

PŘÍLOHA A

Porovnání získaných sekvencí stanovovaných kmenů proti sekvenci kmene *Rhodotorula rubra*.

1.1 Tabulka srovnání kmenů

Tab. 1: Srovnání získaných sekvencí 5,8 ITS2 rDNA oblastí kmenů karotenoidních kvasinek ve srovnání se sekvencí kmene *Rhodotorula rubra*

Kmen	Skóre	Překryv	Hodnota E	Shodnost výběru
<i>Cystofylobasidium capitatum 10-1-1</i>	401	94%	1.00E-116	87%
<i>Cystofylobasidium capitatum 10-1-2</i>	263	90%	7.00E-75	79%
<i>Phaffia rhododyma</i>	300	55%	6.00E-86	92%
<i>Rhodotorula aurantiaca</i>	235	41%	2.00E-66	95%
<i>Rhodotorula glutinis</i>	366	95%	5.00E-106	86%
<i>Sacharomyces cerevisiae</i>	111	22%	4.00E-29	89%
<i>Sporobolomyces salmonicolor</i>	279	94%	7.00E-80	79%
<i>Sporobolomyces shibatanus</i>	270	88%	4.00E-77	79%
<i>Sporobolomyces roseus</i>	111	22%	4.00E-29	89%

1.2 Porovnání sekvencí 5,8-ITS2 oblastí rDNA

Cystofylobasidium capitatum 10-1-1

Query	8	TGTGATTGCAG-TTCAGTGATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTC	66
Sbjct	8	TGTGATTGCAGATTCAGTGATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTC	67
Query	67	CGTGGAGCATGCCTGTTTGARTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGATTG	126
Sbjct	68	CGTGGAGCATGCCTGTTTGAGTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGATTG	127
Query	127	AAKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTTTA--CGGTCTAKCTCCGTCGWAATGC	184
Sbjct	128	AAKASGWGKTTGGWTTTSYGAAYGCTGCTGGCCTTTAAACGATATAGA-CCGTA--AAGGG	184
Query	185	ATTARCATCCGAAACCRAACTTCTCATTGATCATTAAGAAAGAGGAGGGCTGAAKTATTC	244
Sbjct	185	ATTACGCTC-GAAACCRAACTTCTCATTGATCTTTARKAAAGAAGAAGGTTGAAGTATTC	243
Query	245	ATGACACTCTCACAGGCAAGCCCCGGGGAGTACCATGGAGCGCAWGGTGCWTCAWAKAT	304
Sbjct	244	ATGACASTCTMACAGGCAAGCTCCGCGGAGTACCAWGGARCGCWGGWCGTTCAWAGAT	303
Query	305	TCTATGAATCMTGAATTCTGCAAYTCGSATTACTTATCGCATTCTCKCTGCGTTCTTCAT	364
Sbjct	304	TCKATGATTCACTGAATTCTGMAATTTCGSATTACTTATCGCATTCTCSYTACGATCTTCAT	363

Cystofilobasidium capitatum 10-1-2

Query	8	TGTGATTGCAGTTCAGTGATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTATTCC	67
Sbjct	8	TGTGATTGCAGTTCAGTGATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTATTCC	67
Query	68	GTGGAGCATGCCTGTTTGARTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGATTGA	127
Sbjct	68	GTGGAGCMTGYCTGTTTGARTGKYATGAATACTTCMACCCTCCTCTTTCWTAATGATTGA	127
Query	128	AKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTTTACGGTCTAKCT---CCGTC--GWAAT	182
Sbjct	128	AKASGWGGTTSGATTGCGGAYGCTAATG-CATT-ACGAACGAGCTAGACCGTAMRGGCCG	185
Query	183	GCATTARCATCCGAAACCRAACTTCTCATTGATCATTAAGAAAGAGGAGGGCTGAAKTAT	242
Sbjct	186	GCAKCG-C-TCASAAACCAAACCTCTTCWATCATTAARAAAAAAGAGGGTTGAATGAT	243
Query	243	TCATGACACTCTCACAGGCAAGCCCCGGGGAGTACCATGGAGCGCAWGGTGCGWTCAWAK	302
Sbjct	244	TCATGACACTCWWACAGGCATGCTCCGCGGAAKACCAWGAACGCWAGGWGCCCTTAAAK	303
Query	303	ATTCTATGAATCAMPATGAATTCTGCAAYTCGSATTACTTATCGCATT	348
Sbjct	304	ATTCRATGKATCACTGAATTCTGMAATTCGGATTACTTATCGCATT	349

Phaffia rhododyma

Query	8	TGTGATTGCAGTTCAGTGATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTATTCC	67
Sbjct	8	TGTGATTGCARTTCAGTGATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTATTCC	67
Query	68	GTGGAGCATGCCTGTTTGARTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGATTGA	127
Sbjct	68	GTGGAGCATGCCTGTTTGAGTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGATTGA	127
Query	128	AKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTTTACGGTCTAKCTCCGTCGWAATGCATT	187
Sbjct	128	AGAGGTGTTTGGTTTSYGARCGTGCTGGCCTTTACGGTCTAKCTCGTTCGTAATGCATT	187
Query	188	ARCATCCGAAACCRAACTTCTCATTGA	214
Sbjct	188	ASCATCCGCAATCRAACTTCKGATTGA	214

Rhodotorula aurantiaca

Query	8	TGTGATTGCAG-TTCAGTGATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTATTCC	66
Sbjct	8	TGTGATTGCAGATTTCAGTGATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTATTCC	67
Query	67	CGTGGAGCATGCCTGTTTGARTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGATTG	126
Sbjct	68	CGTGGAGCATGCCTGTTTGARTGKCATGAATACTTCAACCCTCCTCTTCTTCTTAATGATTG	127
Query	127	AAKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTTTA	162
Sbjct	128	AAKAGGWGTTTGGWTTSCGAAYGCTGCTGGCCATTA	163

Rhodotorula glutinis

Query	8	TGTGATTGCAGTTCAGTG-ATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTC	66
Sbjct	8	TGTGATTGCAGTTCAGTGAATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTC	67
Query	67	CGTGGAGCATGCCTGTTTGARTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGATTG	126
Sbjct	68	CGTGGAGCATGCCTGTTTGAGTGTGTCATGAATACTTCAACCCTCCTCTTTTWTAAATGATTG	127
Query	127	AAKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTTTA-CGGTCTAKCTCCGTCGWAATG-C	184
Sbjct	128	AAKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTTTAACGAGCTAGA-CCG-CSRGGGGSC	185
Query	185	ATTARCATCCGAAACCRAACTTCTCATTGATCATTAAGAAAGAGGAGGGCTGAAKTATTC	244
Sbjct	186	AKCG-C-TC-GAAAACMAACTTCTCATCGATCTTTARSAAAGAAGARGGTTGAAGGAKTC	242
Query	245	ATGACACTCTCACAGGCAAGCCCCGGGGAGTACCATGGAGCGCAWGGTGCGWTCAWAKAT	304
Sbjct	243	ATGAYACTCTMAGAGGCATGCTCCGGGGAATAYCAWGGAGCGCAWGGWGCWTCWAGKAT	302
Query	305	TCTATGAATCMTGAATTCTGCAAYTCGSATTACTTATCGCATTCTCKCTGCGTTCTTCAT	364
Sbjct	303	TCTATGAATCACTGAATTCYMAAYTCGYATTACTTATCGCATTCTCKTAGCGWTCCTCAT	362
Query	365	A 365	
Sbjct	363	A 363	

