

Table 13 List of new species found in this study.

Strain	GenBank Accession No.	Nearest Species with Accession No. of DNA DataBank	Nucleotide Identity (%)	No. of Nucleotide Different (No. of Gap)	Remark
Ascomycetous yeast					
ST-370	DQ404513	<i>Candida ambrosiae</i> AY013716	530/559 (94.8)	29 (1)	<i>C. ambrosiae</i> ≠ <i>C. tanzawaensis</i> (Eight nucleotides are different between 2 species)
		<i>Candida tanzawaensis</i> U44811	530/559 (94.8)	29 (1)	
ST-249	DQ404488	<i>Candida asparagi</i> AY450920	453/532 (85.2)	79 (22)	-
ST-19	DQ400365	<i>Candida azya</i> U62312	549/553 (99.3)	4	-
ST-239	DQ404486	<i>Candida berthetii</i> U62298	567/574 (98.9)	7 (4)	-
ST-29	DQ400367	<i>Candida</i> cf.. <i>etchellsii</i> AY257048	451/482 (93.6)	31 (1)	-
ST-449	DQ404525	<i>Candida</i> cf.. <i>glabrata</i> UWO(PS)98-110.4 AF313362	581/594 (97.8)	13 (1)	-
ST-33	AY845350	<i>Candida coipomoensis</i> U45747	553/562 (98.4)	9	-
ST-22	AY228492	<i>Candida etchellsii</i> UWO(PS)00-226.2 AF313353	472/501 (94.2)	29 (1)	-
ST-60	DQ400376	<i>Candida fermentati</i> AY187283	553/557 (99.3)	4 (1)	-
ST-253	DQ404490	<i>Candida fermentati</i> AY187283	552/556 (99.3)	4 (4)	-
ST-377	DQ404514	<i>Candida floricola</i> U45710	481/486 (98%)	5 (3)	-
ST-390	DQ404518	<i>Candida floricola</i> U45710	481/485 (99.2)	4 (2)	-
ST-331	DQ404502	<i>Candida friedrichii</i> U45781	534/548 (97.4)	14 (1)	-
ST-43	DQ400371	<i>Candida friedrichii</i> U45781	504/547 (92.1)	43 (12)	-

Table 13 (Continued)

Strain	GenBank Accession No.	Nearest Species with Accession No. of DNA DataBank	Nucleotide Identity (%)	No. of Nucleotide Different (No. of Gap)	Remark
ST-300	DQ404493	<i>Candida friedrichii</i> U45781	541/547 (98.9)	6	} ST-300 = ST-365 = ST-366
ST-365	DQ404511	<i>Candida friedrichii</i> U45781	542/548 (98.9)	6	
ST-366	DQ404512	<i>Candida friedrichii</i> U45781	541/547 (98.9)	6	
ST-328	DQ404499	<i>Candida friedrichii</i> U45781	539/547 (98.5)	8	} ST-328 = ST-329 = ST-333
ST-329	DQ404500	<i>Candida friedrichii</i> U45781	539/547 (98.5)	8	
ST-333	DQ404503	<i>Candida friedrichii</i> U45781	539/547 (98.5)	8	
ST-451	DQ404526	<i>Candida musae</i> U44814	496/534 (92.9)	38 (11)	-
ST-238	DQ404485	<i>Candida insectalens</i> U62304	331/338 (97.9)	7 (1)	-
ST-211	DQ404478	<i>Candida intermedia</i> AJ508588	451/516 (80.4)	65 (8)	-
ST-246	DQ404487	<i>Candida llanquihuensis</i> U70190	534/554 (96.4)	20	-
ST-164	DQ404469	<i>Candida membranifaciens</i> U45792	529/542 (97.6)	13	-
ST-79	DQ400380	<i>Candida mokoensis</i> AY559042	570/574 (99.3)	4	-
ST-337	DQ404506	<i>Candida musae</i> U44814	453/532 (85.2)	79 (22)	-
ST-380	DQ404515	<i>Candida natalensis</i> U45818	563/567 (99.3)	4 (1)	-
ST-95	DQ404454	<i>Candida palmarum</i> AY197725	414/488 (84.8)	74 (9)	-
ST-18	DQ400364	<i>Candida parapsilosis</i> U45754	531/571 (93.0)	40 (3)	-
ST-234	DQ404482	<i>Candida pseudointermedia</i> AF533069	514/518 (99.2)	4 (1)	-
ST-387	DQ404516	<i>Candida rancensis</i> AJ508580	481/510 (94.3)	29 (1)	-

