Supplementary Material

Plastid phylogenomics of the Eriostemon group (Rutaceae; Zanthoxyloideae): support for major clades and investigation of a backbone polytomy

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Table S1. Assembly statistics for plastome sequences of each sample in the genome-skimming dataset.

Taxon	Collector number		GC %	GC % Mean read		
Acronychia laevis	PIF33410	mapped 151370	0 368	<u>depth</u> 142 23		
Asterolasia asterisconhora	MIB2564	129955	0.300	122.25		
Asterolasia drummondii	BIM330	110755	0.372	104.08		
Roronia edwardsii	MIR1074	261050	0.38	251.36		
Boronia edwardsh Poronia imlanansis	MJD1974 MID2005	201039	0.421	231.30		
Boronia imayensis	MJB2003	019091	0.38	371.32		
Boronia ternata	MJB1931	384024	0.372	304.05		
Brombya platynema	PIF34088	254887	0.388	229.72		
Chorilaena anceps	BJM475	63507	0.369	60.55		
Chorilaena euphemiae	BJM424	681616	0.381	623.56		
Chorilaena quercifolia	MJB1954	210902	0.371	200.34		
Correa alba	MJB1876	167251	0.374	161.08		
Correa glabra	MJB2476	32489	0.378	30.91		
Correa lawrenceana var. grampiana	MJB1988	142325	0.372	127.93		
Correa lawrenceana var. latrobeana	MJB2567	150816	0.376	140.44		
Crowea angustifolia var. platyphylla	MJB1953	131807	0.368	126.12		
Crowea exalata subsp. exalata	D Ohlsen s.n.	88272	0.372	82.40		
Crowea exalata var. revoluta	MJB1992	176094	0.378	165.71		
Crowea saligna	D Ohlsen s.n.	73379	0.376	68.31		
Cyanothamnus anemonifolius	MJB2562	11657	0.376	11.22		
Diplolaena drummondii	MJB1956	323773	0.369	310.46		
Diplolaena obovata	MJB1908	16778	0.368	15.39		
Drummondita calida	PIF22556	211112	0.368	194.97		
Drummondita fulva	AMarkey6212	69438	0.372	64.41		
Drummondita hassellii	MJB1925	79421	0.376	74.06		
Eriostemon australasius	PIF34192	55082	0.367	51.80		
Eriostemon banksii	PIF33960	58061	0.368	78.08		
Euodia pubifolia	PIF25751	128623	0.373	120.40		
Geleznowia verrucosa	MJB1910	85504	0.381	79.10		
Geleznowia verrucosa	BM344	222976	0.369	208.93		
Halfordia kendack	Sanko3019	37386	0.37	35.12		
Halfordia kendack	PIF34073	50147	0.365	47.00		
Halfordia kendack	DGF10829	126943	0.368	120.00		
Halfordia kendack	PIF34090	187726	0.366	177.91		
Halfordia kendack	PIF34580	273385	0.368	258.51		
Leionema beckleri	PIF33439	63703	0.369	55.88		
Leionema ellipticum	PIF25021	193942	0.37	220.07		
Leionema lamprophyllum subsp. obovatum	MJB2563	253789	0.373	241.16		
Leionema rotundifolium	PIF34469	48048	0.366	45.57		
Medicosma cunninghamii	PIF33501	103895	0.369	96.70		
Melicope havesii	PIF36183	67494	0.368	63.32		
Muiriantha hassellii	BJM474	574565	0.379	539.37		
Myrtopsis sp.	Munz3458	107718	0 385	92.87		
Nematolenis nhebalioides	AMarkev6215	218082	0.369	204 36		
Nematolenis sauamea	PIF34811	32152	0.37	33.13		
Nematolenis wilsonii	MIB2568	48693	0.374	A7 48		
1. Charlotepis musolili	110102300	-1007J	0.577	T1.T0		

Taxon	Collector number	Total reads mapped	GC %	Mean read denth	
Neobyrnesia suberosa	MJB1904	179925	0.373	170.12	
Neoschmidia pallida	PHW3303	146185	0.365	136.47	
Phebalium clavatum	BJM398	78434	0.366	74.08	
Phebalium elegans	BJM403	33611	0.369	31.11	
Phebalium longifolium	PIF25088	56140	0.376	51.69	
Phebalium multiflorum	RB1280	25207	0.359	47.73	
Phebalium stenophyllum	MJB2560	12155	0.367	14.18	
Phebalium tuberculosum	BJM375	576767	0.378	519.30	
Phebalium whitei	PIF34467	134112	0.372	126.22	
Philotheca angustifolia subsp. angustifolia	MJB1990	91721	0.374	86.37	
Philotheca difformis subsp. smithiana	MJB s.n.	18519	0.38	17.33	
Philotheca fitzgeraldii	MJB1942	116288	0.375	110.91	
Philotheca gardneri	MJB1949	36539	0.368	34.46	
Philotheca myoporoides subsp. myoporoides	MJB2565	71828	0.374	67.62	
Philotheca nodiflora subsp. lasiocalyx	MJB1962	107475	0.378	99.38	
Philotheca pinoides	MJB11	39589	0.365	35.56	
Philotheca pungens	MJB1872	121381	0.374	115.87	
Philotheca spicata	MJB1907	94192	0.378	92.89	
Philotheca tomentella	MJB1913	248796	0.373	237.79	
Philotheca trachyphylla	MJB1900	16916	0.374	15.78	
Picrella glandulosa	MJB2104	92891	0.372	87.34	
Zieria arborescens subsp. arborescens	MJB2566	164404	0.376	155.98	

