

Table S3. Statistics specific to the neutral loci used in the IMfor2 analyses.

Gene	Comparison	S	S1	S2	Ss	Sf	Fst	MinDist ¹	K _s ²	Recombination ³
<i>adh1</i>	crassa vs 19	7	2	4	1	0	0.431759	0.011236	0.03136	Yes
	crassa vs waco	7	2	4	1	0	0.482819	0.011236	0.03464	Yes
	crassa vs ala	10	2	7	1	0	0.391892	0.011236	0.03287	Yes
	19 vs waco	8	3	3	2	0	0.251327	0.011236	0.03209	Yes
<i>adh2</i>	crassa vs 19	14	4	5	5	0	0.152594	0	0.05593	Yes
	crassa vs waco	13	4	4	5	0	0.164641	0	0.05814	Yes
	crassa vs ala	15	4	6	5	0	0.158369	0	0.05678	Yes
	19 vs waco	11	2	1	8	0	-0.00553578	0	0.04269	Yes
<i>adh3</i>	crassa vs 19	7	5	0	2	0	0.372727	0.0104167	0.0212	Yes
	crassa vs waco	8	5	0	3	0	0.144828	0.0104167	0.02808	Yes
	crassa vs ala	8	5	0	3	0	0.282192	0.0104167	0.02349	Yes
	19 vs waco	2	0	0	2	0	0	0	0.01053	No
<i>lal8</i>	crassa vs 19	4	2	2	0	0	0.464384	0	0.04866	No
	crassa vs waco	3	1	1	1	0	0.252508	0	0.02863	No
	crassa vs ala	4	1	2	1	0	0.318622	0	0.0378	No
	19 vs waco	3	1	1	1	0	0.316299	0	0.02696	No
<i>MS</i>	crassa vs 19	7	3	4	0	0	0.366176	0	0.0274	No
	crassa vs waco	6	3	3	0	0	0.403774	0	0.02714	No
	crassa vs ala	9	3	6	0	0	0.382542	0	0.02729	No
	19 vs waco	6	3	2	1	0	0.0102368	0	0.0154	No
<i>MtN21a</i>	crassa vs 19	3	1	1	0	1	0.821612	0.0208333	0.0266	No
	crassa vs waco	3	1	2	0	0	0.731444	0	0.02548	No
	crassa vs ala	4	1	3	0	0	0.784789	0	0.02618	No
	19 vs waco	3	1	1	1	0	-2.61E-17	0	0.0044	No
<i>MtN21b</i>	crassa vs 19	5	2	0	3	0	0.38293	0.0208333	0.05271	Yes
	crassa vs waco	6	3	1	2	0	0.435654	0.0208333	0.05709	Yes
	crassa vs ala	6	2	1	3	0	0.399489	0.0208333	0.05417	Yes
	19 vs waco	4	1	1	2	0	-0.0281924	0	0.02132	Yes
<i>PRK</i>	crassa vs 19	10	3	4	2	1	0.561002	0.0285714	0.06711	No
	crassa vs waco	10	2	4	3	1	0.620419	0.056338	0.07078	Yes
	crassa vs ala	10	2	4	3	1	0.599179	0.0285714	0.06862	Yes
	19 vs waco	6	0	1	5	0	0.0175288	0	0.04158	No
Average ⁴	crassa vs 19	57	22	20	13	2	0.444148	0.0114863	0.04137125	n/a
	crassa vs waco	56	21	19	15	1	0.404511	0.012353	0.0412475	n/a
	crassa vs ala	66	20	29	16	1	0.414634	0.00888217	0.0409	n/a
	19 vs waco	43	11	10	22	0	0.070208	0.00140449	0.02437125	n/a

Notes: statistics calculated on synonymous sites

¹ Minimum pairwise sequence divergence between the two groups.² Average number of nucleotide substitutions per site between populations with Jukes and Cantor correction.³ According to the Hudson and Kaplan test.⁴ The S statistics represent the sum of all loci and not the average.