

**Table S2.** Sequence characteristics of the nine loci studied.

Gene	Subset	Length <sup>1</sup> (total / syn.)	GC %	N <sup>2</sup>	S <sup>3</sup>	Number of mutations <sup>3</sup> (syn. / non-syn. / total)	$\theta_w$ (total/syn. sites)	$\pi$ (total/syn. sites)	Tajima's D <sup>4</sup>	Fu & Li D*
<i>adh1</i>	total	378 / 91	41.9	26	13	11 / 2 / 13				
	Waco			6	7	6 / 1 / 7	0.00809 / 0.02888	0.00686 / 0.02484	-0.88407	-0.99519
	Hatton			7	6	5 / 1 / 6	0.00646 / 0.02244	0.00628 / 0.02302	-0.14112	-0.07313
	crassa			13	2	2 / 0 / 2	0.00170 / 0.0071	0.00284 / 0.01186	1.88482	0.95275
<i>adh2</i>	total	348 / 85	37.9	37	18	16 / 2 / 18				
	Waco			10	11	9 / 2 / 11	0.01117 / 0.03758	0.01328 / 0.0428	0.84513	0.44989
	Hatton			16	13	11 / 2 / 13	0.01126 / 0.03916	0.01092 / 0.04066	-0.11591	0.06329
	crassa			11	11	9 / 2 / 11	0.01079 / 0.03629	0.01526 / 0.05068	1.77992	<b>1.46041*</b>
<i>adh3</i>	total	399 / 96	40.8	17	9	8 / 1 / 9				
	Waco			2	2	2 / 0 / 2	0.00501 / 0.02094	0.00501 / 0.02094	N/A	N/A
	Hatton			4	0	0 / 0 / 0	0 / 0	0 / 0	N/A	N/A
	crassa			11	8	7 / 1 / 8	0.00685 / 0.02498	0.00674 / 0.02623	-0.06124	0.00208
<i>lal8</i>	total	135 / 29	35.5	34	21	4 / 17 / 21				
	Waco			14	6	2 / 4 / 6	0.01429 / 0.02149	0.01190 / 0.01391	-0.59987	0.02019
	Hatton			12	10	2 / 8 / 10	0.02509 / 0.02271	0.01882 / 0.02221	-1.02689	-1.34389
	crassa			8	12	2 / 10 / 12	0.03214 / 0.02641	0.04031 / 0.02813	0.75375	0.37278
<i>MS</i>	total	315 / 70	47.1	43	13	9 / 4 / 13				
	Waco			16	5	3 / 2 / 5	0.00478 / 0.01286	0.00540 / 0.01374	0.42248	1.21439
	Hatton			18	4	4 / 0 / 4	0.00369 / 0.01660	0.00365 / 0.01638	-0.03254	1.12320
	crassa			9	5	3 / 2 / 5	0.00584 / 0.01567	0.00776 / 0.01892	1.39246	0.68670
<i>MtN21a</i>	total	192 / 48	44.2	51	10	4 / 6 / 10				
	Waco			13	7	2 / 5 / 7	0.01175 / 0.01357	0.00868 / 0.00645	-0.99041	-1.40193
	Hatton			18	4	1 / 3 / 4	0.00606 / 0.00607	0.00875 / 0.00231	1.33286	0.21103
	crassa			20	3	1 / 2 / 3	0.00440 / 0.00585	0.00688 / 0.00699	1.50169	1.00649
<i>MtN21b</i>	total	198 / 49	42.1	28	17	7 / 10 / 17				
	Waco			5	8	2 / 6 / 8	0.01969 / 0.01965	0.02256 / 0.02046	1.02753	1.02753
	Hatton			10	7	2 / 5 / 7	0.01269 / 0.01462	0.01630 / 0.02070	1.20402	0.87945
	crassa			13	11	6 / 5 / 11	0.01818 / 0.03976	0.02078 / 0.04533	0.57766	0.31659
<i>PRK</i>	total	324 / 71	41.9	51	13	12 / 1 / 13				
	Waco			13	8	7 / 1 / 8	0.00796 / 0.03178	0.00847 / 0.03470	0.24882	0.88217
	Hatton			18	7	7 / 0 / 7	0.00538 / 0.02866	0.00968 / 0.04419	1.83765	1.30779
	crassa			20	5	5 / 0 / 5	0.00435 / 0.01990	0.00362 / 0.01657	-0.51165	0.38667
<i>lal2</i>	total	626 / 127	41.7	148	432	55 / 25 / 69 (for 180 sites <sup>5</sup> )				
	Waco	626 / 130		62	355	68 / 46 / 114 (for 297 sites <sup>5</sup> )	0.12812 / n.a.	0.14062 / 0.16634	-1.16019	-0.00179
	Hatton	626 / 128		50	348	53 / 62 / 115 (for 300 sites <sup>5</sup> )	0.13258 / n.a.	0.13352 / 0.15249	-1.31858	-0.10672
	crassa	626 / 129		36	307	71 / 72 / 143 (for 375 sites <sup>5</sup> )	0.12527 / n.a.	0.13552 / 0.17705	-0.88434	0.25828

<sup>1</sup> Exon sequence length of complete codons

<sup>2</sup> Number of alleles sampled

<sup>3</sup> Segregating sites excluding sites with gaps / missing data

<sup>4</sup> Calculated on the whole coding region

<sup>5</sup> Sites with gaps or with complex codons were not analysed

\*  $p < 0.05$