

Table S3 Characteristics of alignments of 68 protein-coding genes involved in the phylogenetic analyses.

Gene	Aligned length (bp)	No. of variable sites (divergence, %)	No. of parsimony informative sites (divergence, %)
<i>accD</i>	1,518	1,004 (54.51)	769 (41.75)
<i>atpA</i>	1,500	361 (23.69)	254 (16.67)
<i>atpB</i>	402	352 (23.37)	248 (16.47)
<i>atpE</i>	576	106 (26.57)	62 (15.54)
<i>atpF</i>	246	153 (27.57)	97 (17.48)
<i>atpH</i>	744	43 (17.48)	26 (10.57)
<i>atpI</i>	1,694	167 (22.63)	104 (14.09)
<i>ccsA</i>	1,104	405 (41.67)	268 (27.59)
<i>cemA</i>	1,512	232 (33.33)	150 (21.55)
<i>clpP</i>	363	409 (59.53)	284 (41.34)
<i>matK</i>	1,381	793 (49.04)	548 (33.89)
<i>ndhE</i>	306	80 (26.85)	37 (12.42)
<i>petA</i>	2,276	269 (27.93)	177 (18.38)
<i>petB</i>	1,185	120 (18.52)	81 (12.50)
<i>petD</i>	516	84 (17.39)	55 (11.39)
<i>petG</i>	477	21 (18.42)	12 (10.53)
<i>petL</i>	664	23 (23.95)	9 (9.38)
<i>petN</i>	972	11 (12.22)	6 (6.67)
<i>psaA</i>	648	407 (18.06)	254 (11.27)
<i>psaB</i>	474	391 (17.73)	278 (12.61)
<i>psaC</i>	114	59 (23.98)	38 (15.45)
<i>psaI</i>	96	29 (26.13)	14 (12.61)
<i>psaJ</i>	90	33 (25.58)	24 (18.60)
<i>psbA</i>	2,254	148 (13.98)	92 (8.69)
<i>psbB</i>	2,205	364 (23.98)	254 (16.73)
<i>psbC</i>	246	255 (17.93)	172 (12.10)
<i>psbD</i>	111	178 (16.76)	123 (11.58)
<i>psbE</i>	126	33 (13.10)	21 (8.33)
<i>psbF</i>	1,062	14 (11.67)	9 (7.50)
<i>psbH</i>	1,527	67 (29.78)	45 (20.00)
<i>psbI</i>	1,503	23 (20.72)	13 (11.71)
<i>psbJ</i>	1,062	15 (12.20)	7 (5.69)
<i>psbK</i>	252	48 (25.40)	30 (15.87)
<i>psbL</i>	120	13 (11.11)	7 (5.98)
<i>psbM</i>	231	24 (22.86)	16 (15.24)
<i>psbN</i>	111	22 (16.67)	15 (11.36)
<i>psbT</i>	123	23 (22.55)	17 (16.67)
<i>psbZ</i>	204	36 (19.05)	23 (12.17)

Gene	Aligned length (bp)	No. of variable sites (divergence, %)	No. of parsimony informative sites (divergence, %)
<i>rbcL</i>	117	314 (21.90)	215 (14.99)
<i>rpl2</i>	105	88 (10.55)	45 (5.40)
<i>rpl14</i>	132	103 (27.91)	62 (16.80)
<i>rpl16</i>	102	107 (25.48)	67 (15.95)
<i>rpl20</i>	189	119 (33.62)	76 (21.47)
<i>rpl22</i>	1437	157 (43.98)	104 (29.13)
<i>rpl23</i>	828	25 (8.68)	12 (4.17)
<i>rpl32</i>	369	56 (35.22)	40 (25.16)
<i>rpl33</i>	366	79 (37.62)	46 (21.90)
<i>rpl36</i>	368	24 (21.05)	15 (13.16)
<i>rpoA</i>	386	296 (35.75)	194 (23.43)
<i>rpoB</i>	210	825 (25.65)	485 (15.08)
<i>rpoC1</i>	114	560 (26.90)	306 (14.70)
<i>rpoC2</i>	936	1517 (35.20)	938 (21.76)
<i>rps2</i>	3,246	192 (26.12)	122 (16.60)
<i>rps3</i>	1,380	256 (37.93)	162 (24.00)
<i>rps4</i>	4,229	178 (28.25)	107 (16.98)
<i>rps7</i>	699	54 (11.54)	31 (6.62)
<i>rps8</i>	609	148 (36.54)	88 (21.73)
<i>rps11</i>	468	155 (37.17)	102 (24.46)
<i>rps12</i>	417	37 (9.20)	20 (4.98)
<i>rps14</i>	435	97 (32.01)	59 (19.47)
<i>rps15</i>	383	124 (45.42)	76 (27.84)
<i>rps16</i>	305	74 (28.03)	44 (16.67)
<i>rps18</i>	279	86 (24.71)	52 (14.94)
<i>rps19</i>	372	102 (36.56)	68 (24.37)
<i>ycf1</i>	7,953	4984 (62.59)	3024 (37.98)
<i>ycf2</i>	8,358	1517 (20.30)	758 (10.14)
<i>ycf3</i>	516	87 (16.67)	46 (8.81)
<i>ycf4</i>	555	219 (38.83)	122 (21.63)
Total	61,841	19395 (31.36)	12125 (19.61)