

Supplemental Figure Legends.

Figure S1. Scanning electron micrograph of *Parengyodontium torokii* CBS 368.72 strain. (A) Zigzag rachides of the fertile conidiogenous cells. **(B)** Subcylindrical to ellipsoidal, hyaline single-celled conidia.

Figure S2. Molecular phylogenetic analysis of the ITS region from *Parengyodontium* spp. and related taxa in the Cordycipitaceae. Phylogram of the most likely tree ($-\ln L = 1622.37$) from a ML analysis of 24 sequences based on the ITS region (568 bp) using IQ-TREE. Numbers refer to UFBootstrap support values $\geq 90\%$ based on 5000 replicates. Nodes ≥ 95 are considered strongly supported. Bayesian posterior probabilities $\geq 95\%$ are denoted as thickened branches. *Isaria coleopterora* (CBS 110.73) is used outgroup. ET designates ex-type isolates. Newly described species is in bold and highlighted. Bar indicates nucleotide substitutions per site.

Figure S3. Molecular phylogenetics of concatenated loci, two ribosomal (ITS and LSU) and one protein-coding locus (β -tubulin) from *Parengyodontium* spp. and related taxa in the Cordycipitaceae. Phylogram of the most likely tree ($-\ln L = 3824.45$) from a ML analysis of 22 sequences based on the combined regions of ITS, LSU and TUB (1435 bp) using IQ-TREE. Numbers refer to UFBootstrap support values $\geq 90\%$ based on 5,000 replicates. Nodes ≥ 95 are considered strongly supported. Bayesian posterior probabilities $\geq 95\%$ are denoted as thickened branches. *Isaria coleopterora* (CBS 110.73) is used outgroup. ET designates ex-type isolates. Newly described species is in bold and highlighted. Bar indicates nucleotide substitutions per site.

Phylogram of the most likely tree ($-\ln L = 1622.37$) from a ML analysis of 24 sequences based on the ITS region (568 bp) using IQ-TREE. Numbers refer to UFBootstrap support values $\geq 90\%$ based on 5000 replicates. Nodes ≥ 95 are considered strongly supported. Bayesian posterior probabilities $\geq 95\%$ are denoted as thickened branches. *Isaria coleopterora* (CBS 110.73) is used outgroup. ET designates ex-type isolates. Newly described species is in bold and highlighted. Bar indicates nucleotide substitutions per site.

Figure S4. Biofilm structures of *P. torokii* FJII-L10-SW-P1 strain. (A) A thick layer of biofilm mat containing conidial spores and fungal mycelia. White arrow is pointing the sheath of fungal biofilm mat. **(B)** Arrow pointing to the white material where conidial spores are positioned. **(C)** Arrow pointing to a pair of conidia that were attached to the white fibrous material. **(D)** A thin sheet of fungal biofilm mat containing only conidia. Note only conidial spores are associated with these structures and not fungal mycelia.

Figure S5. Mitogenome of *Parengyodontium torokii*. The circular map of the mitochondrial genome of *P. torokii* was drawn with OGDRAW and core genes related to the electron transport chain, ribosomal protein, transfer RNAs, putative additional ORFs and introns are displayed.

Figure S6. Genomic annotations of secreted proteins among Cordycipitaceae species. Total number of predicted secreted proteins for each individual species were plotted using bar graphs.

Figure S7. Comparative genomic analysis of predicted Secondary Metabolite Cluster among 9 Cordycipitaceae genomes. The secondary metabolite clusters were predicted and annotated using the antiSMASH 6 pipeline. All predicted clusters were countered and plotted in a heatmap.