Scheme	e		Maximum Likelihood Model (IQ-TREE)	Bayesian Inference Model (MrBayes)
Jnpart	itioned	l	TVM+F+R5	GTR+F+I+G4
°D6. n	on and	ing	TVM + E + D2	CTD + E + I + CA + CTD + E + I + CA
JD5, II	on-cou	ing	TVM+F+R5	01K+1+1+04, 01K+1+1+04
Codon	positio	n (1+2); codon position (3); non-coding	TVM+F+R2;	GTR+F+I+G4; GTR+F+I+G4;
			TVM+F+R3;	GTR+F+I+G4
			TVM+F+R5	
Amino	acid		Q.bird+F+R3	-
Locus	1	accD CDS	TVM+F+R3	-
	2	accD gene-psaI gene spacer	K3Pu+F+R2	-
	3	atpA CDS	TIM+F+I+G4	-
	4	atpA gene-atpF gene spacer	K3Pu+F+G4	-
	5	atpB CDS	K3Pu+F+R2	-
	6	atpB gene-rbcL gene spacer	TVM+F+R2	-
	7	atpE CDS	K3P+G4	-
	8	atpF CDS	GTR+F+R3	-
	9	atpF gene-atpH gene spacer	K3Pu+F+R2	-
	10	atpH CDS	K2P+I	-
	11	atpH gene-atpI gene spacer	GTR+F+R3	-
	12	atpI CDS	K3Pu+F+G4	-
	13	atpI gene-rps2 gene spacer	K3Pu+F+R2	-
	14	ccsA CDS	TVM+F+R3	-
	15	ccsA gene-ndhD gene spacer	TVM+F+R2	-
	16	cemA CDS	TVM+F+R2	-
	17	cemA gene-petA gene spacer	K3Pu+F+G4	-
	18	clpP1 CDS	K3P+I	-
	19	clpP1 gene-psbB gene spacer	K3Pu+F+R3	-
	20	matK CDS	TVM+F+R3	-
	21	matK gene-rps16 gene spacer	K3Pu+F+R4	-
	22	ndhA CDS	TVM+F+R3	-
	23	ndhB CDS	K3Pu+F+I	-
	24	ndhB gene-rps7 gene spacer	F81+F	-
	25	ndhC CDS	TVM+F+R2	-
	26	ndhC gene-trnV-UAC gene spacer	K3Pu+F+R3	-
	27	ndhD CDS	GTR+F+R2	-
	28	ndhD gene-psaC gene spacer	K3Pu+F+R3	-
	29	ndhE CDS	IVM+F+G4	-
	30	ndhE gene-ndhG gene spacer	K3Pu+F+G4	-
	31	ndhG CDS	G1R+F+R2	-
	32	nanG gene-nani gene spacer	1 VM+F+R2	-
	33 24	nunn CDS	$1 \text{ V IVI} + \Gamma + KZ$ $K = 2 \text{ Dr} + \Gamma + C A$	-
	34 25	nunn gene-rps15 gene spacer	KJPU+F+G4 TDM2+E+C4	-
	33 24	ndhl gong ndh (gong grader	$1 \Gamma W O + \Gamma + U 4$ $W 2 D_{W} + \Gamma$	-
	30 27	ndh I CDS	K3Fu+F K3Pu⊥F+D2	-
	31	ndhl gene-ndhk gene specer	ΚΟΙ U⊤Γ+Κ∠ ΤΡΜ2⊥ΕιΙ	-
	30 20	ndhy CDS	$TI WI \angle \top \Gamma \top I$ $TDM3_{\perp}E \downarrow D3$	-
	<u> </u>	ndhK gene-ndhC gene spacer	TIM+F	-
	<u>40</u> <u>41</u>	netA CDS	$K3P_{11}+F+R^{2}$	_
	42	petA gene-nshI gene spacer	TVM+F+R3	-
	43	petB CDS	K3Pu+F+R2	-
	44	petB gene-petD gene spacer	TVM+F+R2	-
	45	petD CDS	K3Pu+F+R2	-
	46	petD gene-rpoA gene spacer	K3Pu+F+R2	-
	47	petG CDS	HKY+F	-
	48	petG gene-trnW-CCA gene spacer	K3P+G4	-
	49	petL CDS	K3P	-
	50	petL gene-petG gene spacer	K3Pu+F+R2	-
	51	petN CDS	K2P	-
	52	petN gene-psbM gene spacer	TVM+F+R3	-
	53	psaA CDS	K3Pu+F+R2	-
	54	psaA gene-ycf3 gene spacer	K3Pu+F+R2	-
	55	psaB CDS	TVM+F+R2	-
	56	psaB gene-psaA gene spacer	K2P+I	-
	57	psaC CDS	K2P+R2	-
	58	psaC gene-ndhE gene spacer	K3Pu+F+G4	-

59	psaI CDS	HKY+F	-
60	psaI gene-ycf4 gene spacer	K3Pu+F+G4	-
61	psaJ CDS	K2P+G4	-
62	psaJ gene-rpl33 gene spacer	TIM+F+R2	-
63	psbA CDS	HKY+F+I+G4	-
64	psbA gene-trnK-UUU gene spacer	K3Pu+F+R3	-
65	psbB CDS	K3Pu+F+R2	-
66	psbB gene-psbT gene spacer	K3Pu+F+G4	-
67	psbC CDS	K3Pu+F+R2	-
68	psbC gene-trnS-UGA gene spacer	TVMe+R3	-
69	psbD CDS	K3Pu+F+R2	-
70	psbE CDS	K3P+I	-
71	psbE gene-petL gene spacer	TVM+F+R3	-
72	psbF CDS	K3P+I	-
73	psbF gene-psbE gene spacer	K2P+I	-
74	psbH CDS	K2P+G4	-
75	psbH gene-petB gene spacer	K3Pu+F+R2	-
76	psbI CDS	K2P+I	-
77	psbI gene-trnS-GCU gene spacer	K3Pu+F+G4	-
78	psbJ CDS	TIM3+F	-
79	psbJ gene-psbL gene spacer	TPM2+F+G4	-
80	psbK CDS	TPM3+F+G4	-
81	psbK gene-psbI gene spacer	TVM+F+G4	-
82	psbL CDS	HKY+F	-
83	psbL gene-psbF gene spacer	K3P	-
84	psbM CDS	HKY+F+G4	-
85	psbM gene-trnD-GUC gene spacer	TVM+F+R2	-
86	psbN CDS	K2P+G4	-
87	psbN gene-psbH gene spacer	K3Pu+F+G4	-
88	psb1 CDS	HKY+F+I	-
89	psb1 gene-psbN gene spacer	JC+G4	-
90	psbZ CDS	HKY+F+G4	-
91		KSP+KS	-
92	roch gene-acch gene spacer	$1 \text{ V} \text{ IV} + \Gamma + \text{K} 2$ $\text{HV} \text{V} + \Gamma + C 4$	-
95	rp114 CDS	$\mathbf{T}\mathbf{D}\mathbf{M}2 + \mathbf{F} + \mathbf{G}4$	-
94	rp116 CDS	$K_{2}P_{1}+F_{2}+P_{3}$	-
96	rpl16 gene_rps3 gene spacer	K3Pu+F+G4	_
97	rp12 CDS	$K3P_{0}\pm F$	_
98	rpl2 cD5 rpl2 gene-rpl23 gene spacer	K3P+I	_
99	rpl20 CDS	K3Pu+F+R2	_
100	rpl20 ceps rpl20 gene-rps12 gene spacer	TIM+F+R3	_
101	rpl22 gene-rps19 gene spacer	JC+I	_
102	rpl23 CDS	F81+F	_
103	rpl23 gene-trnM-CAU/trnI-CAU gene	TPM2+F+R2	-
	spacer		
104	rpl32 CDS	TPM2+F+R2	-
105	rpl32 gene-trnL-UAG gene spacer	TVM+F+G4	-
106	rpl33 CDS	GTR+F+G4	-
107	rpl33 gene-rps18 gene spacer	TVM+F+R2	-
108	rpl36 CDS	K2P+G4	-
109	rpl36 gene-rps8 gene spacer	K3Pu+F+G4	-
110	rpoA CDS	TVM+F+R2	-
111	rpoA gene-rps11 gene spacer	TPM3+F+I	-
112	rpoB CDS	TVM+F+R3	-
113	rpoB gene-trnC-GCA gene spacer	K3Pu+F+R3	-
114	rpoC1 CDS	TVM+F+R3	-
115	rpoCl gene-rpoB gene spacer	HKY+F+R2	-
116	rpoC2 CDS	TVM+F+R3	-
117	rpoC2 gene-rpoC1 gene spacer	K3P	-
118	rps11 CDS	TIMe+I	-
119	rps11 gene-rp136 gene spacer	IVM+F+K2	-
120	rps12 CDS	K2P+I K2D+C4	-
121	rps12 gene-cipP1 gene spacer	K3P+04 $K2D_{01}+E+D2$	-
122	110514 CDS	KJFU+F+KZ K3P+G4	-
123	rps14 gene-psab gene spacer	KJF+04 K3Pu±F±C4	-
124	rps15 cene-vcf1 gene spacer	$TIM + F + P^{2}$	-
125	rns16 CDS	$K3P_{11}+F+G4$	_
127	rps16 gene_trnO_HIIG gene_spacer	$K3P_{11}+F+P_{12}$	_
128	rps18 CDS	TN+F+R3	_
129	rps18 gene-rp]20 gene spacer	TPM3+F+G4	_
130	rps19 CDS	K3Pu+F+G4	_
131	rps19 gene-rpl2 gene spacer	K3Pu+F+I	-

