

Supplementary Material 10. Statistics of mitochondrial polymorphisms within lineages and sublineages estimated for each gene.

		Lineage ^{*2}															
Gene		B	C	C1	C2	D	D1	D2	D3	F	G	H	I	Ss	Ss -J1	Ss -J2	Sk
16S 466 bases ^{*1}	N	2	99	27	72	28	19	6	3	134	30	16	39	71	29	42	45
	N _P	5	21	7	16	8	3	0	0	15	8	1	11	14	10	5	15
	N _S	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
	N _R	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
	N _H	2	24	7	18	6	4	1	1	16	7	2	12	13	9	6	13
	H	1.000	0.668	0.746	0.554	0.635	0.298	0.000	0.000	0.565	0.462	0.400	0.731	0.518	0.712	0.344	0.668
	π (%)	1.100	0.210	0.257	0.168	0.433	0.068	0.000	0.000	0.142	0.140	0.086	0.239	0.152	0.234	0.089	0.242
	D	n.a.	-2.30**	-1.03	-2.35**	-0.06	-1.72	n.a.	n.a.	-2.02*	-2.06*	0.65	-1.74	-2.17*	-1.83*	-1.62	-2.10*
	F _S	n.a.	-28.84***	-2.29	-20.99***	0.31	-2.68	n.a.	n.a.	-15.93***	-4.41*	0.87	-8.48***	-11.79***	-5.01**	-4.16*	-9.45***
COXI 561 bases	N	2	99	27	72	28	19	6	3	134	30	16	39	71	29	42	45
	N _P	0	50	20	32	25	6	2	2	37	35	6	47	33	14	18	38
	N _S ^{*3}	0	50	20	32	25	6	2	2	37	35	6	46	33	14	18	39
	N _R ^{*3}	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
	N _H	1	46	17	29	12	7	3	2	37	23	7	31	28	13	15	27
	H	0.000	0.902	0.957	0.820	0.775	0.544	0.600	0.667	0.529	0.975	0.625	0.969	0.901	0.847	0.786	0.902
	π (%)	0.000	0.509	0.510	0.290	0.985	0.113	0.119	0.238	0.132	0.766	0.153	0.582	0.616	0.256	0.252	0.449
	D	n.a.	-2.24**	-1.60	-2.40**	-0.50	-2.05*	n.a.	n.a.	-2.68***	-1.88*	-1.80*	-2.52***	-1.58	-2.00*	-2.14*	-2.47**
	D _{Syn}	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	-2.51***	n.a.	n.a.	n.a.	n.a.
	F _S	n.a.	-33.41***	-11.31***	-33.69***	-0.80	-5.56**	n.a.	n.a.	-68.15***	-17.33***	-4.73	-36.12***	-16.69***	-9.64***	-11.18***	-27.20***

N_P: number of polymorphic sites; N_S: number of synonymous changes; N_R: number of replacement changes; N_H: number of haplotypes; H: unbiased haplotype diversity (Nei, 1987); π: per-cent nucleotide diversity (Nei, 1987); D: Tajima's (1989) neutrality statistic; D_{Syn}: Tajima's D estimated for synonymous sites; F_S: Fu's (1997) neutrality statistic. The significance of the neutrality statistics is indicated by asterisks: * (P < 0.05), ** (P < 0.01), and *** (P < 0.001). For Lineage B and two of the Lineage D sublineages (D2 and D3), the neutrality statistics were not estimated due to small sample sizes (n.a.). D_{Syn} is shown only for gene-lineage/sublineage combinations with one or more replacement polymorphisms (N_R).

^{*1}Length after multiple alignment and sequence trimming (see main text).

^{*2}Ss = *S. spathulata* (Lineage J) and Sk = *S. kegaki*. Lineage L (N = 1) was omitted from the analyses.

^{*3}Incompletely sequenced codons (5'- and 3'-end) were excluded.

^{*4}Stop codons in *NAD3* (TAA or TAG) were excluded.

