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Article

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Culturable mycota on bats in central and southern Yunnan Province, China

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Abstract

Bats represent the second largest mammal group, with over 1400 known species dispersed across six continents. Bats are unique in many ways. Notably, their incredible longevity, with a life span of up to ten times longer than what might be expected from their body size and a unique ability to tolerate viruses without displaying any symptoms, means they provide an area of particular importance from a disease risk perspective. In addition, the warm, humid environments in which bats occur provide ideal habitats for fungi to grow, and the bats potentially carry various

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pathogens that can threaten plants, animals, and humans. Whilst the role of bats as reservoir of viruses is well known, their role as a host to various fungi has been largely neglected. To explore this gap, we investigated the culturable mycota isolated from bats in the diverse Yunnan Province, China. In total, 164 samples from 104 bats were collected, and 164 fungal strains, representing 25 species, were isolated using the dilution plate method. The majority of these species were discovered for the first time from bats, and 14 new species and 11 new records are described in this paper. Some species were previously known from other environments, as pathogens of plants, animals, or humans. Based on morphology and multigene phylogeny, we conclude that bats host a high fungal diversity, including a number of previously unknown species. Novel species described in this paper include *Amphichorda yunnanensis*, *Apiospora xishuangbannaensis*, *Clonostachys rhinolophicola*, *Fusarium hipposidericola*, *F. menglaense*, *F. rhinolophicola*, *F. yunnanense*, *F. xishuangbannaense*, *Neopestalotiopsis xishuangbannaensis*, *Phialemoniopsis hipposidericola*, *Ph. xishuangbannaensis*, *Trichoderma hipposidericola*, *T. rhinolophicola* and *T. xishuangbannaense.*

Keywords – 11 new records – 14 new species –*Ascomycota* – Bat fungi – Caves – Microfungi – Morphology – Phylogeny – Plant pathogens

Introduction

Bats (*Chiroptera*), the only mammal with powered flight, are the second most species-rich mammal order, with more than 1400 species described (Jones et al. 2009, Prothero 2017, Wilson & Mittermeier 2019, Jiang et al. 2020, Ogórek et al. 2020, Poofery et al. 2021, Simmons & Cirranello 2023). Bats inhabit all continents except Antarctica, with diversity peaking in the tropics and subtropics (Jones et al. 2009, Prothero 2017, Ogórek et al. 2020). Bats are well known for their unique immune systems and the diverse viruses they can carry which can result in human and animal diseases, such as Severe acute respiratory syndrome (SARS), SARS-coronavirus disease 2019 (SARS-CoV-2), Ebola virus disease (EV), Hendra virus disease (HeV), Nipah virus infection (NV), Marburg virus disease (MV), the Middle East respiratory syndrome (MERS), Puumala virus infection (PUUV) and Rabies (RV) (He 2014, Leng & Gao 2020, Magnino et al. 2020, Zhou et al. 2020, 2021, Poofery et al. 2021).

In addition to viruses, bats also carry various fungal species, some of which have been responsible for mass mortalities in bats, such as White Nose Syndrome (WNS) caused by *Pseudogymnoascus destructans* (Blehert & Gargas) Minnis & D.L. Lindner (*Thelebolales, Ascomycota*), leading to the death of more than seven million bats in North America (Blehert et al. 2009, Warnecke et al. 2012, Sharma et al. 2019, Magnino et al. 2020, Zhang et al. 2020, Liu et al. 2021, White-nose syndrome 2022). Identifying bat-associated fungi is important as some species associated with bats might be plant or animal pathogens. For example, *Aspergillus fumigatus* Fresen, *A. sydowii* (Bainier & Sartory) Thom & Church, *Candida glabrata* (H.W. Anderson) S.A. Mey. & Yarrow and *Rhodotorula mucilaginosa* (A. Jörg.) F.C. Harrison cause human diseases, *Paecilomyces formosus* Sakag., May. Inoue & Tada ex Houbraken & Samson can result in plant and human diseases, and *Fusarium equiseti* (Corda) Sacc. and *F. incarnatum* (Desm.) Sacc. cause plant diseases (Swezey & Garrity 2011, Shah-Hosseini et al. 2012, Warnecke et al. 2012, Cunha et al. 2020, Magnino et al. 2020), that could pose an underappreciated threat. Bats can also roost in colonies of up to millions of individuals in thermally stable, moist conditions, which provide ideal habitats for fungal growth and transmission. The need for further study of bats and cave fungi has been highlighted with the emergence of WNS in North America in 2006 (Warnecke et al. 2012, Kokurewicz et al. 2016, Cunha et al. 2020, Zhang et al. 2020, Liu et al. 2021).

Some of the earliest reports of bat-associated fungi came from Columbia (Grose & Marinkelle 1966), but subsequent studies described a high diversity of fungi associated with bats in other regions. For example, in a recent study, 36 species of bat-associated fungi were isolated in Northeastern Brazil (Cunha et al. 2020). Research on bat-associated fungi has largely focused on Australia, Europe, the USA, and Brazil (Kokurewicz et al. 2016, Holz et al. 2018, Lorch et al.

2018, Nováková et al. 2018, Cunha et al. 2020, Ogórek et al. 2020). In China, Karunarathna et al. (2020) conducted the first and only study on bat fungi, and reported seven fungal species from bat carcasses in Yunnan Province, China, highlighting the fact that the fungi are commonly associated with bats.

Yunnan provides an ideal location for the study of bats and bat-associated fungi as it has a highly heterogenous landscape. Although Yunnan experiences summer monsoon rainfall patterns, it is divided into distinct climate zones. Northern Yunnan reaches elevations of more than 5000 m.a.s.l, with subalpine environments, central Yunnan, which forms part of Yunnan-Guizhou Plateau, has an elevation of about 1900 m.a.s.l, and is characterized by a temperate climate. Southern Yunnan lies in the lower elevations and has sub-tropical to tropical climate zones. This variation in climate types creates a varied landscape with multiple habitats and a high species diversity index. There are more than 6000 species of fungi already recorded in Yunnan (Feng & Yang 2018), however, the number of bat species in Yunnan has not been properly estimated yet since there are numerous undescribed bat species and unstudied habitats.

Little is known about the taxonomy, diversity, and ecological roles of bat-associated fungi. We aim to fill the knowledge gap relating to the study of bat-associated fungi with our descriptions of new and known fungal species found on bats in the central and southern parts of Yunnan Province, China, and provide detailed morphological descriptions and phylogenetic analyses of the fungal species that we isolated from bats in Yunnan.

Materials & methods

Sample collection

Fieldwork was conducted in four sites from May to September 2020 (Fig. 1, Table 1) using four bank harp traps and a set of selected mist nets (4 shelves, 4 m high). Bats were collected as part of a broader study investigating the diversity of bat species in Yunnan Province, by a team of experts from the Xishuangbanna Tropical Botanical Gardens, Chinese Academy of Sciences. Bats were handled according to standard protocols (Cunha et al. 2020, Kim et al. 2023) and were not harmed during the sampling process. Bats were released after the sampling procedures and data gathering were completed. Morphological features were measured using digital calipers based on standard measurements, while the bats were photographed from the side. The front wing tissue samples were collected using a 3 mm biopsy punch and stored in 99% ethanol for later DNA verification at the Southwest Barcoding Center (Chornelia et al. 2022). From each individual, swabs (used for sampling of fungi) were taken from three areas on the bat's body, namely feet, fur (belly and back) and patagium (ventral and dorsal surface) (Cunha et al. 2020, Kim et al. 2023) (Fig. 2). Bat morphology combined with DNA barcoding was used to identify the bat species and measurements were checked with Francis (2009). Samples were collected using sterile swabs pre-moistened with sterilized chloramphenicol (0.1 mg/L) solution. These were rolled back and forth three times across the bat fur and wing membrane. Swabs were then individually placed in sterilized 50 mL conical centrifuge tubes containing 15 mL chloramphenicol (0.1 mg/L) solution, labelled, and stored at 4 °C (Cunha et al. 2020). In total, 14 bat species were sampled in the course of this work (Supplementary Table 1).

Fungal isolations

In the laboratory, the conical centrifuge tubes were shaken to mix the 15 mL chloramphenicol solution, and then the suspension was spread using a sterilized cotton bud on potato dextrose agar (PDA, Oxoid, England) plates containing amoxicillin (50 µg/mL), the procedure was performed in triplicate. The PDA plates were incubated at room temperature until individual fungal colonies were visible. Fast-growing fungi were subcultured into new plates in one to three days' time, while slow-growing ones were subcultured after one month. Individual fungal colonies were subcultured on new PDA plates in triplicate and incubated at room temperature. All fungal strains were stored at 4 °C for further studies.

Figure 1 – Sampling locations in Yunnan Province of China. Location names are denoted by numbers and full names (Table 1). Source: The original map was extracted from Baidu.

Table 1 Information of the sampled locations. The rainforest and limestone forest sampling areas listed in the table are both located in the subtropical area of Xishuangbanna; Shiliansi is a temperate forest area in central Yunnan; and long cave refers to a cave system found in central Yunnan. The number of samples referred to in the table indicate how many samples were taken in total for each area.

Site	Sampling area	Location	Longitude	Latitude	Altitude (m)	Samples
1	Rainforest	XFBG, Xishuangbanna, Yunnan Province	101.27156ºE	21.91890ºN	570.0	46
2	Limestone forest	XFBG, Xishuangbanna, Yunnan Province	101.28240ºE	21.90760ºN	520.0	49
3	Shiliansi	Pubei Village, Yimen County, Yuxi, Yunnan Province	102.1633ºE	24.61746ºN	616.2	48
4	Long cave	Xishan District, Kunming, Yunnan Province	102.6005ºE	24.50839ºN	1988.3	21

Morphological observations

Morphological characteristics of the cultures sporulated on PDA after 60–80 days were examined. Morphological observations were performed using an Olympus SZ61 (Japan) Series stereomicroscope and photographed using an OLYMPUS SZ2-ILST and Industrial Digital Camera 16NP USB3.0 (Panasonic, Japan) microscope imaging system. Measurements were arranged using the Tarosoft Image Framework program (IFW) 0.97, and images were processed with Adobe Photoshop CS3 Extended version 10.0 software (Adobe Systems, USA).

Dry cultures were deposited in the herbarium of the Kunming Institute of Botany Academia Sinica (HKAS), while living cultures were deposited in the Kunming Culture Collection (KUMCC) and China General Microbiological Culture Collection Center (CGMCC), China. The MycoBank numbers (Robert et al. 2005) and Facesoffungi numbers (Jayasiri et al. 2015) were obtained, while fungal records were updated in the Greater Mekong region database (Chaiwan et al. 2021).

Figure 2 – Scenes of visited caves and bats. A An entrance to long cave. B, C Stalactite and stalagmite. D Bat guano. E, G Bat roosts. F–I Examples of handling the bats when collecting samples: F Lateral view of *Scotomanes ornatus* and standard way of holding (this position was also used for foot swabs). H The back of *S. ornatus* (position for fur swabbing). I Wing swab position of *S. ornatus.*

DNA extraction, PCR amplification and sequencing

A biospin Fungus Genomic DNA Extraction Kit-BSC14S1 (BioFlux, P.R. China) was used to extract DNA from pure fungal mycelia following the manufacturer's protocol. The extracted DNA was maintained at -20 °C for long-term storage. Polymerase chain reaction (PCR) was used to amplify three partial gene regions using the primers shown in Table 2. The total volume of PCR mixture per reaction was 25 µL, containing 2 µL DNA (50 ng/µL), 12.5 µL 2×FastTaq Premix (a mixture of FastTaq TM DNA Polymerase, buffer, dNTP Mixture, and stabilizer) (Beijing Qingke Biological Technology Co., Ltd., Beijing, P.R. China), 1 µL of each reverse and forward primer (10 µM) (Beijing Kinco Biotechnology Co., Ltd. Kunming Branch, P.R. China) and 8.5 µL double distilled water (ddH_2O) (Tibpromma et al. 2018). The quality of PCR products was checked on 1% agarose gel electrophoresis stained with TS-GelRed (TSJ002, Beijing Kinco Biotechnology Co., Ltd. Kunming Branch, China). Purification and sequencing of PCR products were performed by Beijing Kinco Biotechnology Co., Ltd. Kunming Branch, P.R. China.

Table 2 Details of genes/loci with PCR primers used in each fungal genus.