132	rps2 CDS	K3Pu+F+G4	-
133	rps2 gene-rpoC2 gene spacer	K3Pu+F+G4	-
134	rps3 CDS	TPM3+F+G4	-
135	rps4 CDS	K3Pu+F+G4	_
136	rps1 c225 rps4 gene-trnT-UGU gene spacer	$TVM+F+R^2$	_
137	rps7 CDS	K3Pu+F+I	_
138	rps7 ceps rps7 gene_trnV_GAC gene spacer	$TIM + F + R^2$	_
130	rps7 gene trnV GAC gene spacer 2	$K_{2}D_{11} + F_{12}D_{2}$	_
139	rps? gene-univ-OAC gene space 2	TVM + E + GA	-
140	rpso CDS	$V_2D_{11} + E + C_4$	-
141	run 16 cono tra E ULC/tra LCAU cono	K3FU+F+O4 K2D+D2	-
142	milo gene-une-uue-uuc/uni-GAU gene	K3P+K2	-
1/2	spacer	IC	
143	rm4.5 gene rm5 gene spacer		-
144	min4.5 gene-min5 gene spacer	$K_2F + K_2$	-
145	tin A LICC same wir 22 same spacer		-
140	trin CCA sense not N some spacer		-
14/	tine-oca gene-petit gene space	$1 \vee M + F + R2$	-
148	tmD-GUC gene-tm I-GUA gene spacer	$1 \vee M + F + K2$ K = 2D + F + D2	-
149	tmE-UUC gene-tm1-GGU gene spacer	KSPU+F+KS	-
150	trnE-UUC/trnI-GAU gene-trnA-UGC	JC	-
1 = 1	gene spacer		
151	trnF-GAA gene-ndnJ gene spacer	IVM+F+K2	-
152	trnIM-CAU gene-rps14 gene spacer	HKY+F+G4	-
153	trnG-UCC gene-trnR-UCU gene spacer	K3PU+F+K2	-
154	trnH-GUG gene-psbA gene spacer	TVM+F+R3	-
155	trnL-CAA gene-ndhB gene spacer	K3Pu+F+G4	-
156	trnL-UAA gene-trnF-GAA gene spacer	K3Pu+F+R2	-
157	trnL-UAG gene-ccsA gene spacer	TPM3+F+R2	-
158	trnM-CAU gene-atpE gene spacer	TVM+F+R2	-
159	trnM-CAU/trnI-CAU gene-ycf2 gene	JC	-
1.00	spacer	KOD JE CA	
160	trnN-GUU gene-ycf1/ycf1-fragment	K3Pu+F+G4	-
	gene spacer		
161	trnP-UGG gene-psaJ gene spacer	K3Pu+F+R3	-
162	trnQ-UUG gene-psbK gene spacer	K3Pu+F+R3	-
163	trnR-ACG gene-trnN-GUU gene spacer	F81+F+R2	-
164	trnR-UCU gene-atpA gene spacer	TIM+F+R2	-
165	trnS-GCU gene-trnG-UCC gene spacer	GTR+F+R2	-
166	trnS-GGA gene-rps4 gene spacer	K3Pu+F+G4	-
167	trnS-UGA gene-psbZ gene spacer	GTR+F+G4	-
168	trnT-GGU gene-psbD gene spacer	TVM+F+R3	-
169			
170	trn1-UGU gene-trnL-UAA gene spacer	TVM+F+R3	-
	trn1-UGU gene-trnL-UAA gene spacer trnV-GAC gene-rrn16 gene spacer	TVM+F+R3 K2P+I	-
171	trn I-UGU gene-trnL-UAA gene spacer trnV-GAC gene-rrn16 gene spacer trnV-UAC gene-trnM-CAU gene	TVM+F+R3 K2P+I K3Pu+F	- -
171	trn I-UGU gene-trnL-UAA gene spacer trn V-GAC gene-trn16 gene spacer trn V-UAC gene-trnM-CAU gene spacer	TVM+F+R3 K2P+I K3Pu+F	-
171 172	trn I-UGU gene-trnL-UAA gene spacer trnV-GAC gene-trn16 gene spacer trnV-UAC gene-trnM-CAU gene spacer trnW-CCA gene-trnP-UGG gene spacer	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4	-
171 172 173	trn I-UGU gene-trnL-UAA gene spacer trnV-GAC gene-trn16 gene spacer trnV-UAC gene-trnM-CAU gene spacer trnW-CCA gene-trnP-UGG gene spacer trnY-GUA gene-trnE-UUC gene spacer	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4 K3P	- - -
171 172 173 174	trn I-UGU gene-trnL-UAA gene spacer trn V-GAC gene-trn16 gene spacer trn V-UAC gene-trnM-CAU gene spacer trn W-CCA gene-trnP-UGG gene spacer trn Y-GUA gene-trnE-UUC gene spacer ycf1 CDS	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4 K3P TVM+F+R4	- - - -
171 172 173 174 175	tm1-UGU gene-trnL-UAA gene spacer trnV-GAC gene-trn16 gene spacer trnV-UAC gene-trnM-CAU gene spacer trnW-CCA gene-trnP-UGG gene spacer trnY-GUA gene-trnE-UUC gene spacer ycf1 CDS ycf1/ycf1-fragment gene-rpl32 gene	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4 K3P TVM+F+R4 TVM+F+R3	- - - - -
