

## Supplementary Materials for:

### **Mutation rates in plastid genomes: they are lower than you might think.**

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**Supplementary Table S1.** Nucleotide substitution rates between *Micromonas pusilla* CCMP1545 and *Micromonas* sp. RCC299.

**Part A. Mitochondrial DNA-located genes.**

MtDNA gene	# codons	$d_N / d_S$	$d_N$	$d_S$
<i>atp6</i>	249	0.012	0.155	13.366
<i>atp9</i>	73	0.001	0.012	12.069
<i>cob</i>	385	0.008	0.073	9.608
<i>cox1</i>	527	0.013	0.099	7.580
<i>cox2</i>	262	0.013	0.126	9.970
<i>cox3</i>	265	0.002	0.122	61.852
<i>nad1</i>	332	0.001	0.072	60.342
<i>nad2</i>	495	0.029	0.365	12.791
<i>nad3</i>	116	0.002	0.112	50.550
<i>nad4</i>	485	0.002	0.141	60.250
<i>nad4L</i>	99	0.049	0.125	2.561
<i>nad5</i>	670	0.021	0.201	9.465
<i>nad6</i>	262	0.032	0.383	11.802
<i>nad7</i>	397	0.016	0.088	5.595
<i>nad9</i>	177	0.003	0.212	69.797
<i>rpl14</i>	123	0.034	0.284	8.347
<i>rps12</i>	122	0.045	0.148	3.318
<i>rps14</i>	98	0.010	0.448	43.854
<i>rps19</i>	83	0.006	0.351	62.796
<b>Average</b>	<b>274.74</b>	<b>0.02</b>	<b>0.19</b>	<b>27.15</b>
<b>Standard deviation</b>	<b>177.13</b>	<b>0.02</b>	<b>0.12</b>	<b>25.24</b>

**Part B. Plastid DNA-located genes.**

PtDNA genes	# codons	$d_N / d_S$	$d_N$	$d_S$
<i>psaA</i>	750	0.006	0.002	0.312
<i>psaB</i>	733	0.009	0.004	0.383
<i>psbA</i>	352	0.053	0.003	0.047
<i>psbE</i>	83	0.024	0.006	0.239
<i>psbF</i>	37	---	0.000	0.000
<i>psbL</i>	34	---	0.026	0.000
<i>psbZ</i>	61	0.157	0.037	0.238
RNA polymerase alpha	351	0.039	0.091	2.329
RNA polymerase beta chain	1184	0.004	0.349	82.106
RNA polymerase beta subunit	1075	0.041	0.097	2.360
RNA polymerase beta' subunit	764	0.059	0.138	2.363

PtDNA genes	# codons	$d_N / d_S$	$d_N$	$d_S$
<i>rpl14</i>	118	0.025	0.015	0.590
<i>rpl16</i>	138	0.053	0.026	0.489
<i>rpl2</i>	276	0.028	0.019	0.664
<i>rpl23</i>	86	0.054	0.011	0.201
<i>rpl5</i>	183	0.076	0.068	0.899
<i>rps11</i>	129	0.018	0.014	0.768
<i>rps12</i>	123	0.011	0.007	0.654
<i>rps18</i>	69	0.046	0.021	0.462
<i>rps19</i>	91	0.018	0.010	0.530
<i>rps3</i>	210	0.050	0.028	0.549
<i>rps7</i>	155	0.017	0.017	0.971
<i>rps8</i>	121	0.028	0.034	1.215
<i>rps9</i>	127	0.041	0.035	0.846
translation initiation factor 1	83	0.019	0.037	1.925
<i>tufA</i>	407	0.028	0.026	0.960
<i>ycf3</i>	165	0.005	0.008	1.421
<b>Average</b>	<b>292.78</b>	<b>0.04</b>	<b>0.04</b>	<b>3.83</b>
<b>Standard deviation</b>	<b>321.07</b>	<b>0.03</b>	<b>0.07</b>	<b>15.66</b>

**Supplementary Table S2.** Nucleotide substitution rates between *Nannochloropsis gaditana* CCMP527 and *N. salina* CCMP1776.

