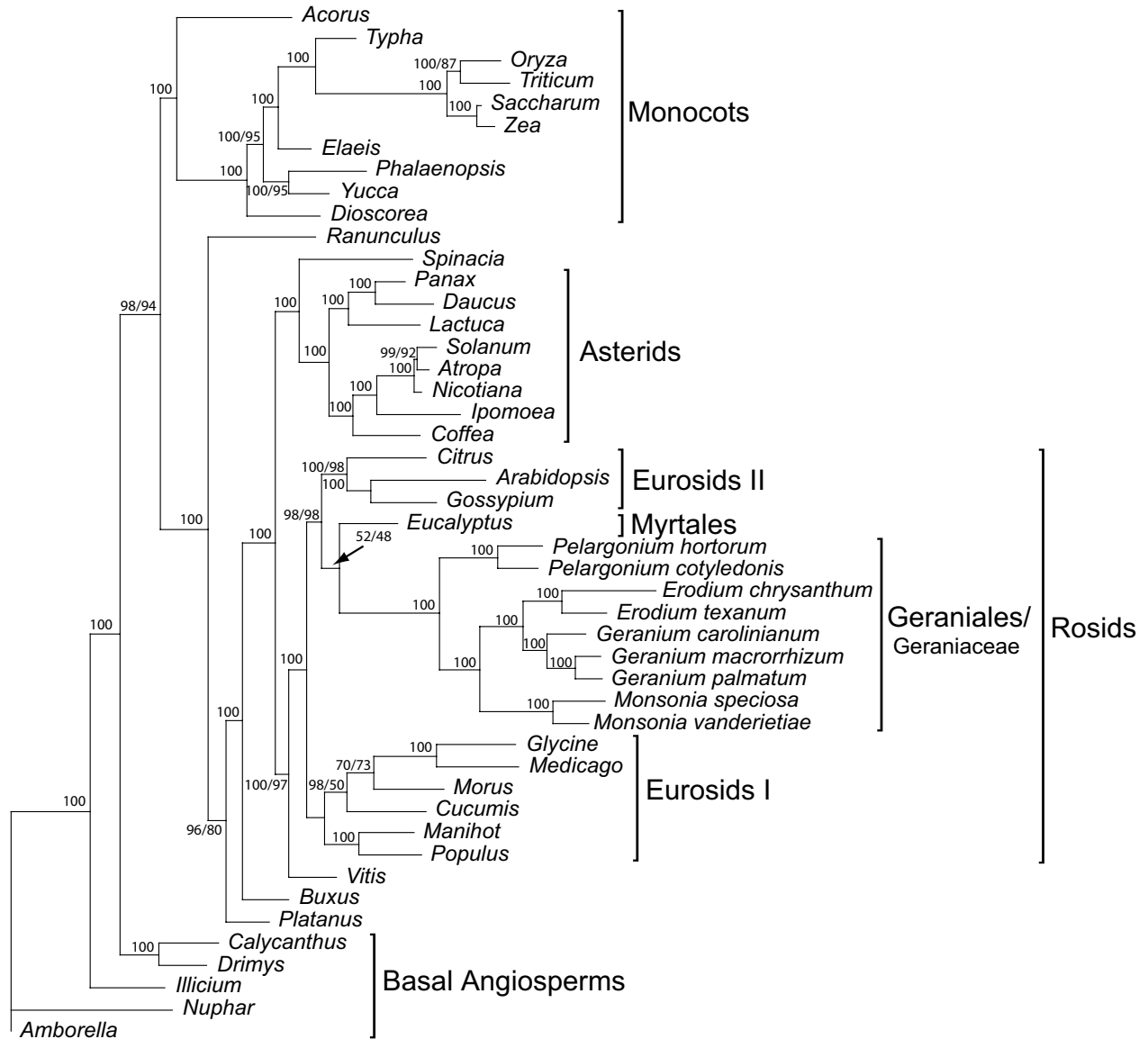


Fig. S1. ML tree inferred from 72 genes from 47 taxa ($-\ln L \mu = 607633.5555$, $\sigma = 0.001$). Bootstrap values for ML and MP, respectively, are shown at nodes. When ML and MP values are the same, only one value is reported.

