

Supplementary Figure 1.

Molecular identification of the isolated strains. Sequences from the D1/D2 domains of the LSU rRNA genes were used in the Megablast program for highly similar sequences in the BLAST suite of National Center for Biotechnology Information (blast.ncbi.nlm.nih.gov) against *Metschnikowia* (taxid:27320) database. Best 10 hits are shown, and alignment to reference strains is included. Due to problems in the D1/D2 amplification, strain P1 was identified using ITS1-5.8S-ITS2 segments of the rDNA repeats against the type species fungal database.

M7 strain

D1/D2 domain sequence, partial. GenBank PP175919

>M7

GCGGCAAAAGCTCAAATTTGAAATCCCCCGGAATTGTAATTTGAAGAGATTTGGGTCCGGCCGGCAG
GGGTAAAGTCCACTGGAAAGTGGCGCCACAGAGGGTGACAGCCCCGTGAACCCCTTCAAAGCCTTCAT
CCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCATCTAAAGCT
AAATACCGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGCACTTTGAAAAGA
GAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAGCAGACACTTAACTGGGCCAGCA
TCGGGGCGGCGGGGAGCAAAACACCGGGGAATGTACCTTTCGAGGATTATAACCCCGGCCCTTACTC
CCATACTGCCCCGAGGCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCGTCTTGAAACA
CGGACC

Megablast alignment against *Metschnikowia* (taxid:27320), first 10 hits

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Metschnikowia pulcherrima isolate 3Y138B large subunit ribosomal RNA gene, partial sequence	Metschnikowia pulcherrima	880	880	100%	0.0	99.59%	786	MT225539.1
✓	Metschnikowia pulcherrima isolate 3Y138A large subunit ribosomal RNA gene, partial sequence	Metschnikowia pulcherrima	880	880	100%	0.0	99.59%	779	MT225531.1
✓	Metschnikowia pulcherrima strain FB002 26S ribosomal RNA gene, partial sequence	Metschnikowia pulcherrima	880	880	100%	0.0	99.59%	507	EF139135.1
✓	Metschnikowia pulcherrima strain CEC RCF-0-39 26S ribosomal RNA gene, partial sequence	Metschnikowia pulcherrima	874	874	100%	0.0	99.38%	544	JX103182.1
✓	Metschnikowia pulcherrima strain D77_2 26S ribosomal RNA gene, partial sequence	Metschnikowia pulcherrima	874	874	100%	0.0	99.38%	492	HM627131.1
✓	Metschnikowia sp. (in Fungi) isolate 1631 large subunit ribosomal RNA gene, partial sequence	Metschnikowia sp. (in budding ye...	870	870	100%	0.0	99.17%	511	MW405494.1
✓	Metschnikowia pulcherrima isolate Soil1 large subunit ribosomal RNA gene, partial sequence	Metschnikowia pulcherrima	869	869	100%	0.0	99.17%	514	MG707676.1
✓	Metschnikowia pulcherrima culture CBS 2243 large subunit ribosomal RNA gene, partial sequence	Metschnikowia pulcherrima	869	869	100%	0.0	99.17%	833	KY108490.1
✓	Metschnikowia sp. (in Fungi) 28S ribosomal RNA gene, partial sequence	Metschnikowia sp. (in budding ye...	869	869	100%	0.0	99.17%	488	KU350434.1
✓	Metschnikowia pulcherrima isolate UTAD201 large subunit ribosomal RNA gene, partial sequence	Metschnikowia pulcherrima	869	869	100%	0.0	99.17%	514	OQ304846.1

Alignment to reference strain *Metschnikowia pulcherrima* culture CBS:5833 large subunit ribosomal RNA gene, partial sequence (ID: KY108497.1)

Score	Expect	Identities	Gaps	Strand
863 bits (467)	0.0	477/482 (99%)	0/482 (0%)	Plus/Plus
Query 1	GCGGCAAAAGCTCAAATTTGAAATCCCCCGGAATTGTAATTTGAAGAGATTTGGGTCCG	60		
Sbjct 134				
Query 61	GCCGGCAGGGGTTAAGTCCACTGGAAAGTGGCGCCACAGAGGGTGACAGCCCCGTGAACC	120		
Sbjct 194				
Query 121	CCTTCAAAGCCTTCATCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAG	180		
Sbjct 254				