**Part A. Mitochondrial DNA-located genes.**

MtDNA genes	# codons	$d_N / d_S$	$d_N$	$d_S$
<i>atp1</i>	519	0.0109	0.0008	0.0733
<i>atp6</i>	261	0.0434	0.0017	0.0403
<i>atp8</i>	104	0.0949	0.0084	0.088
<i>atp9</i>	74	0.001	0.0001	0.0779
<i>cob</i>	385	0.0331	0.0011	0.0344
<i>cox1</i>	505	0.054	0.0068	0.1265
<i>cox2</i>	301	0.001	0	0.0283
<i>cox3</i>	269	0.001	0	0.0307
<i>nad1</i>	325	0.0698	0.0055	0.078
<i>nad2</i>	492	0.0367	0.0035	0.0956
<i>nad3</i>	121	0.001	0.0001	0.0512
<i>nad4</i>	524	0.0312	0.0042	0.133
<i>nad4L</i>	97	0.001	0.0001	0.1422
<i>nad5</i>	673	0.0504	0.0036	0.0717
<i>nad6</i>	194	0.0484	0.0046	0.0955
<i>nad7</i>	397	0.0284	0.0033	0.1145
<i>nad9</i>	188	0.001	0.0001	0.0903

<b>MtDNA genes</b>	<b># codons</b>	<b><math>d_N / d_S</math></b>	<b><math>d_N</math></b>	<b><math>d_S</math></b>
<i>nad11</i>	505	0.1012	0.0101	0.0995
<i>rpl2</i>	274	0.0447	0.0046	0.102
<i>rpl5</i>	178	0.2947	0	0
<i>rpl6</i>	182	0.3321	0.0308	0.0926
<i>rpl14</i>	125	0.001	0	0.013
<i>rpl16</i>	142	0.0548	0.003	0.0541
<i>rps2</i>	211	0.1405	0.0152	0.1084
<i>rps3</i>	419	0.1441	0.0144	0.0998
<i>rps4</i>	240	0.1335	0.0108	0.0809
<i>rps7</i>	144	0.0391	0.0056	0.1436
<i>rps8</i>	127	0.001	0	0.0313
<i>rps10</i>	111	0.2484	0.0238	0.0959
<i>rps11</i>	155	0.0288	0.0058	0.2009
<i>rps12</i>	124	0.001	0.0001	0.0957
<i>rps13</i>	117	0.001	0.0001	0.1202
<i>rps14</i>	97	0.1729	0.0088	0.0506
<i>rps19</i>	84	0.001	0	0.0174
<i>tatC</i>	238	0.0918	0.008	0.0873
<b>Average</b>	<b>254.34</b>	<b>0.067</b>	<b>0.005</b>	<b>0.082</b>
<b>Standard deviation</b>	<b>159.91</b>	<b>0.085</b>	<b>0.007</b>	<b>0.043</b>
<b>Concatenated rRNA genes</b>	3742 nt		$d_i = 0.005$	

### Part B. Plastid DNA-located genes.

<b>PtDNA genes</b>	<b># codons</b>	<b><math>d_N / d_S</math></b>	<b><math>d_N</math></b>	<b><math>d_S</math></b>
<i>atpA</i>	504	0.016	0.001	0.052
<i>atpB</i>	489	0.011	0.001	0.074
<i>atpD</i>	231	0.078	0.006	0.070
<i>atpE</i>	138	0.194	0.003	0.015
<i>atpF</i>	154	0.183	0.006	0.032
<i>atpG</i>	159	0.114	0.003	0.026
<i>atpH</i>	82	0.000	0.000	0.000
<i>atpI</i>	248	0.043	0.002	0.042
<i>cbbX</i>	335	0.030	0.004	0.124
<i>ccsI</i>	422	0.077	0.006	0.077
<i>ccsA</i>	302	0.074	0.004	0.059
<i>chlB</i>	506	0.038	0.004	0.104
<i>chlI</i>	410	0.077	0.007	0.093
<i>chlL</i>	287	0.019	0.001	0.074
<i>chlN</i>	443	0.038	0.005	0.125
<i>clpA</i>	148	0.386	0.017	0.044
<i>clpCI</i>	383	0.019	0.002	0.115