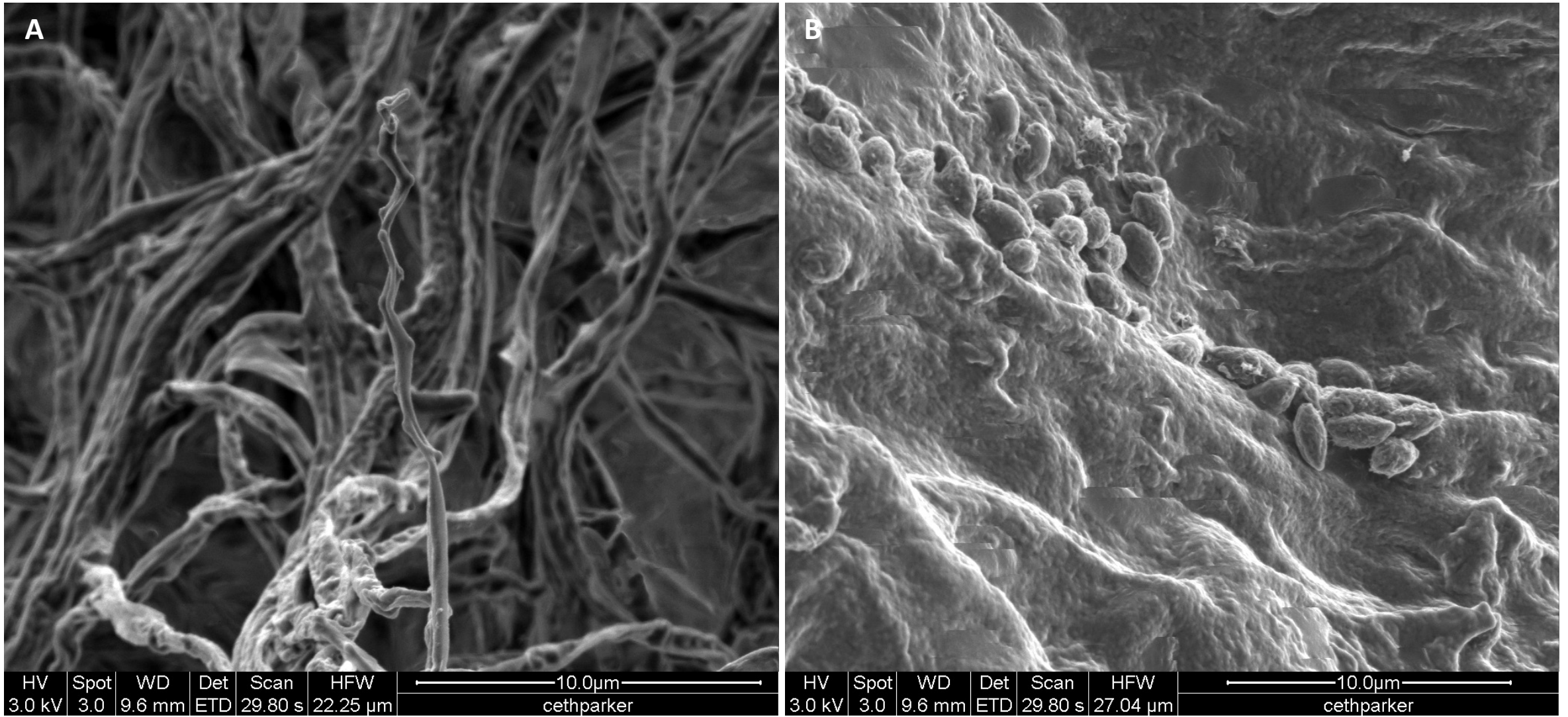
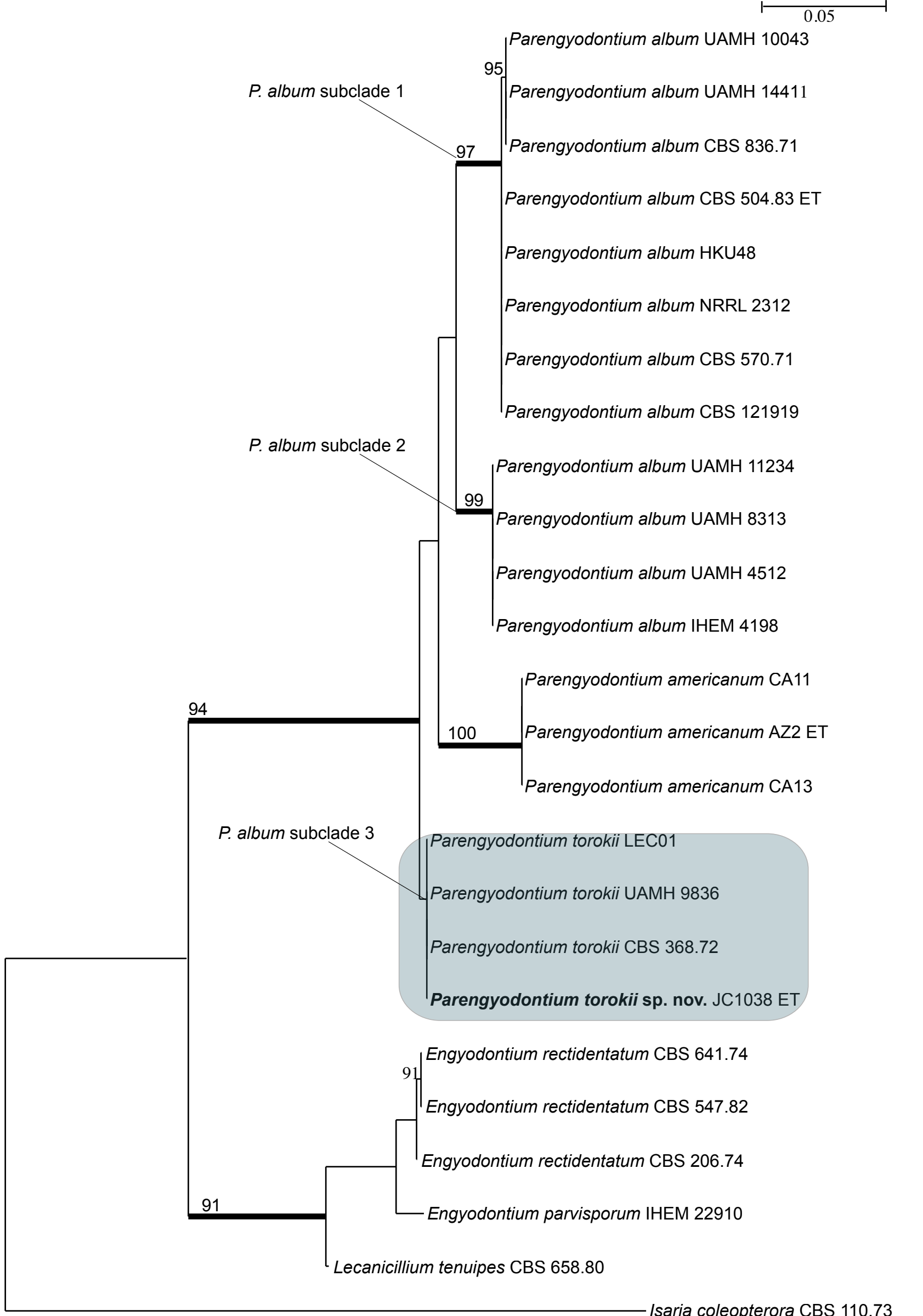


Figure S1. Scanning electron micrography of *Parengyodontium torokii* CBS 368.72 strain. (A) Zigzag rachides of the fertile conidiogenous cells. (B) Subcylindrical to ellipsoidal, hyaline single-celled conidia.