Rhodotorula rubra

Query	8	TGTGATTGCAGTTCAGTGATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTCC	67
Sbjct	8	TGTGATTGCAGTTCAGTGATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTCC	67
Query	68	GTGGAGCATGCCTGTTTGARTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGATTGA	127
Sbjct	68	GTGGAGCATGCCTGTTTGARTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGATTGA	127
Query	128	AKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTTTACGGTCTAKCTCCGTCGWAATGCATT	187
Sbjct	128	AKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTTTACGGTCTAKCTCCGTCGWAATGCATT	187
Query	188	ARCATCCGAAACCRAACTTCTCATTGATCATTAAGAAAGAGGAGGGCTGAAKTATTCATG	247
Sbjct	188	ARCATCCGAAACCRAACTTCTCATTGATCATTAAGAAAGAGGAGGGCTGAAKTATTCATG	247
Query	248	ACACTCTCACAGGCAAGCCCCGGGGAGTACCATGGAGCGCAWGGTGCGWTCAWAKATTCT	307
Sbjct	248	ACACTCTCACAGGCAAGCCCCGGGGAGTACCATGGAGCGCAWGGTGCGWTCAWAKATTCT	307
Query	308	ATGAATCMTGAATTCTGCAAYTCGSATTACTTATCGCATTCTCKCTGCGTTCTTCATARR	367
Sbjct	308	ATGAATCMTGAATTCTGCAAYTCGSATTACTTATCGCATTCTCKCTGCGTTCTTCATARR	367
Query	368	TGCSAGAAA 376	
Sbjct	368	TGCSAGAAA 376	

Sacharomyces cerevisiae

Query	8	TGTGATTGCAGATTCCGTGATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTC	67
Sbjct	8	TGTGATTGCAG-TTCAGTGATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTC	66
Query	68	CAGGGGGCATGCCTGTTTGAGCGTCAT	94
Sbjct	67	CGTGGAGCATGCCTGTTTGARTGTCAT	93

Sporobolomyces salmonicolor

Query	8	TGTGATTGCAG-TTCAGTGATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTC	66
Sbjct	8	TGTGATTGCAGATTTCAGTGATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTC	67
Query	67	CGTGGAGCATGCCTGTTTGARTGTCATGAATACTTCAACCTCCTCTTTCTTAATGATTG	126
Sbjct	68	CGTGGAGCATGCCTGTTTGARTGKCATGAATACTTCMACCTCCTCTTTCWTAATGAKTG	127
Query	127	AAKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTT--TA-CGGTCTAKCTCCGTCGWAATG	183
Sbjct	128	AAKASGAGGTTGGATTGCGGAYGCTRTMG-CATTACTAACGAGCTAGA-CCGTAM-AGGC	184
Query	184	CATTARCA-TCCGAAACCRAACTTCTCATTGATCATTAAGAAAGAGGAGGGCTGAAKTAT	242
Sbjct	185	CGRMAWCGCTCASAACCAACACCTCTTCRATCTTTAAGAAAAGARGGTTGAAGGAK	244
Query	243	TCATGACACTCTCACAGGCAAGCCCCGGGGAG-TACCATGGAGCGCAWGGTGCGWTCAWA	301
Sbjct	245	TCATGAYACTCWTACAGGCATGCTCCGGGGTGGTAYCAWGAACGCAWGGWGCWTAATA	304
Query	302	KATTCTATGAATCMTGAATTCTGCAAYTCGSATTACTTATCGCATTTCKCTGCGTCTCTT	361
Sbjct	305	KATTCSATGAATCAYTGAATTCTGMAATTCGSATTACTTACCGCMTTACYTTGCGWCTCTT	364
Query	362	CA 363	
Sbjct	365	CA 366	

Sporobolomyces shibatanus

Query	8	TGTGATTGCAG-TTCAGTGATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTC	66
Sbjct	8	TGTGATTGCAGATTTCAGTGATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTC	67
Query	67	CGTGGAGCATGCCTGTTTGARTGTCATGAATACTTCAACCTCCTCTTTCTTAATGATTG	126
Sbjct	68	CSTGGASCMTGYCTGTTTGARTGKCATGAATACTTCAACCTCCTCTTTCWTACTGATTG	127
Query	127	AAKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTTTACGGTCTAKCTCCGTCGWAATG-C-	184
Sbjct	128	AAKACGAGGTTTCGATTGCGGATGCTARTG-CATT-ACGAACGAGCTAGACCGTAAAGGCC	185
Query	185	ATTARCA-TCCGAAACCRAACTTCTCATTGATCATTAAGAAAGAGGAGGGCTGAAKTATT	243
Sbjct	186	AGCAGCGCTCASAACCAACACCTCTTCAATCATTAAMAAAAAGAGGGTTGAAGTATT	245
Query	244	CATGACACTCTCACAGGCAAGCCCC-GGGGAGTACCATGGAGCGCAWGGTGCGWTCAWAK	302
Sbjct	246	CATGACACTCWWACAGGCATGCTCCRGGGGA-TACCATGGAACGCAASGWGCGTTCAAAG	304
Query	303	ATTCTATGAATCMTGAATTCTGCAAYTCGSATTACTTA	341
Sbjct	305	AMTCSATGATTCACTGAATTCTGCAATTCCGATTACTTA	343

Sporobolomyces roseus

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Query   8      TGTGATTGCAGATTCCGTGATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTC   67
          |||||
Sbjct   8      TGTGATTGCAG-TTCAGTGATCATCGAATCTTTGAACGCACCTTGCCTCCATGGTATTC   66

Query   68     CAGGGGGCATGCCTGTTTGAGCGTCAT      94
          |  || |||||
Sbjct   67     CGTGGAGCATGCCTGTTTGARTGTCAT      93
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PŘÍLOHA B

Porovnání získaných sekvencí stanovovaných kmenů proti sekvenci kmenu *Rhodotorula rubra*.