PtDNA genes	# codons	$d_N / d_S$	$d_N$	$d_S$
<i>clpC2</i>	448	0.061	0.007	0.106
<i>dnaK</i>	601	0.032	0.003	0.085
<i>ftsH</i>	696	0.049	0.003	0.060
<i>groEL</i>	534	0.045	0.007	0.153
<i>ilvB</i>	591	0.083	0.006	0.066
<i>petA</i>	318	0.016	0.001	0.081
<i>petB</i>	214	0.001	0.000	0.029
<i>petD</i>	159	0.001	0.000	0.023
<i>petF</i>	101	0.001	0.000	0.084
<i>petG</i>	33	0.001	0.000	0.040
<i>petJ</i>	120	0.211	0.004	0.016
<i>petL</i>	30	---	0.017	0.000
<i>petM</i>	30	0.001	0.000	0.308
<i>petN</i>	28	0.001	0.000	0.000
<i>psaA</i>	744	0.001	0.000	0.054
<i>psaB</i>	736	0.019	0.001	0.060
<i>psaC</i>	80	0.106	0.005	0.049
<i>psaD</i>	135	0.001	0.000	0.049
<i>psaE</i>	66	3.980	0.000	0.000
<i>psaF</i>	183	0.014	0.002	0.160
<i>psaI</i>	44	0.001	0.000	0.143
<i>psaJ</i>	40	0.001	0.000	0.057
<i>psaL</i>	171	0.035	0.003	0.073
<i>psaM</i>	29	0.000	0.000	0.000
<i>psb28</i>	112	0.124	0.013	0.108
<i>psbA</i>	359	0.001	0.000	0.006
<i>psbB</i>	508	0.001	0.000	0.082
<i>psbC</i>	468	0.017	0.001	0.055
<i>psbD</i>	355	0.001	0.000	0.044
<i>psbE</i>	82	0.270	0.000	0.000
<i>psbF</i>	42	0.001	0.000	0.108
<i>psbH</i>	66	0.001	0.000	0.048
<i>psbI</i>	37	0.404	0.000	0.000
<i>psbJ</i>	38	0.001	0.000	0.043
<i>psbK</i>	43	0.001	0.000	0.027
<i>psbL</i>	41	0.001	0.000	0.000
<i>psbN</i>	51	0.001	0.000	0.023
<i>psbT</i>	31	0.000	0.014	0.000
<i>psbV</i>	161	0.059	0.003	0.042
<i>psbX</i>	38	0.020	0.000	0.000
<i>psbY</i>	35	0.000	0.000	0.000
<i>psbZ</i>	60	0.001	0.000	0.082