Query 181 TGGGTGGTAAATTCATCTAAAGCTAAATACCGGCGAGAGACCGATAGCGAACAAGTACA 240
Sbjct 314 TGGGTGGTAAATTCATCTAAAGCTAAATACCGGCGAGAGACCGATAGCGAACAAGTACA 373
Query 241 GTGATGGAAAAGATGAAAAGCACCTTTGAAAAGAGAGTGAAAAGTACGTGAAATTGTTGAA 300
Sbjct 374 GTGATGGAAAAGATGAAAAGCACCTTTGAAAAGAGAGTGAAAAGTACGTGAAATTGTTGAA 433
Query 301 AGGGAAGGGCTTGCAAGCAGACACTTAACTGGGCCAGCATCGGGGCGGCGGGGAGCAAAA 360
Sbjct 434 AGGGAAGGGCTTGCAAGCAGACACTTAACTGGGCCAGCATCGGGGCGGCGGGGAGCAAAA 493
Query 361 CCACCGGGGAATGTACCTTTTCGAGGATTATAACCCCGGCCCTTACTCCCATACTGCCCCG 420
Sbjct 494 CCACCGGGGAATGTACCTTTTCGAGGATTATAACCCCGGCCCTTACTCCCATACCACCCCG 553
Query 421 AGGCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCGTCTTGAAACACGGA 480
Sbjct 554 AGGCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCGTCTTGAAACACGGA 613
Query 481 CC 482
Sbjct 614 CC 615

S₁6 strain

D1/D2 domain sequence, partial. GenBank PP175930

GCGAGTGAGCGGCAAAAGCTCAAATTTGAAATCCCCGGGAATTGTAATTTGAAGAGATTTGGGTCCG
GCCGGCGGGGGTTAAGTCCACTGGAAAGTGGCGCCACAGAGGGTGACAGCCCCGTGAACCCCTTTAA
CGCCCTCATCCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCA
TCTAAAGCTAAATACCGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGCACT
TTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAGCAGACACTTAACT
GGGCCAGCATCGGGGCGGCGGGAAACAAACCACCGGGGAATGTACCTTTCGAGGATTATAACCCCG
GTCTCAATTTCTTGTTGCCCGAGGCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCG
TCTTGAAACACGGA

Megablast alignment against Metschnikowia (taxid:27320), first 10 hits

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Metschnikowia fructicola strain UMY553 26S ribosomal RNA gene, partial sequence	Metschnikowia fructicola	896	896	100%	0.0	99.80%	513	KP171590.1
✓	Metschnikowia cf. pulcherrima isolate B14P-2 large subunit ribosomal RNA gene, partial sequence	Metschnikowia cf. pulcherrima	896	896	100%	0.0	99.80%	541	MT749253.1
✓	Metschnikowia aff. fructicola F-b-10 26S ribosomal RNA gene, partial sequence	Metschnikowia aff. fructicola F-b...	896	896	100%	0.0	99.80%	498	FJ842082.1
✓	Metschnikowia sinensis isolate 6-2L large subunit ribosomal RNA gene, partial sequence	Metschnikowia sinensis	891	891	100%	0.0	99.59%	1050	MN123984.1
✓	Metschnikowia pulcherrima isolate UTAD193 large subunit ribosomal RNA gene, partial sequence	Metschnikowia pulcherrima	891	891	100%	0.0	99.59%	518	OQ304841.1
✓	Metschnikowia pulcherrima isolate UTAD10 large subunit ribosomal RNA gene, partial sequence	Metschnikowia pulcherrima	891	891	100%	0.0	99.59%	518	OQ304691.1
✓	Metschnikowia sinensis strain PC-6-49.1 large subunit ribosomal RNA gene, partial sequence	Metschnikowia sinensis	891	891	100%	0.0	99.59%	502	MZ185366.1
✓	Metschnikowia fructicola strain PC-6-12.1 large subunit ribosomal RNA gene, partial sequence	Metschnikowia fructicola	891	891	100%	0.0	99.59%	503	MZ185360.1
✓	Metschnikowia fructicola strain YzA 26S ribosomal RNA gene, partial sequence	Metschnikowia fructicola	891	891	100%	0.0	99.59%	512	HM191666.1
✓	Metschnikowia sinensis isolate 3L2 large subunit ribosomal RNA gene, partial sequence	Metschnikowia sinensis	889	889	100%	0.0	99.59%	970	MN069593.1

Alignment to reference strain *Metschnikowia fructicola* 277 (unitig_213, whole genome shotgun sequence. Sequence ID: [ANFW02000056.1](#)).