Genera name	Genes/loci	Primers (forward/reverse)	References
Amphichorda	ITS	ITS5/ITS4	White et al. (1990)
	RPB1	RPB1A/RPB1B-G2R	Matheny et al. (2002), Hofstetter et al. (2007)
	RPB2	RPB2-5f/RPB2-7cR	Liu et al. (1999)
	TEF1-α	EF1-983F/EF1-2218R	Rehner & Buckley (2005)
Apiospora	ITS	ITS5/ITS4	White et al. (1990)
	LSU	LR0R/LR5	Vilgalys & Hester (1990)
	TUB	Bt-2a/Bt-2b	Glass & Donaldson (1995)
	TEF1-α	EF1-728F/EF-2	O'Donnell et al. (1998), Carbone & Kohn (1999)
Aspergillus	ITS	ITS5/ITS4	White et al. (1990)
	BenA	Bt-2a/Bt-2b	Glass & Donaldson (1995)
	CaM	Cmd5/Cmd6	Hong et al. (2006)
	RPB2	RPB2-5f/RPB2-7cR	Liu et al. (1999)
Clonostachys	ITS	ITS1/ITS4	White et al. (1990)
	TUB	T1/T22	Glass & Donaldson (1995), O'Donnell & Cigelnik (1997)
Fusarium	ITS	ITS5/ITS4	White et al. (1990)
	CaM	CL1/CL2A	O'Donnell et al. (2000)
	RPB2	RPB2-5f/RPB2-7cR	Liu et al. (1999)
	RPB1	RPB1-FA/RPB1-G2R	O'Donnell et al. (2010)
	TUB	T1/T2	O'Donnell & Cigelnik (1997)
	TEF1-α	EF1/EF2	O'Donnell et al. (1998)
Neopestalotiopsis	ITS	ITS5/ITS4	White et al. (1990)
	TUB	Bt-2a/Bt-2b	Glass & Donaldson (1995)
	TEF1-α	EF1-728F/EF1-1567R	Carbone & Kohn (1999), Groenewald et al. (2018)
Penicillium	ITS	ITS5/ITS4	White et al. (1990)
	BenA	Bt-2a/Bt-2b	Glass & Donaldson (1995)
	Cam	Cmd5/Cmd6	Hong et al. (2006)
	RPB2	RPB2-5f/RPB2-7cR	Liu et al. (1999)
Phialemoniopsis	ITS	ITS1/ITS4	White et al. (1990)
	LSU	LR0R/LR5	Vilgalys & Hester (1990)
	ACT	Act1/Act5ra	Voigt & Wostemeyer (2000)
	TUB	TUB-F/TUB-R	Cruse et al. (2002)
Scopulariopsis	ITS	ITS5/ITS4	White et al. (1990)
	LSU	LR0R/LR5	Vilgalys & Hester (1990)
	TUB	Bt-2a/Bt-2b	Glass & Donaldson (1995)
	TEF1-α	EF1-983F/EF1-2218R	Rehner & Buckley (2005)
Trichoderma	ITS	ITS1/ITS4	White et al. (1990)
	RPB2	RPB2-5f/RPB2-7cR	Liu et al. (1999)
	TEF1-α	EF1-728F/TEF1LLErev	Carbone & Kohn (1999), Jaklitsch et al. (2005)

Phylogenetic analyses

Phylogenetic analyses followed the methods in Dissanayake et al. (2020). Newly generated sequence data were initially subjected to blastn search in NCBI to obtain the most probable closely related taxa in the GenBank (http://blast.ncbi.nlm.nih.gov/). Sequence data were retrieved from GenBank based on recent publications (https://www.ncbi.nlm.nih.gov/nuccore/). Forward and reverse sequences were assembled using Geneious Pro.v4.8.5. Single gene sequence datasets were aligned with MAFFT V. 7.215 (https://mafft.cbrc.jp/alignment/server/; Katoh & Standley 2016), trimmed in Trimal.v1.2rev59 and edited manually where necessary in BioEdit V.7.0.5.2 (Hall 1999). The sequence datasets were combined using SequenceMatrix and AliView or BioEdit V.7.0.5.2 (Hall 1999). FASTA datafile formats were transferred to PHYLIP and NEXUS formats by the online tool available on the website ALTER (http://sing.ei.uvigo.es/ALTER/) (Glez-Peña et al. 2010). Phylogenetic trees were based on Randomized Accelerated Maximum Likelihood (ML) and Bayesian inference analyses (BI).

Maximum likelihood trees were generated via RAxM ng the GTR+I+G model of evolution. BI analysis was conducted with MrBayes v. 3.1.2 (Stamatakis 2006, 2014, Stamatakis et al. 2008) in the CIPRES Science Gateway platform to evaluate posterior probabilities (PP) (Rannala & Yang 1996, Zhaxybayeva & Gogarten 2002) by Markov Chain Monte Carlo sampling (MCMC). The GTR+I+G evolution model was also applied in the BI analyses for all gene regions. Six simultaneous Markov chains were run for 2,000,000 to 5,000,000 generations, and trees were sampled at every 100th generation. The resulting trees were visualized in FigTree v. 1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/) and annotated in Microsoft PowerPoint 2019. The ML bootstrap supports (greater than or equal to 60%) and Bayesian posterior probabilities (greater than or equal to 0.90) are shown in the tree and presented under each relevant description. Sequence data of the new strains generated in this study are deposited in the GenBank, and the accession numbers are listed in Supplementary Table 2.

Genealogical concordance phylogenetic species recognition (GCPSR) analysis

We used the genealogical concordance phylogenetic species recognition analysis (GCPSR) to check for significant recombination events (Quaedvlieg et al. 2014). The data were analyzed using the pairwise homoplasy index (PHI) test in SplitsTree 4 to determine the recombination level with closely related species (Bruen et al. 2006, Huson & Bryant 2006, Quaedvlieg et al. 2014). Multi-locus datasets with closely related species were used for the analyses. The pairwise homoplasy index lower than 0.05 ($\Phi w < 0.05$) indicates significant recombination in the dataset. The relationships between closely related taxa were visualized by constructing split graphs from the concatenated datasets using the LogDet transformation and split decomposition options.

Results

Phylogenetic analyses

Aspergillus phylogeny was based on combined ITS, *BenA*, *CaM* and *RPB2* sequence data

The aligned dataset encompassed 205 strains representing 161 taxa, including two new records and the outgroup taxon *Aspergillus nanangensis* Pitt (FRR 6048, type). The trees from the two analyses (ML and BI) showed identical topologies. Multigene phylogenetic analyses based on ITS, *BenA*, *CaM* and *RPB2* show that our new isolates (KUMCC 21-0819 and KUMCC 21-0820) clustered with *Aspergillus creber* Jurjević, S.W. Peterson & B.W. Horn with a relatively high statistical support (ML/BI = 99/1.00) in section *Nidulantes* (Visagie & Houbraken 2020, Visagie et al. 2021), and the new isolates (KUMCC 21-0699 and KUMCC 21-0700) clustered with *As. candidus* with high statistical support (ML/BI = 100/1.00) in section *Candidi* (Visagie & Houbraken 2020, Visagie et al. 2021). The genus *Aspergillus* P. Micheli ex Haller sections are mentioned in the phylogenetic tree as described by Visagie & Houbraken (2020) and Visagie et al. (2021) (Fig. 3).

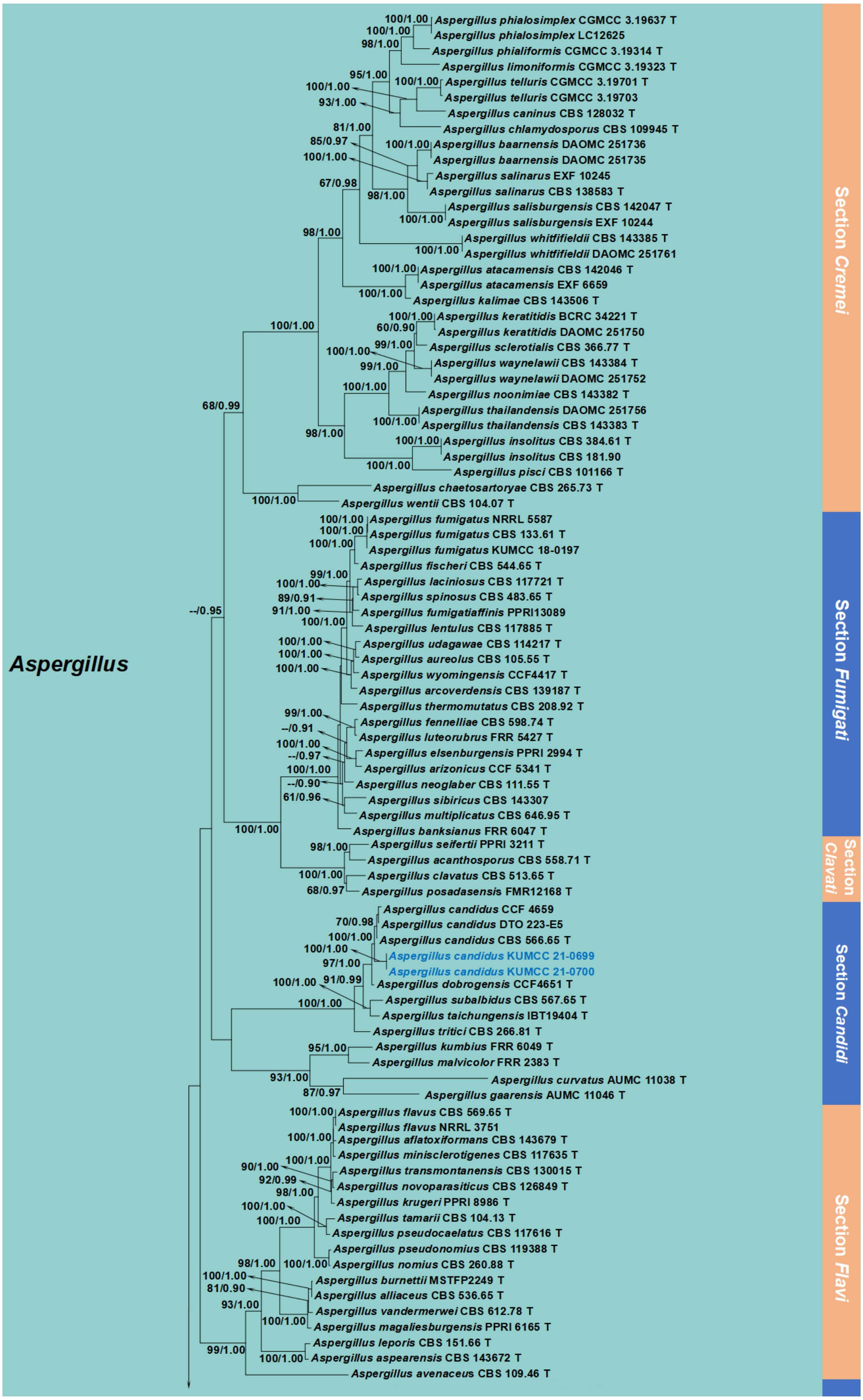


Figure 3 – Consensus phylogram of 1,000 trees resulting from a RAxML analysis of the (ITS+*BenA*+*CaM*+*RPB2*) alignment of the analyzed *Aspergillus* sequences. The RAxML analysis of the combined dataset yielded a best-scoring tree with a final ML optimization likelihood value of -76055.918838 and generated from 622, 516, 670 and 895 base pairs of ITS, *BenA*, *CaM* and *RPB2*

characters, respectively. The matrix comprises 1894 distinct alignment patterns with 19.67% gaps and indeterminate traits. Base frequencies were estimated as follows A = 0.229451, C = 0.271908, G = 0.265799, T = 0.232842 with substitution rates AC = 1.004088, AG = 3.355531, AT = 1.224976, CG = 0.887573, CT = 5.219361, GT = 1.000000; proportion of invariable sites I = 0.303218; gamma distribution shape parameter α = 0.789571. RaxML bootstrap support values (ML equal to or above 60%) and Bayesian inference posterior probabilities (BYPP equal to or above 0.90) are given at the nodes (ML/BYPP). The sequences of the new strains are in blue. The scale bar represents the expected number of changes per site. Type strains are denoted with T.

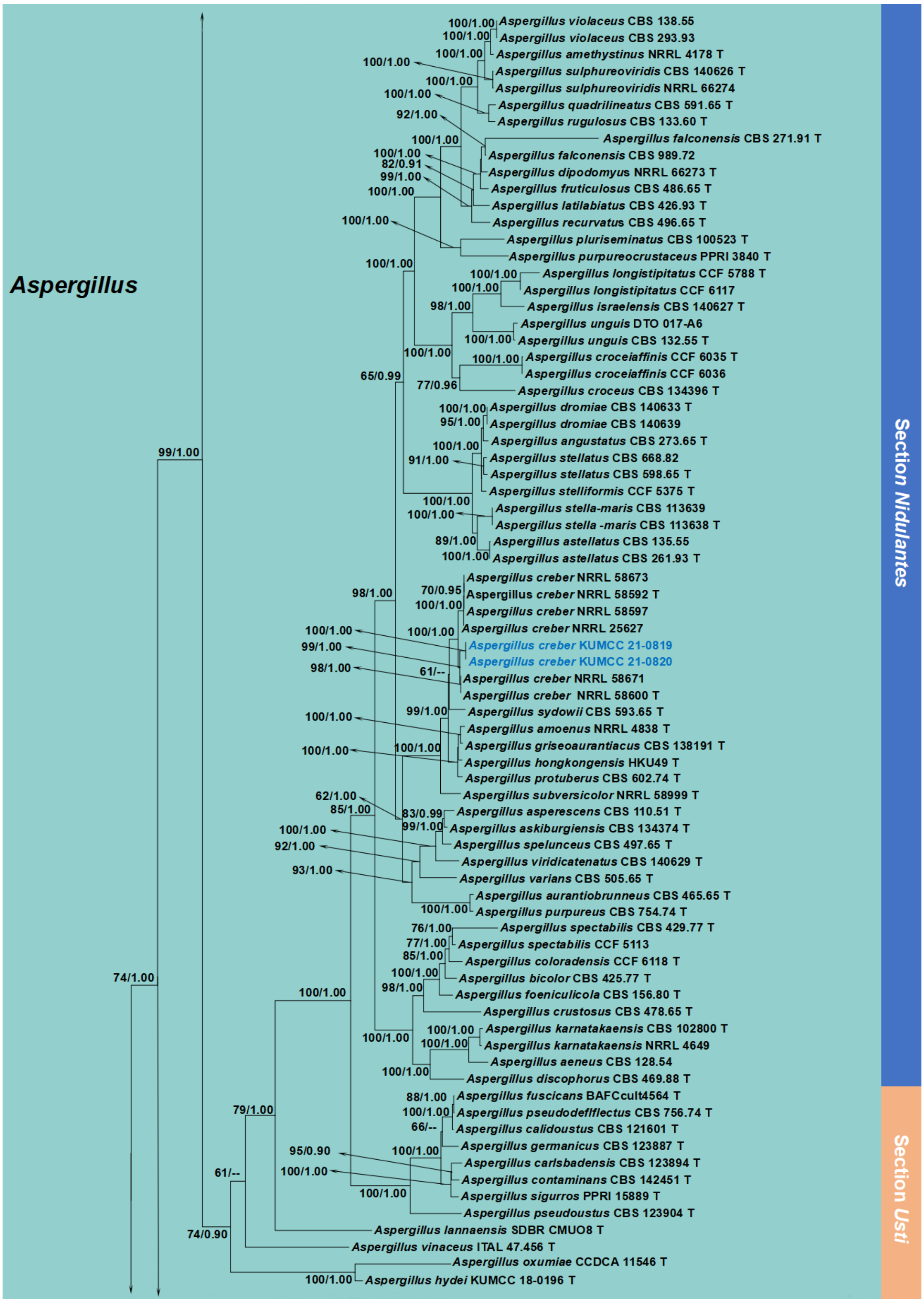


Figure 3 – Continued.

