

Supplementary Material

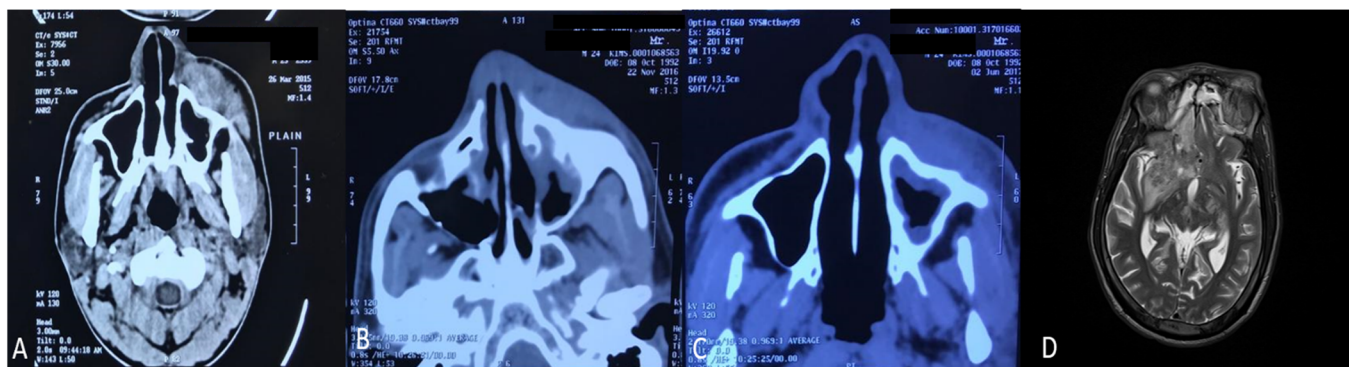


Figure S1. Radiological progression of the lesion over the five years (A) lesion in the skin and subcutaneous tissue of left side of the face (2015) (B, C) progression with involvement of the left maxillary sinus mucosa thickening (2016 & 2017) & (D) Intracranial extension in 2021.