Score Expect Identities Gaps Strand
891 bits (482) 0.0 487/489 (99%) 1/489 (0%) Plus/Minus
Query 1 GCGAGTG-AGCGGCAAAAGCTCAAATTTGAAATCCCCGGGAATTGTAATTTGAAGAGAT 59

Alignment to reference strain *Metschnikowia pulcherrima* culture CBS:5833 large subunit ribosomal RNA gene, partial sequence (ID: KY108497.1).

Score	Expect	Identities	Gaps	Strand
839 bits (454)	0.0	467/473 (99%)	1/473 (0%)	Plus/Plus
Query 1	GCGGCAAAAGCTCAAATTTGAAATCCCCCGGAATTGTAATTTGAAGAGATTGGGTCCG	60		
Sbjct 134	GCGGCAAAAGCTCAAATTTGAAATCCCCCGGAATTGTAATTTGAAGAGATTGGGTCCG	193		
Query 61	GCCGGCAGGGGTTAAGTCCACTGGAAAGTGGCGCCACAGAGGGTGACAGCCCCGTGAACC	120		
Sbjct 194	GCCGGCAGGGGTTAAGTCCACTGGAAAGTGGCGCCACAGAGGGTGACAGCCCCGTGAACC	253		
Query 121	CCCTCAACGCCCTCATCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCTCT-AG	179		
Sbjct 254	CCTTTAAAGCCCTCATCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAG	313		
Query 180	TGGGTGGTAAATTCCATCTAAAGCTAAATACCGCGAGAGACCGATAGCGAACAAGTACA	239		
Sbjct 314	TGGGTGGTAAATTCCATCTAAAGCTAAATACCGCGAGAGACCGATAGCGAACAAGTACA	373		
Query 240	GTGATGGAAAGATGAAAAGCACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAA	299		
Sbjct 374	GTGATGGAAAGATGAAAAGCACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAA	433		
Query 300	AGGGAAGGGCTTGCAAGCAGACACTTAACTGGGCCAGCATCGGGGCGGCGGGAGCAAAA	359		
Sbjct 434	AGGGAAGGGCTTGCAAGCAGACACTTAACTGGGCCAGCATCGGGGCGGCGGGAGCAAAA	493		
Query 360	CCACCGGGGAATGTACCTTTCGAGGATTATAACCCCGGCCCTTACTCCCATACCGCCCCG	419		
Sbjct 494	CCACCGGGGAATGTACCTTTCGAGGATTATAACCCCGGCCCTTACTCCCATACCGCCCCG	553		
Query 420	AGGCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCCGTCTTGAA	472		
Sbjct 554	AGGCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCCGTCTTGAA	606		

Z4 strain

D1/D2 domain sequence, partial. GenBank PP176174

ATGCCTCAGTAACGGCGAGTGAGCGGCAAAAGCTCAAATTTGAAATCCCCCGGAATTGTAATTTGAA
GAGATTTGGGTCCGGCCGGCAGGGGTTAAGTCCACTGGAAAGTGGCGCCACAGAGGGTGACAGCCCC
GTGAACCCCTTTAACGCCCTCATCCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTG
GGTGGTAAATTCCATCTAAAGCTAAATACCGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAA
GATGAAAAGCACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAG
CAGACACTTAACTGGGCCAGCATCGGGGCGGCGGAAACAAACCACCGGGGAATGTACCTTTCGAG
GATTATAACCCCGGCCCTTACTCCCTTGCCACCCCGAGGCCTGCAATCTAAGGATGCTGGCGTAATGGT
TGCAAGTCGCCCCGTCTTGAAACACGGACC