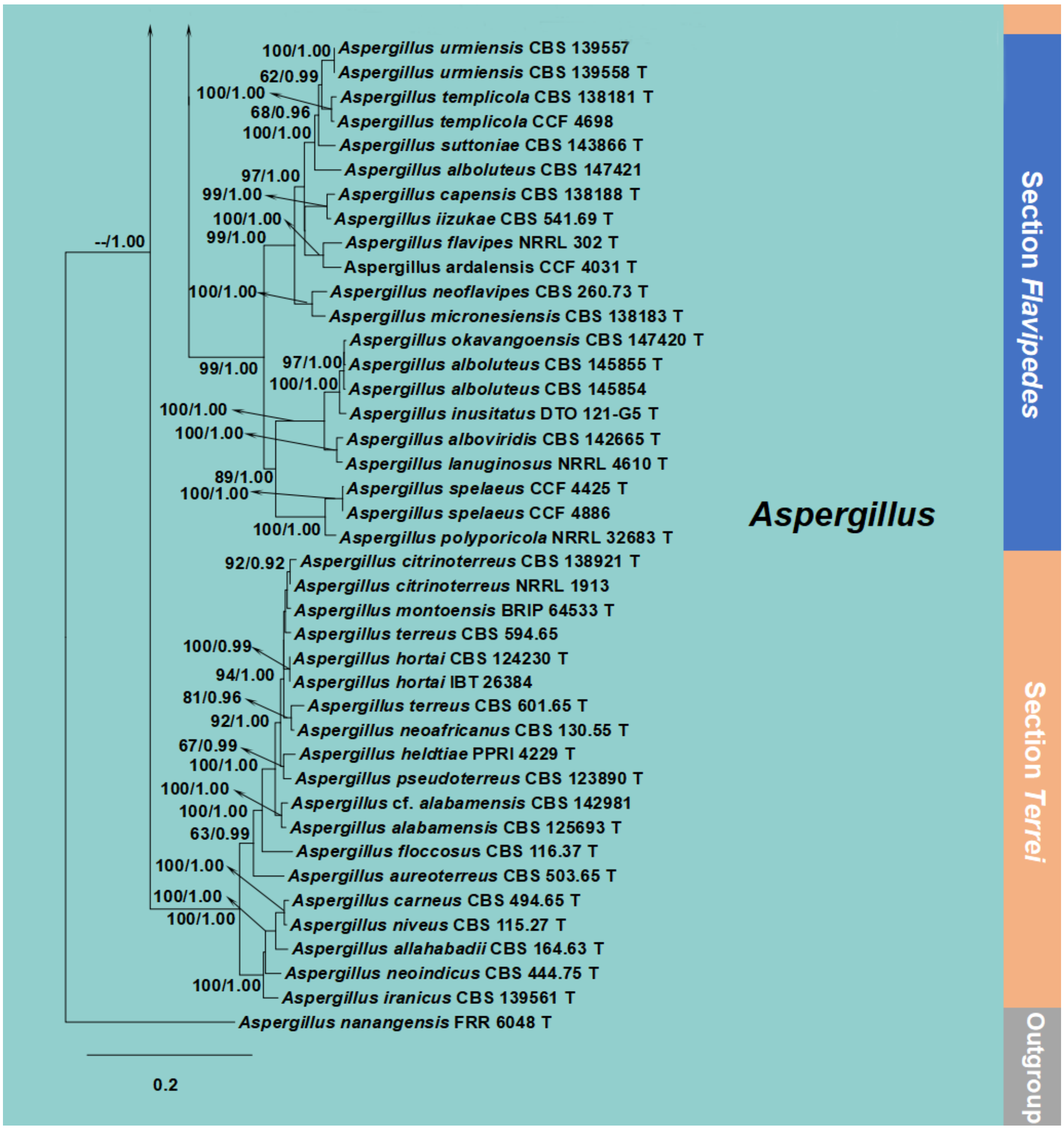


Figure 3 – Continued.

Penicillium phylogeny was based on combined ITS, *BenA*, *Cam* and *RPB2* sequence data

The aligned dataset encompassed 144 strains representing 98 taxa, including the new record and the outgroup taxon *Penicillium sacculum* E. Dale (CBS 23.61). The trees from the two analyses (ML and BI) showed identical topologies. Multigene phylogenetic analyses based on ITS, *BenA*, *Cam* and *RPB2* show our new isolates (KUMCC 21-0762, KUMCC 21-0763, KUMCC 21-0764, KUMCC 21-0765, KUMCC 21-0766, KUMCC 21-0767, KUMCC 21-0768 and KUMCC 21-0769) clustered with *Penicillium brevicompactum* Dierckx with relatively high statistical support (ML/BI = 95/1.00) in section *Brevicompacta*. *Penicillium* Link sections in the phylogenetic tree (Fig. 4) were followed by Houbraken et al. (2014, 2016, 2020) and Ramos et al. (2021).

Apiospora phylogeny was based on combined LSU, ITS, *TUB* and *TEF1-α* sequence data

The combined alignment encompassed 170 strains representing 109 taxa, including *Apiospora* Sacc. (142 strains, 83 taxa), *Arthrinium* Kunze (13 strains, 11 taxa), *Nigrospora* Zimm. (14 strains, 14 taxa) and the outgroup taxon *Sporocadus trimorphus* F. Liu, L. Cai & Crous (CBS 114203). The trees from the two analyses (ML and BI) showed identical topologies. Phylogenetically, *Apiospora* is very similar to *Arthrinium*, and most species of *Apiospora* were synonymized under *Arthrinium* by Pintos & Alvarado (2021) and Tian et al. (2021). Multigene phylogenetic analyses based on LSU, ITS, *TUB* and *TEF1-α* showed the taxonomic placements of our strains belonging to *Apiospora* (Fig. 5). *Apiospora xishuangbannaensis* formed a distinct branch separated from *Ap. septata* (Y. Feng & Jian K. Liu) X.G. Tian & Tibpromma, *Ap. gelatinosa* (Y. Feng & Z.Y. Liu) X.G. Tian & Tibpromma and *Ap. biserialis* (Y. Feng and Z.Y. Liu) X.G. Tian and Tibpromma with high statistical support (ML/BI = 90/1.00). In addition, our two strains KUMCC 21-0697 and KUMCC 21-0698 clustered with *Apiospora arundinis* (Corda) Pintos & P. Alvarado (CBS 449.92 and CBS 133509), KUMCC 21-0693 AND KUMCC 21-0694 clustered together with *Ap. marii* (Larrondo & Calvo) Pintos & P. Alvarado (CBS 113535 and CBS 114803), and KUMCC 21-0428 and KUMCC 21-0429 clustered together with *Ap. vietnamensis* (Hol.-Jech.) Pintos & P. Alvarado (IMI 99670, type).

Neopestalotiopsis **phylogeny was based on combined ITS,** ***TEF1-α*** **and** ***TUB*** **sequence data**

The combined alignment encompassed 137 strains representing 80 taxa, including of *Neopestalotiopsis* Maharachch. et al. (134 strains, 77 taxa), and three outgroup taxon *Pseudopestalotiopsis cocos* Maharachch., K.D. Hyde & Crous (CBS 272.29, type), *Ps. indica* Maharachch., K.D. Hyde & Crous (CBS 459.78, type) and *Ps. theae* (Sawada) Maharachch., K.D. Hyde & Crous (MFLUCC12-0055, type). The trees from ML and BI analyses showed identical topologies. Multigene phylogenetic analyses based on ITS, *TEF1-α* and *TUB* showed our strains belong to *Neopestalotiopsis* (Fig. 6). *Neopestalotiopsis xishuangbannaensis* formed a distinct clade closely related to *N. mianyangensis* W.L. Li & Jian with high statistical support (ML/BI = 100/1.00) (Fig. 6).

Clonostachys **phylogeny was based on ITS and** ***TUB*** **sequence data**

The combined alignment encompassed 73 strains representing 62 taxa, including the new species and the outgroup taxa *Fusarium acutatum* Nirenberg & O'Donnell (CBS 402.97) and *Nectria cinnabarina* (Tode) Fr. (CBS 279.48). The trees from two analyses (ML and BI) showed identical topologies. Multigene phylogenetic analyses based on ITS and *TUB* show our new species formed a distinct clade sister to *Clonostachys pityrodes* Schroers with high statistical support (ML/BI = 99/1.00) (Fig. 7).

Amphichorda **phylogeny was based on combined ITS,** ***RPB1, RPB2*** **and** ***TEF1-α*** **sequence data**

The combined alignment encompassed 77 strains representing 42 taxa, including *Amphichorda* Fr. (nine strains, four taxa), *Beauveria* Vuill. (45 strains, 24 taxa), *Cordyceps* Fr. (13 strains, eight taxa), *Hevansia* Luangsa-ard, Hywel-Jones & Spatafora (eight strains, five taxa) and the outgroup taxa with *Purpureocillium lilacinum* (Thom) Luangsa-ard, Houbraken, Hywel-Jones & Samson (CBS 284-36) and *Pu. Lilacinum* (CBS 431-87). The trees from two analyses (ML and BI) showed identical topologies. *Amphichorda* is closely related to *Beauveria, Cordyceps* and *Hevansia* based on molecular phylogenetic analyses. Multigene phylogenetic analyses based on ITS, *RPB1*, *RPB2* and *TEF1-α* show that our new species belongs to *Amphichorda*, and formed a distinct clade sister to *Am. cavernicola* Z.F. Zhang & L. Cai. and *Am. guana* Z.F. Zhang, F. Liu & L. Cai. with high statistical support (ML/BI = 100/1.00) (Fig. 8).

Trichoderma **phylogeny was based on combined ITS,** ***RPB2*** **and** ***TEF1-α*** **sequence data**

The combined alignment encompassed 159 strains representing 93 taxa, including *Trichoderma* (146 strains, 82 taxa), *Arachnocrea* Z. Moravec (two strains, two taxa), *Hypomyces* (Fr.) Tul. & C. Tul. (five strains, five taxa), *Protocrea* Petch (five strains, three taxa) and the outgroup taxon *Nectria eustromatica* Jaklitsch & Voglmayr (CBS 125578). The trees from the two analyses (ML and BI) showed identical topologies. Multigene phylogenetic analyses based on ITS, *RPB2* and *TEF1-α* show that our strains belong to *Trichoderma* (Fig. 9). *Trichoderma hipposiderocola* formed a distinct clade sister to *T. atroviride* P. Karst. with high statistical support (ML/BI = 98/1.00), and *T. rhinolophicola* formed a distinct clade in the *Atroviride* clade. *Trichoderma xishuangbannaense* formed a distinct clade with high statistical support (ML/BI = 100/1.00) in the basal *Longibrachiatum* clade. The strain KUMCC 21-0806 clustered together with

T. inconspicuum Z.F. Yu & X. Du (YMF 1.04623, type), and the strains KUMCC 21-0807, KUMCC 21-0808, KUMCC 21-0809, KUMCC 21-0810 and KUMCC 21-0811 clustered together with *T. obovatum* Z.F. Yu & Y.F. Lv (YMF 1.06211 (type) and YMF 1.06212). The eight clades of *Trichoderma* are labelled in the phylogenetic tree (Fig. 9) (Rodríguez et al. 2021, Zheng et al. 2021).

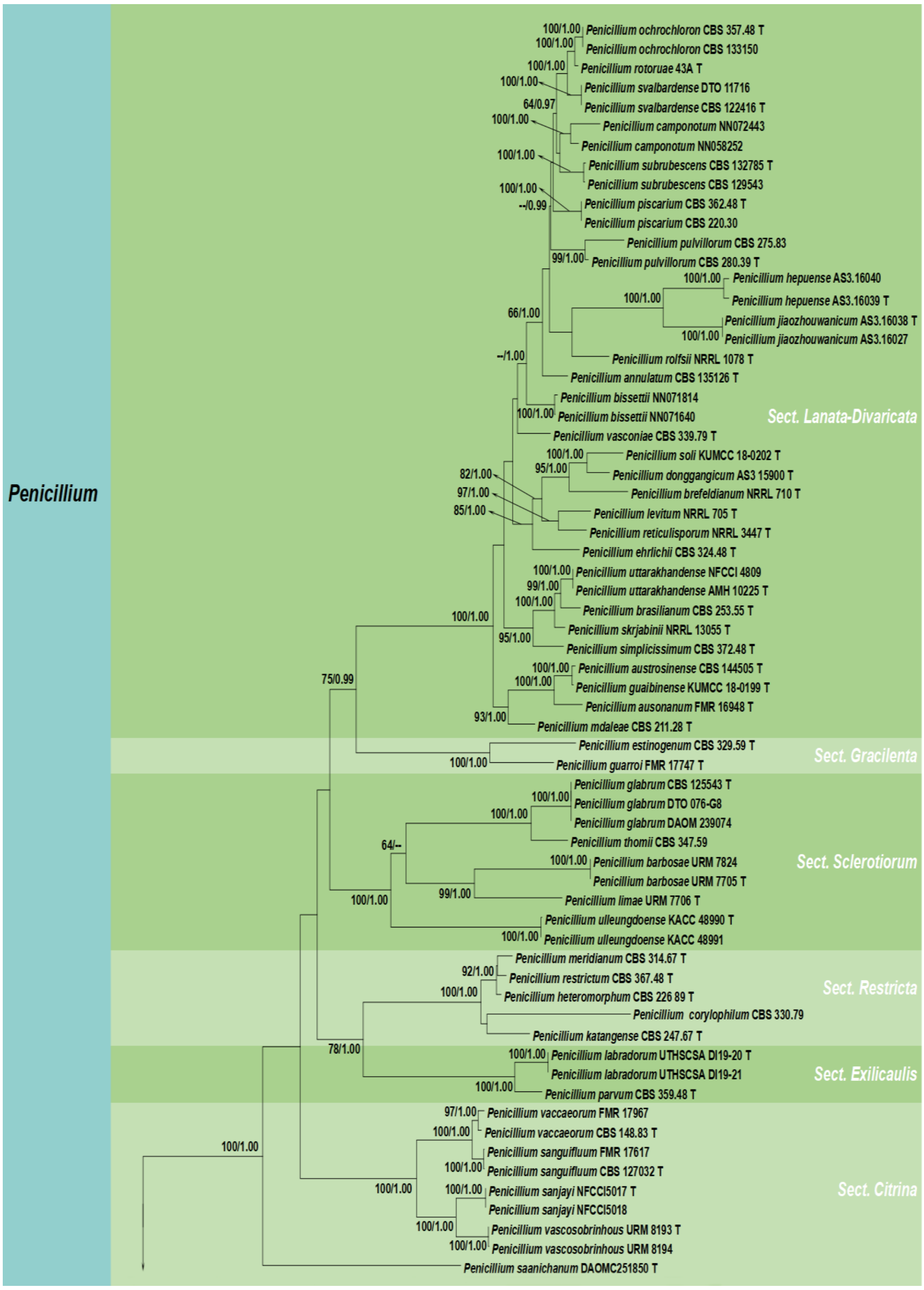


Figure 4 – Consensus phylogram of 1,000 trees resulting from a RAxML analysis of the (ITS+*BenA*+*Cam*+*RPB2*) alignment of the analyzed *Penicillium* sequences. The RAxML analysis of the combined dataset yielded the best scoring tree with a final ML optimization likelihood value of -51877.688097 and generated from 646, 494, 579 and 1121 base pairs of ITS, *BenA*, *Cam* and *RPB2* characters, respectively. The matrix comprises 1808 distinct alignment patterns with 20.41% gaps and indeterminate traits. Base frequencies were estimated as follows A = 0.227750, C = 0.274333, G = 0.263453, T = 0.234465 with substitution rates AC = 1.219666, AG = 3.226510, AT