1.1 Tabulka srovnání kmenů

Tab. 2: Srovnání získaných sekvencí D1/D2 rDNA oblastí kmenů karotenoidních kvasinek ve srovnání se sekvencí kmene *Rhodotorula rubra*

Kmen	Skóre	Překryv	Hodnota E	Shodnost výběru
<i>Cystofylobasidium capitatum 10-1-1</i>	368	93%	5,00E-107	99%
<i>Cystofylobasidium capitatum 10-1-2</i>	375	93%	3,00E-109	99%
<i>Phaffia rhododyma</i>	342	96%	3,00E-99	94%
<i>Rhodotorula aurantiaca</i>	372	93%	4,00E-108	99%
<i>Rhodotorula glutinis</i>	383	97%	2,00E-111	99%
<i>Sacharomyces cerevisiae</i>	137	51%	1,00E-37	88%
<i>Sporobolomyces salmonicolor</i>	259	92%	3,00E-74	90%
<i>Sporobolomyces shibatanus</i>	387	97%	1,00E-112	99%
<i>Sporobolomyces rozeus</i>	355	93%	4,00E-103	97%

1.2 Porovnání sekvencí D1/D2 oblastí rDNA

Cystofilobasidium capitatum 10-1-1

Query	15	TGGGCGTCCGCACCATATACGGGGGTCTCACCACCTATGCCGCTGTATTCCAACAGACTTG	74
Sbjct	17	TGGGCGTCCGCACCATATACGGGGGTCTCACCACCTATGCCGCTGTATTCCAACAGACTTG	76
Query	75	TGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAGGTGCCAG	134
Sbjct	77	TGTGCRGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACMCCGAAGGTGCCAG	136
Query	135	ATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTT	194
Sbjct	137	ATTATAAATTTGAGCTCTTCCCGCTTCRCTCGCCGCTACTAGGGGAATCCTTGTTAGTTT	196
Query	195	CTTTTCCTCCGCTTATTGATATGGC	219
Sbjct	197	CTTTTCCTCCGCTTATTGATATGGC	221

Cystofilobasidium capitatum 10-1-2

Query	15	TGGGCGTCCGCACCATATACGGGGGTCTCACCCTATGCCGCTGTATTCCAACAGACTTG	74
Sbjct	13	TGGGCGTCCGCACCATATACGGGGGTCTCACCCTATGCCGCTGTATTCCAACAGACTTG	72
Query	75	TGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAGGTGCCAG	134
Sbjct	73	TGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACMCCGAAGGTGCCAG	132
Query	135	ATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTT	194
Sbjct	133	ATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTT	192
Query	195	CTTTTCCTCCGCTTATTGATATGGC	219
Sbjct	193	CTTTTCCTCCGCTTATTGATATGGC	217

Phaffia rhozodyma

Query	8	aaarCGMTGGGCGTCCGCACCATATACGGGGGTCTCACCCTATGCCGCTGTATTCCAAC	67
Sbjct	7	AAAGCGMTGGGCGTCCGCACCATATACGGGGGTCTCACCCTATGCCGCTGTATTCCAAC	66
Query	68	AGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAG	127
Sbjct	67	AGACTTGTGKGRGASCRRRCGCGGAAAACATTTCTWAGAGATTACAACCTCGGACMCCGAAR	126
Query	128	GTGCCAGATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTG	187
Sbjct	127	GWGCCAGATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAKGGGAATCCTTG	186
Query	188	TTAGTTTCTTTTCCTCCGCTTATTGATATGGC	219
Sbjct	187	TTAGTTTCTTTTCCTCCGCTTATTGATATGGC	218

Rhodotorula aurantiaca

Query	15	TGGGCGTCCGCACCATATACGGGGGTCTCACCCTATGCCGCTGTATTCCAACAGACTTG	74
Sbjct	15	TGGGCGTCCGCACCATATACGGGGGTCTCACCCTATGCCGCTGTATTCCAACAGACTTG	74
Query	75	TGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAGGTGCCAG	134
Sbjct	75	TGTGCRGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAGGTGCCAG	134
Query	135	ATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTT	194
Sbjct	135	ATTATAAATTTGAGCTCTTCCCGCTTCRCTCGCCGCTACTAGGGGAATCCTTGTTAGTTT	194
Query	195	CTTTTCCTCCGCTTATTGATATGGC	219
Sbjct	195	CTTTTCCTCCGCTTATTGATATGGC	219

Rhodotorula glutinis

Query	7	aaaarCGMTGGGCGTCCGCACCATATACGGGGGTCTCACC	ACTATGCCGCTGTATTCCAA	66
Sbjct	6	AAAAGCGMTGGGCGTCCGCACCATATACGGGGGTCTCACC	ACTATGCCGCTGTATTCCAA	65
Query	67	CAGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACA	ACTCGGACACCGAA	126
Sbjct	66	CAGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACA	ACTCGGACACCGAA	125
Query	127	GGTGCCAGATTATAAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTT		186
Sbjct	126	RGTGCCAGATTATAAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTT		185
Query	187	GTTAGTTTCTTTTCCTCCGCTTATTGATATGGC	219	
Sbjct	186	GTTAGTTTCTTTTCCTCCGCTTATTGATATGGC	218	

Sacharomyces cerevisiae

Query	107	ATTACAACCTCGGACACCGAAGGTGCCAGATTATAAAATTTGAGCTCTTCCCGCTTCGCTCG		166
Sbjct	103	ATTACAACCTCGGGCACCGAAGGTACCAGATTTCAAATTTGAGCTTTTGCCGCTTCACTCG		162
Query	167	CCGCTACTAGGGGAATCCTTGTTAGTTTCTTTTCCTCCGCTTATTGATATGGC	219	
Sbjct	163	CCGTTACTAAGCAATCCCGTTGGTTTCTTTTCCTCCGCTTATTGATATGGC	215	

Sporobolomyces salmonicolor

Query	7	aaaarCGMTGGGCGTCCGCACCATATACGGGGGTCTCACC	ACTATGCCGCTGTATTCCAA	66
Sbjct	5	AAAAGCGCTGGGCGTCCGCACCATATACGGGGGTCTCACC	ACTATGCCGCTGTATTCCAA	64
Query	67	CAGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACA	ACTCGGACACCGAA	126
Sbjct	65	CAGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACA	ACTCGGACACCGAA	124
Query	127	GGTGCCAGATTATAAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTT		186
Sbjct	125	GGTGCCAGATTATAAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTT		184
Query	187	GTTAGTTTCTTTTCCTCCGCTTATTGATATGGC	219	
Sbjct	185	GTTAGTTTCTTTTCCTCCGCTTATTGATATGGC	217	

Sporobolomyces shibatanus

Query	15	TGGGCGTCCGCACCATATACGGGGGTCTCACCCTATGCCGCTGTATTCCAACAGACTTG	74
Sbjct	15	TGGGCGTCCGCACCATATRCGGGGGTCTCACCCTATGCCGCTGTATTCCRACAGACTTG	74
Query	75	TGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAGGTGCCAG	134
Sbjct	75	TGKGCGGGCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAGGWGCCAG	134
Query	135	ATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTT	194
Sbjct	135	ATTATAAATTTGAGCTCTTCCCGCTTCRCTCGCCGCTACTAGGGGAATCCTTGTTAGTTT	194
Query	195	CTTTTCCTCCGCTTATTGATATGGC	219
Sbjct	195	CTTTTCCTCCGCTTATTGATATGGC	219

Sporobolomyces roseus

Query	17	GGCGTCCGCACCATATACGGGGGTCTCACCCTATGCCGCTGTATTCCAACAGACTTGTG	76
Sbjct	19	GGCATCCGCACCGTGTACTGGGTCTCACCCTGTGACGCTCCGTTCAGGAGACTTGTG	78
Query	77	TGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAGGTGCCAGAT	136
Sbjct	79	TGCGGTCTGACGCGGAAAACACTTCTCGAGATTACAACCTCGGACGCCGAAAGCGCCAGAT	138
Query	137	TATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTTCT	196
Sbjct	139	TACAAATTTGAGCTTTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTTCT	198
Query	197	TTTCCTCCGCTTATTGATATGGC	219
Sbjct	199	TTTCCTCCGCTTATTGATATGGC	221

PŘÍLOHA C

Identifikace sekvencí 5,8-ITS2 rDNA pomocí databáze NCBI.