<b>PtDNA genes</b>	<b># codons</b>	<b><math>d_N / d_S</math></b>	<b><math>d_N</math></b>	<b><math>d_S</math></b>
<i>rbcL</i>	486	0.021	0.001	0.044
<i>rbcS</i>	88	0.169	0.011	0.063
<i>rpl1</i>	224	0.107	0.008	0.070
<i>rpl2</i>	274	0.062	0.005	0.073
<i>rpl3</i>	203	0.001	0.000	0.117
<i>rpl4</i>	253	0.196	0.010	0.052
<i>rpl5</i>	183	0.115	0.002	0.020
<i>rpl6</i>	179	0.045	0.005	0.104
<i>rpl11</i>	141	0.067	0.003	0.044
<i>rpl12</i>	129	0.063	0.003	0.052
<i>rpl13</i>	144	0.073	0.006	0.078
<i>rpl14</i>	120	0.001	0.000	0.130
<i>rpl16</i>	137	0.001	0.000	0.047
<i>rpl18</i>	103	0.419	0.008	0.019
<i>rpl19</i>	121	0.340	0.015	0.043
<i>rpl20</i>	133	0.141	0.006	0.044
<i>rpl21</i>	148	0.191	0.005	0.029
<i>rpl22</i>	153	0.001	0.000	0.104
<i>rpl23</i>	118	0.044	0.004	0.081
<i>rpl27</i>	107	0.123	0.012	0.096
<i>rpl29</i>	70	0.001	0.000	0.034
<i>rpl31</i>	73	0.001	0.000	0.050
<i>rpl32</i>	54	0.048	0.016	0.330
<i>rpl33</i>	63	0.001	0.000	0.061
<i>rpl34</i>	48	0.000	0.008	0.000
<i>rpl35</i>	63	0.001	0.000	0.076
<i>rpl36</i>	36	0.001	0.000	0.133
<i>rpoA</i>	443	0.146	0.008	0.057
<i>rpoB</i>	1054	0.004	0.000	0.095
<i>rpoC1</i>	749	0.066	0.006	0.094
<i>rpoC2</i>	1317	0.069	0.006	0.084
<i>rps2</i>	249	0.045	0.002	0.036
<i>rps3</i>	85	0.072	0.005	0.069
<i>rps4</i>	207	0.026	0.002	0.079
<i>rps5</i>	176	0.076	0.005	0.062
<i>rps6</i>	105	0.001	0.000	0.104
<i>rps7</i>	157	0.049	0.003	0.053
<i>rps8</i>	131	0.112	0.003	0.029
<i>rps9</i>	135	0.001	0.000	0.227
<i>rps10</i>	114	0.393	0.011	0.029
<i>rps11</i>	126	0.001	0.000	0.089
<i>rps12</i>	124	0.001	0.000	0.084

PtDNA genes	# codons	$d_N / d_S$	$d_N$	$d_S$
<i>rps13</i>	122	0.037	0.003	0.086
<i>rps14</i>	99	0.224	0.009	0.041
<i>rps16</i>	83	0.001	0.000	0.030
<i>rps17</i>	84	0.001	0.000	0.072
<i>rps18</i>	71	0.001	0.000	0.021
<i>rps19</i>	94	0.042	0.004	0.101
<i>rps20</i>	95	0.053	0.004	0.083
<i>secA</i>	867	0.041	0.003	0.080
<i>secY</i>	378	0.227	0.007	0.031
<i>tatC</i>	251	0.068	0.005	0.080
<i>thiG</i>	268	0.092	0.005	0.051
<i>thiS</i>	75	0.162	0.016	0.097
<i>tufA</i>	408	0.012	0.001	0.086
<i>ycf3</i>	166	0.001	0.000	0.071
<i>ycf4</i>	194	0.001	0.000	0.142
<i>ycf12</i>	33	0.129	0.000	0.000
<i>ycf16</i>	282	0.131	0.011	0.085
<i>ycf24</i>	496	0.040	0.003	0.085
<i>ycf34</i>	84	0.056	0.015	0.263
<i>ycf36</i>	165	0.117	0.011	0.092
<i>ycf46</i>	498	0.115	0.009	0.082
<i>ycf49</i>	96	0.362	0.014	0.039
<i>ycf54</i>	106	0.927	0.013	0.014
<i>ycf59</i>	346	0.071	0.005	0.069
<i>ycf66</i>	100	0.001	0.000	0.060
<b>Average</b>	<b>225.26</b>	<b>0.105</b>	<b>0.004</b>	<b>0.068</b>
<b>Standard deviation</b>	<b>221.47</b>	<b>0.370</b>	<b>0.004</b>	<b>0.054</b>
<b>Concatenated rRNA genes</b>	4552 nt		$d_i = 0.004$	

**Supplementary Table S3.** Nucleotide substitution rates between *Ostreococcus* sp. RCC809 and *Ostreococcus tauri* OTTH0595.