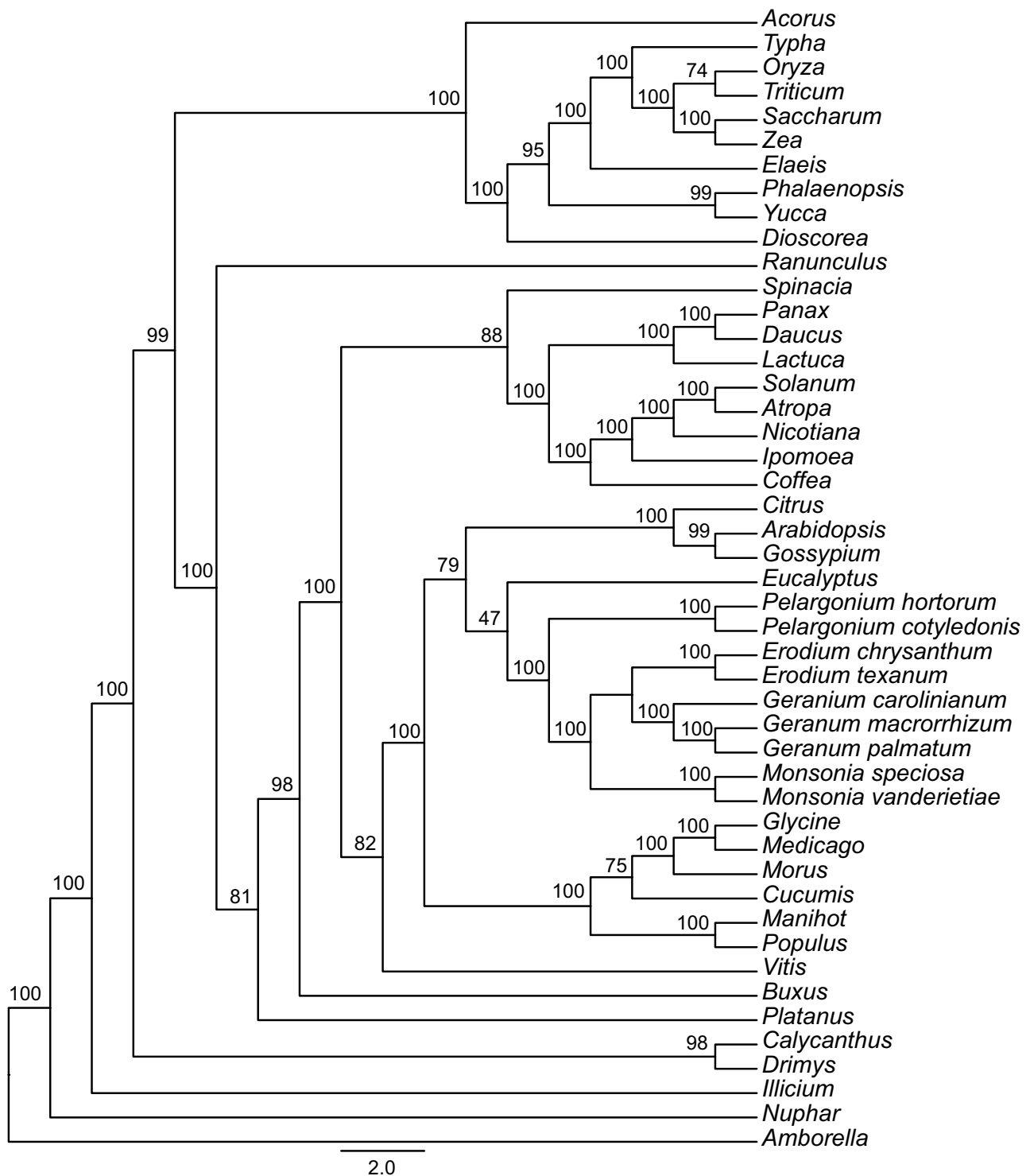


Fig. S2. ML tree inferred from 27 slowly evolving genes for 47 taxa ($-\ln L = 125333.7228$). ML bootstrap values are shown at nodes. Genes included *petA*, *petB*, *petD*, *petG*, *petL*, *petN*, *psaA*, *psaB*, *psaC*, *psal*, *psaj*, *psbA*, *psbB*, *psbC*, *psbD*, *psbE*, *psbF*, *psbH*, *psbl*, *psbj*, *psbK*, *psbL*, *psbM*, *psbN*, *psbT*, *psbZ*, and *rbcl* and were chosen based on Wolfe *et al.* (1) and Moore *et al.* (2).

1. Wolfe KH, Li WH, Sharp PM (1987) Rates of nucleotide substitution vary greatly among plant mitochondrial, chloroplast, and nuclear DNAs. *Proc Natl Acad Sci USA* 84:9054–9058.
2. Moore MJ, Bell CD, Soltis PS, Soltis DE (2007) Using plastid genome-scale data to resolve enigmatic relationships among basal angiosperms. *Proc Natl Acad Sci USA* 104:19363–19638.

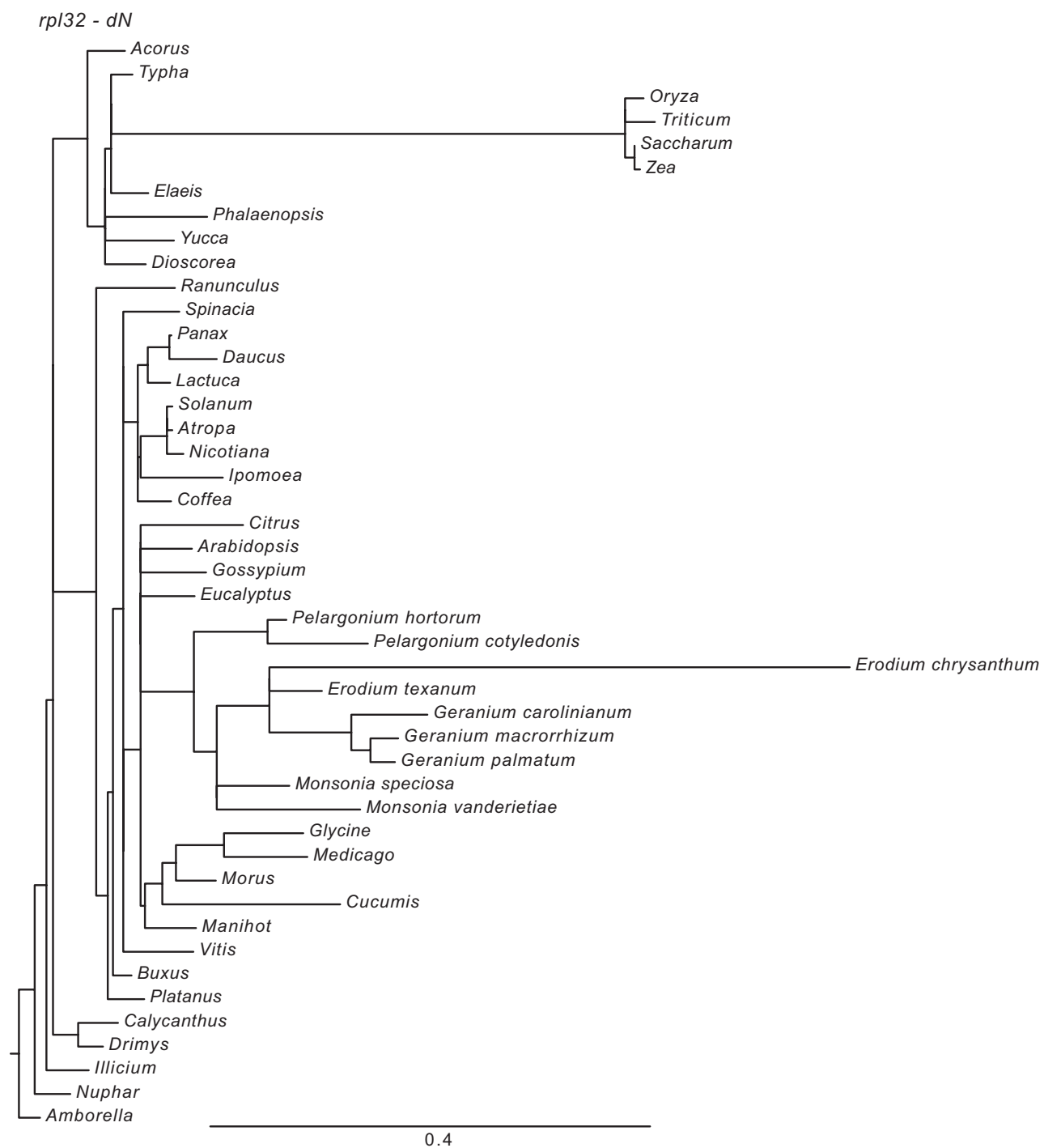


Fig. S3. ML trees from codeml of non-synonymous (*dN*) or synonymous (*dS*) substitutions for the genes *rpl32-dN*, *rpl20-dS*, *rps18-dN*, *rps18-dS*, *psa1-dN*, and *psaC-dS*. The same trees shown in Fig. 4, but taxa names are shown here.