0.05



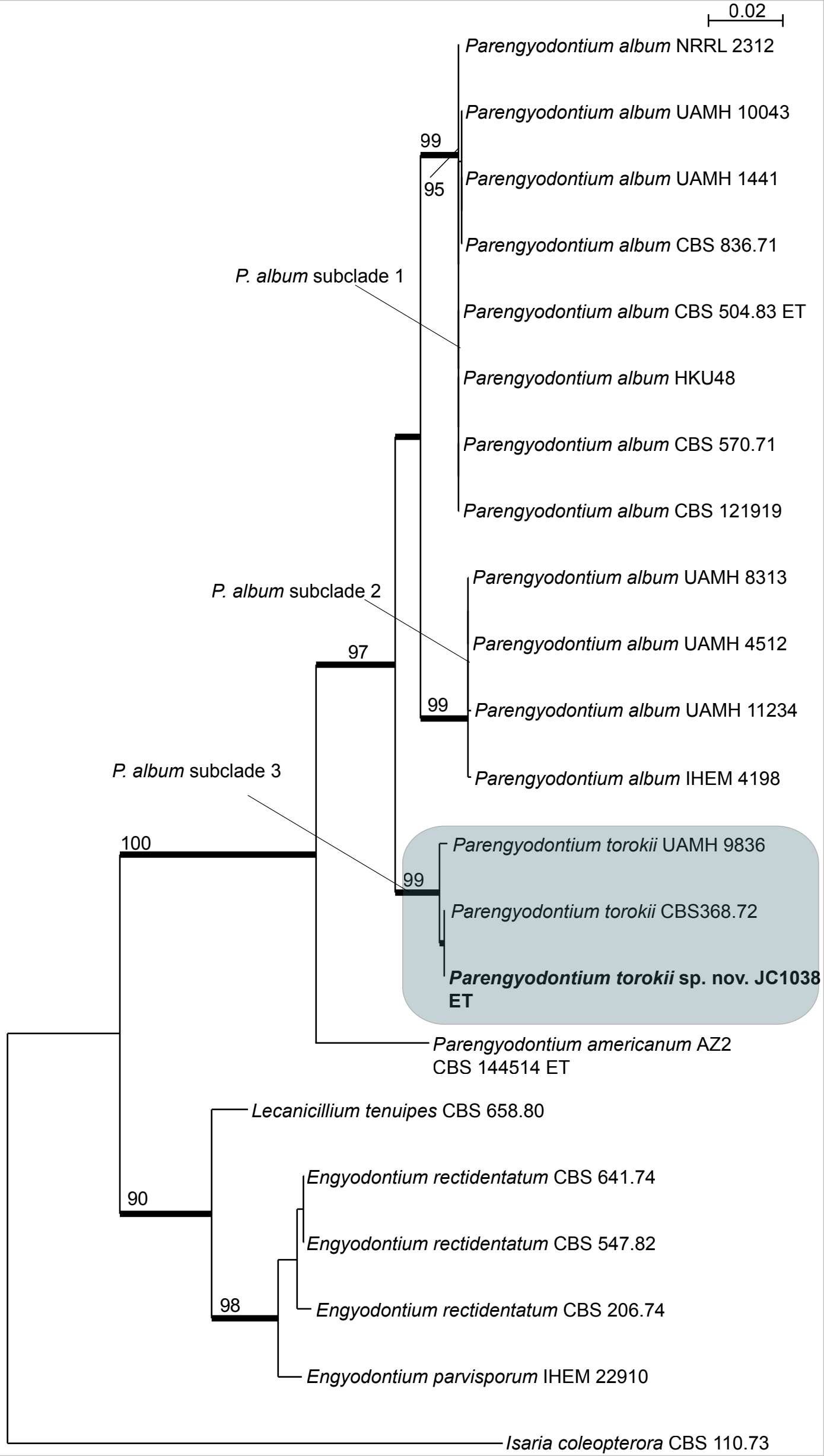
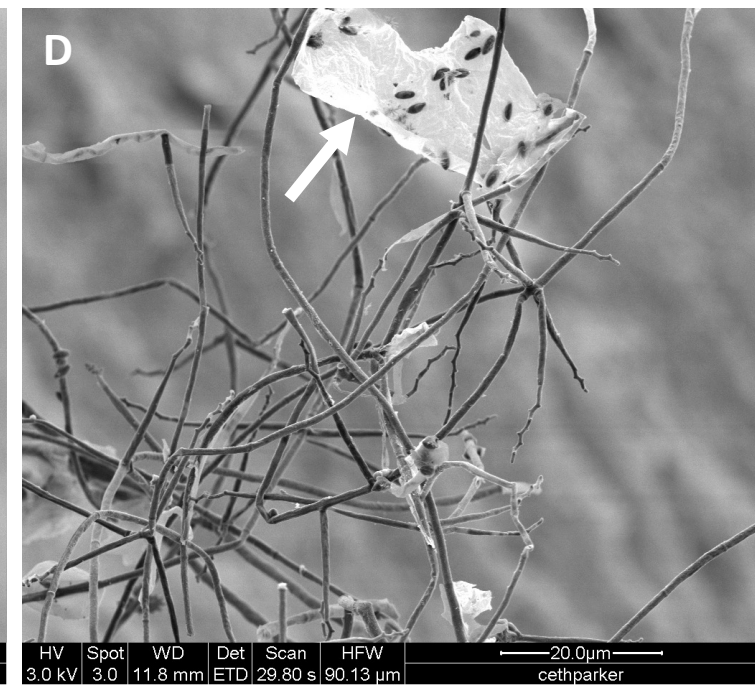
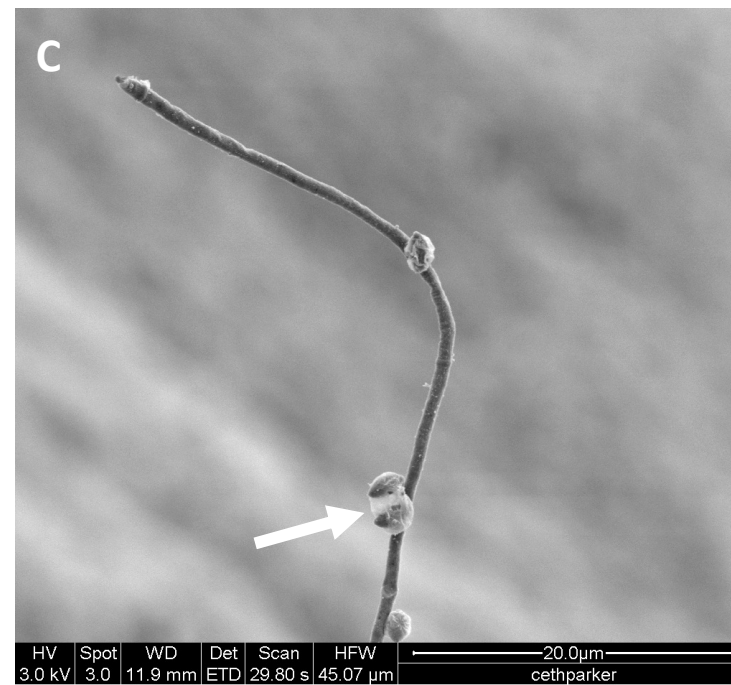