Table 13 (Continued)

Strain	GenBank Accession No.	Nearest Species with Accession No. of DNA DataBank	Nucleotide Identity (%)	No. of Nucleotide Different (No. of Gap)	Remark
ST-330	DQ404501	<i>Candida savonica</i> U62307	451/478 (94.4)	27	-
ST-224	DQ404479	<i>Candida silvanorum</i> U71068	439/522 (84.1)	83 (11)	-
ST-490	DQ404529	<i>Candida sorbosivorans</i> AY008842	489/502 (97.4)	13	-
ST-533	DQ404531	<i>Candida sorbosivorans</i> AY008842	451/462 (97.6)	11	} ST-533 = ST-536
ST-536	DQ404532	<i>Candida sorbosivorans</i> AY008842	436/447 (97.5)	11	
ST-78	DQ400379	<i>Candida tammaniensis</i> AF017243	519/543 (95.6)	21 (3)	-
ST-358	DQ404510	<i>Candida trypodendroni</i> AF017240	525/532 (98.7)	7 (1)	-
ST-388	DQ404517	<i>Candida tammaniensis</i> AF017243	476/515 (92.4)	39 (4)	-
ST-17	AY228491	<i>Candida tsuchiyae</i> U49064	448/514 (87.2)	66 (13)	-
ST-49	DQ400372	<i>Candida tsuchiyae</i> U49064	400/515 (77.7)	105 (8)	-
ST-50	DQ400373	<i>Candida tsuchiyae</i> U49064	403/513 (78.6)	110 (22)	-
ST-431	DQ404522	<i>Candida bolitotheri</i> AY309867	534/556 (96.0)	22 (1)	-
ST-297	DQ404492	<i>Candida</i> sp. BG99-8-18-1-6 AY242348	502/567 (88.5)	65 (9)	-
ST-315	DQ404498	<i>Candida</i> sp. BG99-8-18-1-6 AY242348	517/552 (93.7)	35 (3)	-
ST-32	DQ400369	<i>Candida</i> sp. NRRL Y-17678 AF017237	553/562 (98.4)	11 (3)	-
ST-309	DQ404495	<i>Debaryomyces vanrijiae</i> var. <i>yarrowii</i> U45843	566/570 (99.3)	4	} ST-309 = ST-310
ST-310	DQ404496	<i>Debaryomyces vanrijiae</i> var. <i>yarrowii</i> U45843	566/570 (99.3)	4	
ST-338	DQ404507	<i>Dipodascus ovetensis</i> U40116	399/405 (98.5)	6	-

Table 13 (Continued)

Strain	GenBank Accession No.	Nearest Species with Accession No. of DNA DataBank	Nucleotide Identity (%)	No. of Nucleotide Different (No. of Gap)	Remark
ST-2	DQ400361	<i>Endomyces scopularum</i> AF267231	448/495 (90.5)	47 (1)	-
ST-36	DQ400370	<i>Galactomyces geotrichum</i> U40118	537/548 (98.0)	11 (2)	-
ST-391	DQ404519	<i>Hanseniaspora meyeri</i> AJ 512461	545/569 (94.1)	24 (2)	-
ST-493	DQ404530	<i>Hanseniaspora meyeri</i> AJ 512461	553/577 (96.0)	24 (3)	-
ST-464	DQ404527	<i>Hanseniaspora meyeri</i> AJ 512461	552/572 (96.8)	19	} ST-464 = ST-613
ST-613	DQ414467	<i>Hanseniaspora meyeri</i> AJ 512461	479/498 (96.2)	19 (1)	
ST-476	DQ404528	<i>Hanseniaspora clermontiae</i> AJ512456	568/578 (98.3)	10 (2)	-
ST-250	DQ404489	<i>Hanseniaspora meyeri</i> AJ 512461	552/571 (96.7)	19	ST-250 may be same ST-306
ST-306	DQ404494	<i>Hanseniaspora meyeri</i> AJ 512461	560/569 (98.4)	19 (1)	(One nucleotide is different between 2 species)
ST-314	DQ404497	<i>Issatchenkia</i> sp. NRRL Y-12824 AF017398	513/559 (91.8)	46 (4)	-
ST-343	DQ404509	<i>Kluyveromyces</i> sp. IFO 1884 AB041001	496/516 (96.1)	20 (3)	-
ST-233	DQ404481	<i>Metschnikowia agaveae</i> U84243	520/549 (94.7)	29 (3)	-
ST-57	DQ400374	<i>Metschnikowia drosophilae</i> AF279303	503/537 (93.7)	34 (5)	-
ST-96	DQ404455	<i>Metschnikowia lunata</i> U45733	431/454 (94.9)	23	-
ST-237	DQ404484	<i>Pichia acaciae</i> U45767	563/569 (98.9)	6	-
ST-37	AY634567	<i>Pichia americana</i> U73575	563/569 (98.9)	6	-
ST-236	DQ404483	<i>Pichia anomala</i> AF330115	567/573 (99.0)	4	-