= 1.259285, CG = 0.843272, CT = 5.178371, GT = 1.000000; proportion of invariable sites I = 0.361128; gamma distribution shape parameter α = 0.789719. The trees from three analyses (ML and BI) showed identical topologies. RAxML bootstrap support values (ML equal to or above 60%) and Bayesian inference posterior probabilities (BYPP equal to or above 0.90) are given at the nodes (ML/BYPP). The sequences of new strains are in blue. The scale bar represents the expected number of changes per site. Type strains are denoted with T.

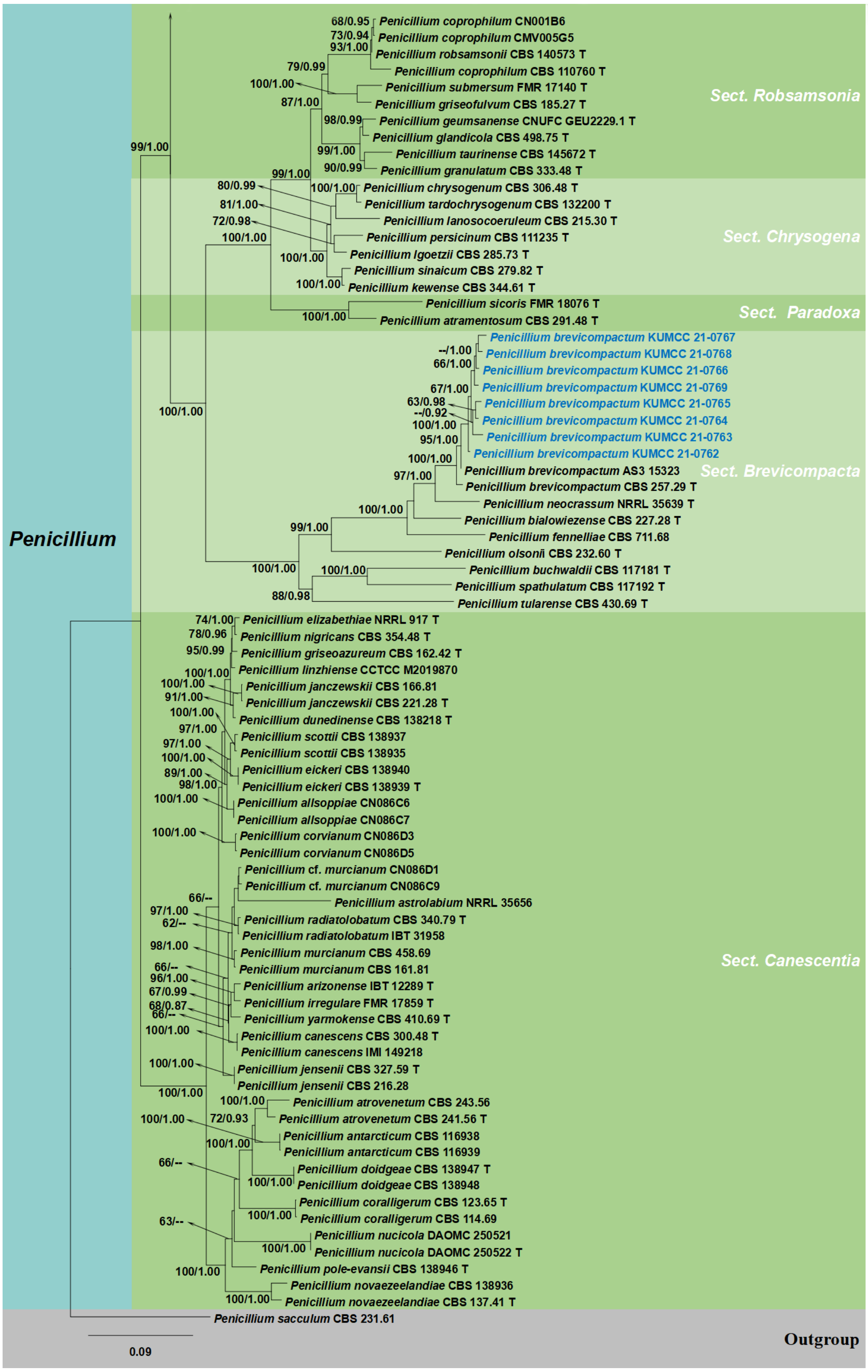


Figure 4 – Continued.

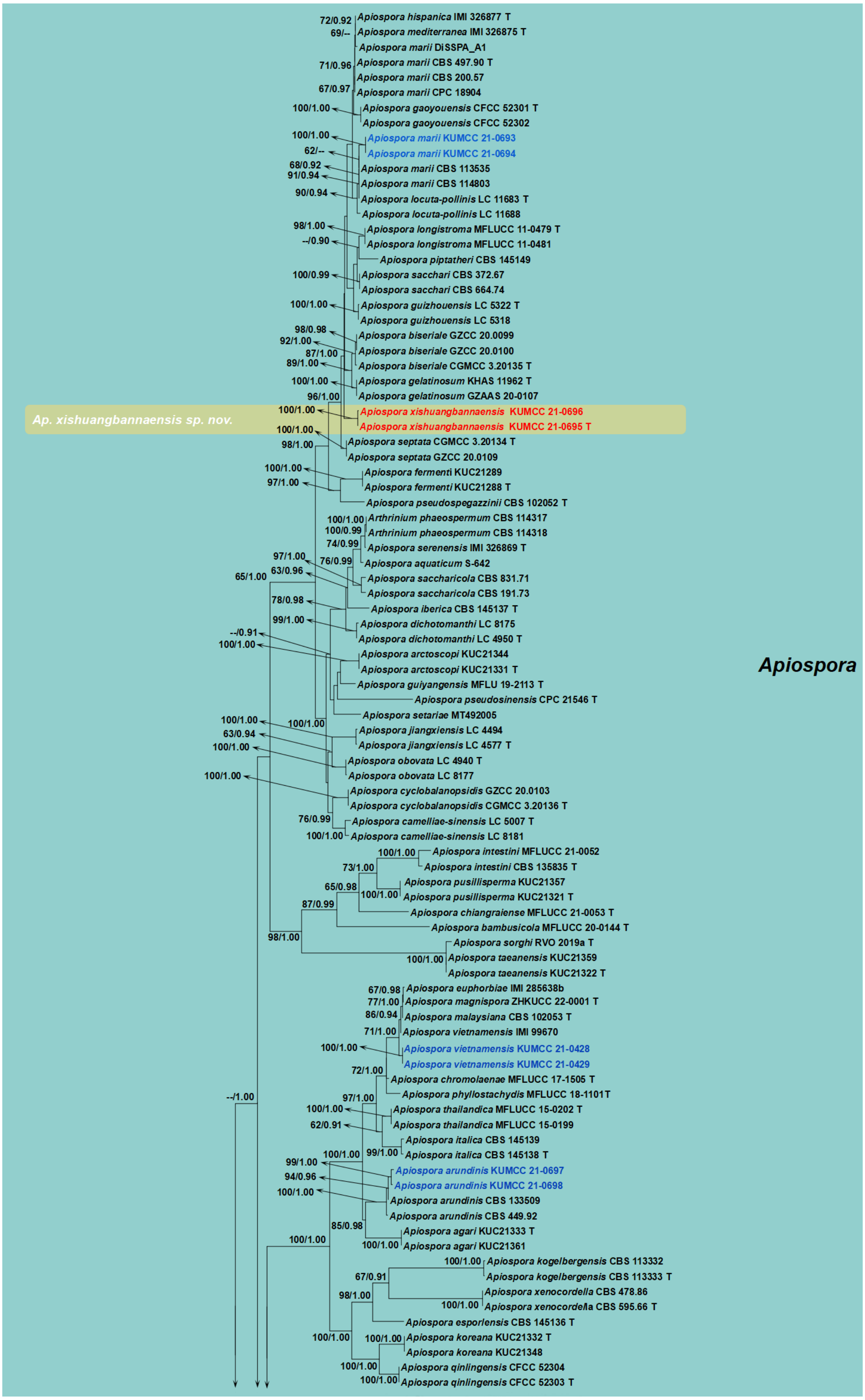


Figure 5 – Consensus phylogram of 1,000 trees resulting from a RAxML analysis of the (ITS+LSU+*TEF1-α*+*TUB*) alignment of the analyzed *Apiospora*. The RAxML analysis of the

combined dataset yielded the best scoring tree with a final ML optimization likelihood value of -36510.216073 and generated from 712, 804, 516 and 800 base pairs of ITS, LSU, *TEF1-α* and *TUB* characters, respectively. The matrix comprises 1724 distinct alignment patterns with 31.19% gaps and indeterminate traits. Base frequencies were estimated as follows A = 0.235767, C = 0.254738, G = 0.254191, T = 0.255304 with substitution rates AC = 1.284023, AG = 3.095908, AT = 1.203994, CG = 1.158116, CT = 4.989142, GT = 1.000000; proportion of invariable sites I = 0.353713; gamma distribution shape parameter α = 0.724256. RAxML bootstrap support values (ML equal to or above 60%) and Bayesian inference posterior probabilities (BYPP equal to or above 0.90) are given at the nodes (ML/BYPP). The ex-type strains are represented in blue bold, and the newly introduced sequences are in red bold. The scale bar represents the expected number of changes per site. Type strains are denoted with T.

Figure 5 – Continued.

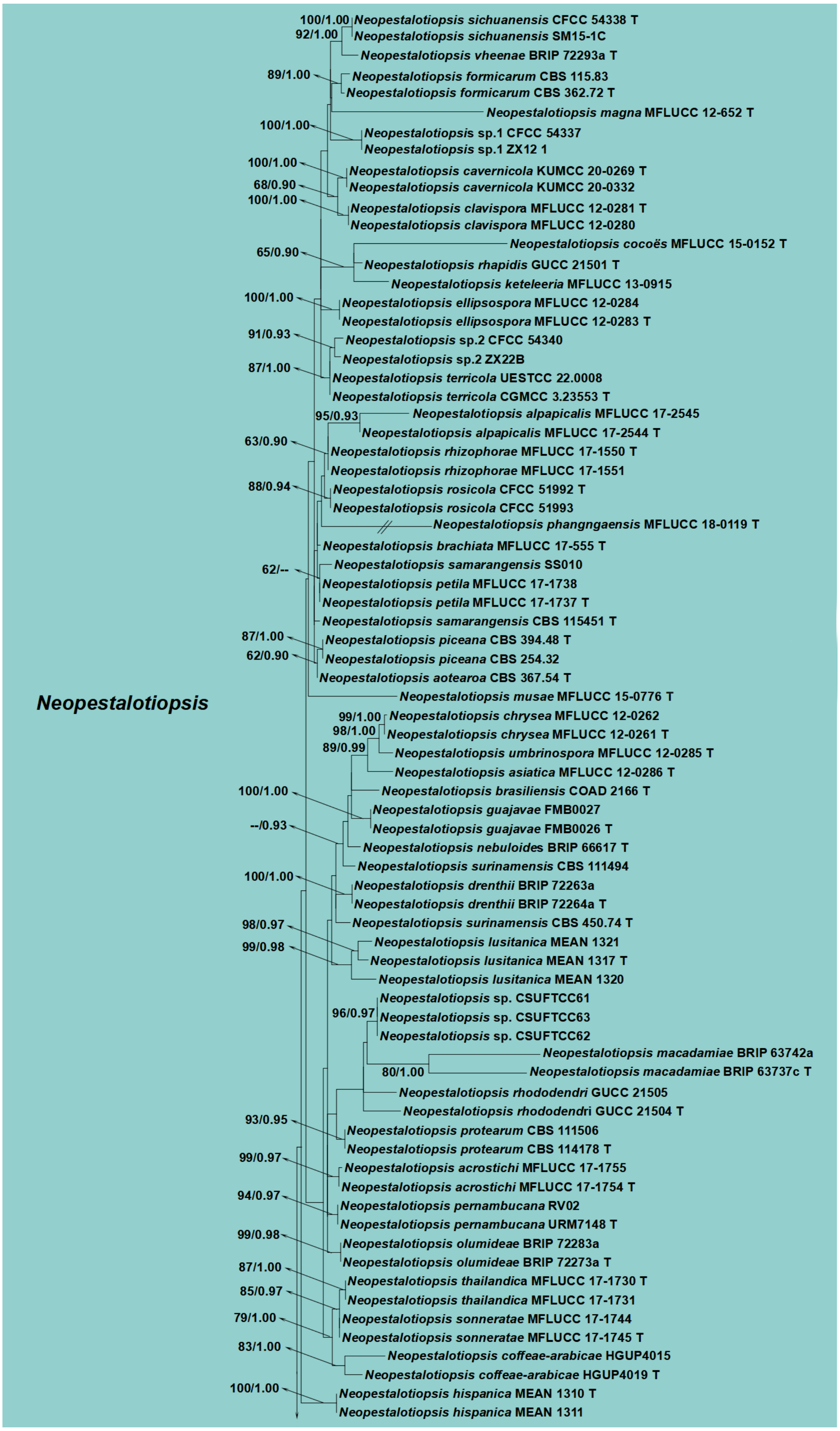


Figure 6 – Consensus phylogram of 1,000 trees resulting from a RAxML analysis of the (ITS+*TEF1-α*+*TUB*) alignment of the analyzed *Neopestalotiopsis* sequences. The RAxML analysis of the combined dataset yielded the best scoring tree with a final ML optimization likelihood value of -11724.008210 and generated from 546, 934 and 771 base pairs of ITS, *TEF1-α* and *TUB*

characters, respectively. The matrix comprises 865 distinct alignment patterns with 27.74% gaps and indeterminate traits. Base frequencies were estimated as follows A = 0.235829, C = 0.27172, G = 0.218698, T = 0.273752 with substitution rates AC = 1.065278, AG = 2.932908, AT = 1.290534, CG = 0.816005, CT = 3.981952, GT = 1.000000; proportion of invariable sites I = 0.369668; gamma distribution shape parameter α = 0.773815. The trees from three analyses (ML and BI) showed identical topologies. RAxML bootstrap support values (ML equal to or above 60%) and Bayesian inference posterior probabilities (BYPP equal to or above 0.90) are given at the nodes (ML/BYPP). The newly introduced sequences are in bold red. The scale bar represents the expected number of changes per site. Type strains are denoted with T.