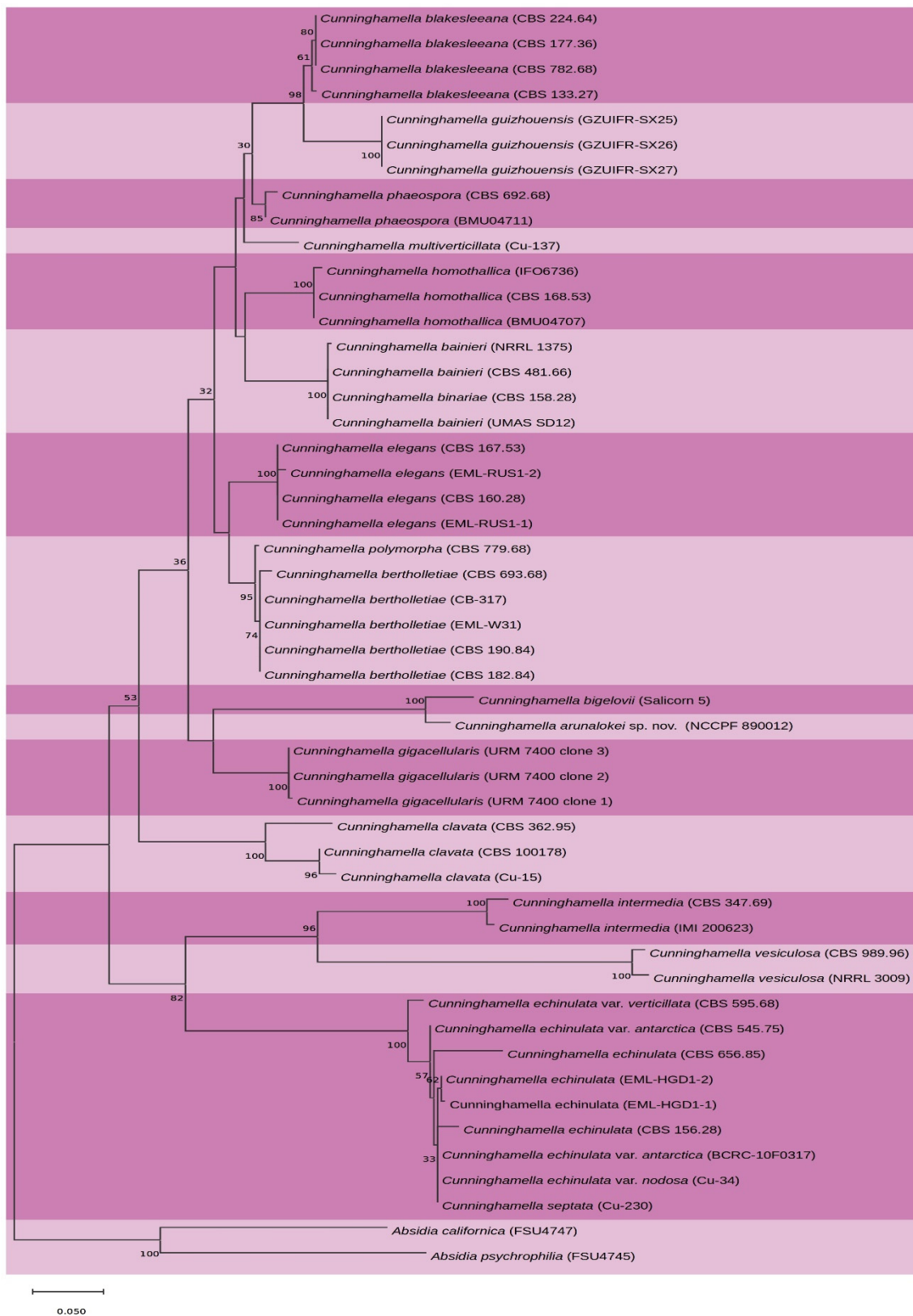


Figure S2: Molecular phylogenetic analysis of *Cunninghamella* species using internal transcribed spacer region. The evolutionary history was inferred by using the Maximum Likelihood method based on the Kimura 2-parameter model. All positions containing gaps and missing data were eliminated.