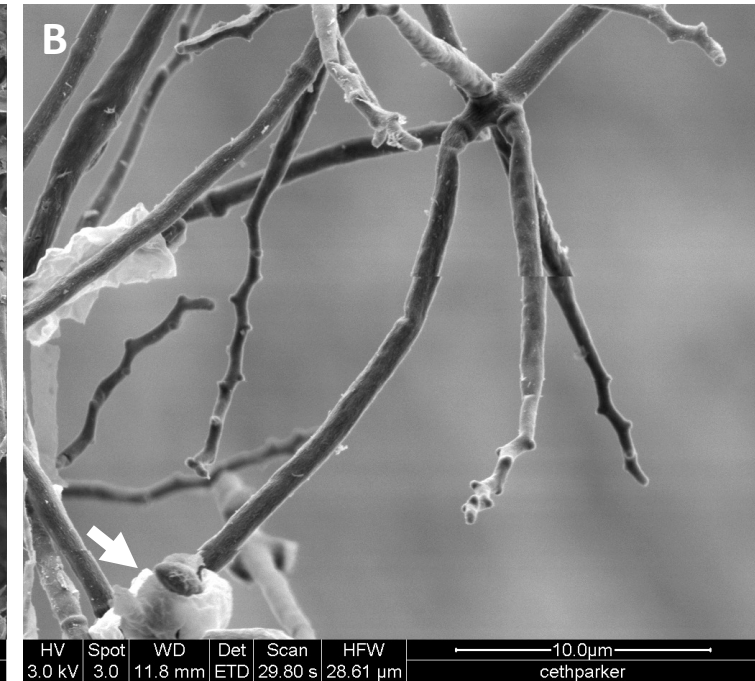
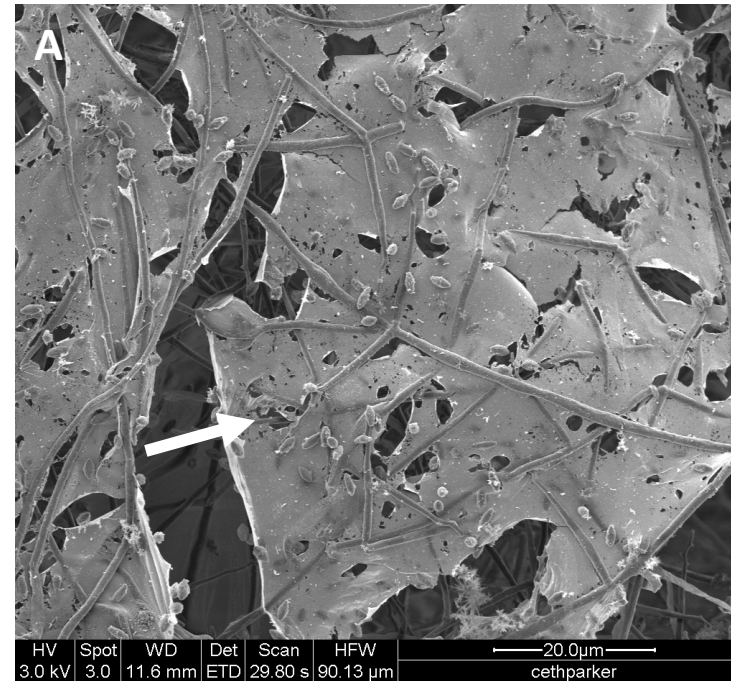
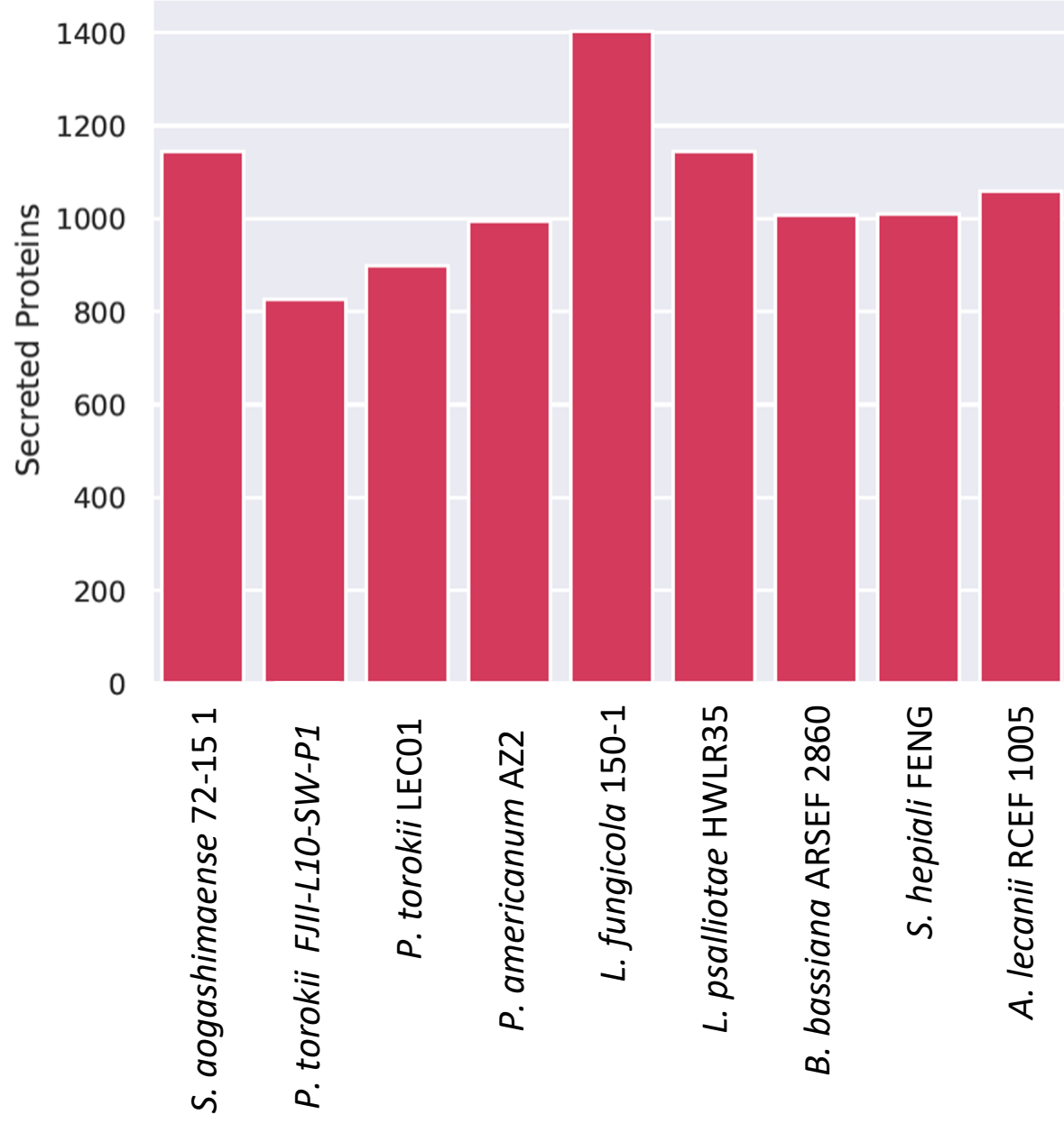
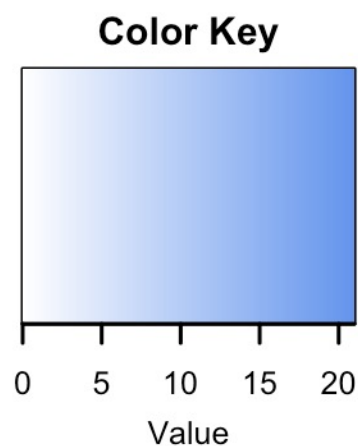