Cystofilobasidium capitatum 10-1-1

Rhodotorula mucilaginosa isolate B-WHX-12-01 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Score	Expect	Identities	Gaps	Strand
233 bits(258)	6e-58	146/159(92%)	3/159(1%)	Plus/Plus

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Query 8 TGTGA-TTGCAGA-TTCAGTGA-TCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA 64
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 208 TGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA 267

Query 65 TTCCGTGGAGCATGCCTGTTTGAGTGTCATGAATACTTCAACCCTCCTCTTTYTTAATGA 124
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 268 TTCCGTGGAGCATGCCTGTTTGAGTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGA 327

Query 125 TTGAAKASGWGKTTGGWTTTSYGAAYGCTGCTGGCCTTTA 163
      ||||| || || ||||| || || || ||||| ||||| |||||
Sbjct 328 TTGAAGAGGTGTTTGGTTTCTGAGCGCTGCTGGCCTTTA 366
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Porovnání sekvence s kmenem *C.capitatum* (NCBI)

Cystofilobasidium capitatum genomic DNA containing ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, strain TSN-59

Score	Expect	Identities	Gaps	Strand
127 bits(140)	4e-32	105/120(88%)	9/120(7%)	Plus/Plus

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Query 8 TGTGA-TTGCAGA-TTCAGTGA-TCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA 64
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 57 TGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTGGTA 116

Query 65 TTCCGTGGAGCATGCCTGTTTGAGTGTCATGAATACT-TCAACCCTCC--TCTTTYTTAA 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 117 TTCCGAAGAGCATGCCTGTTTGAGTGTCATGAA-ACTCTCA--CCTCCAATCTTTTTTAA 173
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Cystofilobasidium capitatum 10-1-2

Rhodotorula mucilaginosa isolate B-WHX-12-01 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand	
		291 bits(322)	3e-75	196/231(85%)	0/231(0%)	Plus/Minus	
Query	135	GTTSGATTGCGGAYGCTAATGCATTACGAACGAGCTAGACCGTAMRGCCGGCAKCGCTC					194
Sbjct	408	GTTCGATTGCGGATGCTAATGCATTACGAACGAGCTAGACCGTAAAGGCCAGCAGCGCTC					349
Query	195	ASAAACCAAACACCTCTTCWATCATTAARAAAAAAGAGGGTTGAATGATTGATGACACTC					254
Sbjct	348	AGAAACCAAACACCTCTTCAATCATTAAAGAAAGAGGAGGGTTGAAGTATTGATGACACTC					289
Query	255	WWACAGGCATGCTCCGCGGAAKACCAWGGAAACGCWAGGWGCCTTAAAAKATTCRATGKAT					314
Sbjct	288	AAACAGGCATGCTCCACGGAATACCATGGAGCGCAAGGTGCGTTCAAAGATTCGATGATT					229
Query	315	CACTGAATTCTGMAATTCGGATTACTTATCGCATTACKCTAAGATCTTCAT					365
Sbjct	228	CACTGAATTCTGCAATTCACATTACTTATCGCATTTGCTGCGTTCTTCAT					178

Porovnání sekvence s kmenem *C.capitatum* (NCBI)

Cystofilobasidium capitatum genomic DNA containing ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, strain TSN-59

		Score 104 bits(114)	Expect 5e-25	Identities 79/93(85%)	Gaps 4/93(4%)	Strand Plus/Plus
Query	8	TGTGA-TTGCAG--TTCAGTGA-TCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA				63
Sbjct	57	TGTGAATTGCAGAATTTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTTTGGTA				116
Query	64	TTCCGTGGAGCMTGYCTGTTTGARTGKYATGAA			96	
Sbjct	117	TTCCGAAGAGCATGCCTGTTTGAGTGTCATGAA			149	

Phaffia rhozodyma

Rhodotorula mucilaginosa strain CBS 9070 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Score	Expect	Identities	Gaps	Strand
414 bits(458)	3e-112	259/284(91%)	4/284(1%)	Plus/Plus

Query	8	TGTGA-TTGCA--TTCAGTGA-TCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA	63
Sbjct	250	TGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA	309
Query	64	TTCCGTGGAGCATGCCTGTTTGTGAGTGTGATGAATACTTCAACCCTCCTCTTTCTTAATGA	123
Sbjct	310	TTCCGTGGAGCATGCCTGTTTGTGAGTGTGATGAATACTTCAACCCTCCTCTTTCTTAATGA	369
Query	124	TTGAAGAGGTGTTTGGTTTTSYGARCGCTGCTGGCCTTTACGGTCTAKCTCGTTCGTAATG	183
Sbjct	370	TTGAAGAGGTGTTTGGTTTCTGAGCGCTGCTGGCCTTTACGGTCTAGCTCGTTCGTAATG	429
Query	184	CATTASCATCCGCAATCRAACTTCKGATTGACTTGGCGTAATAAACTATTCSCTGAAGAA	243
Sbjct	430	CATTAGCATCCGCAATCGAATTCGATTGACTTGGCGTAATAGACTATTTCGCTGAGGAA	489
Query	244	TTGAMATCTTCRGATTAAAGCCCGGTTGGGTTWAARGGAGCGTC	287
Sbjct	490	TTCTAATCTTCGATTAGAGCCCGGTTGGGTTAAAGGAAGCTTC	533

Porovnání sekvence s kmenem *P. rhozodyma* (NCBI)

Phaffia rhodozyma strain zjut 00010 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Score	Expect	Identities	Gaps	Strand
129 bits(142)	1e-32	95/105(90%)	6/105(5%)	Plus/Plus

Query	8	TGTGA-TTGCA--TTCAGTGA-TCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA	63
Sbjct	216	TGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTTGGTA	275
Query	64	TTCCGTGGAGCATGCCTGTTTGTGAGTGTGATG-AATACT-TCAACC	106
Sbjct	276	TTCCGAGGAGCATGCCTGTTTGTGAGTGTGATGAACACTCTCAACC	320

Rhodotorula aurantiaca

Rhodotorula mucilaginosa strain TEMD29 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand
		230 bits(254)	8e-57	146/160(91%)	3/160(1%)	Plus/Plus
Query	8	TGTGA-TTGCAGA-TTCAGTGA-TCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA				64
Sbjct	201	TGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA				260
Query	65	TTCCGTGGAGCATGCCTGTTTGARTGKCATGAATACTTCAACCCTCCTCTTTYTTAATGA				124
Sbjct	261	TTCCGTGGAGCATGCCTGTTTGAGTGTCATGAATACTTCAACCCTCCTCTTCTTCTAATGA				320
Query	125	TTGAAKAGGWGTTTGWTTSCGAAYGCTGCTGGCCATTAA			164	
Sbjct	321	TTGAAGAGGTGTTTGTTTCTGAGCGCTGCTGGCCTTTAA			360	