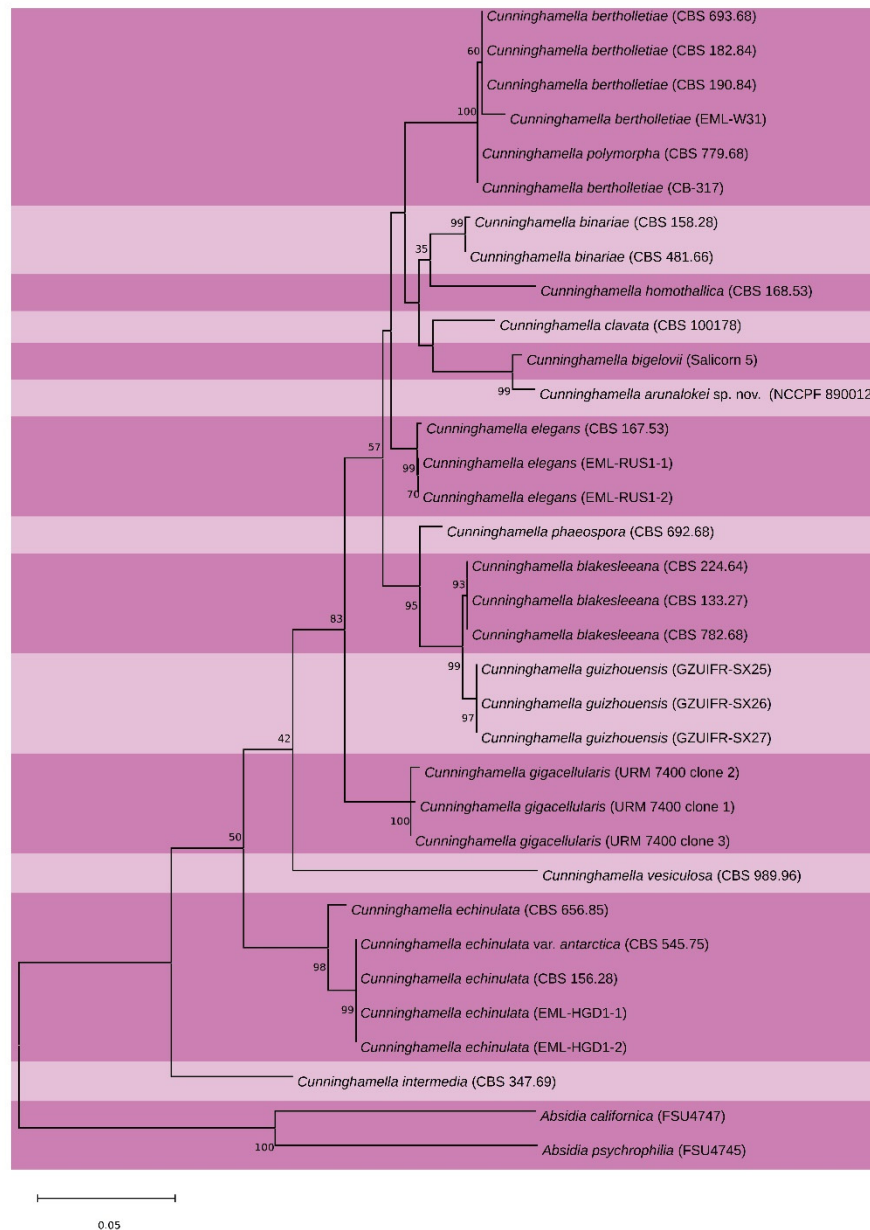


Figure S3: Molecular phylogenetic analysis of *Cunninghamella* species using 28S large ribosomal subunit region. The evolutionary history was inferred by using the Maximum Likelihood method based on the Kimura 2-parameter model. All positions containing gaps and missing data were eliminated.