Table 13 (Continued)

Strain	GenBank Accession No.	Nearest Species with Accession No. of DNA DataBank	Nucleotide Identity (%)	No. of Nucleotide Different (No. of Gap)	Remark
ST-84	DQ404448	<i>Candida</i> sp. BG02-7-15-015A-2-1 AY520326	512/521 (86.2)	8	-
ST-240	AB191049	<i>Pichia dryadoides</i> U75422	464/570 (81.4)	106 (13)	-
ST-335	DQ404505	<i>Pichia mexicana</i> U45797	522/531 (98.3)	9 (1)	-
ST-433	DQ404523	<i>Pichia mississippiensis</i> U74597	522/531 (98.3)	9	-
ST-311	AY634568	<i>Pichia fabianii</i> AF335971	561/570 (98.4)	9	} ST-311 = ST-320 <i>P. fabianii</i> = <i>P. veronae</i>
		<i>Pichia veronae</i> U73576	561/570 (98.4)	9	
ST-320	AY634569	<i>Pichia fabianii</i> AF335971	561/570 (98.4)	9	
		<i>Pichia veronae</i> U73576	561/570 (98.4)	9	
ST-225	AY634570	<i>Pichia japonica</i> U73579	564/570 (98.9)	6	} ST-225 = ST-228 = ST-229
ST-228	AY634571	<i>Pichia japonica</i> U73579	564/570 (98.9)	6	
ST-229	AY634572	<i>Pichia japonica</i> U73579	564/570 (98.9)	6	
ST-3	DQ400362	<i>Pichia pijperi</i> U75418	561/568 (98.8)	7	} ST-3 = ST-4
ST-4	DQ400363	<i>Pichia pijperi</i> U75418	561/568 (98.8)	7	
ST-30	DQ400368	<i>Pichia pijperi</i> U75418	561/568 (98.8)	7 (1)	-
ST-334	DQ404504	<i>Pichia pijperi</i> U75418	562/568 (98.9)	6	-
ST-445	DQ404524	<i>Pichia pijperi</i> U75418	542/551 (98.4)	9	-
ST-339	DQ404500	<i>Pichia</i> sp. UWO(PS)85-301.3 AF530614	547/558 (98.0)	11	-
ST-422	DQ404521	<i>Saccharomyces cerevisiae</i> AY048154	588/595 (98.8)	7 (5)	-

Table 13 (Continued)