**Part A. Mitochondrial DNA-located genes.**

MtDNA genes	# codons	$d_N / d_S$	$d_N$	$d_S$
<i>atp1</i>	506	0.016	0.035	2.214
<i>atp6</i>	381	0.009	0.026	2.830
<i>atp8</i>	165	0.005	0.370	79.057
<i>atp9</i>	73	0.001	0.001	0.570
<i>cob</i>	248	0.007	0.024	3.421
<i>cox1</i>	528	0.008	0.019	2.392
<i>cox2</i>	256	0.017	0.050	3.003

<b>MtDNA genes</b>	<b># codons</b>	<b><math>d_N / d_S</math></b>	<b><math>d_N</math></b>	<b><math>d_S</math></b>
<i>cox3</i>	263	0.032	0.048	1.520
<i>nad1</i>	327	0.007	0.026	3.820
<i>nad2</i>	496	0.022	0.162	7.315
<i>nad3</i>	114	0.004	0.034	8.168
<i>nad4</i>	488	0.015	0.060	4.089
<i>nad4L</i>	99	0.003	0.110	35.642
<i>nad5</i>	667	0.017	0.064	3.819
<i>nad6</i>	255	0.049	0.176	3.604
<i>nad7</i>	393	0.003	0.015	4.937
<i>nad9</i>	184	0.034	0.149	4.415
<i>ndhk</i>	165	0.006	0.035	5.485
<i>rpl14</i>	123	0.023	0.113	4.929
<i>rpl16</i>	132	0.048	0.105	2.208
<i>rpl5</i>	177	0.090	0.320	3.566
<i>rpl6</i>	186	0.003	0.280	85.703
<i>rps10</i>	113	0.005	0.386	74.577
<i>rps11</i>	120	0.041	0.142	3.444
<i>rps12</i>	120	0.022	0.067	3.014
<i>rps13</i>	115	0.030	0.150	5.072
<i>rps14</i>	98	0.003	0.212	79.618
<i>rps19</i>	79	0.002	0.156	77.068
<i>rps2</i>	197	0.043	0.265	6.111
<i>rps3</i>	276	0.012	0.298	25.422
<i>rps4</i>	204	0.021	0.278	13.211
<i>rps7</i>	163	0.064	0.260	4.070
<i>rps8</i>	123	0.072	0.225	3.123
<i>ymf39</i>	179	0.011	0.272	24.845
<b>Average</b>	<b>235.68</b>	<b>0.02</b>	<b>0.15</b>	<b>17.42<sup>a</sup></b>
<b>Standard deviation</b>	<b>151.66</b>	<b>0.02</b>	<b>0.11</b>	<b>27.12</b>

<sup>a</sup>When the eight genes with extremely high  $d_S$  values (>24) are removed from the analysis, the average synonymous-site substitution rate drops to 4.24 (standard deviation = 2.48).

### Part B. Plastid DNA-located genes.

<b>PtDNA genes</b>	<b># codons</b>	<b><math>d_N / d_S</math></b>	<b><math>d_N</math></b>	<b><math>d_S</math></b>
<i>atpA</i>	502	0.052	0.026	0.495
<i>atpB</i>	480	0.021	0.014	0.647
<i>atpE</i>	141	0.034	0.044	1.278
<i>atpF</i>	167	0.067	0.046	0.683
<i>atpH</i>	100	0.037	0.004	0.114
<i>atpI</i>	235	0.011	0.006	0.536
<i>clpP</i>	199	0.002	0.004	1.763
<i>infA</i>	77	0.047	0.040	0.854