171 172 173 174 175	tm1-UGU gene-trnL-UAA gene spacer trnV-GAC gene-trn16 gene spacer trnV-UAC gene-trnM-CAU gene spacer trnW-CCA gene-trnP-UGG gene spacer trnY-GUA gene-trnE-UUC gene spacer ycf1 CDS ycf1/ycf1-fragment gene-rpl32 gene spacer	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4 K3P TVM+F+R4 TVM+F+R3	-
171 172 173 174 175 176	tm1-UGU gene-trnL-UAA gene spacer trnV-GAC gene-trn16 gene spacer trnV-UAC gene-trnM-CAU gene spacer trnW-CCA gene-trnP-UGG gene spacer trnY-GUA gene-trnE-UUC gene spacer ycf1 CDS ycf1/ycf1-fragment gene-rpl32 gene spacer ycf15 CDS	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4 K3P TVM+F+R4 TVM+F+R3 F81+F	-
171 172 173 174 175 176 177	tm1-UGU gene-trnL-UAA gene spacer trnV-GAC gene-trn16 gene spacer trnV-UAC gene-trnM-CAU gene spacer trnW-CCA gene-trnP-UGG gene spacer trnY-GUA gene-trnE-UUC gene spacer ycf1 CDS ycf1/ycf1-fragment gene-rpl32 gene spacer ycf15 CDS ycf15 gene-trnL-CAA gene spacer	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4 K3P TVM+F+R4 TVM+F+R3 F81+F K3Pu+F+R2	- - - - - -
171 172 173 174 175 176 177 178	tm1-UGU gene-trnL-UAA gene spacer trnV-GAC gene-trn16 gene spacer trnV-UAC gene-trnM-CAU gene spacer trnW-CCA gene-trnP-UGG gene spacer trnY-GUA gene-trnE-UUC gene spacer ycf1 CDS ycf1/ycf1-fragment gene-rpl32 gene spacer ycf15 CDS ycf15 gene-trnL-CAA gene spacer ycf2 CDS	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4 K3P TVM+F+R4 TVM+F+R3 F81+F K3Pu+F+R2 K3Pu+F+R2	- - - - - - - - -
171 172 173 174 175 176 177 178 179	tm1-UGU gene-trnL-UAA gene spacer trnV-GAC gene-trn16 gene spacer trnV-UAC gene-trnM-CAU gene spacer trnW-CCA gene-trnP-UGG gene spacer trnY-GUA gene-trnE-UUC gene spacer ycf1 CDS ycf1/ycf1-fragment gene-rpl32 gene spacer ycf15 CDS ycf15 gene-trnL-CAA gene spacer ycf2 CDS ycf2 gene-ycf15 gene spacer	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4 K3P TVM+F+R4 TVM+F+R3 F81+F K3Pu+F+R2 K3Pu+F+R2 JC	- - - - - - - - - - - -
171 172 173 174 175 176 177 178 179 180	tm1-UGU gene-trnL-UAA gene spacer trnV-GAC gene-trn16 gene spacer trnV-UAC gene-trnM-CAU gene spacer trnW-CCA gene-trnP-UGG gene spacer trnY-GUA gene-trnE-UUC gene spacer ycf1 CDS ycf1/ycf1-fragment gene-rpl32 gene spacer ycf15 CDS ycf15 gene-trnL-CAA gene spacer ycf2 CDS ycf2 gene-ycf15 gene spacer ycf3 CDS	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4 K3P TVM+F+R4 TVM+F+R3 F81+F K3Pu+F+R2 K3Pu+F+R2 JC TPM2+F+R3	- - - - - - - - - - - - - - -
171 172 173 174 175 176 177 178 179 180 181	tm1-UGU gene-trnL-UAA gene spacer tmV-GAC gene-trn16 gene spacer tmV-UAC gene-trnM-CAU gene spacer tmW-CCA gene-trnP-UGG gene spacer trnY-GUA gene-trnE-UUC gene spacer ycf1 CDS ycf1/ycf1-fragment gene-rpl32 gene spacer ycf15 CDS ycf15 gene-trnL-CAA gene spacer ycf2 CDS ycf2 gene-ycf15 gene spacer ycf3 CDS ycf3 gene-trnS-GGA gene spacer	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4 K3P TVM+F+R4 TVM+F+R3 F81+F K3Pu+F+R2 K3Pu+F+R2 JC TPM2+F+R3 K3Pu+F+R2	
171 172 173 174 175 176 177 178 179 180 181 182	tm1-UGU gene-trnL-UAA gene spacer tmV-GAC gene-trn16 gene spacer tmV-UAC gene-trnM-CAU gene spacer tmW-CCA gene-trnP-UGG gene spacer trnY-GUA gene-trnE-UUC gene spacer ycf1 CDS ycf1/ycf1-fragment gene-rpl32 gene spacer ycf15 CDS ycf15 gene-trnL-CAA gene spacer ycf2 CDS ycf2 gene-ycf15 gene spacer ycf3 CDS ycf3 gene-trnS-GGA gene spacer ycf4 CDS	TVM+F+R3 K2P+I K3Pu+F K3Pu+F+G4 K3P TVM+F+R4 TVM+F+R3 F81+F K3Pu+F+R2 K3Pu+F+R2 JC TPM2+F+R3 K3Pu+F+R2 TVM+F+R2	