rpl20 - dS

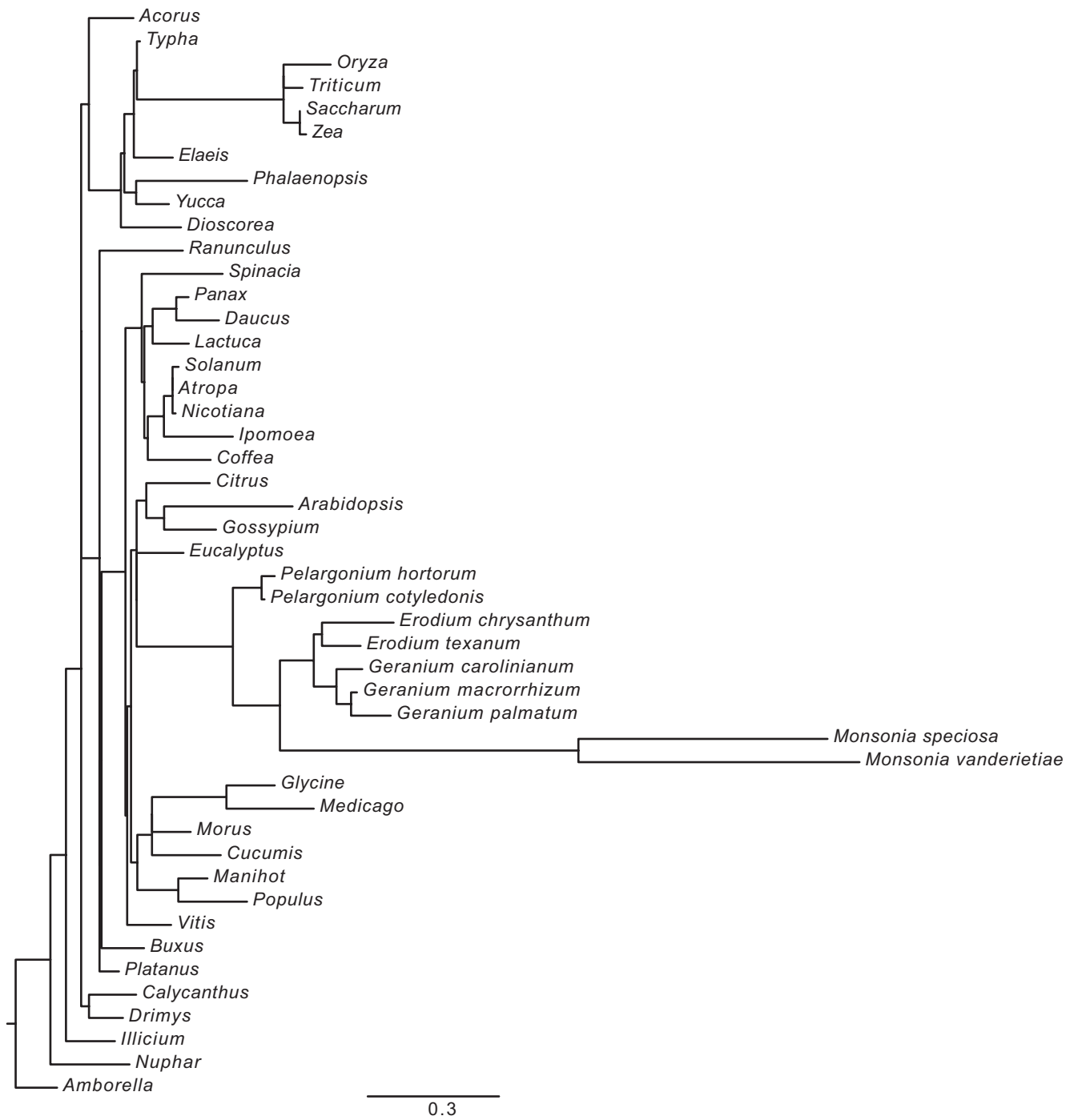
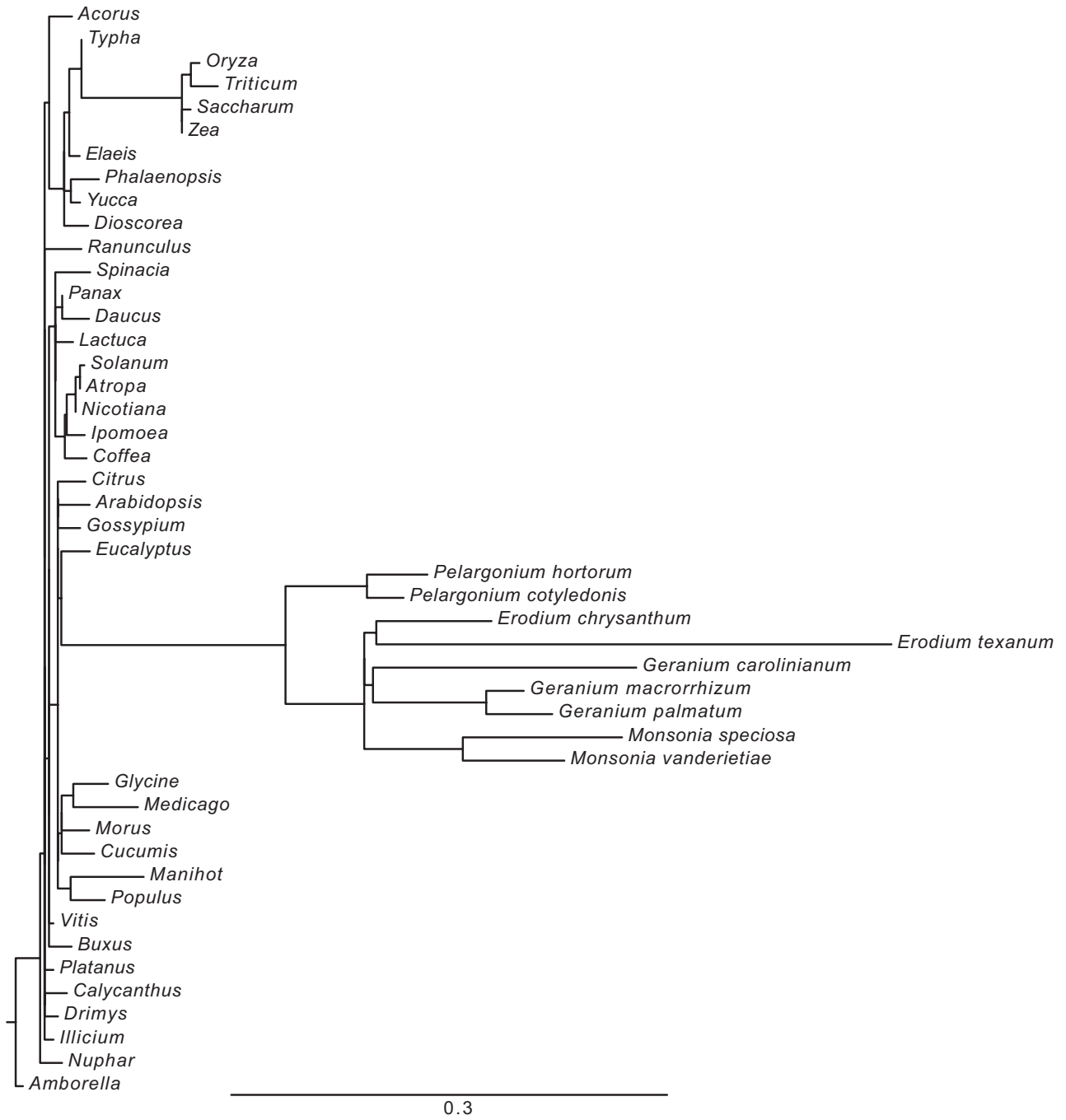


Fig. S3. (continued)