Figure S4. Biofilm structures of *P. torokii* FJII-L10-SW-P1 strain.

(A) A thick layer of biofilm mat containing conidial spores and fungal mycelia. White arrow is pointing the sheath of fungal biofilm mat. **(B)** Arrow pointing to the white material where conidial spores are positioned. **(C)** Arrow pointing to a pair of conidia that were attached to the white fibrous material. **(D)** A thin sheath of fungal biofilm mat containing only conidia. Note only conidial spores are associated with these structures and not fungal mycelia







1	1	1	0	2	1	1	1	1	NAPAA
11	9	9	4	17	7	14	12	14	NRPS
10	4	4	4	10	6	4	8	5	NRPS-like
0	0	0	0	0	0	0	0	2	NRPS,terpene
0	0	1	0	0	0	0	0	0	NRPS-like,terpene
1	2	0	0	0	0	0	0	0	NRPS-like,T1PKS
0	1	1	0	0	1	0	0	0	NRPS,NRPS-like
2	2	4	1	3	3	3	4	2	NRPS,T1PKS
1	0	0	0	1	0	0	0	0	NRPS,betalactone
0	0	0	0	0	1	0	0	0	PKS
11	7	9	6	21	10	10	10	5	T1PKS
1	2	1	3	3	1	1	5	1	T1PKS,NRPS
1	1	3	0	0	0	0	1	0	T1PKS,NRPS-like
0	0	0	0	0	0	0	1	0	T3PKS
0	0	0	0	0	0	1	0	0	T3PKS,T1PKS
4	3	3	3	11	5	7	3	4	terpene
0	0	0	0	0	0	1	0	0	terpene,NRPS
0	0	0	1	0	0	0	0	0	phosphonate
0	0	0	1	0	0	0	0	0	siderophore
1	0	0	0	0	0	0	0	0	betalactone
1	0	0	0	0	0	0	0	0	fungal-RiPP,terpene
1	0	0	0	2	0	0	1	0	indole
<i>S. aogashimaense</i> 72-15 1	<i>P. torokii</i> FJII-L10-SW-P1	<i>P. torokii</i> LEC01	<i>P. americanum</i> AZ2	<i>L. fungicola</i> 150-1	<i>L. psalliotae</i> HWLR35	<i>B. bassiana</i> ARSEF 2860	<i>S. hepiali</i> FENG	<i>A. lecanii</i> RCEF 1005	

Supplemental Table Captions.

Table S1. Interspersed repeats and low complexity DNA sequences deduced by RepeatMasker in the *Parengyodontium torokii* FJII-L10-SW-P1 genome.

Table S2. Carbohydrate-active enzymes (CAZymes) profile of nine Cordycipitaceae fungal species

Table S3. Genes related to formation of biofilm, adherence, and glycosaminoglycan (GAG) biosynthesis characterized in *Aspergillus fumigatus* and identified in the *Parengyodontium torokii* genome.

Table S4. Genes involved in melanin biosynthesis, radioresistance and microgravity resistance and identified in the *Parengyodontium torokii* FJII-L10-SW-P1 genome.

Table S5. Secondary metabolite clusters identified by antiSMASH v6. in the *Parengyodontium torokii* FJII-L10-SW-P1 genome. The genomic scaffold, type, position, most similar known cluster and similarity are listed in the table.

Table S6. LC-MS analysis of *Parengyodontium torokii* FJ11-L10-SW-P1 based on identified biosynthetic gene clusters. Dereplication results of FJ11-L10-SW-P1 grown on rice media compared to an in-house database. Dereplication results of FJ11-L10-SW-P1 grown on oatmeal media compared to in-house database

Table S1 - Genomes download from NCBI and used for comparative genomic analyses
with the novel *Parengyodontium torokii* strain FJII-L10-SW-P1

Species	Strain	accession	Reference (PMID)
<i>Simplicillium aogashimaense</i>	72-15.1	JAALXG000000000.1	32616631
<i>Lecanicillium sp.</i>	LEC01	NIWZ000000000.2	30975820
<i>Parengyodontium americanum</i>	AZ2	PXYO000000000.1	32028048
<i>Lecanicillium fungicola</i>	150-1	FWCC000000000.1	31072880
<i>Lecanicillium psalliotae</i>	HWLR35	PHFE000000000.1	29326219
<i>Beauveria bassiana</i>	ARSEF 2860	ADAH000000000.1	22761991
<i>Samsoniella hepiali</i>	FENG	LNDK000000000.2	Unpublished
<i>Akanthomyces lecanii</i>	RCEF 1005	AZHF000000000.1	27071652

Supplemental Table S2: Interspersed repeats and low complexity DNA sequences deduced by RepeatMasker in the *Parengyodontium torokii* FJII-L10-SW-P1 genome

Characteristics	number of elements	length occupied (bp)	percentage of the genome (%)
Retroelements	257	69,759	0.23
Penelope	2	115	0
LINES	37	7,368	0.02
CRE/SLACS	1	453	0
R1/LOA/Jockey	2	271	0
LTR elements	220	62,391	0.21
Ty1/Copia	49	5,535	0.02
Gypsy/DIRS1	122	45,845	0.15
DNA transposons	185	89,975	0.3
hobo-Activator	16	4,741	0.02
Tc1-IS630-Pogo	58	20,832	0.07
En-Spm	0	0	0
MuDR-IS905	0	0	0
PiggyBac	17	15,249	0.05
Tourist/Harbinger	4	259	0
Other (Mirage, P-element, Transib)	1	85	0
Rolling-circles	1	70	0
Unclassified	220	49,926	0.16
Small RNA	7	5,524	0.02
Simple repeats	6431	239,287	0.79
Low complexity	728	33,542	0.11

Supplemental Table S3. Full Carbohydrate-active enzymes (CAZymes) profile of 9 Cordycipitaceae fungal species

