

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

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Table S2. Results of calculating eight different sequence variability and homoplasy metrics that form the basis for the multiple logistic regression tests of possible effects on the phylogenetic tree inference. Abbreviations used: Length = alignment length; GC = GC content; Polymorphic = fraction of polymorphic sites; Informative = fraction of parsimony-informative sites; CI = consistency index; RI = retention index; RC = rescaled consistency index; P-distance = maximum uncorrected p-distance.

#	Gene	Length	GC	Polymorphic	Informative	CI	RI	RC	P-distance
1	<i>78 CDS</i>	71616	0.394	0.309	0.143	0.86	0.868	0.747	0.379
2	<i>ycf1</i>	6999	0.336	0.999	0.306	0.888	0.891	0.791	0.72
3	<i>rps15</i>	261	0.378	0.284	0.234	0.838	0.882	0.739	0.459
4	<i>rpl32</i>	171	0.332	0.386	0.216	0.94	0.932	0.876	0.497
5	<i>atpE</i>	402	0.428	0.241	0.214	0.879	0.897	0.789	0.436
6	<i>ndhF</i>	2262	0.353	0.28	0.214	0.867	0.888	0.77	0.439
7	<i>rps19</i>	297	0.416	0.323	0.202	0.867	0.917	0.794	0.435
8	<i>infA</i>	246	0.378	0.28	0.199	0.934	0.946	0.884	0.456
9	<i>matK</i>	1536	0.362	0.267	0.197	0.9	0.904	0.813	0.433
10	<i>ccsA</i>	957	0.347	0.262	0.192	0.898	0.912	0.819	0.424
11	<i>rpoC2</i>	4302	0.393	0.292	0.188	0.911	0.922	0.84	0.421
12	<i>rpl20</i>	351	0.416	0.245	0.185	0.947	0.946	0.896	0.434
13	<i>accD</i>	2016	0.376	0.508	0.179	0.904	0.92	0.832	0.476
14	<i>rpl22</i>	375	0.39	0.221	0.173	0.871	0.882	0.769	0.393
15	<i>rpoA</i>	1038	0.38	0.248	0.173	0.889	0.911	0.81	0.392
16	<i>rps11</i>	414	0.465	0.198	0.169	0.918	0.938	0.861	0.384
17	<i>rpoC1</i>	2157	0.397	0.27	0.164	0.934	0.939	0.877	0.425
18	<i>rpl33</i>	204	0.396	0.172	0.162	0.974	0.976	0.951	0.402
19	<i>rps8</i>	396	0.36	0.192	0.157	0.918	0.936	0.859	0.383
20	<i>psbH</i>	237	0.397	0.245	0.156	0.863	0.905	0.781	0.382
21	<i>cemA</i>	687	0.343	0.189	0.151	0.945	0.945	0.893	0.383
22	<i>ndhA</i>	1092	0.379	0.189	0.149	0.867	0.887	0.769	0.368
23	<i>rps3</i>	666	0.373	0.191	0.149	0.882	0.898	0.792	0.365
24	<i>rpoB</i>	3231	0.4	0.187	0.146	0.936	0.94	0.88	0.377
25	<i>atpF</i>	564	0.393	0.202	0.144	0.922	0.926	0.854	0.373
26	<i>psbK</i>	183	0.404	0.202	0.142	0.889	0.907	0.806	0.368
27	<i>rps4</i>	603	0.398	0.163	0.139	0.913	0.93	0.849	0.36
28	<i>ycf4</i>	639	0.398	0.293	0.138	0.881	0.908	0.801	0.376
29	<i>rpl36</i>	111	0.386	0.162	0.135	0.9	0.935	0.842	0.329
30	<i>psbI</i>	108	0.429	0.148	0.13	0.81	0.846	0.685	0.347
31	<i>petA</i>	966	0.402	0.161	0.128	0.867	0.884	0.767	0.336
32	<i>rps16</i>	267	0.375	0.348	0.127	0.932	0.937	0.873	0.371
33	<i>rps18</i>	351	0.353	0.279	0.12	0.964	0.97	0.935	0.372
34	<i>ndhE</i>	303	0.354	0.142	0.119	0.92	0.927	0.853	0.33
35	<i>ycf2</i>	7725	0.381	0.399	0.118	0.964	0.966	0.931	0.396
36	<i>rps2</i>	720	0.413	0.192	0.117	0.937	0.938	0.879	0.35
37	<i>ndhG</i>	558	0.358	0.183	0.111	0.857	0.868	0.744	0.331
38	<i>rps14</i>	300	0.425	0.153	0.11	0.962	0.963	0.927	0.337
39	<i>atpA</i>	1521	0.422	0.147	0.109	0.89	0.907	0.807	0.316
40	<i>rpl14</i>	366	0.406	0.139	0.109	1	1	1	0.305
41	<i>ndhH</i>	1203	0.396	0.155	0.108	0.868	0.896	0.778	0.305
42	<i>ndhJ</i>	474	0.427	0.146	0.108	0.866	0.897	0.777	0.312
43	<i>ndhI</i>	552	0.362	0.161	0.107	0.893	0.897	0.8	0.309
44	<i>ndhK</i>	870	0.401	0.416	0.106	0.944	0.954	0.9	0.369
45	<i>atpB</i>	1494	0.431	0.15	0.104	0.916	0.918	0.841	0.329
46	<i>rpl16</i>	438	0.467	0.24	0.103	0.89	0.898	0.799	0.333
47	<i>rbcL</i>	1425	0.455	0.124	0.101	0.853	0.862	0.735	0.3
48	<i>atpI</i>	744	0.391	0.125	0.099	0.864	0.89	0.769	0.302
49	<i>psaI</i>	111	0.344	0.207	0.099	0.913	0.929	0.848	0.333