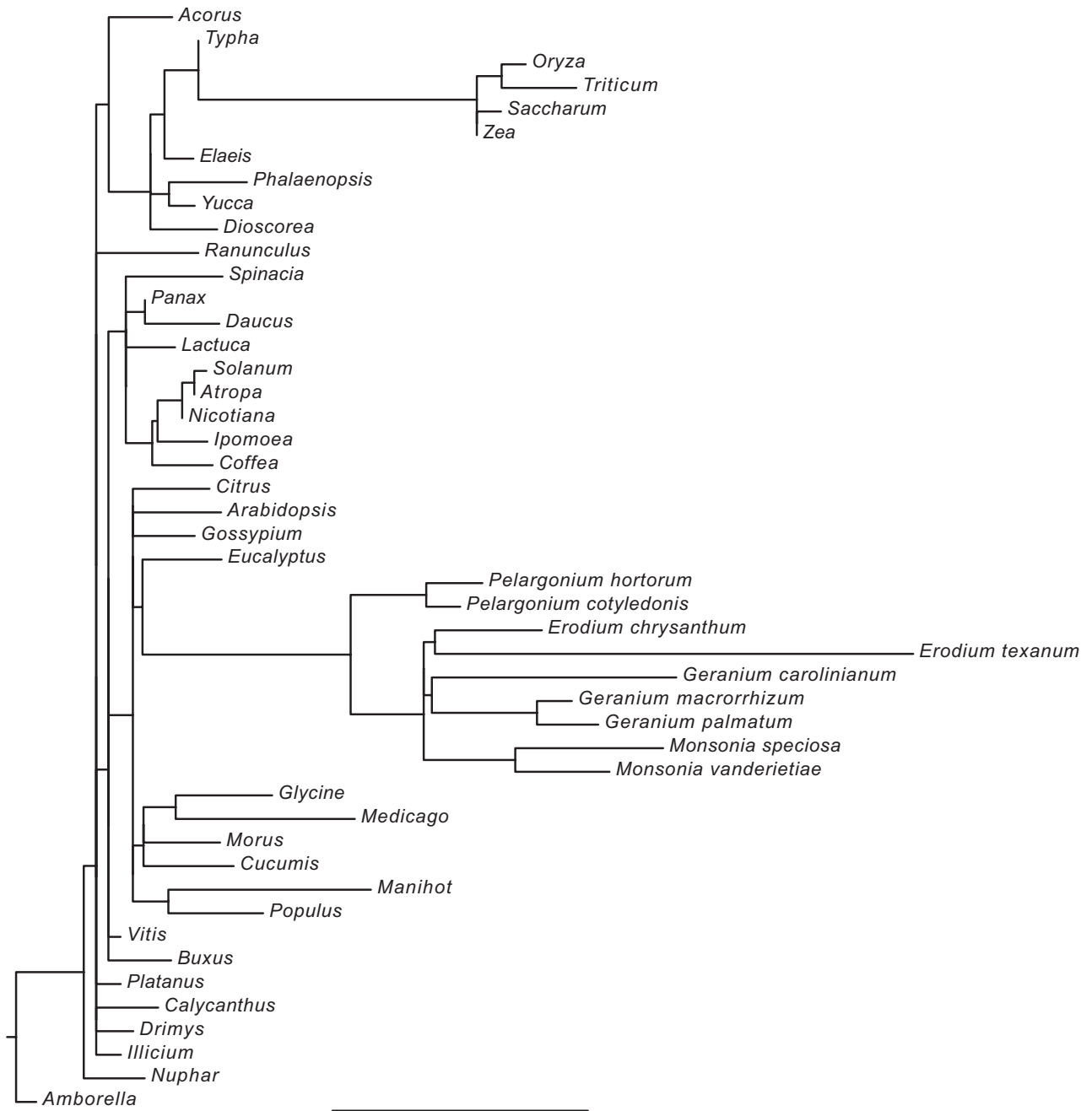
rps18 - dN



0.3

Fig. S3. (continued)

rps18 - dS



0.3

Fig. S3. (continued)

psal - dN

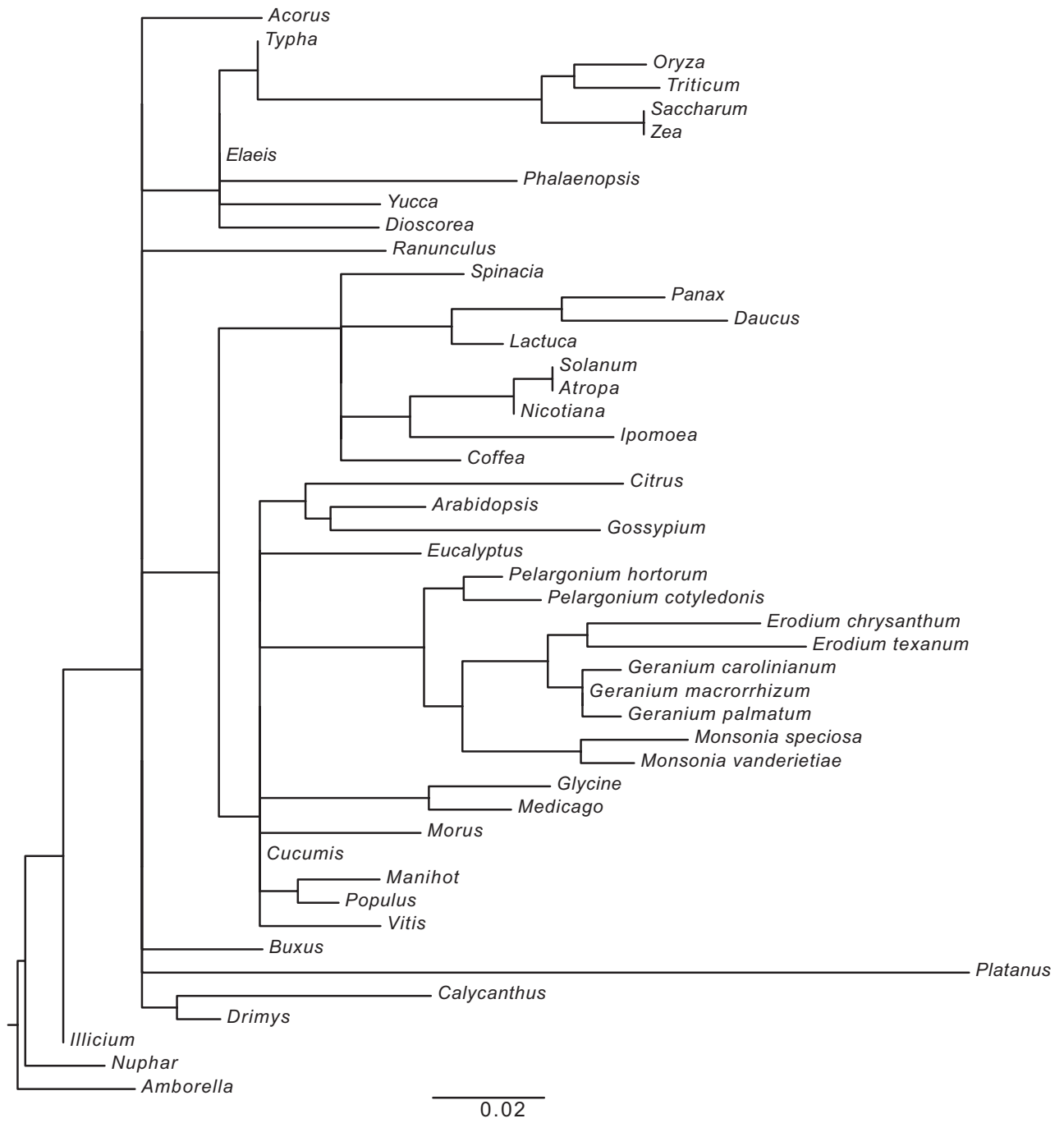


Fig. S3. (continued)

