

TABLE 3. Total pairwise sequence differences and evolutionary distances among fungal sequences examined

Expt and species	Pairwise sequence difference (lightface type) or evolutionary distance (boldface type), avg no. of changes per nucleotide × 100													
	<i>C. albicans</i>	<i>C. viswanathii</i>	<i>C. tropicalis</i>	<i>C. parapsi-</i> <i>losis</i>	<i>C. guillier-</i> <i>mondii</i>	<i>C. lusitaniae</i>	<i>C. krusei</i>	<i>H. poly-</i> <i>morpha</i>	<i>T. glabrata</i>	<i>S. cere-</i> <i>visiae</i>	<i>C. kefyr</i>	<i>K. marxianus</i> var. <i>lactis</i>	<i>Y. lipo-</i> <i>lytica</i>	<i>A. fumi-</i> <i>gatus</i>
Expt 1 ^a														
<i>C. albicans</i>		4	4	6	14	49	86	46	38	55	47	47	117	107
<i>C. viswanathii</i>	0.32		2	2	14	50	82	44	37	52	46	47	117	109
<i>C. tropicalis</i>	0.32	0.16		2	12	50	82	43	36	52	44	46	117	110
<i>C. parapsilosis</i>	0.49	0.24	0.16		12	49	83	43	36	52	44	46	116	109
<i>C. guilliermondii</i>	1.10	1.02	0.93	0.93		48	84	38	36	48	38	42	111	104
<i>C. lusitaniae</i>	3.96	4.05	3.97	3.96	3.75		97	70	63	77	65	68	131	112
<i>C. krusei</i>	6.86	6.51	6.61	6.59	6.55	7.86		71	79	90	80	81	158	146
<i>H. polymorpha</i>	3.61	3.45	3.36	3.36	2.98	5.68	5.52		36	47	42	42	119	113
<i>T. glabrata</i>	3.09	3.01	2.93	2.92	2.80	5.05	6.11	2.81		17	18	21	122	110
<i>S. cerevisiae</i>	4.23	4.15	4.07	4.06	3.75	6.13	7.12	3.69	1.34		27	28	132	121
<i>C. kefyr</i>	3.78	3.70	3.61	3.61	3.06	5.32	6.40	3.33	1.39	2.01		2	123	111
<i>K. marxianus</i> var. <i>lactis</i>	3.85	3.77	3.69	3.68	3.38	5.57	6.55	3.40	1.55	2.17	0.24		124	111
<i>Y. lipolytica</i>	9.86	9.78	9.79	9.77	9.35	11.02	13.66	9.96	10.20	11.07	10.32	10.57		156
<i>A. fumigatus</i>	8.96	9.05	9.15	9.14	8.63	9.34	12.29	9.51	9.10	9.96	99.21	9.28	13.37	
Expt 2 ^b														
<i>C. albicans</i>		11	11	16										
<i>C. viswanathii</i>	0.60		8	11										
<i>C. tropicalis</i>	0.70	0.41		13										
<i>C. parapsilosis</i>	0.95	0.67	0.76											
<i>T. glabrata</i>										41	55	58		
<i>S. cerevisiae</i>											55	59		
<i>C. kefyr</i>										3.31	3.18	5		
<i>K. marxianus</i> var. <i>lactis</i>										3.51	3.37	0.31		

^a Values were obtained using about 1240 unambiguous positions, constrained by the inclusion of the evolutionarily divergent *Y. lipolytica* sequence.^b Values obtained using approximately 1600 positions among the organisms listed.