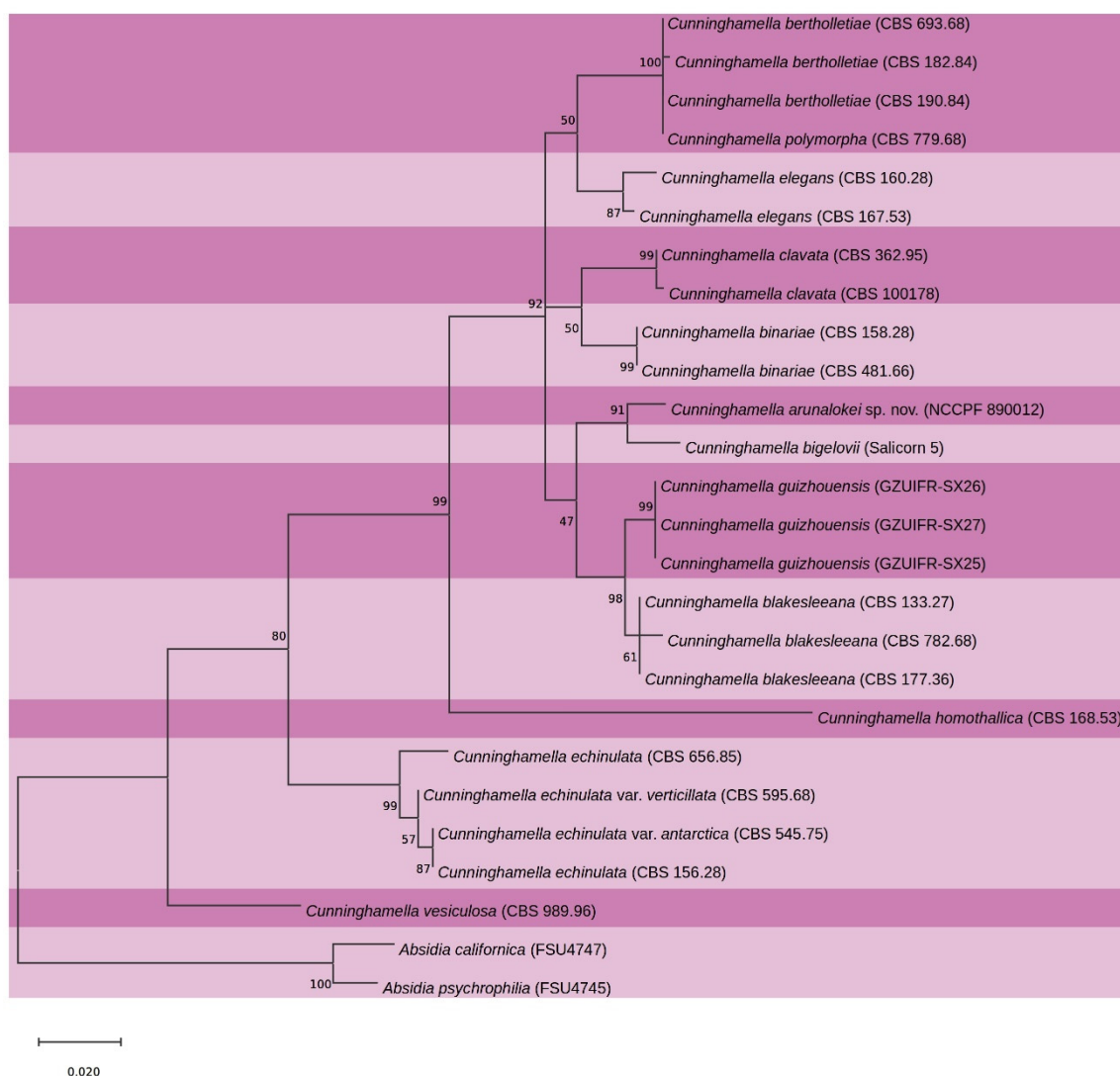


Figure S4. Molecular phylogenetic analysis of *Cunninghamella* species using EF-1 alpha region. The evolutionary history was inferred by using the Maximum Likelihood method based on the Kimura 2-parameter model. All positions containing gaps and missing data were eliminated.

Table S1. Accession numbers of the internal transcribed spacer (ITS) region, large ribosomal subunit (28S) and translation elongation factor-1 alpha (EF-1alpha) of the various *Cunninghamella* species used for phylogenetic analysis in this study.