<b>PtDNA genes</b>	<b># codons</b>	<b><math>d_N / d_S</math></b>	<b><math>d_N</math></b>	<b><math>d_S</math></b>
<i>petA</i>	306	0.047	0.052	1.110
<i>petB</i>	214	0.019	0.010	0.531
<i>petG</i>	36	0.001	0.000	0.242
<i>psaA</i>	750	0.012	0.004	0.360
<i>psaB</i>	732	0.017	0.009	0.553
<i>psaC</i>	80	0.001	0.001	0.851
<i>psaI</i>	35	0.001	0.001	0.703
<i>psaJ</i>	41	0.069	0.045	0.656
<i>psaM</i>	30	0.001	0.000	0.298
<i>psbA</i>	352	0.037	0.004	0.103
<i>psbB</i>	442	0.018	0.007	0.400
<i>psbC</i>	460	0.037	0.015	0.396
<i>psbD</i>	351	0.011	0.004	0.351
<i>psbE</i>	81	0.115	0.032	0.277
<i>psbF</i>	37	0.001	0.000	0.077
<i>psbH</i>	77	0.033	0.012	0.343
<i>psbI</i>	37	0.001	0.000	0.154
<i>psbJ</i>	40	0.211	0.023	0.110
<i>psbK</i>	44	0.063	0.021	0.330
<i>psbL</i>	37	0.001	0.000	0.110
<i>psbN</i>	43	0.015	0.009	0.611
<i>psbT</i>	30	0.193	0.016	0.082
<i>rbcL</i>	474	0.090	0.021	0.232
<i>rpl14</i>	32	0.162	0.044	0.272
<i>rpl16</i>	137	0.028	0.022	0.799
<i>rpl2</i>	276	0.035	0.028	0.813
<i>rpl20</i>	110	0.037	0.052	1.410
<i>rpl23</i>	86	0.022	0.006	0.253
<i>rpl32</i>	71	0.086	0.097	1.127
<i>rpl36</i>	36	0.001	0.001	1.447
<i>rpl5</i>	183	0.061	0.039	0.637
<i>rpoA</i>	355	0.041	0.122	2.961
<i>rpoB</i>	1087	0.024	0.054	2.293
<i>rpoC1</i>	736	0.055	0.102	1.855
<i>rpoC2</i>	1007	0.066	0.227	3.425
<i>rps11</i>	129	0.005	0.003	0.679
<i>rps12</i>	123	0.009	0.007	0.776
<i>rps14</i>	99	0.033	0.027	0.808
<i>rps19</i>	91	0.017	0.010	0.562
<i>rps2</i>	223	0.071	0.076	1.060
<i>rps3</i>	210	0.036	0.024	0.674
<i>rps4</i>	196	0.049	0.048	0.980

PtDNA genes	# codons	$d_N / d_S$	$d_N$	$d_S$
<i>rps7</i>	155	0.021	0.020	0.962
<i>rps8</i>	121	0.068	0.032	0.472
<i>rps9</i>	126	0.064	0.025	0.391
<i>tufA</i>	408	0.051	0.040	0.785
<i>ycf12</i>	118	0.031	0.011	0.361
<i>ycf3</i>	165	0.001	0.002	2.098
<i>ycf9</i>	61	0.024	0.008	0.307
<b>Average</b>	<b>227.56</b>	<b>0.04</b>	<b>0.03</b>	<b>0.76</b>
<b>Standard deviation</b>	<b>243.00</b>	<b>0.04</b>	<b>0.04</b>	<b>0.68</b>