Porovnání sekvence s kmenem *Rhodotorula aurantiaca* (NCBI)

Rhodotorula aurantiaca 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand		
		150 bits(166)	2e-39	256/356(72%)	31/356(8%)	Plus/Plus		
Query	18	ATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCCTCTCTGGTATTCCGGAGAGCAT						77
Sbjct	254	ATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCCTCTTTGGTATTCCGAAGAGTAT						313
Query	78	GTCTGTTTGAGTGTCTATGAATTCTTCAACCCAACTGTTTCTTGTAACAGCT-GGTGT--						134
Sbjct	314	GTCTGTTTGAGTGTCTATGAAACTCTCAACCC--CCTTATTTTGTAATGAGATAAGTGTGG						371
Query	135	--TTGATTCTGAGCGCTGCTGGCTTC-GTGCCTAGCTCGTTTCGTAATACATCAGCATCC						191
Sbjct	372	GCTTGGTTCATGTTGTTGAAGGCTTCACAGTCT-TCTCAACTGAAATACACGAGC-TAC						429
Query	192	CTA----ATACAAGTTTGGATTGACTTGGCGTAATAGACTA-TTCGCTAAGGATTCAATG						246
Sbjct	430	CTATTTTATAATAG-ACGGTTTGACTCGGCGTAATA-ATTATTTGCTGAGGACGTCCTT						487
Query	247	TTCGATTGAGCCAACTTAATTATGGAAGCTTCTAATTGAAAAGTCTACCTTTAGA-TTA						305
Sbjct	488	TTATAATAG-----TAA--ATGG-TGCTTCTAATTCAACA-TC-AATTTAAGATTTA						534
Query	306	GATCTCAAATCAGGCAGGATTACCCGCTGAACTTAAGCATATCAAAAACSGGAGRA						361
Sbjct	535	GACCTCAAATCAGTCAGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA						590

Rhodotorula glutinis

Rhodotorula mucilaginosa strain Sc13 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand	
		239 bits(264)	1e-59	146/159(92%)	3/159(1%)	Plus/Plus	
Query	8	TGTGA-TTGCAG--TTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA					64
Sbjct	249	TGTGAATTGCAGAATTTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA					308
Query	65	TTCCGTGGAGCATGCCTGTTTGAGTGTCATGAATACTTCAACCCTCCTCTTTYWTAATGA					124
Sbjct	309	TTCCGTGGAGCATGCCTGTTTGAGTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGA					368
Query	125	TTGAAKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTTTA			163		
Sbjct	369	TTGAAGAGGTGTTTGGTTTCTGAGCGCTGCTGGCCTTTA			407		

Porovnání sekvence s kmenem *R. glutinis*

Rhodotorula glutinis genomic DNA containing ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate 152b

		Score	Expect	Identities	Gaps	Strand	
		358 bits(396)	8e-101	295/352(84%)	8/352(2%)	Plus/Plus	
Query	18	ATTCAGTGAATCATCGAATCTTTGAACGCATCTTGCGCTCTCTGGTATTCCGGAGAGCAT					77
Sbjct	242	ATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTTGGTATTCCGAGGAGCAT					301
Query	78	GTCTGTTTGAGTGTCATGAATCTTCAACCCAACTGTTTCTT-GT-AAACAGCTGGTGTT					135
Sbjct	302	GCCTGTTTGAGTGTCATGAAATCTTCAACCCACCTCTTTCTTAGTGAATCTGGTGGTGCT					361
Query	136	TGGATTCTGAGCGCTGCT-GGCTTCGTGCCTAGCTCGTTTCGTAATACATCAGCATCCCTA					194
Sbjct	362	TGGTTTCTGAGCGCTGCTCTGCTTCG-GCTTAGCTCGTTTCGTAATGCATTAGCATCCGCA					420
Query	195	ATACAAGTTTGGATTGACTTGGCGTAATAGACTATTCGCTAAGGATTCAATGTTTCGCATT					254
Sbjct	421	ACCGAACTTCGGATTGACTTGGCGTAATAGACTATTCGCTGAGGATTCTA-GTTTAC-TA					478
Query	255	GAGCCAACTT--AATTATGGAAGCTTCTAATTGAAAAGTCTACCTTTAGATTAGATCTCA					312
Sbjct	479	GAGCCGAGTTGGGTAAAGGAAGCTCCTAATCCTAAAGTCTATTTTTGATTAGATCTCA					538
Query	313	AATCAGGCAGGATTACCCGCTGAACCTTAAGCATATCAAAAACSGGAGRAAAA					364
Sbjct	539	AATCAGGTAGGACTACCCGCTGAACCTTAAGCATATCAATAAGCGGAGGAAAA					590

Rhodotorula mucilaginosa

Rhodotorula mucilaginosa isolate B-WHX-12-01 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand	
		289 bits(320)	9e-75	188/211(89%)	4/211(1%)	Plus/Plus	
Query	8	TGTGA-TTGCAG--TTCAGTGA-TCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA					63
Sbjct	208	TGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCATGGTA					267
Query	64	TTCCGTGGAGCATGCCTGTTTGARTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGA					123
Sbjct	268	TTCCGTGGAGCATGCCTGTTTGAGTGTCATGAATACTTCAACCCTCCTCTTTCTTAATGA					327
Query	124	TTGAAKASGWGKTTGGWTTTSYGAACGCTGCTGGCCTTTACGGTCTAKCTCCGTCGWAATG					183
Sbjct	328	TTGAAGAGGTGTTTGGTTTCTGAGCGCTGCTGGCCTTTACGGTCTAGCTCGTTCGTAATG					387
Query	184	CATTARCATCCGAAACCRAACTTCTCATTGA					214
Sbjct	388	CATTAGCATCCGCAATCGAACTTCGGATTGA					418

Sacharomyces cerevisiae

Saccharomyces cerevisiae strain JN30 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

		Score	Expect	Identities	Gaps	Strand		
		345 bits(382)	1e-91	222/241(92%)	3/241(1%)	Plus/Plus		
Query	7	ATGTGA-TTGCAGA-TTCCGTGA-TCATCGAATCTTTGAACGCACATTGCGCCCCTTGGT					63	
Sbjct	253	ATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGT					312	
Query	64	ATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCCTTCTCAAACATTCTGTTTGGTAGTG					123	
Sbjct	313	ATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCCTTCTCAAACATTCTGTTTGGTAGTG					372	
Query	124	AGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCMTTGGAKGTTTTTTTTTT					183	
Sbjct	373	AGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTTTT					432	
Query	184	CCAAAAAAGGTTTCTCCGCGTTTTTGAGGAATAACGAGAAAAAGGYCGTTTTTARGTTTT					243	
Sbjct	433	CCAAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTT					492	
Query	244	A 244						
Sbjct	493	A 493						

Sporobolomyces salmonicolor

Rhodotorula mucilaginosa isolate LM9 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