	S. aogashimae nse 72-15_1	P. toroki JC1038	L. sp. LEC01	Parengyodon ntium_amer icanum	L. fungicola 150-1	Lecanicillium m_psalliotae e_HWLR35	B. bassiana ARSEF_2860	S. hepiali FENG	A. lecanii RCEF_1005
AA1	7	8	9	9	8	7	11	9	6
AA11	3	4	4	5	6	5	4	6	6
AA12	2	2	2	2	3	3	2	2	3
AA13	1	0	0	0	0	0	0	0	0
AA14	1	1	1	1	3	1	0	1	1
AA2	6	2	2	3	2	5	3	3	4
AA3	25	15	15	15	36	15	13	12	13
AA4	2	1	1	1	1	1	2	0	0
AA5	1	2	1	0	4	2	3	2	2
AA6	1	0	1	1	4	1	1	1	1
AA7	19	12	11	13	19	12	16	10	13
AA8	4	4	3	2	4	2	2	2	2
AA9	2	1	1	1	1	1	1	1	1
CBM13	0	0	0	1	1	0	0	0	1
CBM18	0	0	0	0	0	0	0	1	0
CBM20	1	2	2	2	1	0	1	1	0
CBM21	1	1	1	1	1	1	1	1	1
CBM24	1	1	1	1	2	1	0	0	0
CBM32	1	1	1	0	2	1	2	1	1
CBM38	1	0	0	0	0	1	0	0	0
CBM39	0	0	0	0	1	0	0	0	0
CBM42	3	1	1	3	1	4	1	3	4
CBM43	1	1	1	2	1	0	0	0	0
CBM50	2	2	3	6	1	2	3	2	4
CBM52	0	0	0	0	0	1	0	0	0
CBM66	1	1	2	1	5	6	1	3	3
CBM67	1	0	0	2	1	1	0	1	1
CE1	4	3	3	3	4	2	2	2	2
CE10	31	24	27	29	35	19	20	22	23
CE16	4	1	2	2	1	2	1	1	1
CE3	6	3	2	5	2	4	1	3	4
CE4	3	4	4	4	4	3	3	3	3
CE5	8	5	3	2	5	10	5	8	14
CE9	1	1	1	1	1	1	1	1	1
GH1	1	3	3	3	2	1	1	1	2
GH10	0	0	0	0	0	0	1	0	0
GH105	4	2	2	2	9	2	0	1	2
GH109	1	1	1	1	0	0	0	0	1

	S. aogashimae nse 72-15_1	P. toroki JC1038	L. sp. LEC01	Parengyodon ntium_amer icanum	L. fungicola 150-1	Lecanicillium m_psalliotae e_HWLR35	B. bassiana ARSEF_2860	S. hepialii FENG	A. lecanii RCEF_1005
GH11	1	1	1	0	0	0	0	0	0
GH114	2	2	2	2	1	3	1	1	1
GH115	0	1	1	1	0	0	0	0	0
GH12	2	1	1	1	2	0	1	1	1
GH125	3	3	3	3	2	3	3	3	3
GH127	0	0	0	0	1	0	0	0	1
GH128	4	3	3	3	5	9	3	7	7
GH13	8	8	8	7	8	5	4	5	5
GH131	0	0	0	0	0	1	0	0	0
GH132	2	2	2	3	5	2	2	2	2
GH133	1	1	1	1	1	1	1	1	1
GH134	1	0	0	0	0	0	0	0	0
GH135	1	0	0	0	1	1	0	1	0
GH136	1	1	1	0	1	2	1	1	1
GH141	0	0	1	0	0	0	0	0	0
GH142	1	1	1	1	1	1	1	1	1
GH15	1	3	3	2	2	2	2	2	2
GH152	0	0	1	0	1	1	0	0	0
GH154	2	1	1	0	5	1	1	1	1
GH16	18	16	17	16	19	20	20	22	20
GH162	1	0	0	1	1	0	1	1	1
GH17	4	2	2	2	2	2	2	2	2
GH18	28	15	19	21	31	26	19	26	25
GH2	11	9	10	8	10	8	7	8	8
GH20	6	8	8	8	6	8	4	6	7
GH24	4	2	2	4	1	2	0	0	0
GH25	1	1	1	2	2	2	1	2	1
GH27	0	0	0	0	2	0	0	0	0
GH28	2	1	1	1	2	1	1	1	1
GH29	3	3	3	4	1	2	2	2	2
GH3	11	13	12	13	15	14	11	10	12
GH30	2	1	1	1	1	2	0	0	0
GH31	7	5	6	6	8	7	6	5	7
GH32	2	1	1	2	1	2	1	1	1
GH33	0	2	2	3	0	0	0	0	0
GH35	2	2	3	5	3	3	3	3	3
GH36	2	2	2	3	3	2	1	2	2
GH37	2	2	2	2	3	2	2	2	2
GH38	1	1	1	1	3	1	1	1	1
GH4	1	0	0	0	0	0	0	0	0
GH43	6	4	4	4	1	5	2	3	3

	S. aogashimae nse 72-15_1	P. toroki JC1038	L. sp. LEC01	Parengyodon ntium_amer icanum	L. fungicola 150-1	Lecanicillium m_psalliotae e_HWLR35	B. bassiana ARSEF_2860	S. heptali FENG	A. lecanii RCEF_1005
GH45	1	0	0	0	0	1	0	0	1
GH47	8	9	9	9	7	8	7	8	8
GH5	12	9	9	7	13	8	7	8	9
GH51	0	0	1	1	0	0	0	0	0
GH53	0	0	1	0	0	0	0	0	0
GH54	3	1	1	4	1	4	1	3	4
GH55	7	3	3	5	14	9	8	10	4
GH6	1	0	0	0	0	0	0	0	0
GH64	4	2	2	2	2	2	1	2	2
GH65	2	1	1	1	1	1	0	1	1
GH67	0	0	0	1	0	0	0	0	0
GH7	1	0	0	0	0	0	0	0	0
GH71	3	1	1	2	3	1	0	1	2
GH72	5	6	6	6	6	5	6	5	5
GH75	5	4	4	4	25	8	2	5	5
GH76	19	11	12	14	9	11	8	11	11
GH78	2	1	1	3	2	3	0	2	2
GH79	5	1	1	3	3	4	2	4	5
GH81	2	2	2	2	2	2	1	2	2
GH84	1	1	1	1	1	1	1	1	1
GH88	3	3	3	1	7	2	1	1	2
GH89	3	3	2	2	1	2	2	3	2
GH92	4	5	5	5	5	5	4	4	4
GH93	2	2	3	1	0	0	0	1	1
GH95	2	1	1	1	4	1	1	1	1
GT1	5	4	4	4	8	2	5	3	2
GT15	4	4	4	4	3	3	3	3	3
GT17	2	2	2	2	5	2	4	2	2
GT2_Chitin_synth	6	6	6	6	6	6	6	6	6
GT2_Glyco_tranf_2	2	1	2	2	3	2	2	2	2
GT2_Glyco_trans_2	5	2	2	2	0	2	3	2	2
GT2_Glycos_transf	2	2	2	2	2	2	2	2	2
GT20	4	7	7	4	4	4	4	6	4
GT21	1	1	1	1	1	1	1	1	1
GT22	4	4	4	4	4	4	4	4	4
GT24	1	0	0	1	1	1	1	1	0
GT25	1	2	1	5	7	5	5	5	4
GT3	1	1	1	1	1	1	1	1	1
GT31	0	0	0	0	0	1	0	0	0
GT32	4	4	4	5	3	3	4	3	3
GT33	1	1	1	1	0	1	1	1	1