Strain	GenBank Accession No.	Nearest Species with Accession No. of DNA DataBank	Nucleotide Identity (%)	No. of Nucleotide Different (No. of Gap)	Remark
ST-394	DQ404520	<i>Saccharomyces servazzii</i> AF406921	575/591 (97.3)	16 (1)	-
ST-269	DQ404491	<i>Schizoblastosporion chiloense</i> U84347	269/347 (77.5)	78 (40)	-
ST-26	DQ400366	<i>Trichosporonoides spathulata</i> AF335526	289/309 (93.5)	30	-
ST-122	DQ404462	<i>Wickerhamia fluorescens</i> U45719	454/545 (83.3)	91 (26)	-
Basidiomycetous yeast					
ST-144	DQ404464	<i>Bullera pseudovariabilis</i> AF544247	567/610 (92.9)	43 (11)	-
ST-186	DQ404472	<i>Bullera</i> sp. TY-145 AY312997	529/586 (90.3)	57 (1)	-
ST-201	DQ404475	<i>Cryptococcus luteolus</i> AF075482	581/588 (98.8)	7 (1)	-
ST-111	DQ404459	<i>Cryptococcus luteolus</i> AF075482	600/606 (99.0)	6	-
ST-71	DQ400377	<i>Cryptococcus</i> sp. CBS 8507 AF444742	592/600 (98.7)	8	-
ST-73	DQ400378	<i>Cryptococcus</i> sp. CBS 8363 AF444699	582/597 (97.5)	15	-
ST-145	DQ404465	<i>Cryptotrichosporon anacardii</i> AY550003	503/515 (97.7)	12	-
ST-98	DQ404456	<i>Sporidiobolus pararoseus</i> AF189978	582/586 (99.3)	4	} ST-98 = ST-115 = ST-128 = ST-195 = ST-206
ST-115	DQ404460	<i>Sporidiobolus pararoseus</i> AF189978	528/532 (99.2)	4	
ST-128	DQ404463	<i>Sporidiobolus pararoseus</i> AF189978	582/586 (99.3)	4	
ST-195	DQ404473	<i>Sporidiobolus pararoseus</i> AF189978	573/577 (99.3)	4	
ST-206	DQ404477	<i>Sporidiobolus pararoseus</i> AF189978	582/586 (99.3)	4	
ST-87	DQ404449	<i>Sporidiobolus pararoseus</i> AF189978	538/544 (98.9)	6 (1)	-

Table 13 (Continued)

Strain	GenBank Accession No.	Nearest Species with Accession No. of DNA DataBank	Nucleotide Identity (%)	No. of Nucleotide Different (No. of Gap)	Remark
ST-91	DQ404452	<i>Sporidiobolus pararoseus</i> AF189978	558/563 (99.1)	5	-
ST-92	DQ404453	<i>Sporidiobolus pararoseus</i> AF189978	574/580 (98.9)	6	-
ST-102	DQ404457	<i>Sporidiobolus pararoseus</i> AF189978	579/586 (98.8)	4	-
ST-88	DQ404450	<i>Sporidiobolus ruineniae</i> var. <i>ruenie</i> AF070438	572/588 (97.3)	16	} Two nucleotide is different between 2 strains
ST-90	DQ404451	<i>Sporidiobolus ruineniae</i> var. <i>ruenie</i> AF070438	559/575 (97.2)	16	
ST-202	DQ404476	<i>Sporobolomyces bannaensis</i> AY274823	538/560 (96.1)	28 (17)	-
ST-119	DQ404461	<i>Sporobolomyces carnicolor</i> AY070008	549/555 (98.9)	9 (1)	-
ST-151	DQ404466	<i>Sporobolomyces japonicus</i> AY070009	559/564 (91.1)	5	-
ST-156	DQ404468	<i>Sporobolomyces japonicus</i> AY070009	566/572 (99.0)	6 (2)	-
ST-184	DQ404471	<i>Sporobolomyces odoratus</i> AF387125	558/566 (98.6)	8	-
ST-153	DQ404467	<i>Sporobolomyces</i> sp. TY-215 AY313049	555/592 (93.8)	37 (2)	-
ST-198	DQ404474	<i>Sporobolomyces odoratus</i> AF387125	546/552 (98.9)	6	-
ST-226	DQ404480	<i>Sporobolomyces odoratus</i> AF387125	514/518 (99.2)	4	-
ST-173	DQ404470	<i>Tilletiopsis albescens</i> AJ235289	519/584 (88.9)	65 (6)	-
ST-59	DQ400375	<i>Trichosporon faecale</i> AF105395	573/577 (99.3)	4 (2)	-
ST-318	AB164370	<i>Trichosporon loubieri</i> AY101608	710/731 (97.1)	21 (6)	-

Table 14 List of not yet identified species found in this study.