### Part C. Nuclear DNA-located genes.

NucDNA genes	# codons	$d_N / d_S$	$d_N$	$d_S$
RNA homing endonuclease	72	0.001	0.000	0.000
Senescence-associated protein	144	0.474	0.000	0.000
Eif4 eukaryotic translation initiation factor	586	0.025	0.343	13.833
psaL photosystem I subunit XI	200	0.019	0.178	9.192
ATP synthase beta chain, mitochondrial precursor	527	0.002	0.096	61.767
ATP synthase delta subunit 2	176	0.048	0.189	3.934
ATP synthase F1 alpha subunit	562	0.039	0.136	3.509
Chloroplast light-harvesting complex I protein precursor Lhca4	235	0.072	0.167	2.310
Chlorophyll a/b-binding protein CP29	234	0.118	0.179	1.521
Dynein 8 kDa light chain flagellar outer arm	90	0.047	0.156	3.315
rpl9	204	0.062	0.154	2.487
ATP synthase mt F1 assembly factor 2	240	0.036	0.122	3.387
histone H3	119	0.025	0.046	1.878
cytochrome P450	522	0.025	0.066	2.647
ubiquinol cytochrome C reductase	57	0.001	0.077	76.563
rpl9	191	0.034	0.116	3.397
rpl28	146	0.060	0.104	1.738
gpsA glycerol-3-phosphate dehydrogenase	172	0.019	0.071	3.678
psbB oxygen-evolving complex-related	352	0.031	0.061	1.975
acetyl-CoA carboxylase	1130	0.036	0.069	1.903
glucose-6-phosphate phosphate translocator 2	300	0.022	0.037	1.691
glutamine amidotransferase cyclase	537	0.033	0.060	1.815
indole-3-glycerol phosphate lysase	271	0.091	0.113	1.241
ubiquinol-cytochrome-c reductase cytochrome c1	272	0.048	0.098	2.032
rpl2	265	0.059	0.064	1.095
Tpt phosphate/phosphoenolpyruvate	302	0.042	0.070	1.639

<b>NucDNA genes</b>	<b># codons</b>	<b><math>d_N / d_S</math></b>	<b><math>d_N</math></b>	<b><math>d_S</math></b>
translocator				
rpl17	182	0.091	0.095	1.050
chloroplast ribose-5-phosphate isomerase	249	0.019	0.045	2.390
ribulose-1,5-bisphosphate carboxylase small subunit	167	0.107	0.115	1.073
uridine monophosphate synthetase	474	0.029	0.046	1.556
rps1	249	0.058	0.060	1.033
translation elongation factor mitochondrial	420	0.063	0.059	0.932
psaF	228	0.099	0.070	0.707
GTP-binding regulatory protein beta chain	318	0.049	0.049	0.995
rpl27	134	0.033	0.041	1.244
tauri beta tubulin	432	0.012	0.013	1.039
rpl15-2	188	0.033	0.027	0.831
RuBisCO activase	405	0.048	0.039	0.826
rpl3	91	0.066	0.040	0.601
rpl37	128	0.038	0.029	0.755
rps11	299	0.036	0.028	0.770
Ferredoxin-NADP oxidoreductase chloroplast precursor	378	0.067	0.039	0.588
rps29	55	0.045	0.036	0.815
cytochrome b6 f complex subunit4	158	0.026	0.021	0.811
GTP-binding protein sar1	192	0.016	0.013	0.800
rpl35	104	0.043	0.032	0.739
histone H2A	120	0.016	0.011	0.656
rps14	138	0.018	0.010	0.519
adenosylhomocysteinase	481	0.034	0.022	0.641
psaE photosystem I reaction center subunit	53	0.026	0.016	0.601
RNA polymerase II	71	0.039	0.023	0.589
psaD, PSI-D, subunit II, photosystem I protein	131	0.046	0.026	0.566
rpl22	111	0.033	0.029	0.861
rps15	129	0.015	0.010	0.624
EF1 elongation factor 1-alpha	466	0.057	0.028	0.491
H3 and H4	134	0.046	0.020	0.437
rps24	130	0.044	0.022	0.500
rpsL15/L27	146	0.052	0.023	0.447
histone H2B	110	0.005	0.004	0.734
histone H3.3	135	0.001	0.000	0.212
<b>Average</b>	<b>251.87</b>	<b>0.05</b>	<b>0.07</b>	<b>3.93<sup>a</sup></b>
<b>Standard deviation</b>	<b>184.50</b>	<b>0.06</b>	<b>0.06</b>	<b>12.47</b>

<sup>a</sup>When the two genes with extremely high  $d_S$  values (>25) are removed from the analysis, the average synonymous-site substitution rate drops to 1.68 (standard deviation = 2.15).

