

1 The complete chloroplast genome sequence of the *Speiranthra gardenii*: Comparative 2 and adaptive evolutionary analysis

3 **Supplementary Table S4.** Comparison of site models, positive selective amino acid loci and estimation of parameters for five protein-coding genes in the Nolinoideae
4 species.

Protein-coding gene	Model	np	Ln L	Estimates of parameters				Model compared	LRT P-value	Positive sites
ccsA	M3	37	-1751.048	p:	0.14575	0.82907	0.02518	M0 vs. M3	0.000048685	[]
				ω :	0.33548	0.33548	12.4126			
	M0	33	-1763.583	ω_0 :	0.47116					Not Allowed
	M2a	36	-1751.048	p:	0.97482	0	0.02518	M1a vs. M2a	0.001278437	[]
				ω :	0.33548	1	12.4126			
	M1a	34	-1757.710	p:	0.60093	0.39907				Not Allowed
				ω :	0	1				
	M8	36	-1751.050	p0 = 0.97486 (p1 = 0.0251)	p = 50.12233 ω = 12.4261	q = 99.00000		M7 vs. M8	0.001065942	170 D 0.989*, 175 R 0.969*, 178 F 0.764, 184 F 0.978*, 186 D 0.871, 206 R 0.868, 278 S 0.582
	M7	34	-1757.894	p =	0.04406	q =	0.05411			Not Allowed
	M8a	35	-1757.710	p0 = 0.60093 (p1 = 0.3991)	p = 0.00500 ω = 1.00000	q = 1.51348		M8a vs. M8	0.000262727	Not Allowed
	M3	37	-4432.200	p:	0.5974	0.3673	0.0353	M0 vs. M3	0	[]

<i>ndhF</i>			ω :	0.02893	0.58642	5.89282				
	M0	33	-4469.495	ω_0 :	0.33611					Not Allowed
	M2a	36	-4432.209	p:	0.81224	0.1557	0.03206	M1a	vs.	0.000135706 []
				ω :	0.11035	1	6.11525	M2a		
	M1a	34	-4441.114	p:	0.68245	0.31755				Not Allowed
				ω :	0	1				
	M8	36	-4432.201	p0 = 0.96496 (p1 = 0.03504)	p = 0.25532 ω = 5.91012	q = 0.75505		M7 vs. M8	0.000120891	77 V 0.814, 463 K 0.804, 486 A 0.610, 513 G 0.702, 514 R 0.638, 523 H 0.828, 531 T 0.942, 546 V 0.979*, 560 N 0.998**, 584 P 0.726, 586 F 0.947, 588 G 0.550, 590 P 0.961*, 596 L 0.698, 636 G 0.975*, 638 P 0.850, 675 L 0.637, 680 Q 0.871, 728 F 0.830, 729 F 0.720, 732 L 0.973*, 733 F 0.627
	M7	34	-4441.221	p =	0.00582	q =	0.00731			Not Allowed
	M8a	35	-4441.114	p0 = 0.68245 (p1 = 0.3176)	p = 0.00500 ω = 1.00000	q = 2.34031		M8a vs. M8	0.000024187	Not Allowed

<i>rpl20</i>	M3	37	-563.9652	p:	0.34044	0.15434	0.50522	M0 vs. M3	0.98187355	[]
				ω :	0	0	1.1558			
	M0	33	-564.1688	ω 0:	0.5857					Not Allowed
	M2a	36	-563.9653	p:	0.49477	0	0.50523	M1a vs.	0.991598492	[]
				ω :	0	1	1.15579	M2a		
	M1a	34	-563.9737	p:	0.43612	0.56388				Not Allowed
				ω :	0	1				
	M8	36	-563.9652	p0 = 0.49477 (p1 = 0.5052)	p = 0.00962 ω = 1.15579	q = 2.26061		M7 vs.M8	0.966701034	76 Y 0.698
	M7	34	-563.9991	p =	0.0705	q =	0.06306			Not Allowed
	M8a	35	-563.9739	p0 = 0.43612 (p1 = 0.5639)	p = 0.00500 ω = 1.00000	q = 1.27367		M8a vs.M8	0.895206241	Not Allowed
<i>rps2</i>	M3	37	-1163.4474	p:	0.00884	0.98693	0.00423	M0 vs. M3	0	[]
				ω :	0.24037	0.24038	240.8771			
	M0	33	-1217.559	ω 0:	0.09996					Not Allowed
	M2a	36	-1163.446	p:	0.99577	0	0.00423	M1a vs.	0	[]
				ω :	0.24037	1	240.876	M2a		
	M1a	34	-1217.559	p:	0.99999	0.00001				Not Allowed
				ω :	0.09995	1				
	M8	36	-1163.450	p0 = 0.99577 (p1 = 0.0042)	p = 31.43766 ω = 241.456	q = 99.00000		M7 vs.M8	0	32 A 0.524, 131 N 0.504, 199 L 0.612, 237—1.000**
	M7	34	-1217.569	p =	11.12717	q =	99			Not Allowed

rps3	M8a	35	-1217.573	p0 = 0.99999 (p1 = 0.00001)	p = 11.06100 ω = 1.00000	q = 99.00000		M8a vs.M8	0	Not Allowed
	M3	37	-1282.245	p:	0.48965	0.00181	0.50854	M0 vs. M3	0.70129752	[]
				ω:	0	0.51113	0.51158			
	M0	33	-1283.339	ω0:	0.25784					Not Allowed
	M2a	36	-1282.347	p:	0.85452	0.05251	0.09297	M1a vs. 1		[]
				ω:	0.14314	1	1	M2a		
	M1a	34	-1282.347	p:	0.85452	0.14548				Not Allowed
				ω:	0.14315	1				
	M8	36	-1282.267	p0 = 0.99999 (p1 = 0.00001)	p = 0.34957 ω = 1.00000	q = 0.92823		M7 vs.M8	0.999998	30 S 0.571, 86 E 0.568
	M7	34	-1282.267	p =	0.34956	q =	0.92818			Not Allowed
	M8a	35	-1282.278	p0 = 0.99999 (p1 = 0.00001)	p = 0.41550 ω = 1.00000	q = 1.15694		M8a vs.M8	0.87226229	Not Allowed

- 5
- Note:
- 6
- []—No data available
- 7
- np represents the degree of freedom
- 8
- Positively selected sites (* $p > 95\%$; ** $p > 99\%$)