psaC - dS

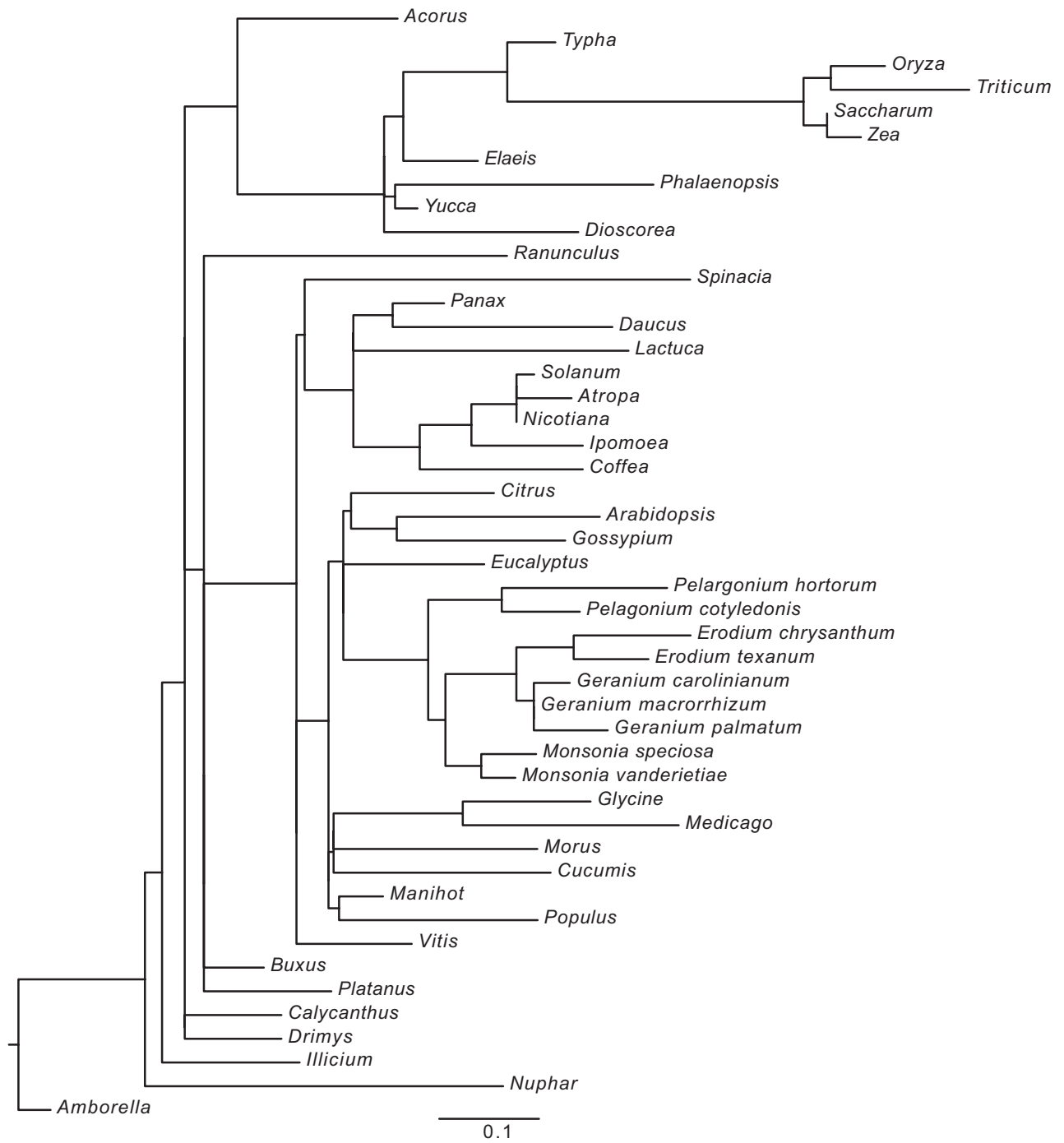


Fig. S3. (continued)

Table S1. Genes sampled for 47 taxa

Gene name	Taxa with missing data
<i>atpA</i>	None
<i>atpB</i>	None
<i>atpE</i>	None
<i>atpF</i>	None
<i>atpH</i>	None
<i>atpI</i>	None
<i>ccsA</i>	None
<i>cemA</i>	None
<i>matK</i>	None
<i>ndhA</i>	<i>Phalaenopsis</i> , <i>E.chrysanthum</i>
<i>ndhB</i>	<i>Phalaenopsis</i>
<i>ndhC</i>	<i>Phalaenopsis</i> , <i>E.chrysanthum</i>
<i>ndhD</i>	<i>Phalaenopsis</i> , <i>E.chrysanthum</i>
<i>ndhE</i>	<i>Phalaenopsis</i> , <i>E.chrysanthum</i>
<i>ndhF</i>	<i>Phalaenopsis</i>
<i>ndhG</i>	<i>Phalaenopsis</i> , <i>E.chrysanthum</i>
<i>ndhH</i>	<i>Phalaenopsis</i> , <i>E.chrysanthum</i>
<i>ndhI</i>	<i>Phalaenopsis</i> , <i>E.chrysanthum</i>
<i>ndhJ</i>	<i>Phalaenopsis</i> , <i>E.chrysanthum</i>
<i>ndhK</i>	<i>Phalaenopsis</i> , <i>E.chrysanthum</i>
<i>petA</i>	None
<i>petB</i>	None
<i>petD</i>	None
<i>petG</i>	None
<i>petL</i>	None
<i>petN</i>	None
<i>psaA</i>	None
<i>psaB</i>	None
<i>psaC</i>	None
<i>psaI</i>	None
<i>psaJ</i>	None
<i>psbA</i>	None
<i>psbB</i>	None
<i>psbC</i>	None
<i>psbD</i>	<i>G.carolinianum</i>
<i>psbE</i>	None
<i>psbF</i>	None
<i>psbH</i>	None
<i>psbI</i>	None
<i>psbJ</i>	None
<i>psbK</i>	None
<i>psbL</i>	None
<i>psbM</i>	None
<i>psbN</i>	None
<i>psbT</i>	None
<i>psbZ</i>	None
<i>rbcL</i>	None
<i>rpl14</i>	None
<i>rpl16</i>	None
<i>rpl2</i>	None
<i>rpl20</i>	None
<i>rpl22</i>	<i>Glycine</i> , <i>Gossypium</i> , <i>Medicago</i>
<i>rpl23</i>	<i>Spinacia</i>
<i>rpl32</i>	<i>Populus</i>
<i>rpl33</i>	None
<i>rpl36</i>	None
<i>rpoA</i>	<i>P.hortorum</i> , <i>P.cotyleonis</i>
<i>rpoB</i>	None
<i>rpoC1</i>	None
<i>rpoC2</i>	None
<i>rps11</i>	None
<i>rps12</i>	None
<i>rps14</i>	None
<i>rps15</i>	None

Gene name	Taxa with missing data
<i>rps16</i>	<i>Dioscorea</i> , <i>Medicago</i> , <i>Populus</i>
<i>rps18</i>	None
<i>rps19</i>	None
<i>rps2</i>	None
<i>rps3</i>	None
<i>rps4</i>	None
<i>rps7</i>	None
<i>rps8</i>	None

E.chrysanthum = *Erodium chrysanthum*, *G.carolinianum* = *Geranium carolinianum*, *P.hortorum* = *Pelargonium X hortorum*, *P.cotyledonis* = *Pelargonium cotyledonis*. Missing data and gene exclusions are described. Two genes, *clpP* and *infA*, were excluded, because we were unable to align either amino acid or nucleotide sequences. Additionally, some genes are missing from various genomes. The majority of the NADH dehydrogenase genes (*ndhA*, *ndhC*, *ndhD*, *ndhE*, *ndhG*, *ndhH*, *ndhI*, *ndhJ*, and *ndhK*) are missing in *E. chrysanthum*. Incomplete genome sequences result in missing data for *psbD* in *G. carolinianum* and 24 nucleotides of *rbcL* in *E. chrysanthum*. In addition, a functional copy of the RNA polymerase gene *rpoA* is missing in *P. cotyledonis* (M. Guisinger, unpublished) and *P. hortorum* (1). Previously published intron losses that were either confirmed in our study or found in additional taxa included the loss of the introns in *rpl16* and *rps16* in all Geraniaceae (1, 2) and in *rpl2* in *Monsonia speciosa* and *M. vanderietiae* (previously *Sarcocaulon vanderietiae*) (3). The loss of the *rpoC1* intron in *E. chrysanthum* has not been previously described. Genes that contain internal stop codons, and are therefore shortened in the alignment, include *atpE* in *Monsonia speciosa* and *M. vanderietiae*, *ndhB* and *ndhF* in *E. chrysanthum*, *rpl22* in *G. palmatum*, *rpl23* in *G. palmatum* and *G. macrorrhizum*, *rpoB* in *G. macrorrhizum*, and *rpoC1* in *G. carolinianum*.