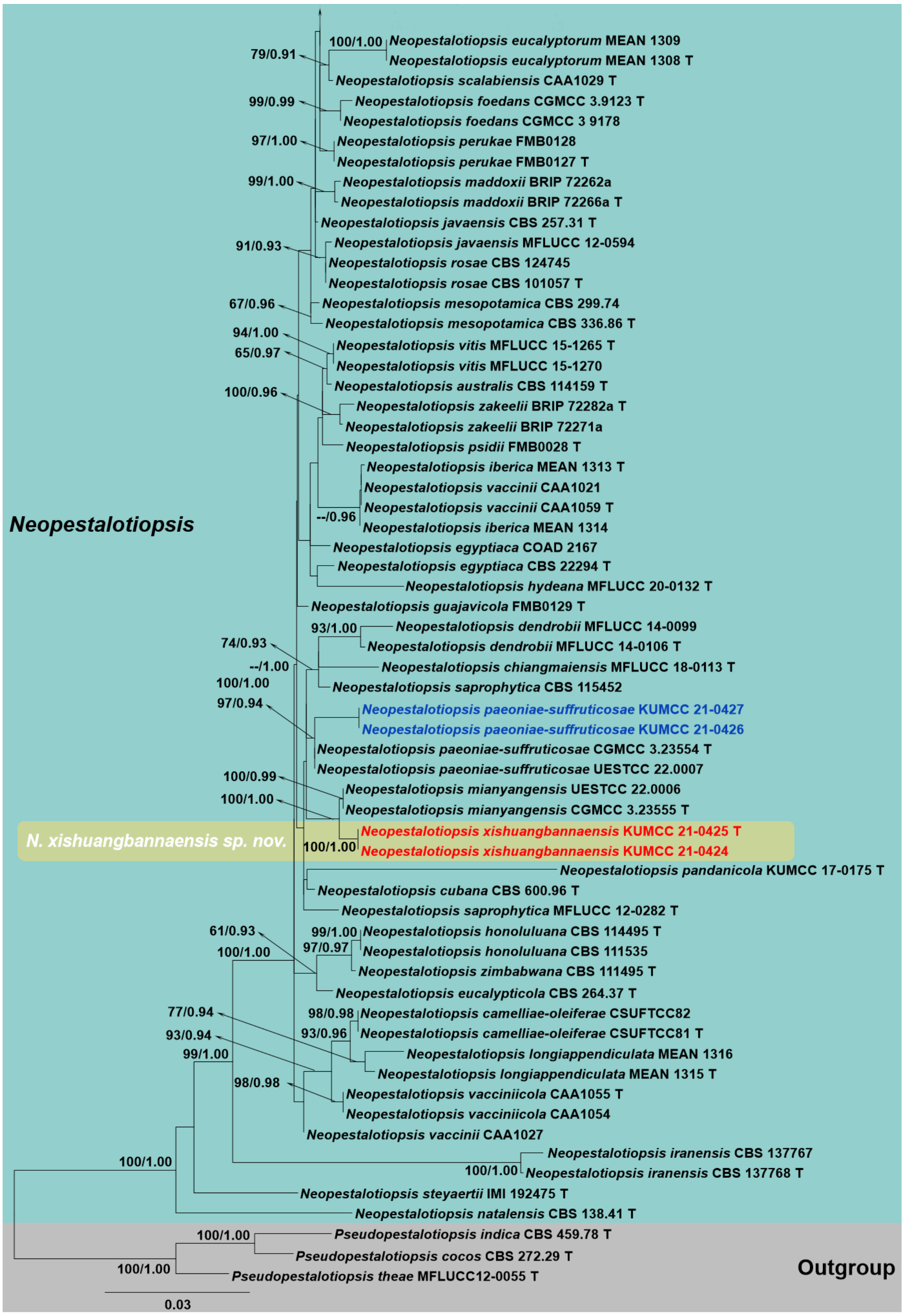


Figure 6 – Continued.

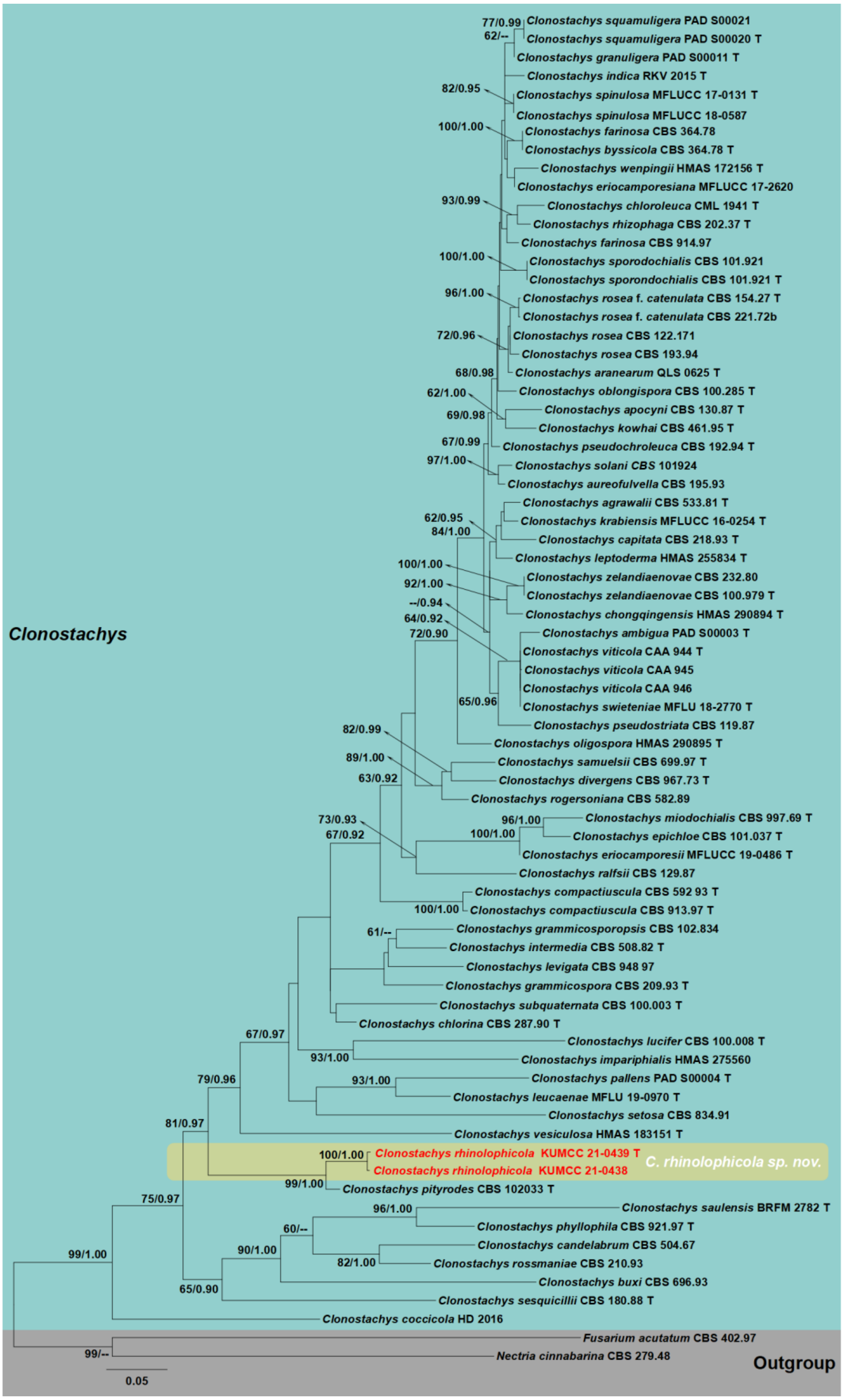


Figure 7 – Consensus phylogram of 1,000 trees resulting from a RAxML analysis of the (ITS+*TUB*) alignment of the analyzed *Clonostachys* sequences. The RaxML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of -12437.722313 and generated from 479 and 602 base pairs of ITS and *TUB* characters, respectively. The matrix comprises 640 distinct alignment patterns with 22.83% gaps and indeterminate traits.

Base frequencies were estimated as follows A = 0.211034, C = 0.282207, G = 0.249578, T = 0.257181 with substitution rates AC = 1.215440, AG = 3.197995, AT = 1.110533, CG = 0.636495, CT = 4.148100, GT = 1.000000; proportion of invariable sites I = 0.315419; gamma distribution shape parameter α = 0.673328. The trees from three analyses (ML and BI) showed identical topologies. RaxML bootstrap support values (ML equal to or above 60%) and Bayesian inference posterior probabilities (BYPP equal to or above 0.90) are given at the nodes (ML/BYPP). The newly introduced sequences are in red bold. The scale bar represents the expected number of changes per site. Type strains are denoted with T.

Fusarium **phylogeny was based on ITS, *RPB2, RPB1, TUB, CAM* and *TEF1-α* sequence data**

The combined alignment encompassed 193 strains representing 113 taxa, including *Fusarium* Link (191 strains, 111 taxa), and the outgroup taxa *Microcera coccophila* Desm. (CBS 310.34) and *M. diploa* (Berk. & M.A. Curtis) Gräfenhan & Seifert (CBS 735.79). The trees from the two analyses (ML and BI) showed identical topologies. Multigene phylogenetic analyses based on ITS, *RPB2, RPB1, TUB, CAM* and *TEF1-α* show that our strains represent one new host record and five new species (*F. hipposidericola, F. menglaense, F. rhinolophicola, F. xishuangbannaensee* and *F. yunnanense*). The 12 *Fusarium* species in the phylogenetic tree were labelled following Sandoval-Denis et al. (2018) and Wang et al. (2020), while the *F. yunnanense* species complex was introduced based on the new species *F. yunnanense* (Fig. 10).

Scopulariopsis **phylogeny was based on ITS, LSU, *TUB* and *TEF1-α* sequence data**

The combined alignment encompassed 88 strains representing 48 taxa, including *Microascus* Zukal (32 strains, 30 taxa), *Scopulariopsis* Bainier (52 strains, 14 taxa), *Yunnania* H.Z. Kong (three strains, three taxa) and the outgroup taxon *Cephalotrichum asperulum* (J.E. Wright & S. Marchand) Sand.-Den., Guarro & Gené (CBS 582.71). The trees from the two analyses (ML and BI) showed identical topologies. Multigene phylogenetic analyses based on ITS, LSU, *TUB* and *TEF1-α* show the taxonomic placements of our total strains belonging to *Scopulariopsis brevicaulis* (Sacc.) Bainier in *Scopulariopsis* group (Fig. 11).

Phialemoniopsis **phylogeny was based on combined ITS, LSU, *Act* and *TUB* sequence data**

The combined alignment encompassed 31 strains representing 14 taxa, including *Phialemoniopsis* Perdomo, Dania García, Gené, Cano & Guarro (21 strains, nine taxa), *Phialemonium* W. Gams & McGinnis (nine strains, four taxa), and the outgroup taxon *Lecythophora lignicola* Nannf. (CBS 267.3). The trees from two analyses (ML and BI) showed identical topologies. Multigene phylogenetic analyses based on ITS, LSU, *Act* and *TUB* showed that *Phialemoniopsis* and *Phialemonium* are closely related, but form separate branches and our strains belong to *Phialemoniopsis* (Fig. 12). *Phialemoniopsis hipposidericola* and *Ph. xishuangbannaensis* each formed a distinct clade sister to *Ph. pluriloculosa* W. Gams & McGinnis with high statistical support.

Overall species summary

In total 25 species of fungi were isolated from 14 bat species (Supplementary Table 1) in this study, representing 14 new fungal species belonging to six families, viz., *Apiosporaceae* K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr, *Bionectriaceae* Samuels & Rossman, *Cordycipitaceae* Kreisel, *Hypocreaceae* De Not., *Nectriaceae* Tul. & C. Tul. and *Sporocadaceae* Corda. The 11 known species represent new host records for bats.

Taxonomy

Chethana et al. (2021) was used as the main reference for introducing new taxa in this study. Each genus was treated using the latest and most comprehensive publications of that particular genus. The introduction of new taxa in *Amphichorda* followed Zhang et al. (2017, 2020), while the new *Apiospora* taxon was introduced following Pintos & Alvarado (2021) and Tian et al. (2021).