Supplemental Table S4. Genes related to formation of biofilm, adherence and glycosaminoglycan (GAG) biosynthesis characterized in *Aspergillus fumigatus* and identified in the *Pare*

gene name in <i>A. fumigatus</i>	gene ID in <i>A. fumigatus</i>	Predicted function	Best match in <i>P. torokii</i>
uge3	Afu3g07910	UDP-glucose epimerase required for GAG synthesis. Null mutants are unable to adhere to abiotic surfaces and exhibit reduced adherence to epithelial cells	H0188_002713
medA	Afu2g13260	Transcription factor that regulates GAG biosynthetic cluster. Null mutants have reduced <i>uge3</i> expression and reduced adhesion	H0188_004544
stuA	Afu2g07900	Transcription factor that regulates GAG biosynthetic cluster. Null mutants have reduced <i>uge3</i> expression and reduced adhesion	H0188_006447
somA	Afu7g02260	Transcription factor, upstream regulator of <i>medA</i> and <i>stuA</i> . Role in GAG biosynthesis regulation. Null mutants have decreased adherence	H0188_006643
mpkA	Afu4g13720	MAP kinase, null mutants have decreased adherence, cell wall integrity	H0188_008493
sitA	Afu6g11470	MpkA-regulating phosphatase, upstream regulator of <i>mpkA</i> in coordinating surface adhesion and cell wall composition	H0188_008416
gtb3	Afu3g07860	Has domain(s) with predicted role in biosynthetic process	X
ega3	AFUA_3G07890	endo- α -1,4-polygalactosaminidase	H0188_003078
sph3	Afu3g07900	α -1,4-galactosaminogalactan hydrolase	X
agd3	Afu3g07870	Extracellular serine rich protein; predicted secretory signal sequence; ortholog of <i>A. nidulans</i> AN2954	H0188_008471
-	Afu2g01700	AMP-activated protein kinase activity	H0188_000928
exg1	Afu1g03600	glucan endo-1,6-beta-glucosidase activity	H0188_003673
bgt1	Afu1g11460	1,3-beta-glucanotransferase	H0188_003464
adh1	Afu7g01010	alcohol dehydrogenase	H0188_004408
acyA	Afu6g08520	Adenylate cyclase of the cAMP-dependent signaling pathway	H0188_005876
rhbA	Afu5g05480	Ras-related signaling protein	H0188_008959
rasA	Afu5g11230	Ras family GTPase protein	H0188_002821
pkcC	Afu2g12200	cAMP-dependent protein kinase catalytic subunit	H0188_008806
mpkA	Afu4g13720	Mitogen-activated protein kinase	H0188_008493
-	Afu6g11010	Ortholog(s) have role in budding cell apical bud growth, cell budding, cell morphogenesis, cellular response to biotic stimulus, cellular response to drug and cellular response to neutral pH	H0188_003706
-	Afu3g14040	Ortholog(s) have role in filamentous growth of a population of unicellular organisms and growth of unicellular organism as a thread of attached cells	H0188_002587
-	Afu3g08050	Ortholog(s) have DNA-binding transcription factor activity, RNA polymerase II-specific, RNA polymerase II transcription regulator recruiting activity, transcription coactivator activity	H0188_004740
-	Afu2g17860	Ortholog(s) have role in cellular response to drug, growth of symbiont in host and positive regulation of cell adhesion involved in single-species biofilm formation	H0188_005262
-	Afu2g10640	Ortholog(s) have chromatin binding, histone acetyltransferase activity, phosphatidylserine binding, sequence-specific DNA binding, transcription coactivator activity, transcription regulator activity	H0188_009550
-	Afu2g03460	Ortholog(s) have DNA-binding transcription activator activity, RNA polymerase II-specific, DNA-binding transcription repressor activity, RNA polymerase II-specific activity	H0188_007512
-	Afu1g17150	Ortholog(s) have role in cellular carbohydrate metabolic process, maltose catabolic process, maltose metabolic process and positive regulation of cell adhesion involved in single-species biofilm formation	H0188_001623
-	Afu1g01850	Ortholog(s) have DNA-binding transcription factor activity, RNA polymerase II-specific activity and role in negative regulation of single-species biofilm formation, negative regulation of transcription by RNA polymerase II	H0188_000557
-	Afu3g13790	Ortholog(s) have calcium transmembrane transporter activity, phosphorylative mechanism, ion transmembrane transporter activity, phosphorylative mechanism activity	H0188_004626
zfpB	Afu1g10230	Putative C2H2 zinc-finger transcription factor	H0188_005857
scw4	Afu6g12380	Ortholog(s) have role in cell adhesion, cell adhesion involved in single-species biofilm formation, cell-substrate adhesion, cellular response to glucose starvation and cellular response to neutral pH,	H0188_003464
mnt1	Afu5g10760	Putative alpha-1,2-mannosyltransferase with a predicted role in protein glycosylation; 1 predicted transmembrane domain	H0188_002879
-	Afu4g04070	Protein of unknown function, phoB-regulated	H0188_005032
sitA	Afu6g11470	Serine/threonine phosphatase required for cell wall integrity, biofilm formation, adhesion and virulence	H0188_008416
-	Afu4g13660	Ortholog(s) have efflux transmembrane transporter activity, polyamine transmembrane transporter activity	H0188_007721
-	Afu3g03190	Ortholog(s) have cation transmembrane transporter activity, efflux transmembrane transporter activity, xenobiotic transmembrane transporter activity (1)	H0188_003803
yvc1	Afu3g13490	Calcium activated cation channel with a predicted role in cellular cation homeostasis	H0188_004780
ptcB	Afu1g09280	Putative type 2C protein phosphatase (PP2C) involved in dephosphorylation of SakA MAP kinase in response to osmotic stress	H0188_004047

Supplemental Table S5 - Genes involved in melanin biosynthesis, radioresistance and microgravity resistance.