S. No	Species	Strain ID	ITS	28S	EF-1alpha
1	<i>C. bainieri</i>	NRRL 1375	AF254935.1	NA	NA
2	<i>C. bainieri</i>	UMAS SD12	KF201293.1	NA	NA
3	<i>C. bertholletiae</i>	CB-317	KX638508.1	KX638507.1	NA
4	<i>C. bertholletiae</i>	CBS 182.84	JN205877.1	MH873434.1	KJ156481.1
5	<i>C. bertholletiae</i>	CBS 190.84	JN205878.1	HM849701.1	KJ156485.1
6	<i>C. bertholletiae</i>	CBS 693.68	AF254931.1	MH870924.1	KJ156490.1
7	<i>C. bertholletiae</i>	EML-W31	MF806022.1	MF806029.1	NA
8	<i>C. bigelovii</i>	Salicorn 5	KJ013403.1	KJ013405.1	KJ395944.1
9	<i>C. echinulata</i>	EML-HGD1-2	MF806024.1	MF806026.1	NA
10	<i>C. echinulata</i> var. <i>antarctica</i>	CBS 545.75	AF254938.1	JN206597.1	KJ156492.1
11	<i>C. elegans</i>	EML-RUS1-2	MF806021.1	MF806028.1	NA
12	<i>A. psychrophilia</i>	FSU4745	AY944874.1	EU736306.1	EU736252.1
13	<i>A. californica</i>	FSU4747	AY944872.1	EU736300.1	EU736246.1
14	<i>C. arunalokei</i>	IL3459	MN431159.1	MN431158.1	This study
15	<i>C. binariae</i>	CBS 158.28	JN205888.1	JN206602.1	KJ156486.1
16	<i>C. blakesleeana</i>	CBS 133.27	AF254932.1	NG_063968.1	KJ156479.1
17	<i>C. blakesleeana</i>	CBS 224.64	JN205870.1	MH870055.1	NA
18	<i>C. blakesleeana</i>	CBS 177.36	JN205868.1	NA	KJ156483.1
19	<i>C. blakesleeana</i>	CBS 782.68	JN205869.1	JN206601.1	KJ156478.1
20	<i>C. clavata</i>	CBS 100178	JN205890.1	HM849696.1	KJ156477.1
21	<i>C. clavata</i>	CBS 362.95	JN205891.1	NA	KJ156473.1
22	<i>C. clavata</i>	Cu-15	AF254942.1	NA	NA
23	<i>C. echinulata</i>	CBS 156.28	JN942997.1	JN939199.1	KJ156500.1
24	<i>C. echinulata</i>	CBS 656.85	JN942996.1	JN939200.1	KJ156491.1
25	<i>C. echinulata</i>	EML-HGD1-1	MF806020.1	MF806025.1	NA
26	<i>C. echinulata</i> var. <i>antarctica</i>	BCRC-10F0317	JQ678764.1	NA	NA
27	<i>C. echinulata</i> var. <i>nodosa</i>	Cu-34	AF346407.1	NA	NA
28	<i>C. echinulata</i> var. <i>verticillata</i>	CBS 595.68	AF254937.1	NA	KJ156475.1
29	<i>C. elegans</i>	CBS 167.53	JN205882.1	HM849700.1	KJ156494.1
30	<i>C. elegans</i>	CBS 481.66	JN205889.1	JN206603.1	KJ156495.1
31	<i>C. elegans</i>	EML-RUS1-1	MF806023.1	MF806027.1	NA
32	<i>C. elegans</i>	CBS 160.28	AF254928.1	NA	KJ156470.1
33	<i>C. gigacellularis</i>	URM 7400 clone 1	KX238886.1	KX238889.1	NA
34	<i>C. gigacellularis</i>	URM 7400 clone 2	KX238887.1	KX238890.1	NA
35	<i>C. gigacellularis</i>	URM 7400 clone 3	KX238888.1	KX238891.1	NA
36	<i>C. guizhouensis</i>	GZUIFR-SX25	MN908596.1	MN908599.1	MN912633.1
37	<i>C. guizhouensis</i>	GZUIFR-SX26	MN908597.1	MN908600.1	MN912634.1
38	<i>C. guizhouensis</i>	GZUIFR-SX27	MN908598.1	MN908601.1	MN912635.1
39	<i>C. homothallica</i>	CBS 168.53	JN205863.1	JN206605.1	KJ156498.1
40	<i>C. homothallica</i>	BMU04707	MN217567.1	NA	NA
41	<i>C. homothallica</i>	IFO6736	AF254941.1	NA	NA
42	<i>C. intermedia</i>	CBS 347.69	AF254940.1	JN206606.1	NA
43	<i>C. intermedia</i>	IMI 200623	AF254939.1	NA	NA
44	<i>C. multiverticillata</i>	Cu-137	AF254933.1	NA	NA
45	<i>C. phaeospora</i>	BMU04711	MG583991.1	NA	NA
46	<i>C. phaeospora</i>	CBS 692.68	AF254934.1	HM849697.1	NA

47	<i>C. polymorpha</i>	CBS 779.68	JN205874.1	JN206599.1	KJ156471.1
48	<i>C. septata</i>	Cu-230	AF346408.1	NA	NA
49	<i>C. vesiculosa</i>	CBS 989.96	JN205897.1	HM849693.1	KJ156474.1
50	<i>C. vesiculosa</i>	NRRL 3009	AF254943.1	NA	NA

Table S2. Details of various Mucorales genomes used for whole-genome phylogeny in this study.