To introduce new *Clonostachys* Corda, Lechat et al. (2020) and Torcato et al. (2020) were followed. *Fusarium* is one of the most widely distributed and complex genera, and the definition of species is still controversial. We describe five new species of *Fusarium* in this work following Crous et al. (2021). *Neopestalotiopsis* is distinguished from *Pestalotiopsis* Steyaert based on multi-gene analyses of ITS, *TEF1-α* and *TUB*, and we describe two new taxa in this paper following Maharachchikumbura et al. (2014). *Phialemoniopsis* was erected by Perdomo et al. (2013), and we followed this paper to introduce two new *Phialemoniopsis* taxa in this paper. Cai & Druzhinina (2021) and Zheng et al. (2021) were followed to introduce three new *Trichoderma* Pers. taxa in this study.

Phylum ***Ascomycota*** Caval.-Sm.
Class ***Eurotiomycetes*** O.E. Erikss. & Winka
Eurotiales G.W. Martin ex Benny & Kimbr.
Aspergillaceae Link

Aspergillaceae was established by Link (1826), with *Aspergillus* as the type genus. Houbraken & Samson (2011) discussed this family based on multi-locus phylogeny, and it was split into seven clades. Some species in this family tolerate extreme conditions, such as high sugar or salt concentrations, low or high temperatures, and low acidity or oxygen levels (Houbraken et al. 2014, Zhang et al. 2020). *Aspergillaceae* species are predominantly saprobic and commonly occur in soil, while a few are plant and animal pathogenic fungi (Houbraken et al. 2014).

Aspergillus P. Micheli ex Haller

Aspergillus (*As.*) was established by Haller (1768) with *Aspergillus glaucus* (L.) Link. as the type species (Wijayawardene et al. 2017, Houbraken et al. 2020). *Aspergillus* is one of the most economically important and widely distributed genera of fungi (Zhang et al. 2020). To date, *Aspergillus*, a large genus of filamentous fungi, contains 428 accepted species (Sklenář et al. 2021, Wijayawardene et al. 2022). According to the traditional classification, this genus is classified into subgenera, sections, and series, and the latest revised and updated overview by Houbraken et al. (2020) shows that the accepted species are distributed across six subgenera, 27 sections, and 75 series (Sklenář et al. 2021). Most members of this genus are terrestrial but were also reported as aquatic fungi. They mainly live as saprophytic fungi in soil, plant, and food, but also include some pathogenic fungi, which are harmful to humans (aspergillosis), animals and plants (Peterson 2008, Sigler et al. 2010, Varga et al. 2010a, b, 2011, Guarro et al. 2012, Jurjević et al. 2012, 2015, Asgari et al. 2014, Samson et al. 2014, Arzanlou et al. 2016, Visagie et al. 2017, Wijayawardene et al. 2017). The typical feature of this genus is the structure of the conidiophore known as aspergillum, which consists of a foot cell, stipe aseptate, and ends in a vesicle (Houbraken et al. 2020). We describe two new records as *Aspergillus candidus* Link and *As. creber* Jurjević, S.W. Peterson & B.W. Horn in this study.

Aspergillus candidus Link, Mag. Gesell. naturf. Freunde, Berlin 3 (1–2): 16 (1809). Fig. 13

MycoBank number: MB 204868; Facesoffungi number: FoF 13414

Asexual morph on PDA: Conidial heads radiate, splitting into 3 or more columns. *Conidiophores* uniseriate, branched at apex. *Stipes* 150–450 × 3–9 µm, hyaline, septate. *Vesicles* 7–28 µm wide, globose to spathulate, smooth. *Metulae* 6–21 × 3–6 µm (x̄ = 9.78× 4.38 µm, n = 30), hyaline to pale brown, uni- to biseriate. *Phialides* 6–16 × 1–3 µm (x̄ = 9.31 × 2.54 µm, n = 30), ampulliform, with minute collarette. *Conidia* 3–5 × 2–5 µm (x̄ = 3.67 ×3.44 µm, n = 60), broadly ellipsoid to globose, smooth-walled, hyaline, arranged in chains. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 20–40 mm after 15 days at room temperature (20–25 ℃), colonies at surface, floccose, wrinkled, with mycelial areas white to cream, greenish grey to yellowish grey; reverse white to yellowish grey. Sporulation moderately dense on PDA after 60 days.

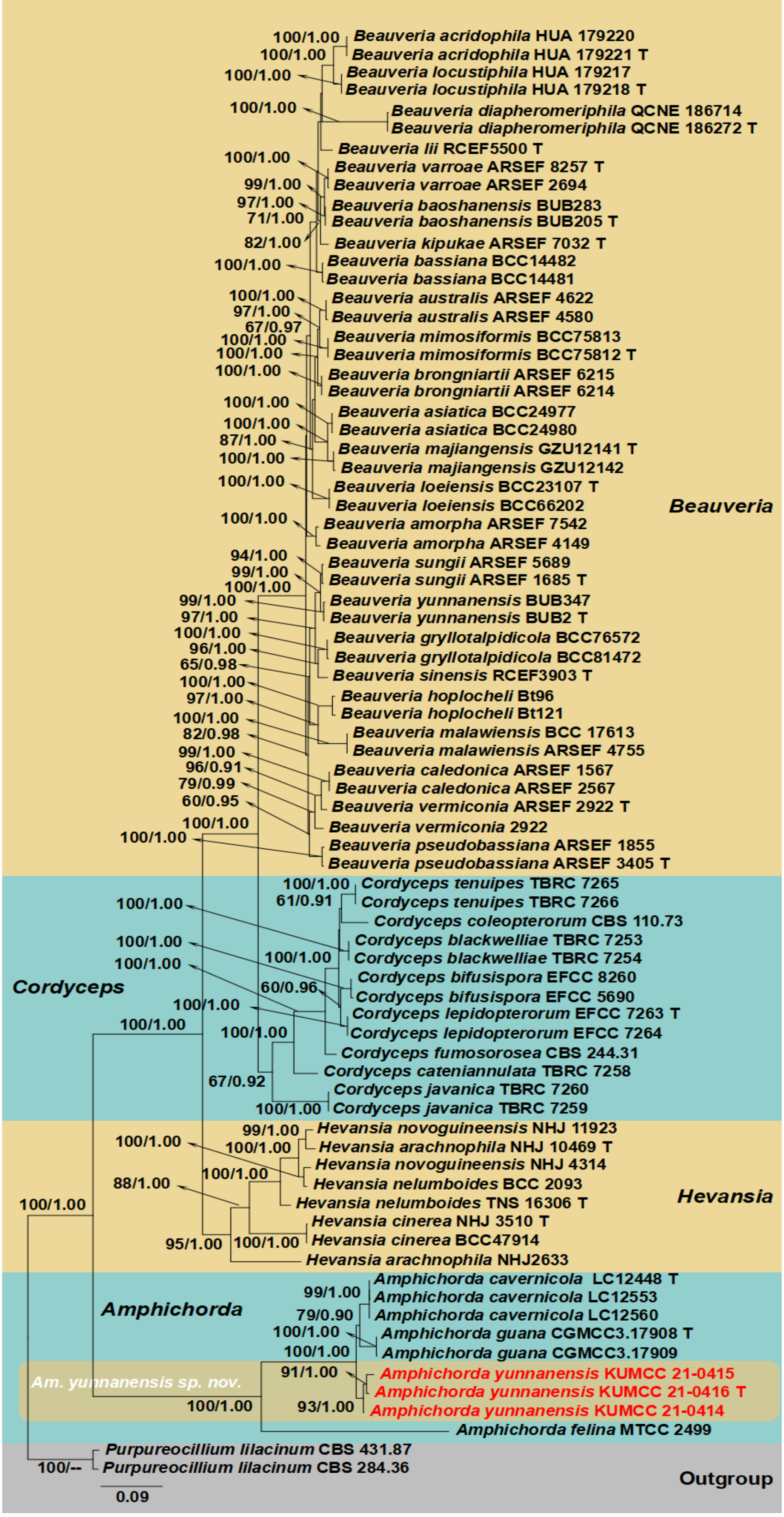


Figure 8 – Consensus phylogram of 1,000 trees resulting from a RAxML analysis of the (ITS+*RPB1*+*RPB2*+*TEF1-α*) alignment of the analyzed *Amphichorda*. The RAxML analysis of the combined dataset yielded the best scoring tree with a final ML optimization likelihood value of -

33516.617816 and generated from 586, 749, 1153 and 975 base pairs of ITS, *RPB1*, *RPB2* and *TEF1-α* characters, respectively. The matrix comprises 2398 distinct alignment patterns with 34.61% gaps and indeterminate traits. Base frequencies were estimated as follows A = 0.239382, C = 0.288878, G = 0.258017, T = 0.213723 with substitution rates AC = 1.084122, AG = 3.455204, AT = 0.832988, CG = 0.988778, CT = 5.225831, GT = 1.000000; proportion of invariable sites I = 0.199312; gamma distribution shape parameter α = 0.661000. The trees from three analyses (ML and BI) showed identical topologies. RAxML bootstrap support values (ML equal to or above 60%) and Bayesian inference posterior probabilities (BYPP equal to or above 0.90) are given at the nodes (ML/BYPP). The newly introduced sequences are in bold red. The scale bar represents the expected number of changes per site. Type strains are denoted with T.

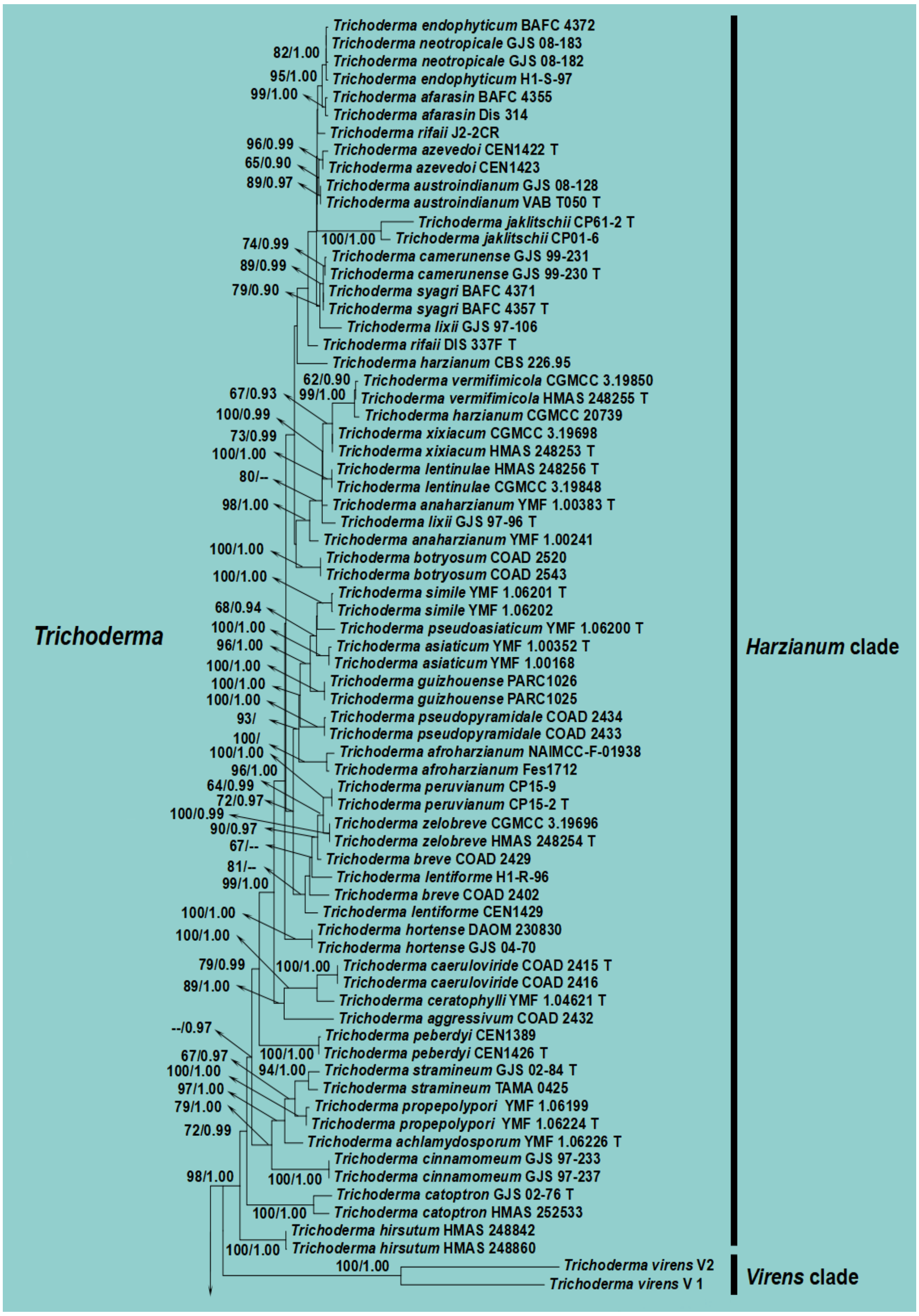
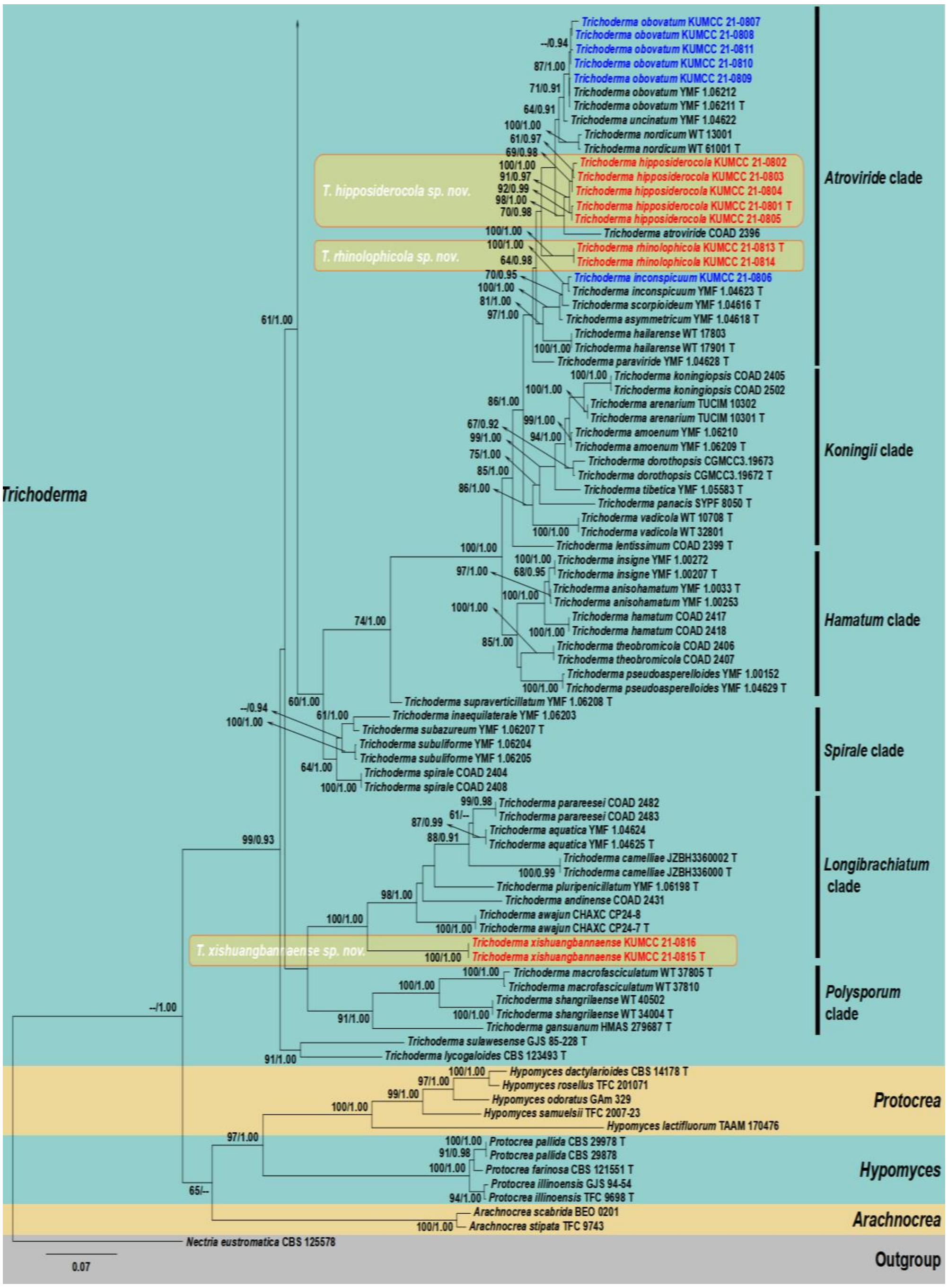