1. Chumley TW, Palmer JD, Mower JP, Fourcade HM, Calie PJ et al. (2006) The complete chloroplast genome sequence of *Pelargonium x hortorum*: organization and evolution of the largest and most highly rearranged chloroplast genome of land plants. *Mol Biol Evol* 23:2175–90.
2. Campagna ML, Downie SR (1998) The intron in chloroplast gene *rpl16* is missing from the flowering plant families Geraniaceae, Goodeniaceae, and Plumbaginaceae. *Trans Ill State Acad Sci* 91:1–11.
3. Downie SR, Olmstead RG, Zurawski G, Soltis DE, Soltis PS et al. (1991) Six independent losses of the chloroplast DNA *rpl2* intron in dicotyledons: molecular and phylogenetic implications. *Evolution* 45:1245–1259.

Table S2. GenBank accession numbers for 47 taxa included in analyses

Taxon	GenBank accession numbers
<i>Acorus americanus</i>	NC_010093
<i>Amborella trichopoda</i>	NC_005086
<i>Arabidopsis thaliana</i>	NC_000932
<i>Atropa belladonna</i>	NC_004561
<i>Buxus microphylla</i>	NC_009599
<i>Calycanthus floridus</i>	NC_004993
<i>Citrus sinensis</i>	NC_008334
<i>Coffea arabica</i>	NC_008535
<i>Cucumis sativus</i>	NC_007144
<i>Daucus carota</i>	NC_008325
<i>Dioscorea elephantipes</i>	NC_009601
<i>Drimys granadensis</i>	NC_008456
<i>Elaeis oleifera</i>	EU016883-EU016962
<i>Erodium chrysanthum</i>	EU922029-EU922091
<i>Erodium texanum</i>	EU922092-EU922163
<i>Eucalyptus globulus</i>	NC_008115
<i>Geranium carolinianum</i>	EU922164-EU922234
<i>Geranium macrorrhizum</i>	EU922235-EU922306
<i>Geranium palmatum</i>	EU922307-EU922378
<i>Glycine max</i>	NC_007942
<i>Gossypium hirsutum</i>	NC_007944
<i>Illicium oligandrum</i>	NC_009600
<i>Ipomoea purpurea</i>	NC_009808
<i>Lactuca sativa</i>	NC_007578
<i>Manihot esculenta</i>	NC_010433
<i>Medicago truncatula</i>	NC_003119
<i>Monsonia speciosa</i>	EU922379-EU922450
<i>Monsonia vanderietiae</i>	EU922451-EU922522
<i>Morus indica</i>	NC_008359
<i>Nicotiana tabacum</i>	NC_001879
<i>Nuphar advena</i>	NC_008788
<i>Oryza sativa</i>	NC_001320
<i>Panax schinseng</i>	NC_006290
<i>Pelargonium cotyledonis</i>	EU922523-EU922593
<i>Pelargonium X hortorum</i>	NC_008454
<i>Phalaenopsis aphrodite</i>	NC_007499
<i>Platanus occidentalis</i>	NC_008335
<i>Populus trichocarpa</i>	NC_008235
<i>Ranunculus macranthus</i>	NC_008796
<i>Saccharum officinarum</i>	NC_006084
<i>Solanum tuberosum</i>	NC_008096
<i>Spinacia oleracea</i>	NC_002202
<i>Triticum aestivum</i>	NC_002762
<i>Typha latifolia</i>	DQ069337-DQ069702, EU017296-EU017315
<i>Vitis vinifera</i>	NC_007957
<i>Yucca schidigera</i>	DQ069337-DQ069702, EU016681-EU016700
<i>Zea mays</i>	NC_001666

Table S3. Status of Geraniaceae plastid genome sequencing

Species name	No. of contigs	Largest contig, bp	IR information (PCR confirmation needed)
<i>Erodium texanum</i>	1	131,840	~ 125 bp
<i>Erodium chrysanthum</i>	8	37,800	unknown
<i>Geranium carolinianum</i>	10	56,075	unknown
<i>Geranium macrorrhizum</i>	4	70,351	unknown
<i>Geranium palmatum</i>	1	137,094	~ 8,300 bp
<i>Monsonia speciosa</i>	1	125,022	~ 5,640 bp
<i>Monsonia vanderietiae</i>	8	53,711	unknown
<i>Pelargonium cotyledonis</i>	2	81,829	unknown

Table S4. Pair-wise Wilcoxon rank sum tests for values of *dN* across gene groups within Geraniaceae (see *Materials and Methods* for grouping of genes)

<i>dN</i> Gene(s)	Individual gene or gene group										
	<i>atp</i>	<i>ccsA</i>	<i>cemA</i>	<i>matK</i>	<i>ndh</i>	<i>pet</i>	<i>psa</i>	<i>psb</i>	<i>rbcL</i>	<i>rpl</i>	<i>rpo</i>
<i>ccsA</i>	0.0034	-	-	-	-	-	-	-	-	-	-
<i>cemA</i>	< 0.0001	0.0001	-	-	-	-	-	-	-	-	-
<i>matK</i>	0.0010	1.0000	0.0041	-	-	-	-	-	-	-	-
<i>ndh</i>	1.0000	0.0011	< 0.0001	0.0003	-	-	-	-	-	-	-
<i>pet</i>	0.0062	< 0.0001	< 0.0001	< 0.0001	0.0002	-	-	-	-	-	-
<i>psa</i>	< 0.0001	< 0.0001	< 0.0001	< 0.0001	< 0.0001	1.0000	-	-	-	-	-
<i>psb</i>	< 0.0001	< 0.0001	< 0.0001	< 0.0001	< 0.0001	0.0013	0.4091	-	-	-	-
<i>rbcL</i>	0.0002	0.0001	< 0.0001	< 0.0001	0.0002	1.0000	1.0000	1.0000	-	-	-
<i>rpl</i>	< 0.0001	1.0000	0.0012	1.0000	< 0.0001	< 0.0001	< 0.0001	< 0.0001	< 0.0001	< 0.0001	-
<i>rpo</i>	< 0.0001	1.0000	0.0009	1.0000	< 0.0001	< 0.0001	< 0.0001	< 0.0001	< 0.0001	1.0000	-
<i>rps</i>	< 0.0001	1.0000	0.0085	1.0000	< 0.0001	< 0.0001	< 0.0001	< 0.0001	< 0.0001	0.1979	1.0000

Bold cells show *P*-values significant after Bonferroni correction ($\alpha = 0.05$).