The amino acid and locus schemes were not analysed with Bayesian Inference, and thus no model search was performed. The amino acid scheme was also analysed under a fixed Q.plant model, which produced results consistent with those of the Q.bird model.

Internet				Cluster 1 Cluster 2				Cluster 3							
mmb dia 1 103 104	Locus	Total	Informative	Invariable	Locus	Locus	Total	Informative	Invariable	Locus	Locus	Total	Informative	Invariable	Locus
1 1	number	sites	sites	sites		number	sites	sites	sites		number	sites	sites	sites	
3 1 1 0 0 1 0 1 0 1 0	1	1530	232	1114	accD CDS	1	59	17	30	atpA gene-atpF gene spacer	1	58	8	38	ndhK gene-ndhC gene spacer
1 1 0 1 0 0 1 0	2	1530	145	1262	atpA CDS	2	405	45	333	atpE CDS	2	117	5	98	petG CDS
4 30 </td <td>3</td> <td>1497</td> <td>143</td> <td>1250</td> <td>atpB CDS</td> <td>3</td> <td>69</td> <td>17</td> <td>34</td> <td>atpF gene-atpH gene spacer</td> <td>3</td> <td>96</td> <td>10</td> <td>77</td> <td>petL CDS</td>	3	1497	143	1250	atpB CDS	3	69	17	34	atpF gene-atpH gene spacer	3	96	10	77	petL CDS
5 500 500 500 600 600 600 600 600 700	4	786	140	502	atpB gene-rbcL gene spacer	4	246	26	198	atpH CDS	4	90	2	82	petN CDS
9 1.41 0.51 0.	5	561	79	417	atpF CDS	5	221	43	143	atpl gene-rps2 gene spacer	5	25	1	24	psaB gene-psaA gene spacer
1 0.00 <t< td=""><td>6</td><td>1219</td><td>337</td><td>622</td><td>atpH gene-atpl gene spacer</td><td>6</td><td>299</td><td>97</td><td>141</td><td>ccsA gene-ndhD gene spacer</td><td>6</td><td>248</td><td>11</td><td>123</td><td>psbC gene-trnS-UGA gene spacer</td></t<>	6	1219	337	622	atpH gene-atpl gene spacer	6	299	97	141	ccsA gene-ndhD gene spacer	6	248	11	123	psbC gene-trnS-UGA gene spacer
9 100	/	/44	/0	598	atpl CDS	/	3/2	36	309	ndhC CDS	/	252	14	226	psbE CDS
No. 133 88 130 98 130 99 130 99 130 99 110 90 90 900	0	726	105	514	com A CDS	0	199	25	222	ndhE CDS	0	120	2	107	psbF CDS
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	10	233	58	128	cemA gene-netA gene spacer	10	125	33	233	ndhL gene_ndhK gene spacer	10	117	15	82	psbH gene-pstB gene spacer
1 4.51 9 2.60 4.51 90 900	10	588	38	510	clnP1 CDS	11	483	50	396	netD CDS	11	111	8	92	nshI CDS
Di Did Bid Did Did <thdid< th=""> Did <thdid< th=""> <thdid< th=""> <thdid< th=""></thdid<></thdid<></thdid<></thdid<>	12	424	78	266	clpP1 gene-psbB gene spacer	12	263	81	130	petD gene-rpoA gene spacer	12	123	6	110	psbl CDS
161 163 163 164 1	13	1605	366	957	matK CDS	13	146	40	74	petG gene-trnW-CCA gene spacer	13	117	6	103	psbL CDS
15 677 64 511 181	14	1663	262	1216	ndhD CDS	14	246	21	208	psaC CDS	14	22	4	13	psbL gene-psbF gene spacer
10 84. 84. 84. 84. 84. 133 14 111 pNN CBR 10 92 </td <td>15</td> <td>477</td> <td>69</td> <td>371</td> <td>ndhJ CDS</td> <td>15</td> <td>145</td> <td>13</td> <td>119</td> <td>psaJ CDS</td> <td>15</td> <td>105</td> <td>9</td> <td>89</td> <td>psbM CDS</td>	15	477	69	371	ndhJ CDS	15	145	13	119	psaJ CDS	15	105	9	89	psbM CDS
11 18 11 19 11 19 10 <th< td=""><td>16</td><td>684</td><td>86</td><td>531</td><td>ndhK CDS</td><td>16</td><td>261</td><td>82</td><td>133</td><td>psbA gene-trnK-UUU gene spacer</td><td>16</td><td>133</td><td>12</td><td>111</td><td>psbN CDS</td></th<>	16	684	86	531	ndhK CDS	16	261	82	133	psbA gene-trnK-UUU gene spacer	16	133	12	111	psbN CDS
Bio OND O	17	963	114	747	petA CDS	17	205	51	113	psbB gene-psbT gene spacer	17	102	7	89	psbT CDS
10 640	18	1070	282	547	petA gene-psbJ gene spacer	18	222	24	176	psbH CDS	18	71	20	41	psbT gene-psbN gene spacer
31 30 45 31 apple provide property 31 46 92 92 94 94 95 95 94 94 95 95 95 94 96 95 <	19	648	60	543	petB CDS	19	125	35	60	psbI gene-trnS-GCU gene spacer	19	456	73	338	rpl20 CDS
11 100 10	20	210	45	133	petB gene-petD gene spacer	20	142	27	90	psbJ gene-psbL gene spacer	20	282	10	262	rpl23 CDS
138 3.3 0.00 prof. graps 2.3 3.7 1 0.1 prof. Graps	21	190	50	107	petL gene-petG gene spacer	21	192	30	142	psbK CDS	21	114	8	96	rpl36 CDS
10 100 101 104 100 101 10	22	1288	330	7/01	petN gene-psbM gene spacer	22	104	12	152	psbN gene-psbH gene spacer	22	26	4	16	rpoCI gene-rpoB gene spacer
11 200 101 100 101 100 101 100 10	23	2253	145	1960	psaA CDS	23	189	12	152	psbZ CDS	23	357	11	341	rps12 CDS
100 101 1000 1000 100 100 100 100 100 100 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 10000 10000 10000 10000 10000 10000 10000 100000 $1000000000000000000000000000000000000$	24	729	16/	433	psaA gene-ycf3 gene spacer	24	369	50	285	rp114 CDS	24	468	1200	451	rps/CDS
and and bit b	25	2203	134	1924	psab CDS	25	121	33	39	rp114 gene-rp116 gene spacer	23	150	1500	141	yeff CDS
9 102 91 90 <td< td=""><td>20</td><td>246 475</td><td>1/3</td><td>232</td><td>psac gene-indife gene spacer</td><td>20</td><td>138</td><td>40</td><td>07 /88</td><td>rp120 gene-rps12 gene spacer</td><td>20</td><td>139</td><td>/</td><td>141</td><td>yci2 gene-yci15 gene spacer</td></td<>	20	246 475	1/3	232	psac gene-indife gene spacer	20	138	40	07 /88	rp120 gene-rps12 gene spacer	20	139	/	141	yci2 gene-yci15 gene spacer
9 127 128 129 128 129 136 140 133 135 134 134 135 135 134 135	28	1062	91	900	pshA CDS	28	192	53	113	rpl32 CDS					