Strain	Nearest Species with Accession No. of DNA DataBank	Nucleotide Identity (%)	No. of Nucleotide Different (No. of Gap)	Remark
Ascomycetous yeast				
ST-446	<i>Candida albicans</i> AF156536	585/587 (99.7)	2	-
ST-108	<i>Candida dendronema</i> U45751	528/530 (99.6)	2 (1)	-
ST-385	<i>Candida floricola</i> U45710	481/484 (99.6)	3 (1)	-
ST-127	<i>Candida maltosa</i> U45745	570/571 (99.8)	2 (1)	-
ST-441	<i>Candida quercitrusa</i> U45831	563/565 (99.8)	2	-
ST-39	<i>Candida rancensis</i> AJ508580	507/510 (99.4)	3 (1)	-
ST-248	<i>Candida</i> sp. BG00-7-5-1-2-1 AY242247	557/560 (99.5)	3	-
ST-116	<i>Debaryomyces</i> sp. NRRL Y-7804 U45771	553/556 (99.1)	3	-
ST-235	<i>Pichia acaciae</i> U45767	562/564 (99.6)	2	-
ST-38	<i>Pichia stipitis</i> U45741	566/568 (99.8)	2	-
ST-14	<i>Torulaspora</i> sp. IFO 11061 AB087395	571/574 (99.5)	3 (1)	-
Basidiomycetous yeast				
ST-172	<i>Bullera sinensis</i> AF189884	571/574 (99.5)	3	ST-172 # ST-181 (Three nucleotide is different between 2 strains)
	<i>Bullera derxii</i> AF189857	571/574 (99.5)	3	
ST-181	<i>Bullera sinensis</i> AF189884	557/560 (99.5)	3	
	<i>Bullera derxii</i> AF189857	557/560 (99.5)	3	
ST-52	<i>Cryptococcus heveanensis</i> AFO75467	605/608 (99.5)	3 (1)	-

Table 14 (Continued)

Strain	Nearest Species with Accession No. of DNA DataBank	Nucleotide Identity (%)	No. of Nucleotide Different (No. of Gap)	Remark
ST-323	<i>Cryptococcus humicola</i> AF189836	603/606 (99.5)	3 (1)	-
ST-213	<i>Exobasidium vexans</i> AJ235288	576/578 (99.6)	2 (2)	-
ST-170	<i>Sporobolomyces japonicus</i> AY070009	583/586 (99.5)	3	} ST-170 = ST-175 = ST-178 = ST-183
ST-175	<i>Sporobolomyces japonicus</i> AY070009	569/572 (99.5)	3	
ST-178	<i>Sporobolomyces japonicus</i> AY070009	583/586 (99.5)	3	
ST-183	<i>Sporobolomyces japonicus</i> AY070009	536/539 (99.4)	3	
ST-94	<i>Sporobolomyces odoratus</i> AF387125	488/490 (99.6)	2 (1)	-
ST-100	<i>Sporobolomyces odoratus</i> AF387125	540/543 (99.4)	3	} ST 100 ≠ ST-123 (4) ST-100 ≠ ST-192 (3) ST-123 ≠ ST-192 (7/4)
ST-123	<i>Sporobolomyces odoratus</i> AF387125	568/571 (99.5)	3	
ST-192	<i>Sporobolomyces odoratus</i> AF387125	552/555 (99.5)	3	
ST-159	<i>Sporobolomyces</i> sp. TY-257 AY313054	571/574 (99.5)	3	-
ST-197	<i>Tilletiopsis</i> sp. TY-363 AY313023	593/595 (99.7)	2	-
ST-121	<i>Trichosporon multisporum</i> AF139984	593/595 (99.7)	2	-
ST-299	<i>Trichosporon mycotoxinivorans</i> AJ601388	600/602 (99.7)	2 (2)	-

Table 15 Nucleotides difference from nearest species of 283 strains of Thai yeast.

No. of Nucleotide Difference	No. of Strains	No. of Species (No. of Genera)	No. of Strains/No. of Species
0-1	139 (49%)	56 (26)	2.3
2-3	28 (10%)	21 (10)	1.3
≥4	116 (41%)	101 (21)	1.1
Nucleotides difference of 116 strains that differed from nearest species by 4 or more nucleotides showed as below.			
4-6 (0.7-1%)	35 (30%)	26	1.3
7-12 (>1-2%)	28 (24%)	25	1.1
13-24 (>2-4%)	19 (17%)	15	1.3
25-60 (>4-10%)	20 (17%)	19	1
61-110 (>10-18%)	14 (12%)	14	1