Table S5. Pair-wise Wilcoxon rank sum tests for values of *dS* across gene groups within Geraniaceae (see Materials and Methods for grouping of genes)

<i>dS</i> Gene(s)	Individual gene or gene group										
	<i>atp</i>	<i>ccsA</i>	<i>cemA</i>	<i>matK</i>	<i>ndh</i>	<i>pet</i>	<i>psa</i>	<i>psb</i>	<i>rbcL</i>	<i>rpl</i>	<i>rpo</i>
<i>ccsA</i>	0.4120	-	-	-	-	-	-	-	-	-	-
<i>cemA</i>	1.0000	1.0000	-	-	-	-	-	-	-	-	-
<i>matK</i>	1.0000	1.0000	1.0000	-	-	-	-	-	-	-	-
<i>ndh</i>	1.0000	0.1311	1.0000	1.0000	-	-	-	-	-	-	-
<i>pet</i>	1.0000	0.0698	1.0000	0.9165	1.0000	-	-	-	-	-	-
<i>psa</i>	1.0000	0.3760	1.0000	1.0000	1.0000	1.0000	-	-	-	-	-
<i>psb</i>	1.0000	0.0417	0.9244	0.6271	1.0000	1.0000	1.0000	-	-	-	-
<i>rbcL</i>	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	-	-	-
<i>rpl</i>	0.8840	1.0000	1.0000	1.0000	0.0283	0.0109	0.4348	< 0.0001	1.0000	-	-
<i>rpo</i>	1.0000	1.0000	1.0000	1.0000	1.0000	0.9881	1.0000	0.2601	1.0000	1.0000	-
<i>rps</i>	0.1511	1.0000	1.0000	1.0000	0.0013	0.0009	0.0531	< 0.0001	1.0000	1.0000	1.0000

Bold cells show *P*-values significant after Bonferroni correction ($\alpha = 0.05$).

Table S6. Pair-wise Wilcoxon rank sum tests for values of dS for branches within Geraniaceae

dS	Branch															
Branch	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
2	0.0001	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3	< 0.001	0.0133	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4	< 0.001	0.0538	1.0000	-	-	-	-	-	-	-	-	-	-	-	-	-
5	< 0.001	0.0014	1.0000	1.0000	-	-	-	-	-	-	-	-	-	-	-	-
6	< 0.001	< 0.001	1.0000	1.0000	1.0000	-	-	-	-	-	-	-	-	-	-	-
7	0.0003	1.0000	0.0244	0.0984	0.0046	< 0.001	-	-	-	-	-	-	-	-	-	-
8	< 0.001	< 0.001	0.2111	0.3515	0.6520	1.0000	< 0.001	-	-	-	-	-	-	-	-	-
9	< 0.001	< 0.001	0.0044	0.0191	0.0350	0.4998	< 0.001	1.0000	-	-	-	-	-	-	-	-
10	1.0000	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	-	-	-	-	-	-	-
11	< 0.001	1.0000	0.0812	0.3305	0.0094	0.0003	1.0000	< 0.001	< 0.001	< 0.001	-	-	-	-	-	-
12	< 0.001	0.0148	1.0000	1.0000	1.0000	1.0000	0.0244	0.5356	0.0127	< 0.001	0.0523	-	-	-	-	-
13	< 0.001	< 0.001	0.0017	0.0079	0.0167	0.2613	< 0.001	1.0000	1.0000	< 0.001	< 0.001	0.0056	-	-	-	-
14	< 0.001	< 0.001	0.2613	0.4517	0.8406	1.0000	< 0.001	1.0000	1.0000	< 0.001	< 0.001	0.5309	1.0000	-	-	-
15	< 0.001	< 0.001	0.7205	0.9713	1.0000	1.0000	< 0.001	1.0000	1.0000	< 0.001	< 0.001	1.0000	0.7205	1.0000	-	-
16	< 0.001	1.0000	1.0000	1.0000	0.4517	0.0094	1.0000	< 0.001	< 0.001	< 0.001	1.0000	0.7921	< 0.001	< 0.001	< 0.001	-
17	< 0.001	0.0003	1.0000	1.0000	1.0000	1.0000	0.0015	1.0000	0.5356	< 0.001	0.0026	1.0000	0.2672	1.0000	1.0000	0.0147

Branch labels are found in Fig. S3a. Bold cells show P -values significant after Bonferroni correction ($\alpha = 0.05$).

Table S7. Pair-wise Wilcoxon rank sum tests for values of dN for branches within Geraniaceae

dN	Branch															
Branch	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
2	1.0000	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3	0.0004	1.0000	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4	0.0024	1.0000	1.0000	-	-	-	-	-	-	-	-	-	-	-	-	-
5	0.0001	0.4998	1.0000	1.0000	-	-	-	-	-	-	-	-	-	-	-	-
6	<0.0001	0.0568	1.0000	1.0000	1.0000	-	-	-	-	-	-	-	-	-	-	-
7	1.0000	1.0000	1.0000	1.0000	1.0000	0.1143	-	-	-	-	-	-	-	-	-	-
8	<0.0001	0.0106	1.0000	1.0000	1.0000	1.0000	0.0279	-	-	-	-	-	-	-	-	-
9	<0.0001	0.0005	0.1553	1.0000	1.0000	1.0000	0.0017	1.0000	-	-	-	-	-	-	-	-
10	1.0000	0.2027	0.0001	0.0001	<0.0001	<0.0001	0.2137	<0.0001	<0.0001	-	-	-	-	-	-	-
11	0.6511	1.0000	1.0000	1.0000	1.0000	0.4531	1.0000	0.0672	0.0065	0.0562	-	-	-	-	-	-
12	0.0025	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.6396	0.0005	1.0000	-	-	-	-	-
13	<0.0001	0.0002	0.1468	0.6230	0.7382	1.0000	0.0009	1.0000	1.0000	<0.0001	0.0041	0.2752	-	-	-	-
14	<0.0001	0.0327	1.0000	1.0000	1.0000	1.0000	0.0949	1.0000	1.0000	<0.0001	0.2963	1.0000	1.0000	-	-	-
15	<0.0001	0.0730	1.0000	1.0000	1.0000	1.0000	0.1792	1.0000	1.0000	<0.0001	0.5485	1.0000	1.0000	1.0000	-	-
16	0.0847	1.0000	1.0000	1.0000	1.0000	0.5029	1.0000	0.0724	0.0029	0.0118	1.0000	1.0000	0.0026	0.3397	0.6511	-
17	0.0003	0.6308	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.0001	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000

Branch labels are found in Fig. S3a. Bold cells show P -values significant after Bonferroni correction ($\alpha = 0.05$).