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50	<i>psbB</i>	1524	0.445	0.124	0.098	0.884	0.904	0.799	0.299
51	<i>psbT</i>	114	0.372	0.228	0.096	0.9	0.933	0.84	0.338
52	<i>petB</i>	660	0.414	0.135	0.092	0.823	0.877	0.722	0.278
53	<i>petG</i>	111	0.351	0.099	0.09	0.917	0.947	0.868	0.3
54	<i>psaB</i>	2202	0.422	0.1	0.086	0.873	0.893	0.78	0.271
55	<i>psaC</i>	243	0.442	0.111	0.086	0.875	0.892	0.78	0.287
56	<i>psbN</i>	129	0.458	0.085	0.085	0.929	0.963	0.894	0.292
57	<i>ndhC</i>	366	0.389	0.137	0.082	0.865	0.889	0.769	0.298
58	<i>psaA</i>	2250	0.437	0.101	0.082	0.895	0.921	0.824	0.278
59	<i>psbC</i>	1419	0.45	0.124	0.08	0.884	0.896	0.792	0.27
60	<i>psbA</i>	1059	0.433	0.101	0.075	0.893	0.901	0.804	0.27
61	<i>psbZ</i>	186	0.343	0.102	0.075	1	1	1	0.284
62	<i>petD</i>	633	0.388	0.321	0.074	0.77	0.806	0.621	0.282
63	<i>psbD</i>	1059	0.442	0.138	0.073	0.875	0.893	0.781	0.242
64	<i>psbF</i>	117	0.427	0.077	0.068	1	1	1	0.261
65	<i>ndhD</i>	1500	0.365	0.754	0.067	0.891	0.875	0.779	0.355
66	<i>atpH</i>	249	0.467	0.173	0.064	0.955	0.963	0.919	0.248
67	<i>rpl2</i>	822	0.441	0.082	0.064	0.903	0.92	0.83	0.247
68	<i>psaJ</i>	132	0.411	0.144	0.061	0.889	0.913	0.812	0.267
69	<i>psbL</i>	114	0.333	0.07	0.061	1	1	1	0.265
70	<i>psbJ</i>	120	0.462	0.1	0.058	0.875	0.909	0.795	0.274
71	<i>rps7</i>	465	0.408	0.06	0.056	1	1	1	0.232
72	<i>petL</i>	93	0.374	0.075	0.054	1	1	1	0.232
73	<i>rps12</i>	372	0.415	0.11	0.054	1	1	1	0.232
74	<i>ycf3</i>	507	0.4	0.063	0.053	0.853	0.891	0.76	0.223
75	<i>psbE</i>	249	0.427	0.068	0.052	0.947	0.95	0.9	0.228
76	<i>petN</i>	96	0.425	0.135	0.042	1	1	1	0.214
77	<i>ndhB</i>	1542	0.377	0.053	0.041	0.959	0.967	0.927	0.196
78	<i>psbM</i>	102	0.334	0.069	0.039	1	1	1	0.221
79	<i>rpl23</i>	288	0.382	0.062	0.024	1	1	1	0.158