Figure 9 – Consensus phylogram of 1,000 trees resulting from a RAxML analysis of the (ITS+*RPB2*+*TEF1-α*) alignment of the analyzed *Trichoderma*. The RAxML analysis of the

combined dataset yielded the best scoring tree with a final ML optimization likelihood value of -39488.402675 and generated from 663, 1064, and 1360 base pairs of ITS, *RPB2* and *TEF1-α* characters, respectively. The matrix comprises 1892 distinct alignment patterns with 32.33% gaps and indeterminate traits. Base frequencies were estimated as follows A = 0.235539, C = 0.281030, G = 0.245910, T = 0.237522 with substitution rates AC = 1.091673, AG = 2.872530, AT = 1.096178, CG = 0.815653, CT = 4.704279, GT = 1.000000; proportion of invariable sites I = 0.247980; gamma distribution shape parameter α = 0.545773. The trees from three analyses (ML and BI) showed identical topologies. RAxML bootstrap support values (ML equal to or above 60%) and Bayesian inference posterior probabilities (BYPP equal to or above 0.90) are given at the nodes (ML/BYPP). The ex-type strains are represented in blue bold, while the newly introduced sequences are in red bold. The scale bar represents the expected number of changes per site. Type strains are denoted with T.



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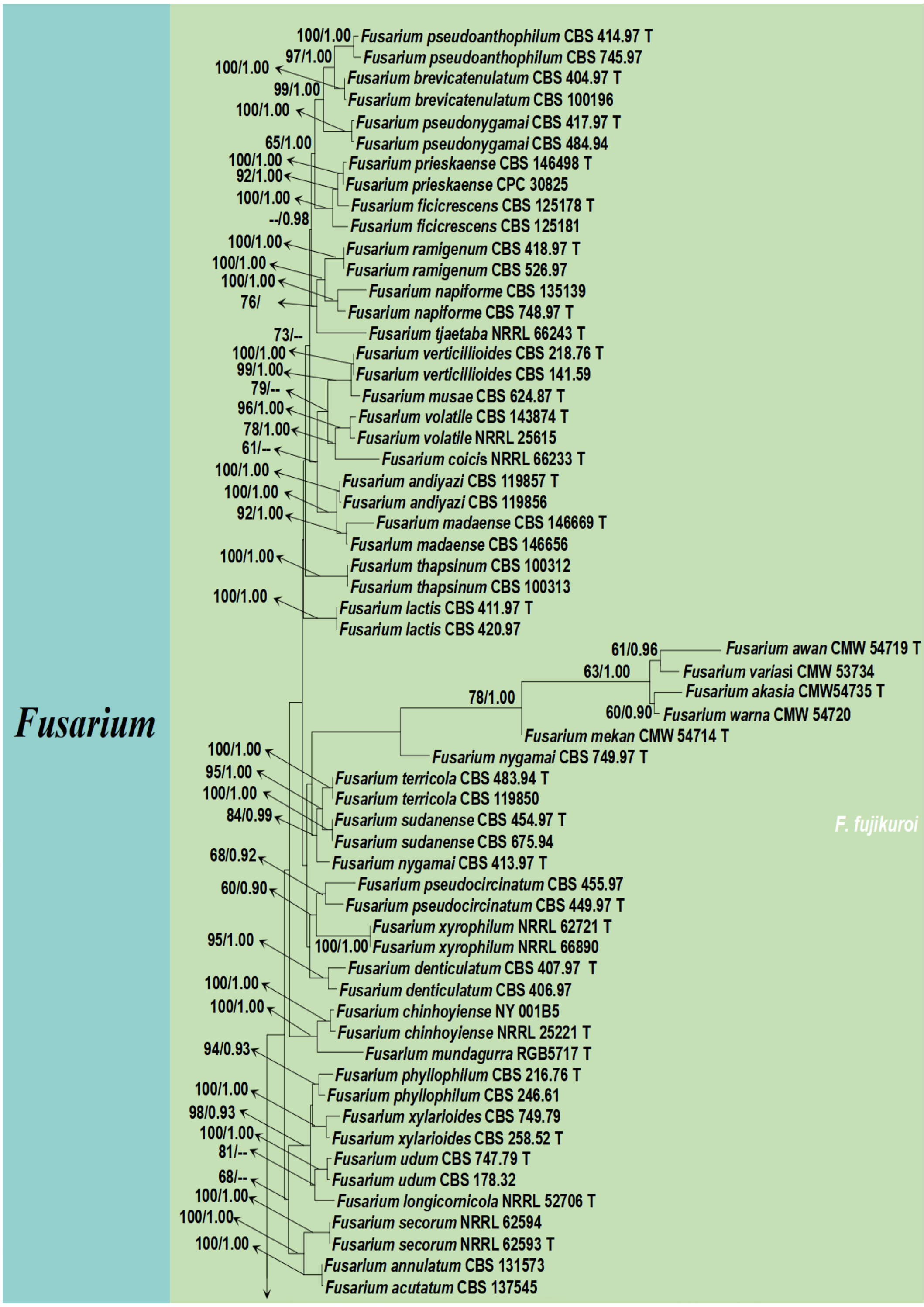

Figure 10 – Consensus phylogram of 1,000 trees resulting from a RAxML analysis of the (ITS+*CaM*+*RPB1*+*RPB2*+*TEF1-α*+*TUB*) alignment of the analyzed *Fusarium*. The RAxML analysis of the combined dataset yielded the best scoring tree with a final ML optimization likelihood value of -65846.059817 and generated from 578, 845, 1598, 555, 728 and 517 base pairs of ITS, *CaM*, *RPB2*, *RPB1*, *TEF1-α* and *TUB* characters, respectively. The matrix comprises 2917 distinct alignment patterns with 31.21% gaps and indeterminate traits. Base frequencies were estimated as follows A = 0.249250, C = 0.257580, G = 0.248502, T = 0.244668 with substitution rates AC = 1.366159, AG = 3.869772, AT = 1.236258, CG = 0.964808, CT = 7.097812, GT = 1.000000; proportion of invariable sites I = 0.178858; gamma distribution shape parameter α = 0.643467. The trees from three analyses (ML and BI) showed identical topologies. RAxML bootstrap support values (ML equal to or above 60%) and Bayesian inference posterior

probabilities (BYPP equal to or above 0.90) are given at the nodes (ML/BYPP). The ex-type strains are in blue bold, while the newly introduced sequences are in red bold. The scale bar represents the expected number of changes per site. Subdivision of the *Fusarium* clade represents the recognized species complexes. Type strains are denoted with T.

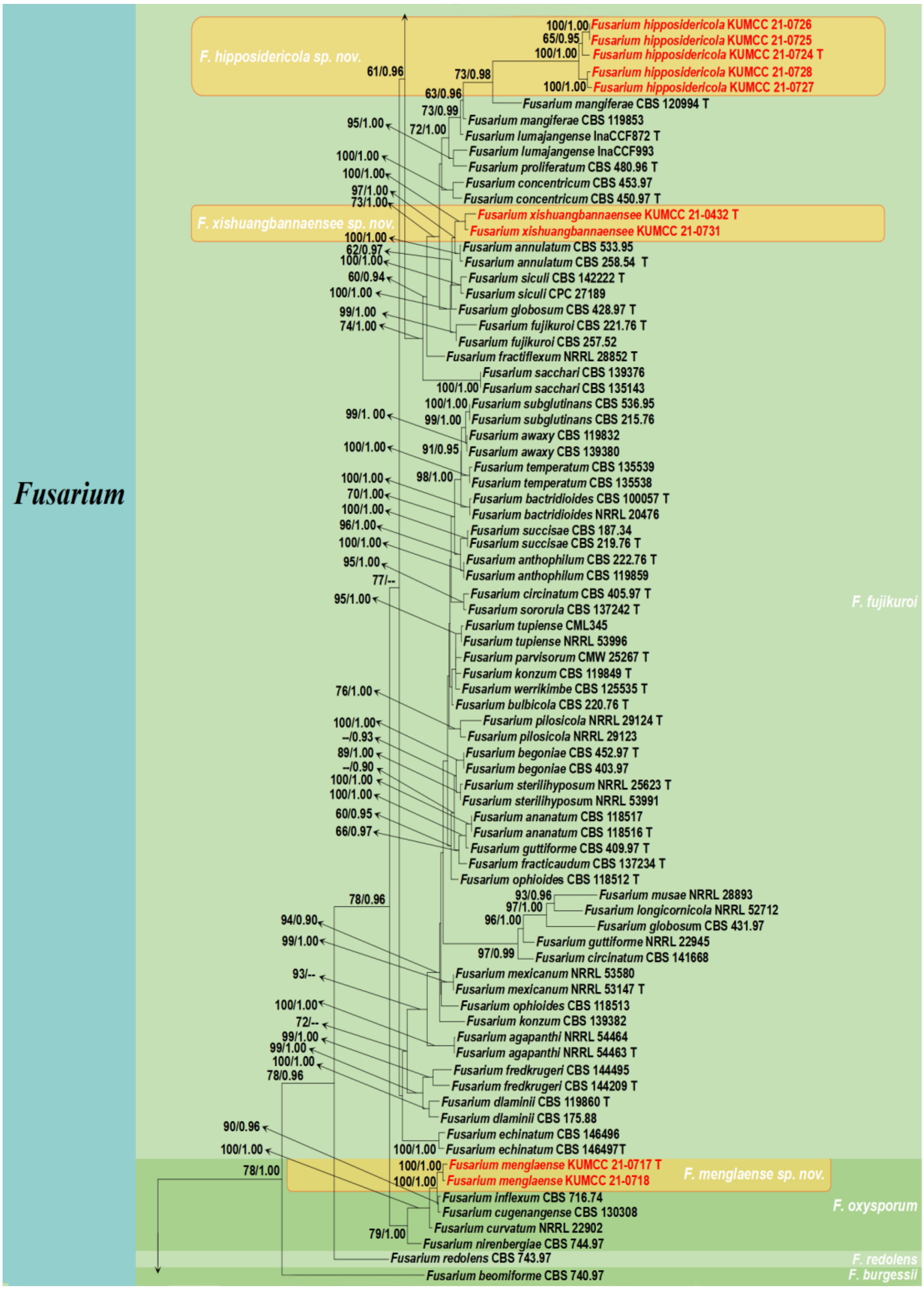

Figure 10 – Continued.

Substrata – Air, animal nests, barley, barn litter, bat droppings, carpets, compost, corn, crawlspace metal duct, dead bees, dung, dust, flooring, fur, human external auditory canal, human toenail, mattresses, mouse excrements in grain store, oats, rice, soil, tunnels of bark beetles, wheat, and wood submerged in seawater.

Distribution – Antarctica, Argentina, Australia, Austria, Bahamas, Bangladesh, Belgium, Brazil, Canada, Chile, China, Cuba, Czechia, Denmark, Egypt, Estonia, Ethiopia, Finland, France, Germany, Ghana, Hungary, India, Indonesia, Iran, Iraq, Israel, Italy, Jamaica, Japan, Kenya, Kuwait, Latvia, Libya, Malaysia, Nepal, Netherlands, New Guinea, New Zealand, Nigeria, North Korea, Pakistan, Poland, Portugal, Romania, Russia, Saudi Arabia, Sierra Leone, Slovakia, Solomon Islands, Somalia, South Africa, Spain, Sri Lanka, Sudan, Syria, Thailand, Trinidad and Tobago, Türkiye, UK, Ukraine, USA, Venezuela and Zambia.