Table S8. Negative log likelihood scores used in likelihood ratio tests (LRT) to test the fit of model H_A to H_0

Taxa included	Gene name	-lnL H_0	-lnL H_A	$2^*(H_0-H_A)$	P-value	d.f.	Bonferroni
all	<i>rpoB</i>	30845.4641	30659.6961	371.5360	0.0000	1	0.0000
all	<i>rpoC1</i>	16928.0848	16701.3552	453.4591	0.0000	1	0.0000
all	<i>rpoC2</i>	49377.1243	49262.4918	229.2651	0.0000	1	0.0000
all	<i>rps11</i>	5150.0430	5076.7273	146.6314	0.0000	1	0.0000
all	<i>rps2</i>	8053.3952	7952.3144	202.1616	0.0000	1	0.0000
all	<i>rps3</i>	10462.9379	10408.0313	109.8131	0.0000	1	0.0000
all	<i>cemA</i>	10539.6248	10501.8909	75.4677	0.0000	1	0.0000
all	<i>atpE</i>	3354.0640	3325.6529	56.8223	0.0000	1	0.0000
all	<i>rpl14</i>	3853.4849	3826.0317	54.9064	0.0000	1	0.0000
all	<i>rps4</i>	5889.9077	5867.5889	44.6376	0.0000	1	0.0000
all	<i>atpB</i>	12795.6739	12775.5249	40.2979	0.0000	1	0.0000
all	<i>rps8</i>	5271.8554	5257.7698	28.1712	0.0000	1	0.0000
all	<i>atpF</i>	5801.0679	5788.2812	25.5733	0.0000	1	0.0000
all	<i>rps19</i>	3566.1481	3553.4543	25.3875	0.0000	1	0.0000
all	<i>rps18</i>	2476.7328	2464.3268	24.8119	0.0000	1	0.0000
all	<i>rps15</i>	2916.0309	2904.8897	22.2823	0.0000	1	0.0000
all	<i>atpH</i>	1783.8555	1772.7967	22.1177	0.0000	1	0.0000
all	<i>rpl36</i>	1175.2563	1164.6501	21.2123	0.0000	1	0.0000
all	<i>rps12</i>	2344.5476	2335.4152	18.2649	0.0000	1	0.0000
no Glyc,Med,Gossy	<i>rpl22</i>	1337.9096	1329.0802	17.6588	0.0000	1	0.0000
no Phal, Echrys	<i>ndhA</i>	12458.2546	12450.0763	16.3567	0.0001	1	0.0072
all	<i>petD</i>	3817.5277	3809.8413	15.3729	0.0001	1	0.0072
no Phal, Echrys	<i>ndhG</i>	6359.7186	6352.4323	14.5726	0.0001	1	0.0072
all	<i>atpA</i>	15118.3301	15111.3373	13.9856	0.0002	1	0.0144
all	<i>rps7</i>	2988.2488	2981.2917	13.9142	0.0002	1	0.0144
no Phal, Echrys	<i>ndhD</i>	16468.8854	16461.9620	13.8467	0.0002	1	0.0144
all	<i>rpl16</i>	4204.1510	4197.8957	12.5107	0.0004	1	0.0288
no Phal, Echrys	<i>ndhH</i>	11863.8184	11857.9901	11.6565	0.0006	1	0.0432
all	<i>petA</i>	10034.6283	10029.0822	11.0920	0.0009	1	0.0648
no Phal, Echrys	<i>ndhK</i>	5982.6134	5977.2846	10.6576	0.0011	1	0.0792
all	<i>ccsA</i>	12220.6267	12215.6045	10.0444	0.0015	1	0.1080
no Pel, Pcoty	<i>rpoA</i>	11459.8231	11454.9034	9.8395	0.0017	1	0.1224
all	<i>petB</i>	4913.6811	4908.8644	9.6333	0.0019	1	0.1368
all	<i>rps14</i>	3128.3874	3123.8029	9.1691	0.0025	1	0.1800
no Phal, Echrys	<i>ndhE</i>	3143.4456	3138.9944	8.9024	0.0028	1	0.2016
no Phal, Echrys	<i>ndhC</i>	3036.0586	3031.6405	8.8361	0.0030	1	0.2160
all	<i>psbB</i>	12542.2190	12538.4331	7.5718	0.0059	1	0.4248
all	<i>petN</i>	549.3180	545.7272	7.1817	0.0074	1	0.5328
no Phal, Echrys	<i>ndhI</i>	4315.1437	4311.6213	7.0449	0.0079	1	0.5688
all	<i>psbT</i>	641.0695	637.7282	6.6826	0.0097	1	0.6984
all	<i>rbcL</i>	12890.5450	12887.5740	5.9420	0.0148	1	1.0000
all	<i>petG</i>	732.1408	729.2326	5.8164	0.0159	1	1.0000
all	<i>psaB</i>	16112.5066	16109.7271	5.5591	0.0184	1	1.0000
all	<i>psbI</i>	860.0936	857.4286	5.3300	0.0210	1	1.0000
no Phal	<i>ndhF</i>	2941.1020	2938.5093	5.1852	0.0228	1	1.0000
all	<i>rpl2</i>	5366.2976	5363.7847	5.0259	0.0250	1	1.0000
all	<i>rpl20</i>	5252.5669	5250.2576	4.6186	0.0316	1	1.0000
no Pop	<i>rpl32</i>	2300.1382	2298.1576	3.9610	0.0466	1	1.0000
no Phal	<i>ndhB</i>	1208.2257	1206.2558	3.9397	0.0472	1	1.0000
no Phal, Echrys	<i>ndhJ</i>	4441.4858	4439.8892	3.1933	0.0739	1	1.0000
all	<i>atpI</i>	6633.9899	6632.4017	3.1764	0.0747	1	1.0000
all	<i>matK</i>	21033.6178	21032.3196	2.5964	0.1071	1	1.0000
all	<i>rpl33</i>	2748.6607	2747.4057	2.5099	0.1131	1	1.0000
all	<i>psbZ</i>	1492.3624	1491.4649	1.7951	0.1803	1	1.0000
all	<i>psbE</i>	1561.7736	1560.8801	1.7869	0.1813	1	1.0000
all	<i>psaA</i>	16841.1913	16840.3392	1.7043	0.1917	1	1.0000
all	<i>psbC</i>	10735.0652	10734.3395	1.4513	0.2283	1	1.0000
no Spin	<i>rpl23</i>	836.0069	835.2962	1.4214	0.2332	1	1.0000
all	<i>psbN</i>	742.7416	742.1411	1.2010	0.2731	1	1.0000
no Diosc,Med,Pop	<i>rps16</i>	1361.1748	1360.6133	1.1230	0.2893	1	1.0000
all	<i>psbJ</i>	958.3703	957.9172	0.9062	0.3411	1	1.0000
no Gcaro	<i>psbD</i>	7049.3826	7048.9460	0.8732	0.3501	1	1.0000
all	<i>psaC</i>	1878.3671	1877.9475	0.8392	0.3596	1	1.0000
all	<i>psbH</i>	2524.8681	2524.5500	0.6362	0.4251	1	1.0000

Taxa included	Gene name	-lnL H0	-lnL HA	2*(H0-HA)	P-value	d.f.	Bonferroni
all	<i>psaJ</i>	1262.9889	1262.6891	0.5996	0.4387	1	1.0000
all	<i>psbF</i>	732.6367	732.4236	0.4263	0.5138	1	1.0000
all	<i>psbL</i>	562.9720	562.8376	0.2688	0.6042	1	1.0000
all	<i>psbA</i>	6815.2708	6815.1778	0.1860	0.6663	1	1.0000
all	<i>psbM</i>	817.2205	817.1431	0.1549	0.6939	1	1.0000
all	<i>psbK</i>	1910.3696	1910.3685	0.0022	0.9627	1	1.0000
all	<i>psaI</i>	1048.1031	1048.1026	0.0010	0.9743	1	1.0000
all	<i>petL</i>	947.8021	947.8021	0.0000	0.9958	1	1.0000

Glyc = *Glycine*, Med = *Medicago*, Gossy = *Gossypium*, Phal = *Phalaenopsis*, Echrys = *Erodium chrysanthum*, Pel = *Pelargonum hortorum*, Pcoty = *Pelargonium cotyledonis*, Pop = *Populus*, Spin = *Spinacia*, Diosc = *Dioscorea*, Gcaro = *Geranium carolinianum*. H₀ and H_A are described.