**Part D. Mitochondrial DNA intergenic regions.**

<b>MtDNA intergenic region</b>	<b>Alignment length (nt)</b>	<b><math>d_i</math></b>
<i>cob / trnQ</i>	52	9
<i>trnH / ndhK</i>	507	2.316
<i>atp9 / trnL</i>	60	1.316
<i>atp6 / trnG</i>	36	1.179
<i>nad9 / atp1</i>	55	2.212
<i>nad4 / nad2</i>	54	0.733
<i>nad5 / nad4</i>	48	0.970
<i>nad6 / atp6</i>	63	0.632
<i>ymf39 / cox1</i>	175	0.466
<i>rps11 / atp9</i>	78	0.557
<i>nad2 / cox3</i>	37	0.503
<i>rrs / trnM</i>	38	0.549
<i>trnG / trnR</i>	289	0.423
<i>rps12 / cob</i>	53	0.652
<b>Average</b>	<b>110.36</b>	<b>1.54</b>
<b>Standard deviation</b>	<b>133.65</b>	<b>2.23</b>

**Part E. Plastid DNA intergenic regions.**

<b>PtDNA intergenic regions</b>	<b>Alignment length (nt)</b>	<b><math>d_i</math></b>
<i>psbA-rrl</i>	442	4.448
<i>psaJ-trnF</i>	117	2.275
<i>trnN-ORF1260</i>	194	4.052
<i>petB-trnK</i>	109	1.601
<i>rbcL-petG</i>	149	1.388
<i>atpE-clpP</i>	110	2.023
<i>rpl32-ORF537</i>	164	1.700
<i>trnL-trnE</i>	92	1.224
<i>trnN-trnT</i>	117	0.894
<i>psaI-ycf12</i>	90	0.933
<i>atpA-rps14</i>	195	1.239
<i>psbN-rps4</i>	152	0.828
<i>psbA-petG</i>	232	0.655
<i>ORF1260-psbE</i>	163	0.682
<i>psaB-petA</i>	338	0.616
<i>trnD-psaA</i>	354	0.627
<i>rps2-rrs</i>	119	0.621
<i>psaC-atpB</i>	180	0.954
<i>rpl20-trnS</i>	77	0.618
<i>rps7-tufA</i>	106	0.627

<b>PtDNA intergenic regions</b>	<b>Alignment length (nt)</b>	<b><math>d_i</math></b>
<i>psbT-psbD</i>	204	0.576
<i>clpP-rpl32</i>	209	0.642
<i>atpB-atpE</i>	59	0.650
<i>psbE-psbF</i>	95	0.586
<i>rps19-rps3</i>	73	0.538
<i>trnM-rpl23</i>	202	0.508
<i>atpI-atpH</i>	179	0.476
<i>psbC-trnR</i>	127	0.469
<i>ycf9-trnM</i>	195	0.712
<i>psbI-psaJ</i>	85	0.429
<i>trnC-rpoB</i>	109	0.402
<i>rps9-trnL</i>	119	0.457
<i>rps4-ycf3</i>	158	0.370
<i>trnS-rpl20</i>	171	0.389
<i>trnF-rbcL</i>	125	0.363
<i>psbJ-petB</i>	143	0.344
<i>rps18-trnE</i>	188	0.348
<i>trnK-psaC</i>	99	0.291
<i>trnS-psbK</i>	105	0.291
<i>atpH-atpF</i>	175	0.284
<i>trnM-trnG</i>	367	0.244
<i>tufa-trnC</i>	327	0.224
<i>trnL-atpI</i>	111	0.272
<i>rps14-trnQ</i>	70	0.257
<i>psaM-trnP</i>	137	0.202
<i>atpF-atpA</i>	169	0.192
<i>psbH-psbN</i>	82	0.142
<i>trnV-psbB</i>	280	0.061
<b>Average</b>	<b>163.81</b>	<b>0.81</b>
<b>Standard deviation</b>	<b>84.87</b>	<b>0.87</b>