		Alignment statistics for match #1					
		Score	Expect	Identities	Gaps	Strand	
		199 bits(220)	1e-47	127/139(91%)	3/139(2%)	Plus/Plus	
Query	8	TGTGA-TTGCAGA-TTCAGTGA-TCATCGAATCTTTGAACGCACCTTGC					64
Sbjct	128	TGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGC					187
Query	65	TTCCGTGGAGCATGCCTGTTTGARTGKCATGAATACTTCMACCCTCCTCTT					124
Sbjct	188	TTCCGTGGAGCATGCCTGTTTGAGTGTGATGAATACTTCAACCCTCCTCTT					247
Query	125	KTGAAKASGAGGTTGGATT		143			
Sbjct	248	TTGAAGAGGTGTTTGGATT		266			

Porovnání sekvence s kmenem *S.salmonicolor*

Sporidiobolus salmonicolor isolate T1Ss internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

		Score 111 bits(122)	Expect 2e-26	Identities 88/104(85%)	Gaps 3/104(2%)	Strand Plus/Plus	
Query	8	TGTGA-TTGCAGA-TTCAGTGA-TCATCGAATCTTTGAACGCACCTTGC					64
Sbjct	192	TGTGAATTGCAGAATTCAAGTGAATCATCGAATCTTTGAACGCATCTTGC					251
		ACTCTCTGGTA					
Query	65	TTCCGTGGAGCATGCCTGTTTGARTGKCATGAATACTTCMACCC				108	
Sbjct	252	TTCCGGAGAGTATGTCTGTTGGAGTGTCAATCTTCAACCC				295	

PŘÍLOHA D

1.2.1 Identifikace sekvencí oblastí D1/D2 srovnáním s databází NCBI.

Cystofilobasidium capitatum 10-1-1

Rhodotorula mucilaginosa strain HY3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand	
		364 bits(197)	1e-97	200/203(99%)	0/203(0%)	Plus/Minus	
Query	17	TGGGCGTCCGCACCATATACGGGGTCTCACCCTATGCCGCTGTATTCCAACAGACTTG					76
Sbjct	754	TGGGCGTCCGCACCATATACGGGGTCTCACCCTATGCCGCTGTATTCCAACAGACTTG					695
Query	77	TGTGCRGTCCAACGCGGAAAACATTTCTAGAGATTACAACGCGACMCCGAAGGTGCCAG					136
Sbjct	694	TGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACGCGACACCGAAGGTGCCAG					635
Query	137	ATTATAAATTTGAGCTCTTCCCGCTTCRCTCGCCGCTACTAGGGGAATCCTTGTTAGTTT					196
Sbjct	634	ATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTT					575
Query	197	CTTTTCCTCCGCTTATTGATATG					219
Sbjct	574	CTTTTCCTCCGCTTATTGATATG					552

Porovnání sekvence s kmenem *C. capitatum*

Cystofilobasidium capitatum genomic DNA containing ITS2 and 28S rRNA gene, isolate 120b

		Score	Expect	Identities	Gaps	Strand	
		200 bits(108)	3e-54	161/188(86%)	3/188(1%)	Plus/Minus	
Query	35	ACGGGGGTCTCA-CCACTATGCCGCTGTATTCCAACAGACTTGTGTGCRGTCCAACGCGG					93
Sbjct	277	ACGGGATTCTCACCTCTATGACGCCCTGTTCGAAGGACTTGTGCACAGGCCAACGCGG					218
Query	94	AAAACATTTCTAGAGATTACAACGCGAC-MCCGAAG-GTGCCAGATTATAAATTTGAGC					151
Sbjct	217	AAAACACTTCTCGAGATTACAATTCGGACAATCGTAGACTGCCAGATTTTAAATTTGAGC					158
Query	152	TCTTCCCGCTTCRCTCGCCGCTACTAGGGGAATCCTTGTTAGTTTCTTTTCCTCCGCTTA					211
Sbjct	157	TCTTCCCGCTTCACTCGCCGTTACTAGGGGAATCCTTGTTAGTTTCTTTTCCTCCACTTA					98
Query	212	TTGATATG					219
Sbjct	97	TTGATATG					90

Cystofilobasidium capitatum 10-1-2

Rhodotorula mucilaginosa genomic DNA containing ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, culture collection ZIM:2404, isolate BGAL2-Y32

		Score	Expect	Identities	Gaps	Strand	
		377 bits(204)	2e-101	206/208(99%)	0/208(0%)	Plus/Minus	
Query	8	AGCGMTGGGCGTCCGCACCATATACGGGGGTCTCACC					67
Sbjct	750	AGCGCTGGGCGTCCGCACCATATACGGGGGTCTCACC					691
		ACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACA					127
Sbjct	690	ACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACA					631
		GCCAGATTATAAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTT					187
Sbjct	630	GCCAGATTATAAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTT					571
		AGTTTCCTTTCTCCGCTTATTGATATG		215			
Sbjct	570	AGTTTCCTTTCTCCGCTTATTGATATG		543			

Porovnání sekvence s kmenem *C.capitatum*

Cystofilobasidium capitatum genomic DNA containing ITS2 and 28S rRNA gene,
isolate 120b

		Score	Expect	Identities	Gaps	Strand		
		196 bits(106)	4e-53	161/188(86%)	3/188(1%)	Plus/Minus		
Query	31	ACGGGGGTCTCA-CCACTATGCCGCTGTATTCCAACAGACTTGTGTGCGGTCCAACGCGG						89
Sbjct	277	ACGGGATTCTCACCTCTATGACGCCCTGTTCCAAGGGAAGTGTGCACAGGCCAACGCGG						218
Query	90	AAAACATTTCTAGAGATTACAACTCGGAC-MCCGAAG-GTGCCAGATTATAAATTTGAGC						147
Sbjct	217	AAAACACTTCTCGAGATTACAATTTCGGACAATCGTAGACTGCCAGATTTTAAATTTGAGC						158
Query	148	TCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTTCTTTTCTCCGCTTA						207
Sbjct	157	TCTTCCCGCTTCACTCGCCGTTACTAGGGGAATCCTTGTTAGTTTCTTTTCTCCACTTA						98
Query	208	TTGATATG	215					
Sbjct	97	TTGATATG	90					

Phaffia rhozodyma

Rhodotorula mucilaginosa genomic DNA containing ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, culture collection ZIM:2404, isolate BGAL2-Y32

Score	Expect	Identities	Gaps	Strand
344 bits(186)	2e-91	199/211(94%)	0/211(0%)	Plus/Minus

Query	6	CAAAGCGMTGGGCGTCCGCACCATATACGGGGGTCTCACCCTATGCCGCTGTATTCCAA	65
Sbjct	753	CAAAGCGCTGGGCGTCCGCACCATATACGGGGGTCTCACCCTATGCCGCTGTATTCCAA	694
Query	66	CAGACTTGTGKGCRCGASCRRCGCGGAAAACATTTCTWAGAGATTACAACCTCGGACMCCGAA	125
Sbjct	693	CAGACTTGTGTCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAA	634
Query	126	RGWGCCAGATTATAAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAKGGGAATCCTT	185
Sbjct	633	GGTGCCAGATTATAAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTT	574
Query	186	GTTAGTTTCTTTTCCTCCGCTTATTGATATG	216
Sbjct	573	GTTAGTTTCTTTTCCTCCGCTTATTGATATG	543