Melanin biosynthesis

DHN-melanin pathway

Gene ID in <i>Aspergillus fumigatus</i>	Gene ID in <i>Aspergillus niger</i>	Homologue in <i>Parengyodontium torokii</i>
pksP/Afu2g17600	An03g05440	H0188_000958
ayg1/Afu2g17550	An14g05350	H0188_005280
arp2/Afu2g17560	An02g00220	H0188_009464
arp1/Afu2g17580	An08g09920	X
abr2/Afu2g17530	An01g1366	H0188_000003
abr1/Afu2g17540	An14g05370	H0188_005715

DOPA-melanin pathway

melC2/Afu3g01070	An01g09220	H0188_002942
melO/Afu1g17430	An12g01670	H0188_005733
tpcJ/Afu4g14490	An12g05810	H0188_002651

L-Tyrosine degradation pathway

tat/Afu2g13630	An02g05540	H0188_009650
hppD/Afu2g04200	An11g02200	H0188_004175
hmgA/Afu2g04220	An11g02180	H0188_000361
fahA/Afu2g04230	An11g02170	H0188_000334
maiA/Afu2g04240	An11g02160	H0188_008130

Radioresistance genes

rad51/Afu1g10410		H0188_003614
rad54/Afu6g12910		H0188_003451
rad54b/Afu1g15120		H0188_004866
rdh54/Afu1g15120		H0188_003451
rad9/Afu5g04020		H0188_001584
rad9b/Afu2g10710		H0188_005646

Microgravity resistance gene*

Proteinase K (<i>Parengyodontium album</i>) - X14689.1		H0188_006801/H0188_008610
Floculin A (<i>Saccharomyces pastorianus</i>) - 4LHK_A		X
Floculin B (<i>Saccharomyces pastorianus</i>) - 4LHK_B		X
DNA repair protein rad9 (<i>Schizosaccharomyces pombe</i>) - P26306		H0188_005646
Daughter-specific expression protein 2 (<i>Saccharomyces cerevisiae</i>) - P38844.1		H0188_008471
Daughter-specific expression protein 1 (<i>Saccharomyces cerevisiae</i>) - P40077		X

* Query genes were selected from multiple fungal species

Table S6. Secondary metabolite clusters identified by antiSMASH v6. in the *Parengyodontium torokii* FJII-L10-SW-P1 genome.

Region (genomic Scaffold)	Type	From	To	Most similar known cluster		Similarity
Region 1.1	NRPS	235,392	283,546			
Region 1.2	NRPS-like	499,503	542,84			
Region 1.3	T1PKS	545,554	593,164			
Region 2.1	NRPS	504,787	537,693			
Region 7.1	NRPS-like,T1PKS	288	35,258			
Region 7.2	T1PKS,NRPS	211,319	263,478	equisetin	NRP + Polyketide	45%
Region 8.1	NRPS-like	14,078	57,416			
Region 9.1	terpene	186,065	207,624			
Region 13.1	NAPAA	185,108	218,998			
Region 14.1	NRPS-like	79,895	123,667			
Region 19.1	NRPS	74,496	126,369			
Region 21.1	T1PKS	155,29	201,697			
Region 24.1	T1PKS	126,575	173,852			
Region 25.1	T1PKS	169,887	206,955			
Region 37.1	NRPS,NRPS-like	66,329	160,996	cephalosporin C	NRP	71%
Region 45.1	T1PKS	1	41,374			
Region 46.1	T1PKS,NRPS	81,864	134,547			
Region 49.1	NRPS-like,T1PKS	87,657	160,102	EQ-4	NRP	100%
Region 70.1	terpene	86,187	107,762	squalestatin S1	Terpene	40%
Region 76.1	NRPS	13,728	64,552	curvupallide-B	NRP + Polyketide	50%
Region 78.1	NRPS,T1PKS	1	41,975	cytochalasin E / cytochalasin K	NRP + Polyketide:iterative type I	15%
Region 98.1	NRPS	16,327	63,391			
Region 103.1	NRPS	1	45,747			
Region 108.1	NRPS,T1PKS	9,595	61,452	pyranonigrin E	Polyketide	100%
Region 109.1	NRPS-like	27,908	71,988			
Region 111.1	T1PKS	61,274	92,081			
Region 132.1	terpene	39,107	60,084			
Region 135.1	T1PKS,NRPS-like	21,748	71,69			
Region 161.1	NRPS	1	41,834			
Region 208.1	NRPS	1	45,777			
Region 213.1	T1PKS	1	37,438			
Region 220.1	NRPS	11,41	42,442	dimethylcoprogen	NRP	100%

Supplemental Table S7. LC-MS analysis of *Parengyodontium torokii* FJ11-L10-SW-P1 based on identified biosynthetic gene clusters.

Name of Compound	Standard m/z	Standard d RT	Experiment al m/z	Experiment al RT	Library fragmentation Data										Experimental Fragmentation Data									
					Frg 1	Frg 2	Frg 3	Frg 4	Frg 5	Frg 6	Frg 7	Frg 8	Frg 9	Frg 10	Frg 1	Frg 2	Frg 3	Frg 4	Frg 5	Frg 6	Frg 7	Frg 8	Frg 9	Frg 10
Rice																								
5,8-Epidioxyergosta-6,9(11),22-trien-3-ol	427.32	7.9	427.3197	7.78	409	391	381	363	339	303	285	267	175	147	409	391	381	339	311	301	285	283	267	239
(E)-2,3-dihydroxypropyl octadec-6-enoate	357.2996	7.98	357.2994	7.95	339	283	265	247	177	163	151	149	135	121	339	283	265	247	191	165	151	149	135	121
Betulinan C	291.1018	5.64	291.1011	5.72	291	276	273	263	260	259	258	245	231	213	291	276	273	263	260	259	258	245	231	213
6,9-Octadecadienoic acid	281.2476	7.25	281.2473	7.21	264	263	246	245	221	163	151	149	135	121	264	263	246	245	185	180	176	166	150	136
Cyclo (L-Pro-L-Leu)	211.1437	1.89	211.1436	1.96	211	194	183	155	138	127	86	70			194	183	167	166	155	138	127	86	70	69
Ergosta-4,6,8(14),22-tetraen-3-ol, (3 β ,22E)-	395.3303	8.82	395.3298	8.82	377	325	311	307	293	269	253	251			377	335	325	311	307	293	271	269	253	251
Cyclo (Pro-Phe)	245.1281	2.29	245.128	2.32	245	228	217	200	172	154	131	120	70		227	217	213	204	200	181	146	120		
Oatmeal																								
5,8-Epidioxyergosta-6,9(11),22-trien-3-ol	427.32	7.9	427.3196	7.79	409	391	381	363	339	303	285	267	175	147	427	410	409	391	382	339	301	285	283	267
Cephalochromin	519.1267	5.45	519.127	5.47	519	501	477	476	473	459	260	245	219	218	519	501	500	478	477	459	261	260	245	184
(E)-2,3-dihydroxypropyl octadec-6-enoate	357.2996	7.98	357.2994	8.07	339	283	265	247	177	163	151	149	135	121	339	283	265	247	177	165	163	149	135	121
Cyclo (L-Pro-L-Leu)	211.1437	1.89	211.1437	1.74	211	194	183	155	138	127	86	70			194	193	183	170	166	155	138	127	86	70