Name	Strain	NCBI Genome Accession	SRA ID	SRX ID
<i>A. glauca</i>	CBS 101.48 substr. RVII-324 met-	GCA_900079185.1	-	-
<i>A. repens</i>	NRRL 1336	GCA_002105175.1	-	-
<i>A. elegans</i>	B7760	GCA_000696995.1	-	-
<i>A. ossiformis</i>	NRRL A-21654	GCA_014839865.1	-	-
<i>A. trapeziformis</i>	B9324	GCA_000696975.1	-	-
<i>A. variabilis</i>	NCCPF 102052	GCA_002749535.1	-	-
<i>C. cucurbitarum</i>	KUS-F28377	GCA_001683725.1	-	-
<i>C. recurvatus</i>	B5483	GCA_000697235.1	-	-
<i>C. antarctica</i>	NRRL 6534	-	SRR7686432	SRX4546928
<i>C. arunalokei</i> sp. nov.	IL3459	This study	This study	This study
<i>C. bertholletiae</i>	175	GCA_000697215.1	-	-
<i>C. bertholletiae</i>	B7461	GCA_000697315.1	-	-
<i>C. bertholletiae</i>	NRRL 1380	-	SRR9718426	SRX6476271
<i>C. bertholletiae</i>	NRRL 1377	-	SRR9719771	SRX6477469
<i>C. echinulata</i>	RSA 2017+	-	SRR10125925	SRX6854350
<i>C. echinulata</i>	RSA 2018-	-	SRR10125928	SRX6854353
<i>C. echinulata</i>	NRRL 1385	-	SRR9719880	SRX6477578
<i>C. echinulata</i>	NRRL 1386	-	SRR9720690	SRX6478239
<i>C. echinulata</i>	NRRL 1387	-	SRR9721137	SRX6478686
<i>C. elegans</i>	NRRL 1392	-	SRR9719892	SRX6477590
<i>C. elegans</i>	NRRL 1388	-	SRR9719893	SRX6477591
<i>C. elegans</i>	NRRL 1390	-	SRR9719896	SRX6477594
<i>C. elegans</i>	NRRL 1391	-	SRR9719906	SRX6477604
<i>C. elegans</i>	NRRL 1393	-	SRR9719909	SRX6477607
<i>C. polymorpha</i>	NRRL 6428	-	SRR12691406	SRX9171364
<i>Gigaspora rosea</i>	DAOM 194757	GCA_003550325.1	-	-
<i>Glomus cerebriforme</i>	DAOM 227022	GCA_003550305.1	-	-
<i>Gongronella</i> sp.	w5	GCA_001650995.1	-	-
<i>Hesseltinella vesiculosa</i>	NRRL 3301	GCA_002104935.1	-	-
<i>Lichtheimia corymbifera</i>	FSU 9682	GCA_000723665.1	-	-
<i>Lichtheimia ramosa</i>	KPH11	GCA_008728235.1	-	-
<i>Linnemannia elongata</i>	AG-77	GCA_001651415.1	-	-
<i>Mortierella alpina</i>	ATCC 32222	GCA_000240685.2	-	-
<i>Mortierella hygrophila</i>	NRRL 2591	GCA_015680625.1	-	-
<i>Mucor ambiguus</i>	NBRC 6742	GCA_000950595.1	-	-
<i>Mucor circinelloides</i>	JCM 22480	GCA_001599575.1	-	-
<i>Mucor irregularis</i>	B50	GCA_000587855.1	-	-
<i>Mucor lusitanicus</i>	MU402	GCA_010203745.1	-	-
<i>Mucor racemosus</i>	B9645	GCA_000697255.1	-	-
<i>Mucor velutinosus</i>	B5328	GCA_000696895.1	-	-

<i>Phycomyces blakesleeanus</i>	NRRL 1555(-)	GCA_001638985.2	-	-
<i>Podila verticillata</i>	NRRL 6337	GCA_000739165.1	-	-
<i>Rhizomucor miehei</i>	CAU432	GCA_000611695.1	-	-
<i>Rhizomucor pusillus</i>	-	GCA_900175165.2	-	-
<i>Rhizophagus irregularis</i>	DAOM 197198	GCA_000439145.3	-	-
<i>Rhizopus azygosporus</i>	CBS 357.93	GCA_003325435.1	-	-
<i>Rhizopus delemar</i>	RA 99-880	GCA_000149305.1	-	-
<i>Rhizopus microsporus</i>	ATCC 52813	GCA_002708625.1	-	-
<i>Rhizopus oryzae</i>	99-892	GCA_000697725.1	-	-
<i>Rhizopus stolonifer</i>	B9770	GCA_000697035.1	-	-
<i>Saksenaea oblongispora</i>	B3353	GCA_000697495.1	-	-
<i>Saksenaea vasiformis</i>	B4078	GCA_000697055.1	-	-
<i>Syncephalastrum contaminatum</i>	UoMD18-1	GCA_013461545.1	-	-
<i>Syncephalastrum monosporum</i>	B8922	GCA_000697355.1	-	-
<i>Syncephalastrum racemosum</i>	NRRL 2496	GCA_002105135.1	-	-
<i>Thermomucor indicae-seudaticae</i>	HACC 243	GCA_000787465.1	-	-