Megablast alignment against Metschnikowia (taxid:27320), first 10 hits

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Metschnikowia pulcherrima isolate YQY_A20_26S large subunit ribosomal RNA gene, partial sequence	Metschnikowia p...	902	902	100%	0.0	99.01%	512	OP643941.1
✓	Metschnikowia pulcherrima strain M53 26S ribosomal RNA gene, partial sequence	Metschnikowia p...	902	902	99%	0.0	99.01%	513	GU080051.1
✓	Metschnikowia pulcherrima isolate UTAD182 large subunit ribosomal RNA gene, partial sequence	Metschnikowia p...	900	900	100%	0.0	98.82%	518	QQ304834.1
✓	Metschnikowia pulcherrima strain M320 26S ribosomal RNA gene, partial sequence	Metschnikowia p...	896	896	99%	0.0	98.81%	513	GU478324.1
✓	Metschnikowia pulcherrima isolate CABM7C large subunit ribosomal RNA gene, partial sequence	Metschnikowia p...	891	891	98%	0.0	99.00%	664	MF783068.1
✓	Metschnikowia pulcherrima culture CBS 5833 large subunit ribosomal RNA gene, partial sequence	Metschnikowia p...	891	891	99%	0.0	98.61%	693	KY108497.1
✓	Metschnikowia aff. pulcherrima P01A016 small subunit ribosomal RNA gene, partial sequence, internal transcribe...	Metschnikowia af...	891	891	99%	0.0	98.61%	1203	JX188181.1
✓	Metschnikowia pulcherrima strain NRRL Y-7111 small subunit ribosomal RNA gene, partial sequence, internal tran...	Metschnikowia p...	891	891	99%	0.0	98.61%	1179	JX188179.1
✓	Metschnikowia pulcherrima strain XJ-73 large subunit ribosomal RNA gene, partial sequence	Metschnikowia p...	889	889	99%	0.0	98.61%	513	MN371967.1
✓	Metschnikowia sp. (in budding yeasts) 26S ribosomal RNA gene, partial sequence	Metschnikowia s...	889	889	98%	0.0	98.99%	537	KT922942.1

Alignment to reference strain *Metschnikowia pulcherrima* culture CBS:5833 large subunit ribosomal RNA gene, partial sequence (ID: KY108497.1).

Score	Expect	Identities	Gaps	Strand
891 bits (482)	0.0	497/504 (99%)	1/504 (0%)	Plus/Plus
Query 2	TGCCTCAGTAACGGCGAGTG-AGCGGCAAAAGCTCAAATTTGAAATCCCCCGGGAATTGT	60		
Sbjct 112	TGCCTCAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCCCCCGGGAATTGT	171		
Query 61	AATTTGAAGAGATTTGGGTCCGGCCGGCAGGGTTAAGTCCACTGGAAAGTGGCGCCACA	120		
Sbjct 172	AATTTGAAGAGATTTGGGTCCGGCCGGCGGGGTTAAGTCCACTGGAAAGTGGCGCCACA	231		
Query 121	GAGGGTGACAGCCCCGTGAACCCCTTTAAGCCCTCATCCAGATCTCCAAGAGTCGAGT	180		
Sbjct 232	GAGGGTGACAGCCCCGTGAACCCCTTTAAGCCCTCATCCAGATCTCCAAGAGTCGAGT	291		
Query 181	TGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCATCTAAAGCTAAATACCGGCGAG	240		
Sbjct 292	TGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCATCTAAAGCTAAATACCGGCGAG	351		
Query 241	AGACCGATAGCGAACAAGTACAGTGATGGAAGATGAAAAGCACTTTGAAAAGAGAGTGA	300		
Sbjct 352	AGACCGATAGCGAACAAGTACAGTGATGGAAGATGAAAAGCACTTTGAAAAGAGAGTGA	411		
Query 301	AAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAGCAGACACTTAACTGGGCCAGC	360		
Sbjct 412	AAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGCAAGCAGACACTTAACTGGGCCAGC	471		
Query 361	ATCGGGGCGGCGGAAACAAAACCACCGGGGAATGTACCTTTCGAGGATTATAACCCCGG	420		
Sbjct 472	ATCGGGGCGGCGGAGCAAAACCACCGGGGAATGTACCTTTCGAGGATTATAACCCCGG	531		
Query 421	CCCTTACTCCCTTGCCACCCCGAGGCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAA	480		
Sbjct 532	CCCTTACTCCCATACACCCCGAGGCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAA	591		
Query 481	GTCGCCCCGTCTTGAAACACGGACC	504		
Sbjct 592	GTCGCCCCGTCTTGAAACACGGACC	615		

P1 strain

ITS sequence. GenBank PP176176

TCCGTAGGTGAACCTGCGGAAGGATCATTAATATTGTTATTACACCCTTTTAGGCACAACTCTAAATCT
TTACCGTCAATAACTCAATCAAAAACTTTCAACAACGGATCTCTTGTTCTCGCATCGATGAAGAACGC
AGCGAATTGCGATACGTAATATGACTTGACAGACGTGAATCATTGAATCTTTGAACGCACATTGCGCCCC
GGGGTATTCCCCAGGGCATGCGTGGGTGAGCGATATTTACTCTCAAACCTCCGGTTTGGTCTGCTTCG
GCCTAATATCAACGGCGCTAGAATAAGTTTTAGCCCCATTCTTCTCCTCACCTCGTAAGACTACCCGC
TGAACCTAAGCATATCAATAAGCGGAGGA

Megablast alignment against fungal ITSs, type strains database (rRNA_typestrains/
ITS_RefSeq_Fungi).

