SUPPLEMENTAL MATERIAL

Why the monophyly of Nymphaeaceae currently remains indeterminate: An assessment based on gene-wise plastid phylogenomics

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Table S1. Results of calculating the fractions of polymorphic sites of the three codon positions across the 78 protein-coding plastome genes under study that form the basis for the multiple logistic regression tests of possible effects on the phylogenetic tree inference as well as the overall and pairwise comparisons of the mean fraction values using parametric and non-parametric statistical tests. Also displayed are the best-fitting nucleotide substitution models identified for each of the plastome genes under study. Abbreviations used: CodonOne = fraction of polymorphic sites of codon 1; CodonTwo = fraction of polymorphic sites of codon 2; CodonThree = fraction of polymorphic sites of codon 3; Model = best-fitting nucleotide substitution model; Hypo = hypothesis.

#	Gene	CodonOne	CodonTwo	CodonThree	Model	HypoA	HypoB	HypoC
1	78 CDS	0.276	0.252	0.4	GTR+G+I	1	0	0
2	ycf1	0.998	0.999	0.999	GTR+G	1	0	0
3	rps15	0.23	0.195	0.425	GTR+G	1	0	0
4	rpl32	0.333	0.333	0.491	HKY+G	1	0	0
5	atpE	0.179	0.119	0.425	HKY+G	0	1	0
6	ndhF	0.24	0.176	0.423	GTR+G	1	0	0
7	rps19	0.232	0.253	0.485	HKY+G	1	0	0
8	infA	0.268	0.232	0.341	GTR+G	0	0	1
9	matK	0.256	0.191	0.354	GTR+G	1	0	0
10	ccsA	0.223	0.176	0.389	GTR+G	0	1	0
11	rpoC2	0.265	0.216	0.396	GTR+G	0	1	0
12	rpl20	0.197	0.205	0.333	GTR+I	0	1	0
13	accD	0.485	0.479	0.56	GTR+G	1	0	0
14	rpl22	0.168	0.144	0.352	GTR+G	0	1	0
15	rpoA	0.208	0.182	0.353	GTR+G	1	0	0
16	rps11	0.138	0.109	0.348	SYM+I	0	1	0
17	rpoC1	0.232	0.217	0.362	GTR+G	1	0	0
18	rpl33	0.118	0.118	0.279	GTR	1	0	0
19	rps8	0.121	0.129	0.326	HKY+G	0	0	1
20	psbH	0.203	0.165	0.367	HKY+I	0	1	0
21	cemA	0.179	0.105	0.284	GTR	0	0	1
22	ndhA	0.146	0.096	0.324	GTR+G	0	1	0
23	rps3	0.162	0.09	0.32	GTR+G	0	0	1
24	rpoB	0.148	0.119	0.293	GTR+I	0	1	0
25	atpF	0.165	0.149	0.293	GTR	0	1	0
26	psbK	0.148	0.148	0.311	HKY+G	1	0	0
27	rps4	0.129	0.07	0.289	GTR+G	1	0	0
28	ycf4	0.216	0.244	0.418	HKY+I	1	0	0
29	rpl36	0.135	0.054	0.297	K80	0	0	0
30	psbI	0.028	0.028	0.389	K80+I	1	0	0
31	petA	0.087	0.075	0.323	GTR+G	0	0	1
32	rps16	0.303	0.315	0.427	HKY	1	0	0
33	rps18	0.248	0.248	0.342	HKY+I	1	0	0
34	ndhE	0.069	0.03	0.327	GTR+I	1	0	0
35	ycf2	0.406	0.391	0.4	GTR+G	1	0	0
36	rps2	0.142	0.142	0.292	GTR+G	0	1	0
37	ndhG	0.14	0.124	0.285	GTR+G+I	0	0	1
38	rps14	0.12	0.07	0.27	HKY+G	0	0	1
39	atpA	0.093	0.059	0.288	GTR+G	0	1	0
40	rpl14	0.049	0.041	0.328	GTR+I	1	0	0
41	ndhH	0.102	0.067	0.294	GTR+I	1	0	0
42	ndhJ	0.12	0.082	0.234	GTR+I	0	0	1
43	ndhI	0.114	0.098	0.272	GTR+G	0	0	0
44	ndhK	0.379	0.369	0.5	GTR+I	1	0	0
45	atpB	0.09	0.05	0.309	GTR+G	1	0	0
46	rpl16	0.192	0.144	0.384	HKY+I	1	0	0
47	rbcL	0.076	0.029	0.267	GTR+G+I	0	1	0
48	atpI	0.069	0.036	0.27	GTR+I	0	1	0
49	psaI	0.27	0.081	0.27	HKY	0	1	0

#	Gene	CodonOne	CodonTwo	CodonThree	Model	HypoA	HypoB	HypoC
50	*psbB*	0.057	0.031	0.283	GTR+G	1	0	0
51	*psbT*	0.237	0.158	0.289	K80	1	0	0
52	*petB*	0.059	0.036	0.309	HKY+I	0	1	0
53	*petG*	0	0.081	0.216	HKY	0	0	0
54	*psaB*	0.04	0.014	0.248	GTR+I	0	0	1
55	*psaC*	0.025	0.012	0.296	K80+G	1	0	0
56	*psbN*	0.047	0.047	0.163	K80+I	0	1	0
57	*ndhC*	0.098	0.066	0.246	GTR+G	0	0	1
58	*psaA*	0.044	0.017	0.241	GTR+I	0	1	0
59	*psbC*	0.063	0.04	0.268	GTR+I	0	1	0
60	*psbA*	0.04	0.008	0.255	GTR+I	0	0	0
61	*psbZ*	0.097	0.032	0.177	HKY+I	0	1	0
62	*petD*	0.261	0.251	0.45	GTR+I	0	1	0
63	*psbD*	0.085	0.059	0.269	GTR+I	1	0	0
64	*psbF*	0.026	0.026	0.179	JC	0	0	0
65	*ndhD*	0.728	0.728	0.806	GTR+G	0	0	1
66	*atpH*	0.12	0.108	0.289	SYM	1	0	0
67	*rpl2*	0.044	0.055	0.146	HKY+G	0	0	1
68	*psaJ*	0.045	0.091	0.295	K80+I	1	0	0
69	*psbL*	0.026	0.053	0.132	HKY+I	0	0	0
70	*psbJ*	0.15	0.025	0.125	JC+I	0	1	0
71	*rps7*	0.065	0.045	0.071	HKY+I	0	0	1
72	*petL*	0.032	0.129	0.065	K80+I	0	0	0
73	*rps12*	0.065	0.097	0.169	F81+I	0	1	0
74	*ycf3*	0.012	0.024	0.154	GTR+I	0	0	1
75	*psbE*	0.036	0.024	0.145	K80+I	0	0	1
76	*petN*	0.156	0.094	0.156	JC	0	0	0
77	*ndhB*	0.035	0.049	0.074	GTR+I	1	0	0
78	*psbM*	0.029	0.029	0.147	JC	0	0	0
79	*rpl23*	0.062	0.062	0.062	F81	0	0	0

Table S1