

Table 3 Major reference genomes of the methylotroph and basal lineages

Species	Strain	Genome size (Mb) ^a	No. of chromosomes ^b	Total no. of CDS ^c	Reference or source
Methylotrophs					
Phaffomycetaceae					
<i>Komagataella phaffii</i>	CBS 7435	9.4	4	5325	Küberl <i>et al.</i> (2011)
<i>Candida sorboxylosa</i>	JCM1536	(10.7)	(37)	4724	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma unpublished data ^d
Pichiaceae and related Saccharomycetales incertae sedis					
<i>Dekkera bruxellensis</i>	CBS 2499	13.4	—	5208	Piškur <i>et al.</i> , (2012)
<i>Dekkera anomala</i>	YV396	(12.9)	(30)	5241	Y. Vervoort, B. Herrera-Malaver, S. Mertens, V. Guadalupe Medina, J. Duitama, L. Michiels, G. Derdelinckx, K. Voordeckers and K. J. Verstrepen unpublished data ^e
<i>Dekkera naardensis</i>	CBS7540	(11.3)	(76)	—	H. Jiang, unpublished data ^f
<i>Nakazawaea peltata</i>	JCM9829	(11.7)	(11)	5620	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma unpublished data ^d
<i>Pichia membranifaciens</i>	NRRL Y-2248 ^T	(11.6)	(11)	5546	Riley <i>et al.</i> (2016)
<i>Kuraishia capsulata</i>	CBS 1993 ^T	11.4	7	6029	Morales <i>et al.</i> (2013)
<i>Ogataea polymorpha</i>	NCYC495 leu1.1	(9.0)	7	5177	Riley <i>et al.</i> (2016)
<i>Ogataea parapolyomorpha</i>	DL-1	9.1	7	5325	Ravin <i>et al.</i> (2013)
<i>Ogataea methanolica</i>	JCM10240	(15.1)	(32)	6063	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma unpublished data ^d
<i>Candida boidinii</i>	JCM9604	(19.4)	(32)	6053	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma, unpublished data ^d
<i>Ambrosiozyma kashinagacola</i>	JCM15019	(12.3)	(23)	5787	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma, unpublished data ^d
<i>Candida succiphila</i>	JCM9445	(12.1)	(22)	5455	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma, unpublished data ^d
<i>Candida arabinofementans</i>	NRRL YB-2248 ^T	(13.2)	(62)	5861	Riley <i>et al.</i> (2016)
<i>Pachysolen tannophilus</i>	CBS 4044	(12.2)	(34)	5546	Liu <i>et al.</i> (2012)
Basal lineages					
Dipodascaceae, Trichomonascaceae, and related Saccharomycetales incertae sedis					
<i>Geotrichum candidum</i>	CLIB918	24.2	(134) ^g	6804	Morel <i>et al.</i> (2015)
<i>Yarrowia lipolytica</i>	CLIB122 (E150)	20.6	6	6582	Dujon <i>et al.</i> (2004)
<i>Yarrowia keelungensis</i>	JCM14894	(21.8)	(41)	6618	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma unpublished data ^d
<i>Yarrowia deformans</i>	JCM1694	(20.9)	(44)	6704	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma unpublished data ^d
<i>Starmerella bombicola</i>	JCM9596	(9.6)	(16)	4887	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma unpublished data ^d
<i>Starmerella (Candida) apicola</i>	NRRL Y-50540	(9.8)	(40)	3818 ^h	Vega-Alvarado <i>et al.</i> (2015)
<i>Sporopachydermia quercuum</i>	JCM9486	(16.4)	(15)	5992	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma unpublished data ^d
<i>Blastobotrys adenivorans</i>	LS3	11.8	4	6150	Kunze <i>et al.</i> (2014)
<i>Blastobotrys attinorum</i>	NRRL Y27639	(14.0)	(14)	6184	J. K. Magnuson unpublished data ⁱ
<i>Trichomonascus petasosporus</i>	NRRL YB2093	(14.5)	(79)	6567	J. K. Magnuson unpublished data ⁱ
<i>Sugiyamaella lignohabitans</i>	CBS 10342	16.0	4	6820	Bellasio <i>et al.</i> (2016)
<i>Sugiyamaella americana</i>	NRRL YB2067	(16.5)	(48)	6288	J. K. Magnuson unpublished data ⁱ
<i>Wickerhamiella domercqiae</i>	JCM9478	8.5	4	4928	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma unpublished data ^d

(continued)

Table 3, continued

Species	Strain	Genome size (Mb) ^a	No. of chromosomes ^b	Total no. of CDS ^c	Reference or source
<i>Zygoascus hellenicus</i>	Y7136	(12.2)	(11)	5430	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma unpublished data ^d
<i>Candida infanticola</i>	DS02	(8.1)	(22)	—	H. Lee, C. Han, G. Park, W. Jeon, H. Lee and J. Ahn. unpublished data ⁱ
<i>Nadsonia fulvescens</i> var. <i>elongata</i>	DSM6958	(13.7)	(20)	5657	Riley <i>et al.</i> (2016)
<i>Tortispora caseinolytica</i>	NRRL Y-17796 ^T	9.2	6	4657	Riley <i>et al.</i> (2016)
Early branching^k					
Ascoideaceae					
<i>Ascoidea rubescens</i>	NRRL Y-17699 ^T	(17.5)	(63)	6802	Riley <i>et al.</i> (2016)
<i>Ascoidea asiatica</i>	JCM7603	(20.3)	(71)	7694	R. Manabe, R. Endoh, S. Uzuhashi, G. Okada, M. Takashima and M. Ohkuma unpublished data ^d
Lipomycetaceae					
<i>Lipomyces starkeyi</i>	NRRL Y-11557	(21.3)	(117) ^g	8192	Riley <i>et al.</i> (2016)

The table lists the yeast species of indicated families under the same conditions as specified in Table 1. Strain numbers correspond to the reference indicated. Species in which several isolates have been sequenced in complete form or permanent drafts are indicated by bold type, and only one isolate is listed (the first one or the best one).

^a Genome sizes are indicated in bold type when determined from complete sequences and in brackets when deduced from scaffolds in assemblies (figures are haploid equivalent in case of known diploid strains). Sizes ignore rDNA, mtDNA, and plasmids.

^b Numbers of chromosomes are indicated in bold type when known. Figures in brackets correspond to numbers of scaffolds in assemblies.

^c Total numbers of predicted protein-coding genes (CDS) are taken from original publications or subsequent annotations, as most appropriate. Data not found indicated by —.

^d Unpublished data taken from the National BioResource Project (www.jcm.riken.jp/cgi-bin/nbrp/nbrp_list.cgi).

^e Unpublished data taken from GenBank: LCTY00000000.1.

^f Unpublished data taken from GenBank: MDSA00000000.1.

^g *G. candidum* and *L. starkeyi* are listed here despite their large number of scaffolds because each genome represents the only reference available, so far, in its respective lineage.

^h Automated prediction based on comparisons to the CTG clade.

ⁱ Unpublished data taken from <http://genome.jgi.doe.gov> (nonpublic).

^j Unpublished data taken from GenBank: LWLF00000000.1.

^k These are listed here for convenience and are the few sequenced yeast species not included in the four major subgroups of Saccharomycotina defined in this review. See Shen *et al.* (2016) for a recent genome-based phylogenetic reconstruction. The Lipomycetaceae family is basal to all Saccharomycotina.