

Table S1.1 Estimates of sequence divergence between genera in *Saccharomycetaceae*.

	No. of species included	Intragenomic nucleotide changes ^a		Intergeneric nucleotide changes ^b												
		No. of base differences	No. of base differences per site	<i>Kaz.</i>	<i>Nak.</i>	<i>Ere.</i>	<i>Han.</i>	<i>Zyg.</i>	<i>Z'tor.</i>	<i>Sac.</i>	<i>Tet.</i>	<i>Lac.</i>	<i>Tor.</i>	<i>Nau.</i>	<i>Klu.</i>	<i>Van.</i>
<i>Kazachstania</i>	19	29.44	0.064		47.46	55.93	50.20	40.95	50.58	27.80	66.98	39.21	30.27	28.21	47.83	34.00
<i>Nakaseomyces</i>	4	44.33	0.108	0.09		60.50	60.46	42.79	45.25	42.07	69.45	45.60	41.40	40.88	53.58	47.75
<i>Eremothecium</i>	5	17.80	0.042	0.11	0.12		59.54	52.93	62.00	49.26	76.00	39.72	46.48	44.20	47.53	47.50
<i>Hanseniaspora</i>	7	30.76	0.076	0.10	0.12	0.12		52.83	63.14	48.71	78.20	45.71	39.29	42.29	54.69	40.86
<i>Zygosaccharomyces</i>	6	21.07	0.056	0.08	0.08	0.10	0.10		46.17	34.83	68.67	35.83	35.30	32.75	47.19	37.25
<i>Zygorulaspota</i>	2	20.00	0.045	0.10	0.09	0.12	0.12	0.09		46.50	76.10	45.00	44.90	40.25	52.42	50.25
<i>Saccharomyces</i>	7	12.10	0.029	0.05	0.08	0.10	0.09	0.07	0.09		63.69	34.74	21.97	23.43	42.60	23.07
<i>Tetrapispora</i>	5	48.30	0.108	0.13	0.13	0.15	0.15	0.13	0.15	0.12		68.04	62.76	61.30	71.77	69.20
<i>Lachancea</i>	5	16.50	0.033	0.08	0.09	0.08	0.09	0.07	0.09	0.07	0.13		28.36	27.10	37.33	27.50
<i>Torulaspota</i>	5	5.20	0.013	0.06	0.08	0.09	0.08	0.07	0.09	0.04	0.12	0.06		16.90	32.00	20.60
<i>Naumovozyma</i>	2	7.00	0.021	0.05	0.08	0.09	0.08	0.06	0.08	0.05	0.12	0.05	0.03		35.75	24.75
<i>Kluyveromyces</i>	6	9.20	0.022	0.09	0.10	0.09	0.11	0.09	0.10	0.08	0.14	0.07	0.06	0.07		45.08
<i>Vanderwaltozyma</i>	2	12.00	0.023	0.07	0.09	0.09	0.08	0.07	0.10	0.04	0.13	0.05	0.04	0.05	0.09	

Data were calculated based on Kurtzman [15].

^a Number of base differences per sequence averaging overall sequence pairs within each group.

^b Upper right, Number of base differences per sequence averaging overall sequence pairs between groups; Lower left, The p-distance averaging overall sequence pairs between groups.

All positions containing gaps and missing data were eliminated.

There were a total of 515 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [24].

Table S1.2 Estimates of sequence divergence between genera *Derxomyces*, *Dioszegia*, *Filobasidiella* and *Hannaella* .

	No. of species included	Intragenomic nucleotide changes ^a		Intergeneric nucleotide changes ^b			
		No. of base differences	No. of base differences per site	<i>Der.</i>	<i>Dio.</i>	<i>Fil.</i>	<i>Han.</i>
<i>Derxomyces</i>	11	13.58	0.024		49.60	75.59	46.05
<i>Dioszegia</i>	13	15.05	0.026	0.09		90.23	56.76
<i>Filobasidiella</i>	4	18.83	0.033	0.12	0.16		68.96
<i>Hannaella</i>	7	28.57	0.050	0.08	0.10	0.12	

Data were calculated based on Fig 100.8C of "The Yeasts, A Taxonomic Study" 5th ed. [17].