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Metschnikowia pulcherrima NRRL Y-7111 ITS region: from TYPE material	Metschnikowia pulcherrima	658	658	100%	0.0	98.14%	434	NR_164379.1
✓	Metschnikowia ziziphicola CBS 10358 ITS region: from TYPE material	Metschnikowia ziziphicola	658	658	99%	0.0	98.40%	387	NR_166218.1
✓	Metschnikowia sinensis CBS 10357 ITS region: from TYPE material	Metschnikowia sinensis	580	580	99%	4e-166	94.67%	390	NR_155404.1
✓	Metschnikowia shanxiensis CBS 10359 ITS region: from TYPE material	Metschnikowia shanxiensis	580	580	99%	4e-166	94.67%	388	NR_155403.1
✓	Metschnikowia chrysoperlae ATCC MYA-4304 ITS region: from TYPE material	Metschnikowia chrysoperlae	566	566	100%	1e-161	93.68%	381	NR_111376.1
✓	Metschnikowia pimensis ATCC MYA-4306 ITS region: from TYPE material	Metschnikowia pimensis	560	560	100%	5e-160	93.42%	381	NR_111377.1
✓	Metschnikowia vanudenii CBS 9134 ITS region: from TYPE material	Metschnikowia vanudenii	438	438	100%	2e-123	87.76%	540	NR_155405.1
✓	Metschnikowia chrysomelidarum ATCC MYA-4344 ITS region: from TYPE material	Metschnikowia chrysomelidarum	436	436	100%	9e-123	87.56%	386	NR_111396.1
✓	Metschnikowia rancensis CBS 8174T ITS region: from TYPE material	Metschnikowia rancensis	431	431	100%	4e-121	87.43%	392	NR_155369.1
✓	Metschnikowia cibodasensis UICC Y-335 ITS region: from TYPE material	Metschnikowia cibodasensis	394	394	98%	5e-110	85.82%	389	NR_138172.1

Alignment to *Metschnikowia pulcherrima* NRRL Y-7111 ITS region; from TYPE material
(Sequence ID: NR_164379.1).

Score	Expect	Identities	Gaps	Strand
658 bits (356)	0.0	370/377 (98%)	0/377 (0%)	Plus/Plus
Query 1	TCCGTAGGTGAACCTGCGGAAGGATCATTAATATTGTTATTACACCCTTTTAGGCACAAA	60		
Sbjct 17	TCCGTAGGTGAACCTGCGGAAGGATCATTAATATTGTTTTTACACCCTTTTAGGCACAAA	76		
Query 61	CTCTAAATCTTTACCGTCAATAACTCAATCAAAAAACCTTCAACAACGGATCTCTTGGTT	120		
Sbjct 77	CTCTAAATCTTTAACCCTCAATAACACAATTAAAAACCTTCAACAACGGATCTCTTGGTT	136		
Query 121	CTCGCATCGATGAAGAACGCAGCGAATTGCGATACGTAATATGACTTGCAGACGTGAATC	180		
Sbjct 137	CTCGCATCGATGAAGAACGCAGCGAATTGCGATACGTAATATGACTTGCAGACGTGAATC	196		
Query 181	ATTGAATCTTTGAACGCACATTGCGCCCGGGGTATTCCCAGGGCATGCGTGGGTGAGC	240		
Sbjct 197	ATTGAATCTTTGAACGCACATTGCGCCCGGGGTATTCCCAGGGCATGCGTGGGTGAGC	256		
Query 241	GATATTTACTCTCAAACCTCCGGTTTGGTCCTGCTTCGGCCTAATATCAACGGCGCTAGA	300		
Sbjct 257	GATATTTACTCTCAAACCTCCGGTTTGGTCCTGCTTCGGCCTAATATCAACGGCGCTAGA	316		
Query 301	ATAAGTTTGTAGCCCCATTCTTCTTCCTCACCTCGTAAGACTACCCGCTGAACCTAAGCA	360		
Sbjct 317	ATAAGTTTGTAGCCCCATTCTTCTTCCTCACCTCGTAAGACAACCCGCTGAACCTAAGCA	376		
Query 361	TATCAATAAGCGGAGGA	377		
Sbjct 377	TATCATTAAGCGGAGGA	393		