10 135 107 172 64C 05 10 11 103 114 103 104 103 104 </td <td>29</td> <td>1527</td> <td>128</td> <td>1298</td> <td>psbR CDS</td> <td>29</td> <td>216</td> <td>24</td> <td>163</td> <td>rpl32 CDS</td> <td></td> <td></td> <td></td> <td></td> <td></td>	29	1527	128	1298	psbR CDS	29	216	24	163	rpl32 CDS					
11 1002 6.4 9.64 9.05 11 58 14 9.9 Track structure 13 15 16	30	1386	107	1173	psbC CDS	30	198	53	114	rp133 gene-rps18 gene spacer					
12 17.6 1.41 7.6 1.42 9.6 rpt. ² precept. ² precept. 1.1 1	31	1062	64	946	psbD CDS	31	58	14	39	rpoA gene-rps11 gene spacer					
31 381 152 180 pick gene pik gene piker 33 420 53 186 rpil CDS 34 566 156 pikk gene piker 35 16 35 pike pi	32	1376	341	765	psbE gene-petL gene spacer	32	178	42	96	rpoC2 gene-rpoC1 gene spacer					
34 356 156 156 156 151 25 11 25 36 11 25 37 121 14 155 14 25 37 121 14 155 14 25 37 14 155 157 110 150 111 25 37 131 14 150 14 155 14 155 14 155 14 155 14 155 14 155 14 155 14 155 14 155 14 155 14 155 14 155 14 155 14 155 14 155 14 155 14 155 165 155 165 155	33	383	125	180	psbK gene-psbI gene spacer	33	420	53	318	rps11 CDS					
35 447 123 123 rhd, CDS 35 111 25 99 rpl 2 genc/pH2 genc spacer 35 53 10 328 rhd, CDS 35 111 25 99 rpl 2 genc/pH2 genc/pH2 genc/pH2 rescharter 35 131 142 140	34	586	136	356	psbM gene-trnD-GUC gene spacer	34	129	31	69	rps11 gene-rpl36 gene spacer					
36 57 116 38 thd_gene-sub-Degne support 30 32 24 pi4 cmc 5M 37 60 39 101 GUN 39 91 914 CMS 914 cmc 5M Ber support 38 1 10 10 10 pl 2 per opl2 spec spect 39 372 33 318 pi4 per 5M Ber support 41 343 115 163 pi2 gene-spi2 gene spect 40 270 16 243 pi9 9 CDS 41 343 115 163 pi2 gene-spi2 gene spect 41 270 16 244 pi2 gene-spi2 gene spect 44 101 101 723 piA CDS 41 700 92 104 pi2 gene-spi2 gene spect 45 304 103 pi2 constructure 43 104 104 pi2 constructure 44 104 1	35	1437	123	1212	rbcL CDS	35	111	25	59	rps12 gene-clpP1 gene spacer					
37 402 00 39 pld CDS 37 148 23 98 ppl4 gene pake the space t	36	557	116	328	rbcL gene-accD gene spacer	36	303	32	234	rps14 CDS					
38 8.11 21 760 rpl2 gase-rpl2 gase space 38 27 32 98 rpl4 CDS 41 13 15 13 73 72 34 13 13 15 13 73 74 73 74	37	462	60	359	rpl16 CDS	37	148	23	93	rps14 gene-psaB gene spacer					
39 18 1 10 mpl gener mL/G gene spacer 31 113 mpl 8 UD8 41 63 212 260 102 104 102 mpl 14 Gene spacer 104 104 mpl 8 gene mL/G gene spacer 42 1017 161 202 tpo A CDS 104 mpl 8 gene mL/G agene spacer 104 mpl 8 gene mL/G agene spacer 44 1219 341 633 mpl 8 gene mL/G agene spacer 104 mpl 8 gene mL/G agene spacer 45 2046 205 163 mpl 8 gene mL/G agene spacer 110 L/A gene spacer 46 437 677 316 mpl 4 gene mL/G agene spacer 110///////////////////////////////////	38	831	21	766	rpl2 CDS	38	267	32	198	rps16 CDS					
au b.3 2.1.5 2.3.6 pi.3.2 pi.3.4 pi.3.2 pi.3.4 pi.3.2 pi.3.4	39	18	1	16	rpl2 gene-rpl23 gene spacer	39	372	33	313	rps18 CDS					
11 10 <th10< th=""> 10 10 <th1< td=""><td>40</td><td>033</td><td>212</td><td>293</td><td>rpi32 gene-trnL-UAG gene spacer</td><td>40</td><td>255</td><td>04</td><td>145</td><td>rps18 gene-rpi20 gene spacer</td><td></td><td></td><td></td><td></td><td></td></th1<></th10<>	40	033	212	293	rpi32 gene-trnL-UAG gene spacer	40	255	04	145	rps18 gene-rpi20 gene spacer					
14 2115 340 257 inpla CDS 43 41 20 41 500 inpla CDS inpla CDS <t< td=""><td>41</td><td>545 1017</td><td>115</td><td>105</td><td>rpiso gene-rps8 gene spacer</td><td>41</td><td>279</td><td>10</td><td>245</td><td>rps19 CDS</td><td></td><td></td><td></td><td></td><td></td></t<>	41	545 1017	115	105	rpiso gene-rps8 gene spacer	41	279	10	245	rps19 CDS					
14 129 341 63 pp8 grow-fm-GCA gene spacer 44 170 92 174 mp7 grow-mW-GAA gene spacer 45 2046 205 163 mpC CDS 46 366 102 193 unLUAA gene-mG-GAA gene spacer 47 282 44 96 mp15 gene-scA gene spacer 108 194 unLUAA gene-mG-GAA gene spacer 48 357 128 152 mp15 gene-scA gene spacer 48 185 54 94 unW-CGA gene spacer 50 711 91 550 mp2 (DS 36 42 ycf3 CDS 51 637 100 507 mp2 (DS espacer 49 138 0 228 ycf3 CDS 52 357 105 185 mp4 gene-tm1-UG gene spacer 44 94 178 ycf3 CDS 53 617 30 552 mp2 gene-tm1-UG gene spacer 44 94 179 gene spacer 54 405 71 920 ps8 gene-tm1-UG gene spacer 44 45 170 gene-tp14 gene spacer 55<	42	3213	340	2567	moB CDS	42	612	52	500	rps2 gene-rpoC2 gene spacer					
145 2046 205 1633 rpcCl CDS 45 366 102 103 rmL-UAA gene-mTe-GAA gene spacer 47 322 44 196 rp15 CDS 47 351 108 194 rmcUAA gene-spacer spacer 47 47 48 357 128 132 rps15 CDS 47 351 108 194 rmcUCA gene-spake gene spacer 49 795 236 379 rp16 gene-spacer 49 138 0 128 ycl3 CDS 51 687 101 507 rp34 CDS 50 104 20 104	43	1219	341	653	rpoB gene-trnC-GCA gene spacer	43	1770	92	1574	rps7 gene-trnV-GAC gene spacer					
46 4377 677 3165 mpC2 CDS 46 97 32 52 mL/AC gene-sch/age report 47 282 44 96 mpl 5 gene-yell gene spacer 48 151 108 104 tmQ-U/G gene-paker gene spacer 48 357 128 152 mpl 5 gene-yell gene spacer 48 185 54 94 tmQ-U/G gene-spacer 49 138 0 128 yell 5 CDS 47 310 36 422 yell 5 CDS 47 31 37 31 52 357 105 185 mpd gene-tm1-UG1 gene spacer 45 45 47 37 mpd gene-tm1-VGA gene spacer 45 45 17 290 mpd gene-tm1-VGA gene spacer 45 45 17 363 62 17 93 77 mpd gene-tm1-VGA gene spacer 45 45 45 18 46 18 mmd-CA gene spacer 45 45 18	45	2046	205	1653	rpoC1 CDS	45	366	102	193	trnL-UAA gene-trnF-GAA gene spacer					