^a Number of base differences per sequence averaging overall sequence pairs within each group.

^b Upper right, Number of base differences per sequence averaging overall sequence pairs between groups; Lower left, The p-distance averaging overall sequence pairs between groups.

All positions containing gaps and missing data were eliminated. There were a total of 583 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [24].

Table S1.3 Estimates of sequence divergence between yeast groups in the Microbotryomycetes of the Pucciniomycotina.

	No. of species included	Intra-group nucleotide changes ^a			Inter-group nucleotide changes ^b											
		No. of base differences	No. of base differences per site	<i>yam. / L. ant.</i>	Leucosporidiales	Microbotryales	<i>van.</i>	<i>Cur.</i>	<i>Col.</i>	<i>hyl.</i>	<i>H. pyc.</i>	<i>jav.</i>	<i>Rho.</i>	mixed <i>Rho. / Spo.</i>	<i>Spo.</i>	<i>son.</i>
<i>yamatoana / Leucosporidium antarcticum</i>	21	32.28	0.060		38.71	48.13	34.43	45.43	47.11	56.62	55.76	58.90	60.93	61.01	63.02	86.76
Leucosporidiales	8	10.71	0.020	0.07		33.02	21.63	41.00	55.79	65.38	64.00	69.00	59.68	52.79	71.45	91.75
Microbotryales	12	21.03	0.039	0.09	0.06		37.38	49.71	58.24	67.92	65.33	76.33	60.19	52.95	72.24	86.58
<i>vanillica</i>	2	5.00	0.009	0.06	0.04	0.07		31.25	51.75	60.00	58.50	58.50	56.58	52.39	66.32	87.50
<i>Curvibasidium</i>	4	11.50	0.021	0.08	0.08	0.09	0.06		55.75	63.25	67.75	65.75	62.50	58.97	68.93	85.25
<i>Colacogloea</i>	6	30.93	0.057	0.09	0.10	0.11	0.09	0.10		61.67	64.33	62.50	66.69	70.61	74.32	92.17
<i>Rhodotorula hylophila</i>	1	n/c		0.11	0.13	0.14	0.12	0.13	0.12		58.00	61.00	66.69	70.89	68.12	88.00
<i>Heterogastridium pycnidioideum</i>	1	n/c		0.11	0.12	0.12	0.11	0.13	0.12	0.12		68.00	81.38	84.00	79.76	101.00
<i>Rhodotorula javanica</i>	1	n/c		0.11	0.13	0.14	0.11	0.12	0.12	0.12	0.13		71.31	77.78	79.94	102.00
<i>Rhodospordium</i>	13	24.74	0.047	0.12	0.11	0.11	0.11	0.12	0.13	0.13	0.15	0.13		40.78	66.71	90.15
mixed <i>Rhodospordium / Sporidiobolus</i>	9	19.86	0.038	0.12	0.10	0.10	0.10	0.11	0.13	0.14	0.16	0.15	0.08		57.56	83.78
<i>Sporidiobolus</i>	17	20.75	0.039	0.12	0.14	0.14	0.13	0.13	0.14	0.14	0.15	0.15	0.13	0.11		83.53
<i>Rhodotorula sonckii</i>	1	n/c		0.16	0.17	0.16	0.16	0.16	0.17	0.18	0.19	0.19	0.17	0.16	0.16	

Data were calculated based on Fig 100.7C of "The Yeasts, A Taxonomic Study" 5th ed. [17].

^a Number of base differences per sequence averaging overall sequence pairs within each group.

^b Upper right, Number of base differences per sequence averaging overall sequence pairs between groups; Lower left, The p-distance averaging overall sequence pairs between groups.

All positions containing gaps and missing data were eliminated. There were a total of 569 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [24].

The presence of n/c in the results denotes cases in which it was not possible to estimate evolutionary distances.