Porovnání sekvence s kmenem *Phaffia rhozodyma*

Phaffia rhodozyma strain CBS5905 26S ribosomal RNA gene, partial sequence

Score	Expect	Identities	Gaps	Strand
168 bits(186)	7e-45	144/180(80%)	3/180(1%)	Plus/Minus

Query	32	ACGGGGGTCTCACCA-CTATGCCGCTGTATTCCAACAGACTTGTGKGCRCGASCRRCGCGG	90
Sbjct	180	ACGGGATTCTCACCTCTATGACGCCCTATTCCAAGGGACTTGTACACAGGCCGGCACGG	121
Query	91	AAAACATTTCTWAGAGATTACAACCTCGGACM-CCGAARG-WGCCAGATTATAAAATTTGAGC	148
Sbjct	120	AAAACGCTTCTCTAGTTTACAACCTCGGACAACCGGAGGCTGCCAGATTTCAAATTTGAGC	61
Query	149	TCTTCCCGCTTCGCTCGCCGCTACTAKGGGAATCCTTGTTAGTTTCTTTTCCTCCGCTTA	208
Sbjct	60	TCATCCCGCTTCACTCGCCGTTACTAGGGGAATCCTTGTTAGTTTCTTTTCCTCCGCTTA	1

Rhodotorula aurantiaca

Rhodotorula mucilaginosa strain HY3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Score	Expect	Identities	Gaps	Strand
372 bits(201)	8e-100	203/205(99%)	0/205(0%)	Plus/Minus

Query	13	GCTGGGCGTCCGCACCATATACGGGGGTCTCACCACCTATGCCGCTGTATTCCAACAGACT	72
Sbjct	756	GCTGGGCGTCCGCACCATATACGGGGGTCTCACCACCTATGCCGCTGTATTCCAACAGACT	697
Query	73	TGTGTGCRGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAGGTGCC	132
Sbjct	696	TGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAGGTGCC	637
Query	133	AGATTATAAATTTGAGCTCTTCCCGCTTCRCTCGCCGCTACTAGGGGAATCCTTGTTAGT	192
Sbjct	636	AGATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGT	577
Query	193	TTCTTTTCTCCGCTTATTGATATG	217
Sbjct	576	TTCTTTTCTCCGCTTATTGATATG	552

Porovnání sekvence s kmenem R.aurantiaca

Rhodotorula aurantiaca strain CBS317 26S ribosomal RNA gene, partial sequence

Score	Expect	Identities	Gaps	Strand
200 bits(108)	1e-54	154/178(87%)	1/178(0%)	Plus/Minus

Query	35	ACGGGGGTCTCA-CCACTATGCCGCTGTATTCCAACAGACTTGTGTGCRGTCCAACGCGG	93
Sbjct	178	ACGGGGTCTCACCCTCTATGACGCTGTATTCCAACAGACTCATACACATGCCAGCGCGG	119
Query	94	AAAACATTTCTAGAGATTACAACCTCGGACMCCGAAGGTGCCAGATTATAAATTTGAGCTC	153
Sbjct	118	AAAACATTTCTCGAGACTACAACCTCGGACAGCGAAGCTGCCAGATTACAAAGTTGAGCTT	59
Query	154	TTCCCGCTTCRCTCGCCGCTACTAGGGGAATCCTTGTTAGTTTCTTTTCTCCGCTTA	211
Sbjct	58	TTCCCACTTCACTCGCCGTTACTAGGGGAATCCTTGTTAGTTTCTTTTCTCCGCTTA	1

Rhodotorula glutinis

Rhodotorula mucilaginosa strain HY3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand	
		381 bits(206)	1e-102	208/210(99%)	0/210(0%)	Plus/Minus	
Query	7	AAAGCGMTGGGCGTCCGCACCATATACGGGGGTCTCACCACATATGCCGCTGTATTCCAAC					66
Sbjct	761	AAAGCGCTGGGCGTCCGCACCATATACGGGGGTCTCACCACATATGCCGCTGTATTCCAAC					702
Query	67	AGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAR					126
Sbjct	701	AGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAG					642
Query	127	GTGCCAGATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTG					186
Sbjct	641	GTGCCAGATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTG					582
Query	187	TTAGTTTCTTTTCTCCTCCGCTTATTGATATG		216			
Sbjct	581	TTAGTTTCTTTTCTCCTCCGCTTATTGATATG		552			

Porovnání sekvence s kmenem R. glutinis

Rhodotorula glutinis strain AGG711 26S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand	
		352 bits(390)	2e-99	200/206(97%)	0/206(0%)	Plus/Minus	
Query	14	CGMTGGGCGTCCGCACCATATACGGGGGTCTCACCACATATGCCGCTGTATTCCAACAGAC					73
Sbjct	216	CGCTGGGCGTCCGCACCATATACGGGGGTTCACCACATATGCCGCTGTATTCCAACAGAC					157
Query	74	TTGTGTGCRGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACMCCGAAGGTGC					133
Sbjct	156	TTGTGTGCGGTCCAACGCGGAAAACACTTCTAGAGATTACAACCTCGGACACCGAAGGTGC					97
Query	134	CAGATTATAAATTTGAGCTCTTCCCGCTTCRCTCGCCGCTACTAGGGGAATCCTTGTTAG					193
Sbjct	96	CAGATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAG					37
Query	194	TTTCTTTTCTCCTCCGCTTATTGATATG		219			
Sbjct	36	TTTCTTTTCTCCTCCGCTTATTGATATG		11			

Rhodotorula mucilaginosa

Rhodotorula mucilaginosa strain HY3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Score	Expect	Identities	Gaps	Strand
381 bits(206)	1e-102	208/210(99%)	0/210(0%)	Plus/Minus

Query	8	AAARCGMTGGGCGTCCGCACCATATACGGGGGTCTCACCACATATGCCGCTGTATTCCAAC	67
Sbjct	761	AAAGCGCTGGGCGTCCGCACCATATACGGGGGTCTCACCACATATGCCGCTGTATTCCAAC	702
Query	68	AGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAG	127
Sbjct	701	AGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACAACCTCGGACACCGAAG	642
Query	128	GTGCCAGATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTG	187
Sbjct	641	GTGCCAGATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTG	582
Query	188	TTAGTTTCTTTTCTCCGCTTATTGATATG	217
Sbjct	581	TTAGTTTCTTTTCTCCGCTTATTGATATG	552

Sacharomyces cerevisiae

Saccharomyces cerevisiae genomic DNA containing ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, culture collection ZIM:2447, isolate ZG7-Y178

Score	Expect	Identities	Gaps	Strand
368 bits(199)	1e-98	199/199(100%)	0/199(0%)	Plus/Plus

Query	15	ACTCCTCGCCACACGGGATTCTCACCCTCTATGACGTCCTGTTCCAAGGAACATAGACAA	74
Sbjct	364	ACTCCTCGCCACACGGGATTCTCACCCTCTATGACGTCCTGTTCCAAGGAACATAGACAA	423
Query	75	GGAACGGCCCCAAAGTTGCCCTCTCCAAATTACAACCTCGGGCACCGAAGGTACCAGATTT	134
Sbjct	424	GGAACGGCCCCAAAGTTGCCCTCTCCAAATTACAACCTCGGGCACCGAAGGTACCAGATTT	483
Query	135	CAAATTTGAGCTTTTGCCGTTCACTCGCCGTTACTAAGGCAATCCCGGTTGGTTTCTTT	194
Sbjct	484	CAAATTTGAGCTTTTGCCGTTCACTCGCCGTTACTAAGGCAATCCCGGTTGGTTTCTTT	543
Query	195	TCCTCCGCTTATTGATATG	213
Sbjct	544	TCCTCCGCTTATTGATATG	562