Supplementary Material 9. *Continued.*

		Lineage ^{*2}															
Gene		B	C	C1	C2	D	D1	D2	D3	F	G	H	I	Ss	Ss -J1	Ss -J2	Sk
COX3 765 bases	<i>N</i>	2	99	27	72	28	19	6	3	134	30	16	39	71	29	42	45
	<i>N_P</i>	0	74	13	56	28	12	4	3	69	48	16	63	51	19	33	47
	<i>N_S^{*3}</i>	0	68	19	49	25	11	4	2	59	45	14	63	51	19	33	44
	<i>N_R^{*3}</i>	0	6	0	6	3	1	0	1	11	3	2	0	2	1	1	3
	<i>N_H</i>	1	59	14	45	18	10	5	3	60	29	12	35	37	15	22	36
	<i>H</i>	0.000	0.939	0.895	0.899	0.878	0.737	0.933	1.000	0.902	0.998	0.967	0.991	0.944	0.823	0.921	0.987
	π (%)	0.000	0.580	0.346	0.295	0.607	0.165	0.174	0.260	0.313	0.924	0.344	0.719	0.869	0.250	0.624	0.455
	<i>D</i>	<i>n.a.</i>	-2.25**	-1.64	-2.66***	-1.29	-2.30**	<i>n.a.</i>	<i>n.a.</i>	-2.56***	-1.55	-1.79	-2.28**	-1.31	-2.19**	-1.37	-2.36**
	<i>D_{Syn}</i>	<i>n.a.</i>	-2.18**	<i>n.a.</i>	-2.61***	-1.19	-2.27**	<i>n.a.</i>	<i>n.a.</i>	-2.49***	-1.56	-1.89*	<i>n.a.</i>	-1.25	-2.21**	-1.32	-2.32**
	<i>F_S</i>	<i>n.a.</i>	-67.92***	-6.94**	-67.84***	-8.06***	-7.42**	<i>n.a.</i>	<i>n.a.</i>	-88.41***	-26.45***	-7.80***	-36.75***	-18.44***	-10.82***	-9.16***	-44.46***
NAD3 354 bases	<i>N</i>	2	99	27	72	28	19	6	3	134	30	16	39	71	29	42	45
	<i>N_P</i>	0	37	9	28	9	4	1	0	27	25	7	36	30	15	16	32
	<i>N_S^{*4}</i>	0	33	8	25	8	4	1	0	24	24	4	36	26	12	13	27
	<i>N_R^{*4}</i>	0	4	1	3	0	0	0	0	3	1	3	1	5	3	3	4
	<i>N_H</i>	1	37	10	27	8	5	2	1	26	23	8	27	27	13	14	25
	<i>H</i>	0.000	0.910	0.838	0.851	0.696	0.386	0.533	0.000	0.398	0.963	0.842	0.910	0.880	0.766	0.764	0.906
	π (%)	0.000	0.883	0.412	0.545	0.416	0.119	0.151	0.000	0.134	0.773	0.355	0.671	0.724	0.411	0.434	0.691
	<i>D</i>	<i>n.a.</i>	-1.75	-1.20	-2.09*	-1.15	-1.86*	<i>n.a.</i>	<i>n.a.</i>	-2.63***	-2.02*	-1.42	-2.56***	-1.91*	-2.10*	-1.87*	-2.26**
	<i>D_{Syn}</i>	<i>n.a.</i>	-1.65	-1.04	-2.07*	<i>n.a.</i>	<i>n.a.</i>	<i>n.a.</i>	<i>n.a.</i>	-2.59***	-1.98*	-1.55	-2.55***	-1.73	-1.95*	-1.66	-2.14**
	<i>F_S</i>	<i>n.a.</i>	-30.16***	-5.08**	-25.45***	-2.54*	-3.57*	<i>n.a.</i>	<i>n.a.</i>	-46.74***	-24.00***	-4.73**	-31.37***	-20.27***	-9.56***	-8.75***	-23.13***