

Table S2. The selective pressure of peanut chloroplast gene using codeml.

Gene categories	Gene	dn	ds	dn/ds	ts/tv
Photosystem I	<i>psaA</i>	0.0009	0.0078	0.11738	4.26905
	<i>psaB</i>	0.0000	0.0049	0.00010	1.09968
	<i>psaC</i>	0.0000	0.0002	0.00010	0.00010
	<i>psaI</i>	0.0000	0.0001	0.29236	2.03338
	<i>psaJ</i>	0.0000	0.0001	0.39110	1.99922
Photosystem II	<i>psbA</i>	0.0000	0.0276	0.00010	2.19588
	<i>psbC</i>	0.0000	0.0002	0.00010	0.00010
	<i>psbE</i>	0.0000	0.0001	0.08281	1.51375
	<i>psbF</i>	0.0000	0.0001	0.19840	2.03057
	<i>psbH</i>	0.0000	0.0001	0.14205	2.08796
	<i>psbI</i>	0.0000	0.0001	0.00010	1.74915
	<i>psbJ</i>	0.0000	0.0001	0.52203	2.06485
	<i>psbK</i>	0.0000	0.0002	0.00010	0.00010
	<i>psbL</i>	0.0000	0.0001	0.13514	1.87574
	<i>psbM</i>	0.0000	0.0001	0.00010	1.26601
	<i>psbN</i>	0.0000	0.0001	0.27056	1.97383
	<i>psbZ</i>	0.0000	0.0001	0.39998	2.00000
RuBisCO large subunit	<i>rbcL</i>	0.0000	0.0028	0.00010	304.712
Cytochrome b/f complex	<i>petB</i>	0.0000	0.0088	0.00010	0.00010
	<i>petD</i>	0.0028	0.0208	0.13444	646.080
	<i>petG</i>	0.0000	0.0605	0.00010	0.00010
c-type cytochrome	<i>ccsA</i>	0.0036	0.0075	0.48371	0.00010
ATP synthase	<i>atpB</i>	0.0000	0.0002	0.00010	0.00010
	<i>atpE</i>	0.0000	0.0001	0.18572	1.75995
	<i>atpF</i>	0.1716	0.5252	0.32675	0.64903
	<i>atpI</i>	0.0000	0.0123	0.00010	1.25983
NADH dehydrogenase	<i>ndhA</i>	0.0047	0.0091	0.51982	0.94759
	<i>ndhB</i>	0.1541	0.2653	0.58095	0.94584
	<i>ndhC</i>	0.0036	0.0270	0.13434	3.51268
	<i>ndhD</i>	0.0000	0.0068	0.00010	1.10592
	<i>ndhF</i>	0.0057	0.0217	0.26054	1.16489
	<i>ndhH</i>	0.0021	0.0050	0.41775	0.92841
	<i>ndhI</i>	0.0000	0.0001	0.33657	2.00128
	<i>ndhJ</i>	0.0000	0.0002	0.00010	0.59237
	<i>ndhK</i>	4.1292	8.6219	0.47892	1.58000
Assembly/stability of photosystem I	<i>ycf3</i>	0.0500	0.2265	0.22082	0.48335
	<i>ycf4</i>	0.0047	0.0180	0.26276	1.71848
RNA polymerase genes	<i>rpoA</i>	0.0052	0.0107	0.47980	1.86694
	<i>rpoB</i>	0.0012	0.0048	0.25119	1.61900
	<i>rpoCl</i>	0.0371	0.0976	0.38038	1.36740

	<i>rpoC2</i>	0.0140	0.0156	0.89652	0.67955
	<i>rpl2</i>	0.0563	0.0612	0.92049	2.67673
	<i>rpl23</i>	0.0000	0.0001	0.04132	2.60832
	<i>rpl32</i>	0.0000	0.0002	0.00010	0.00010
Ribosomal protein	<i>rpl33</i>	0.0000	0.0001	0.46871	0.00010
	<i>rps8</i>	0.0033	0.0118	0.28020	1.84263
	<i>rps14</i>	0.0000	0.0002	0.00010	1.40338
	<i>rps18</i>	0.0000	0.0000	650.584	606.459
Acetyl-CoA carboxylase subunit	<i>accD</i>	0.0049	0.0000	146.010	1.22978
Proteolysis subunit	<i>clpP</i>	0.0364	0.0314	1.16086	0.12456
Carbon metabolism	<i>cemA</i>	0.0000	0.0001	0.00010	2.34633
Conserved reading frames	<i>ycf1</i>	0.0213	0.0180	1.18700	1.06362
	<i>ycf2</i>	0.0017	0.0042	0.40000	1.99999