47 282 44 96 "nsl 5 CDS 47 351 108 194 unD-UCG gene-ph8k gene spacer 48 37 128 379 psl 6 gene-yd1 gene spacer 49 138 0 128 umD-UCG gene-sph2Ge gene spacer 49 138 0 128 ycl 5 CDS 50 71 90 50 792 CDS 50 510 647 101 507 rpsl 5 gene-rm2 (Jg ene spacer 50 510 642 ycl 5 CDS 52 667 30 552 rpsl gene-rm2 (Jg ene spacer 55 514 42 77 rpsl gene-rm2 (Jg ene spacer 55 515 42 77 rpsl gene-space spacer 55 514 42 77 rpsl gene-space spacer 55 514 42 77 rpsl gene-space spacer 55 56 719 173 370 100-CG gene-space spacer 55 56 719 173 100 100-GG gene space respacer 55 56 128 47 148 100-GG gene space respacer 55 56 128 100 100-GG gene space spacer	46	4377	677	3165	rpoC2 CDS	46	97	32	52	trnL-UAG gene-ccsA gene spacer					
48 357 128 152 rps15 gene-yn0 upg ene spacer 48 185 54 94 umW-CCA gene-imP-UGG gene spacer 50 711 91 550 rps2 CDS 50 50 36 442 ycB 2 CDS 51 647 105 185 rps4 gene-im7-UGU gene spacer 50 50 36 442 ycB 2 CDS 52 357 105 185 rps4 gene-im7-UGU gene spacer 55 56 71 200 rps4 CDS 55 56 71 200 rps4 CDS 56 56 71 200 rps4 CDS 56 56 71 70 rps4 gene-im7-UGU gene spacer 56 57 56 71 73 377 rmC-GCA gene-peN gene spacer 56 57 56 71 131 230 rmF-GAA gene spacer 56 56 57 14 40 rmB-UGC gene-rm-GAU gene spacer 56 56 57 68 60 50 97 181 rmF-GAA gene spacer 56 56 56 56 56 68 23 rmF-GAA gene spacer <td< td=""><td>47</td><td>282</td><td>44</td><td>196</td><td>rps15 CDS</td><td>47</td><td>351</td><td>108</td><td>194</td><td>trnQ-UUG gene-psbK gene spacer</td><td></td><td></td><td></td><td></td><td></td></td<>	47	282	44	196	rps15 CDS	47	351	108	194	trnQ-UUG gene-psbK gene spacer					
49 795 236 379 rps16 gene-tmQ-UUG gene spacer 49 138 0 128 yef15 CDS 50 711 91 500 rps2 CDS 50 50 36 442 yef15 CDS 51 687 101 507 rps3 CDS yef3 CDS yef3 CDS 52 357 105 153 rps4 gene-m1-GU gene spacer yef3 CDS yef3 CDS 54 407 71 rps8 gene-m1-GU gene spacer yef3 CDS yef3 CDS yef3 CDS 55 154 42 77 rps8 gene-m1-GU gene spacer yef3 CDS yef3 CDS yef3 CDS 56 179 173 377 rp64 GCA gene-gebR gene spacer yef3 CDS yef3 CDS yef3 CDS 57 469 125 241 tmD-GU gene-spage ges spacer yef3 CDS yef3 CDS yef3 CDS yef3 CDS 61 614 41 491 tmR-ACG gene-space ges spacer yef3 CDS yef3 CDS yef3 CDS yef3 CDS 62 193 77 61 mR/ACQ gene-space ges spacer yef3 CDS	48	357	128	152	rps15 gene-ycf1 gene spacer	48	185	54	94	trnW-CCA gene-trnP-UGG gene spacer					
50 711 91 50 50 50 36 442 ycf3 CDS 51 687 101 507 93 CDS	49	795	236	379	rps16 gene-trnQ-UUG gene spacer	49	138	0	128	ycf15 CDS					
51 687 101 507 rp3 205 52 357 105 185 rp4 gene-tm1-UGU gene spacer 53 607 30 552 rp4 gene-tm1-UGU gene spacer 54 405 71 290 rp8 CDS 55 154 42 77 rp8 gene-mp1l4 gene spacer 56 719 173 377 tm0-GCA gene-phg gene spacer 57 469 125 241 tm0-GCA gene-phg gene spacer 58 467 131 230 tm6-GA gene-aplE gene spacer 60 350 97 181 tm1-CAU gene-aplE gene spacer 61 614 41 491 tmR-CAC gene-rbs-Gu gene spacer 62 193 77 61 tmR-UCU gene-spacer 64 355 68 223 tm3-UGA gene-pbd gene spacer 65 1238 279 711 tmT-GGU gene-spacer 66 1000 292 494 tmT-UGA gene spacer 67 165 48 93 tmTu-UGA gene spacer 68 792	50	711	91	550	rps2 CDS	50	510	36	442	ycf3 CDS					
52 357 105 185 rps4 gene-tmT-UGU gene spacer 53 607 30 552 rps7 gene-tmT-VGAC gene spacer 54 405 71 290 rps8 gene-rp114 gene spacer 55 154 42 77 rps8 gene-rp114 gene spacer 56 719 173 377 tmC-GCA gene-ptN gene spacer 57 469 125 241 tmD-GUC gene-tmN-GUI gene spacer 58 467 131 230 tmP-GAA gene-spader spacer 59 234 47 148 tmM-CAU gene-spader 61 614 41 491 tmR-MC gene-tmN-GUU gene spacer 62 193 77 61 tmR-UC gene-spadere 64 355 68 233 tmS-GG gene-spade gene spacer 65 1238 279 71 tmT-GG gene-spade gene spacer 66 1000 292 494 tmT-GG gene-spader 67 165 48 93 tmT-GA gene spacer 68 792 47 683 yef2 gene-tmS-GGA gene spacer	51	687	101	507	rps3 CDS										
53 607 30 552 ps8 CDS 54 405 71 290 ps8 CDS 55 154 42 77 ps8 cpen-pell gene spacer 56 719 173 377 tmC-GCA gene-pelV gene spacer 57 469 125 241 tmC-GCA gene-pelV gene spacer 58 467 131 230 tmF-GAA gene-palge gene spacer 59 234 47 148 tmM-GAU gene-apage gene spacer 61 614 41 491 tmR-GAC gene-malge gene spacer 62 193 77 61 tmR-GC gene-malge gene spacer 63 180 48 93 tmS-GG gene-ps4 gene spacer 64 355 68 223 tmS-GG gene-ps4 gene spacer 65 128 279 711 GG gene-ps4 gene spacer 66 1000 292 494 tmT-GGU gene-spacer 67 165 48 93 tmM-CAG gene spacer 68 792 47 680 ycf2 gene-tmL-CAA gene spacer 70	52	357	105	185	rps4 gene-trnT-UGU gene spacer										
34 405 /1 290 rps8 CDS 55 154 42 77 rps8 gene-rpl14 gene spacer 56 719 173 377 tmC-GCA gene-tpr14 gene spacer 57 469 125 241 tmD-GUC gene-tmV-GUA gene spacer 58 467 131 230 tmF-GA gene-anb1 gene spacer 60 350 97 181 tmA-CG gene-tpsaJ gene spacer 61 614 41 491 tmR-CG gene-tpsaJ gene spacer 62 193 77 61 tmR-UCG gene-tpsaJ gene spacer 63 180 48 93 tmS-GGA gene-psaJ gene spacer 64 355 68 223 tmS-UGA gene-psaJ gene spacer 65 1238 279 721 tmT-GU gene-psaJ gene spacer 66 1000 292 494 tmT-UGU gene-spacer 68 792 47 680 ycf2 gene-tmL-CAA gene spacer 69 7071 214 654 gene spacer 55 71 558 73 415 gene-tmL-CAA gene spacer 72 </td <td>53</td> <td>607</td> <td>30</td> <td>552</td> <td>rps7 gene-trnV-GAC gene spacer</td> <td></td>	53	607	30	552	rps7 gene-trnV-GAC gene spacer										
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	Mean	400 954 57	141 014	698.36	yor+ gene-centra gene spacer		276.4	43.62	198 40			377 73	66.23	266.69	