Sporobolomyces salmonicolor

Rhodotorula mucilaginosa strain HY3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand	
		388 bits(210)	8e-105	210/210(100%)	0/210(0%)	Plus/Minus	
Query	6	AAAGCGCTGGGCGTCCGCACCATATACGGGGGTCTCACC					65
Sbjct	761	AAAGCGCTGGGCGTCCGCACCATATACGGGGGTCTCACC					702
Query	66	AGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACA					125
Sbjct	701	AGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAGATTACA					642
Query	126	GTGCCAGATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTG					185
Sbjct	641	GTGCCAGATTATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTG					582
Query	186	TTAGTTTCTTTTCCTCCGCTTATTGATATG		215			
Sbjct	581	TTAGTTTCTTTTCCTCCGCTTATTGATATG		552			

Porovnání sekvence s kmenen S.salmonicolor

Sporidiobolus salmonicolor genomic DNA containing ITS2 and 28S rRNA gene, isolate 49-1

		Score	Expect	Identities	Gaps	Strand	
		255 bits(138)	4e-70	180/201(90%)	0/201(0%)	Plus/Minus	
Query	15	GGCGTCCGCACCATATACGGGGGTCTCACC					74
Sbjct	212	GGCATCCGCACCGTGTA					153
Query	75	TGCGGTCCAACGCGGAAAACATTTCTAGAGATTACA					134
Sbjct	152	TGCGGTCTGACGCGGAAAACACTTCTCGAGATTACA					93
Query	135	TATAAATTTGAGCTCTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTTCT					194
Sbjct	92	TACAAATTTGAGCTTTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTTCT					33
Query	195	TTTCCTCCGCTTATTGATATG		215			
Sbjct	32	TTTCCTCCGCTTATTGATATG		12			

Sporobolomyces shibatanus

Rhodotorula mucilaginosa strain HY3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand	
		359 bits(194)	6e-96	204/211(97%)	1/211(0%)	Plus/Minus	
Query	7	AAAGCCGCTGGGCGTCCGCACCATATRCGGGGGTCTCACC					66
Sbjct	761	AAAG-CGCTGGGCGTCCGCACCATATACGGGGGTCTCACC					703
Query	67	CAGACTTGTGKCGGGCCAACGCGGAAAACATTTCTAGAG					126
Sbjct	702	CAGACTTGTGTGCGGTCCAACGCGGAAAACATTTCTAGAG					643
Query	127	GGWGCCAGATTATAAAATTTGAGCTCTTCCCGCTTCRCT					186
Sbjct	642	GGTGCCAGATTATAAAATTTGAGCTCTTCCCGCTTCGCT					583
Query	187	GTTAGTTTCTTTTCCTCCGCTTATTGATATG					217
Sbjct	582	GTTAGTTTCTTTTCCTCCGCTTATTGATATG					552

Porovnání sekvence s kmenen S.shibatanus

Sporidiobolus pararoseus strain TA200 26S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand	
		230 bits(124)	9e-63	174/201(87%)	0/201(0%)	Plus/Minus	
Query	17	GGCGTCCGCACCATATRCGGGGGTCTCACC					76
Sbjct	202	GGCATCCGCATCGTGTACTGGGTCTCACC					143
Query	77	KGCGGGCCAACGCGGAAAACATTTCTAGAG					136
Sbjct	142	TGCGGTCTATCACGGAACACTTCTCGAG					83
Query	137	TATAAATTTGAGCTCTTCCCGCTTCRCTCGCCGCTACTAGGGGAATCCTTGTTAGTTTCT					196
Sbjct	82	TACAAATTTGAGCTTTTCCCGCTTCGCTCGCCGCTACTAGGGGAATCCTTGTTAGTTTCT					23
Query	197	TTTCCTCCGCTTATTGATATG					217
Sbjct	22	TTTCCTCCGCTTATTGATATG					2

Sporobolomyces roseus

Sporidiobolus salmonicolor isolate z3 26S ribosomal RNA gene, partial sequence

		Score	Expect	Identities	Gaps	Strand	
		381 bits(206)	1e-102	206/206(100%)	0/206(0%)	Plus/Minus	
Query	14	CATCAGGCATCCGCACCGTGTACTGGGTTCTCACC		ACTGTGACGCTCCGTTCCAGGAGAC			73
Sbjct	207	CATCAGGCATCCGCACCGTGTACTGGGTTCTCACC		ACTGTGACGCTCCGTTCCAGGAGAC			148
Query	74	TTGTGTGCGGTCTGACGCGGAAAACACTTCTCGAG		ATTACAACTCGGACGCCGAAAGCGC			133
Sbjct	147	TTGTGTGCGGTCTGACGCGGAAAACACTTCTCGAG		ATTACAACTCGGACGCCGAAAGCGC			88
Query	134	CAGATTACAAATTTGAGCTTTTCCCGCTTCGCTCG		CCGCTACTAGGGGAATCCTTGTTAG			193
Sbjct	87	CAGATTACAAATTTGAGCTTTTCCCGCTTCGCTCG		CCGCTACTAGGGGAATCCTTGTTAG			28
Query	194	TTTCTTTTCCTCCGCTTATTGATATG		219			
Sbjct	27	TTTCTTTTCCTCCGCTTATTGATATG		2			

Porovnání sekvence s kmenen Sporobolomyces roseus

Sporobolomyces roseus genomic DNA containing ITS2 and 28S rRNA gene, isolate 91

		Score	Expect	Identities	Gaps	Strand	
		311 bits(344)	2e-86	190/202(94%)	0/202(0%)	Plus/Minus	
Query	18	AGGCATCCGCACCGTGTACTGGGTTCTCACC		ACTGTGACGCTCCGTTCCAGGAGACTTGT			77
Sbjct	298	AGGCATCCGCATCGTGTACTGGGTTCTCACC		ACTATGACGCTCTGTTCCAAGAGACTTGT			239
Query	78	GTGCGGTCTGACGCGGAAAACACTTCTCGAG		ATTACAACTCGGACGCCGAAAGCGCCAGA			137
Sbjct	238	ATGCGGTCTATCACGGAACACTTCTCGAG		ATTACAACTCGGACGTCGTAGACGCCAGA			179
Query	138	TTACAAATTTGAGCTTTTCCCGCTTCGCTCG		CCGCTACTAGGGGAATCCTTGTTAGTTTC			197
Sbjct	178	TTACAAATTTGAGCTTTTCCCGCTTCGCTCG		CCGCTACTAGGGGAATCCTTGTTAGTTTC			119
Query	198	TTTTCCTCCGCTTATTGATATG		219			
Sbjct	118	TTTTCCTCCGCTTATTGATATG		97			