Table S3. Detailed information on the clusters identified by analysis of tree space.

377.73 66.23 266.69

Table S4. Results of topology tests on possible resolutions of the polytomy.

Tree	logL	deltaL	bp-RELL		p-SH		p-WKH		p-WSH		c-ELW		p-AU	
Most likely	-494970.83	1.16E-10	0.13	+	0.934	+	0.305	+	0.639	+	0.163	+	0.764	+
Hard polytomy	-494975.27	4.446	9.00E-05	_	0.225	+	0.124	+	0.648	+	0.00808	_	0.0218	-
1	-494974.05	3.2185	0.0496	+	0.381	+	0.216	+	0.688	+	0.047	+	0.347	+
2	-494975.18	4.3504	0.00198	_	0.24	+	0.132	+	0.59	+	0.0102	_	0.0701	+
3	-494973.93	3.1049	0.0546	+	0.407	+	0.221	+	0.686	+	0.0486	+	0.334	+
4	-494974.38	3.5497	0.0222	+	0.34	+	0.188	+	0.658	+	0.0283	+	0.191	+
5	-494971.58	0.7469	0.161	+	0.782	+	0.313	+	0.786	+	0.129	+	0.606	+
6	-494974.77	3.9455	0.0096	_	0.287	+	0.161	+	0.64	+	0.0192	+	0.109	+
7	-494975.48	4.6497	0.00076	_	0.207	+	0.0982	+	0.585	+	0.0067	_	0.00179	-
8	-494974.6	3.7669	0.0141	_	0.316	+	0.169	+	0.616	+	0.0215	+	0.119	+
9	-494975.38	4.5493	0.00112	_	0.216	+	0.119	+	0.643	+	0.00739	_	0.0387	-
10	-494971.85	1.0255	0.0809	+	0.746	+	0.255	+	0.719	+	0.0884	+	0.163	+
11	-494974.25	3.418	0.043	+	0.364	+	0.197	+	0.684	+	0.0373	+	0.353	+
12	-494974.89	4.0631	0.00958	_	0.278	+	0.149	+	0.592	+	0.0158	_	0.0444	-
13	-494971.96	1.1339	0.133	+	0.758	+	0.31	+	0.744	+	0.11	+	0.499	+
14	-494972.09	1.2629	0.109	+	0.742	+	0.284	+	0.72	+	0.0953	+	0.441	+
15	-494970.83	0	0.179	+	1	+	0.687	+	0.979	+	0.163	+	0.798	+

"+" and "-" apply to the test in the column to the left. The SH and AU tests return *P*-values, thus a tree is rejected if P < 0.05 (denoted by "-" if rejected, or "+" if accepted). The bp-RELL and c-ELW return posterior weights, and "+" is assigned to those largest values which accumulate above 0.95 (thus forming the confidence set of trees).

IQ-TREE single most likely tree, unpartitioned



IQ-TREE single most likely tree, partitioned by region (CDS, Non-codir



Q-TREE single most likely tree, partitioned by codon position (Codons 1 & 2, Codon 3, Non-coding)





MrBayes 50% majority-rule consensus tree, unpartitioned



MrBayes 50% majority-rule consensus tree, partitioned by region (CDS, Non-coding



MrBayes 50% majority-rule consensus tree, partitioned by codon position (Codons 1 & 2, Codon 3, Non-coding)



ASTRAL



Fig. S1. Comparison of phylogenies (as cladograms) produced by various analyses of the basic alignment. Red branches indicate posterior probability < 1 in MrBayes trees, local posterior probability < 1 in the ASTRAL tree and < 95 % UFBoot and SH-aLRT in IQ-TREE trees.

ena, Phebalium



Fig. S2. ASTRAL polytomy test. Branch support values are p-values, where i > 0.05 for a given branch corresponds with a failure to reject the null hypothesis that the branch is a true (hard) polytomy.



Fig. S3. Comparison of phylogenies produced by IQ-TREE analysis of concatenated genes in Clusters 1, 2 and 3. Branches with less than 95% UFBoot support are collapsed.



Fig. S4. Boxplots comparing length and branch support of RAxML gene trees across three topology clusters. Horizontal lines represent medians, boxes show interquartile ranges (IQR) and whiskers show the full range excluding outliers (denoted by open circles; these are values that fall outside whiskers, i.e. greater than $1.5 \times IQR + Q3$ and less than $1.5 \times IQR - Q3$).



Fig. S5. Scanning Electron Micrographs of staminal filaments in *Philotheca coateana* (*K.H. Coate 292*; MEL 2278579A) at $20\times$, $60\times$ and $100\times$ magnification. Images show a mature flower with sepals and petals removed. The filaments (F) are free from each other at their bases.



Fig. S6. Phylogeny produced from IQ-TREE analysis of the CDS loci from the basic alignment, translated to amino acids. Branch support is quantified by UFBoot values, gene concordance (gCF) or site concordance (sCF).

Methods and results of analyses of *18S–5.8S–26S* nuclear ribosomal cistron sequences from shotgun-sequenced samples

Sequence assembly, editing and alignment

Raw Illumina reads were *de-novo* assembled into contigs with CLC Genomics Workbench (ver. 9.5.1, Qiagen) using default settings. Contigs and raw reads were imported into Geneious Prime (ver. 2021.1.1, see <u>http://www.geneious.com</u>) and plastome sequences for all samples were assembled in this software. Initially, the draft cistron sequence of *Acronychia laevis* was constructed using the nrDNA cistron sequence of *Eremophila macdonnellii* (GenBank: MN411575.1) as a reference. Following this, reads were re-mapped to the draft assembly multiple times with manual checking and corrections to produce a final cistron sequence. To assemble the remaining cistron sequences we adopted an approach of using a closely related, already-assembled sequence as the reference for the next assembly in the same manner as that used to assemble plastome sequences (beginning with *A. laevis* cistron sequence). Assemblies were carried out following the same protocol and settings used for the plastome sequences. Sequences were then aligned using MAFFT (ver. 7.450) with default settings, and to reduce the potential for inclusion of non-homologous sites, sites with more than 30% gaps were removed to produce a final alignment 5,810 bp long.

Phylogenetic analyses

The nrDNA sequence alignment was analysed using Maximum Likelihood and Bayesian Inference approaches in IQ-TREE (ver. 2.1.3) and MrBayes (ver. 3.2.7a). For both analyses, the alignment file was partitioned by marker, resulting in a total of five partitions for the markers: *18S* rRNA, *5.8S* rRNA, *26S* rRNA, *ITS1*, *ITS2*. Best-fit models were estimated in IQ-TREE using ModelFinder, with models for MrBayes selected using the '-mset' option to restrict model searches to only those implemented in MrBayes. The MrBayes analysis was run for 100,000 generations, with a 25% burn-in and manual checking to ensure that the standard deviation of split frequencies reached below 0.01. We assessed convergence in Tracer (ver. 1.7.2) to ensure effective sample sizes (ESS) were above 200 for all parameters. Support for branches in the IQ-TREE phylogeny was estimated using ultrafast bootstrap (UFBoot) and SH-aLRT with each set to 1000 replicates. Branch support for the MrBayes phylogeny was assessed using posterior probability.



Figure S7. Maximum likelihood phylogeny from IQ-TREE analysis of nrDNA cistron sequences. Branch support values are SH-aLRT/UFBoot.



Figure S8. Bayesian inference 50% majority-rule consensus phylogeny from MrBayes analysis of nrDNA cistron sequences. Branch support values are posterior probabilities.