Material examined – China, Yunnan Province, Kunming, Xishan District, Long cave, *Hipposideros armiger* collected from the wing surfaces, 102.60045 E, 24.838887 N, Alice Hughes, XS-1-B2 (HKAS122854), living culture KUMCC 21-0699; *ibid*., XS-1-B2-2, living culture KUMCC 21-0700.

GenBank numbers – KUMCC 21-0699 = ITS: OQ928957, *BenA*: OQ927579, *CaM*: OR022042, *RPB2*: OR022027; KUMCC 21-0700 = ITS: OQ928958, *BenA*: OQ927580, *CaM*: OR022043, *RPB2*: OR022028.

Notes – *Aspergillus candidus* was introduced by Link (1809). Based on multi-locus phylogenetic analyses (ITS+*BenA*+*CaM*+*RPB*2), our isolates clustered together with *As. candidus* (CCF 4659, DTO 223-E5 and CBS 566.65 (type)) and close to *As. dobrogensis* A. Nováková et al. In the sequence comparisons, our isolate (KUMCC 21-0699) was different from *As. candidus* (CBS 566.65, type) in 12/636 bp (1.89%) of the ITS, 7/524 bp (1.34%) of the *BenA*, 9/469 bp (1.91%) of *CaM* and 10/1014 bp (0.99%) of *RPB2*. Compared to *As. dobrogensis* (CCF4651, type) in 12/636 bp (1.89%) of the ITS, 9/456 bp (1.97%) of the *BenA*, 14/469 bp (2.99%) of *CaM* and 12/1014 bp (1.18%) of *RPB2*. Morphologically, the new isolate (KUMCC 21-0734) is differed from *As. dobrogensis* by the latter having shorter phialides (6–16 × 1–3 µm vs (5–)6–9(–12) × 2.5–3.5(–4) µm), smaller wedge-shaped to cylindrical metulae (6–21 × 3–6 µm vs (3–)4–17(–36) × (3–)4–10(–16) µm) (Hubka et al. 2018). Based on both phylogeny and morphology, the new isolates (KUMCC 21-0819 and KUMCC 21-0820) are identified as *As. candidus*. This is the first report of *As. candidus* isolated from bats in China.

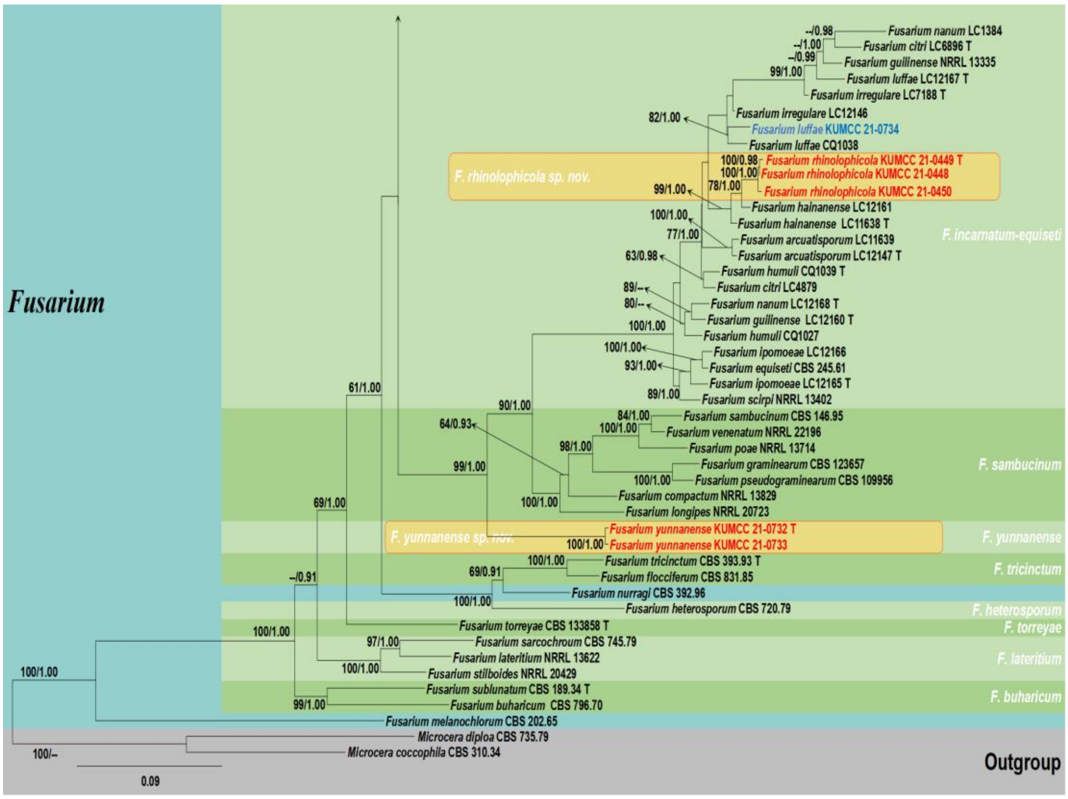

Figure 10 – Continued.

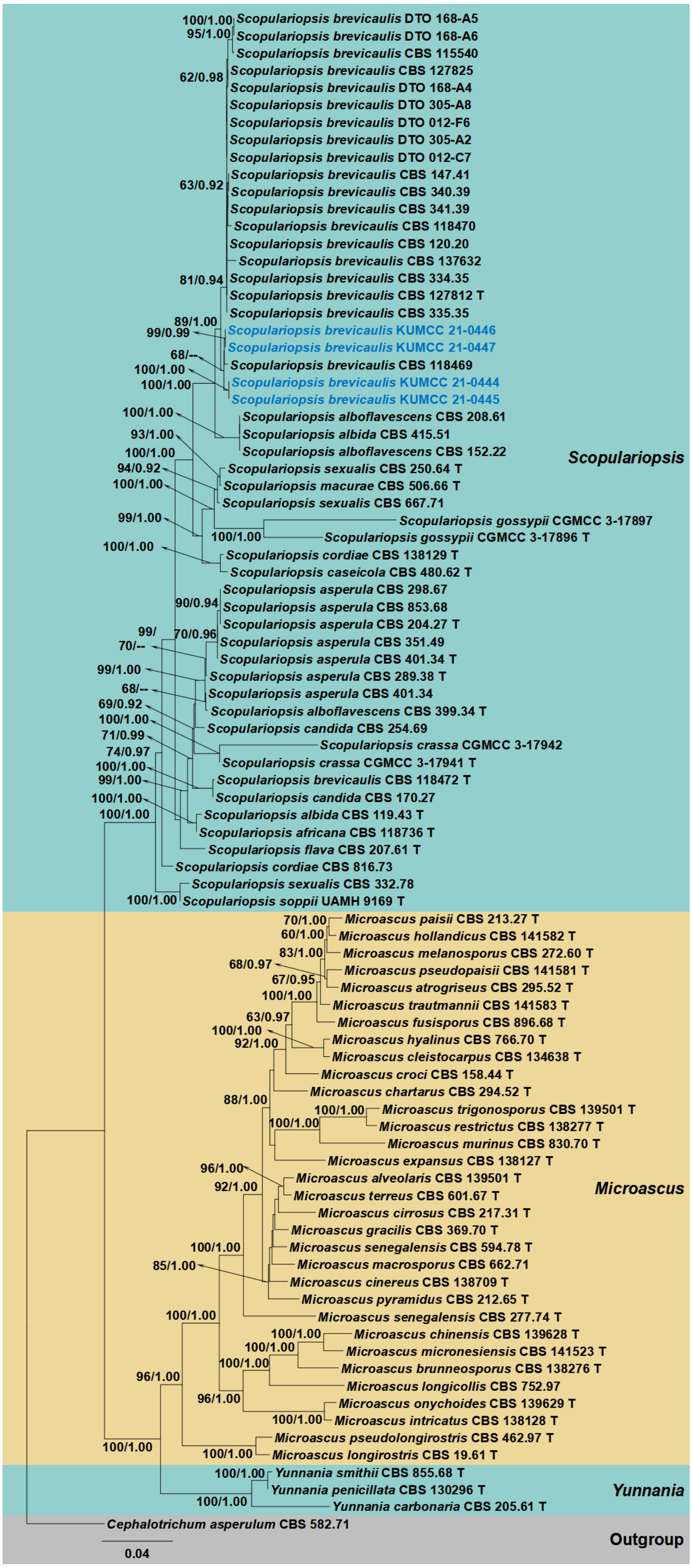

Figure 11 – Consensus phylogram of 1,000 trees resulting from a RAxML analysis of the (ITS+LSU+*TEF1-α*+*TUB*) alignment of the analyzed *Scopulariopsis* sequences. The RAxML

analysis of the combined dataset yielded the best scoring tree with a final ML optimization likelihood value of -21567.579786 and generated from 852, 608, 520 and 910 base pairs of ITS, LSU, *TEF1-α* and *TUB*) characters, respectively. The matrix comprises 1130 distinct alignment patterns with 18.17% gaps and indeterminate traits. Base frequencies were estimated as follows A = 0.214585, C = 0.306434, G = 0.274428, T = 0.204552 with substitution rates AC = 0.870016, AG = 2.055798, AT = 1.420918, CG = 1.014776, CT = 4.598943, GT = 1.000000; proportion of invariable sites I = 0.348651; gamma distribution shape parameter α = 0.591395. RAxML bootstrap support values (ML equal to or above 60%) and Bayesian inference posterior probabilities (BYPP equal to or above 0.90) are given at the nodes (ML/BYPP). The new strains are in blue. The scale bar represents the expected number of changes per site. Type strains are denoted with T.

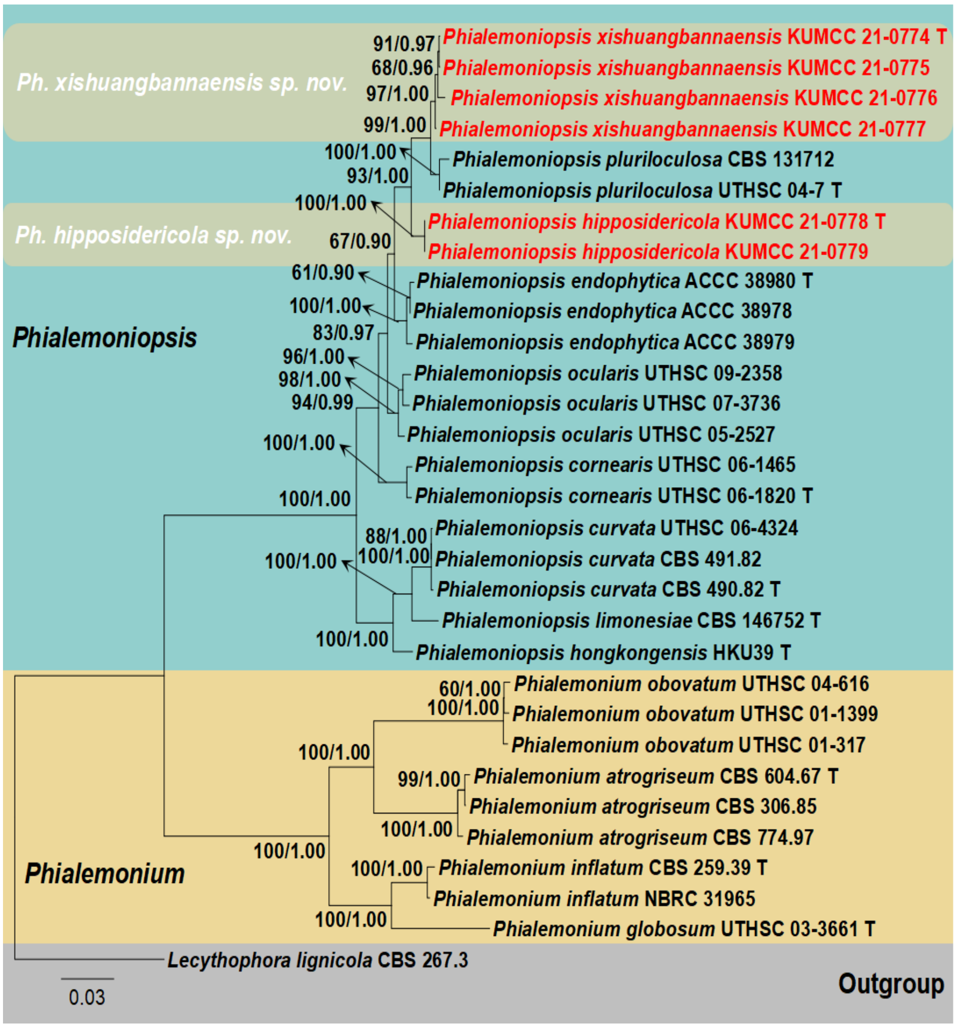

Figure 12 – Consensus phylogram of 1,000 trees resulting from a RAxML analysis of the (ITS+LSU+*Act*+*TUB*) alignment of the analyzed *Phialemoniopsis*. The RAxML analysis of the combined dataset yielded the best scoring tree with a final ML optimization likelihood value of -36643.289170 and generated from 906, 468, 704 and 390 base pairs of ITS, LSU, *Act* and *TUB* characters, respectively. The matrix comprises 1987 distinct alignment patterns with 40.11% gaps and indeterminate traits. Base frequencies were estimated as follows A = 0.218041, C = 0.286820, G = 0.257607, T = 0.237532 with substitution rates AC = 0.759580, AG = 1.946459, AT = 1.203373, CG = 0.953560, CT = 6.268516, GT = 1.000000; proportion of invariable sites I = 0.500216; gamma distribution shape parameter α = 0.531412. The trees from three analyses (ML and BI) showed identical topologies. RAxML bootstrap support values (ML equal to or above 60%) and Bayesian inference (BYPP equal to or above 0.90) are given at the nodes (ML/BYPP). The newly introduced sequences are in bold red. The scale bar represents the expected number of changes per site. Type strains are denoted with T.

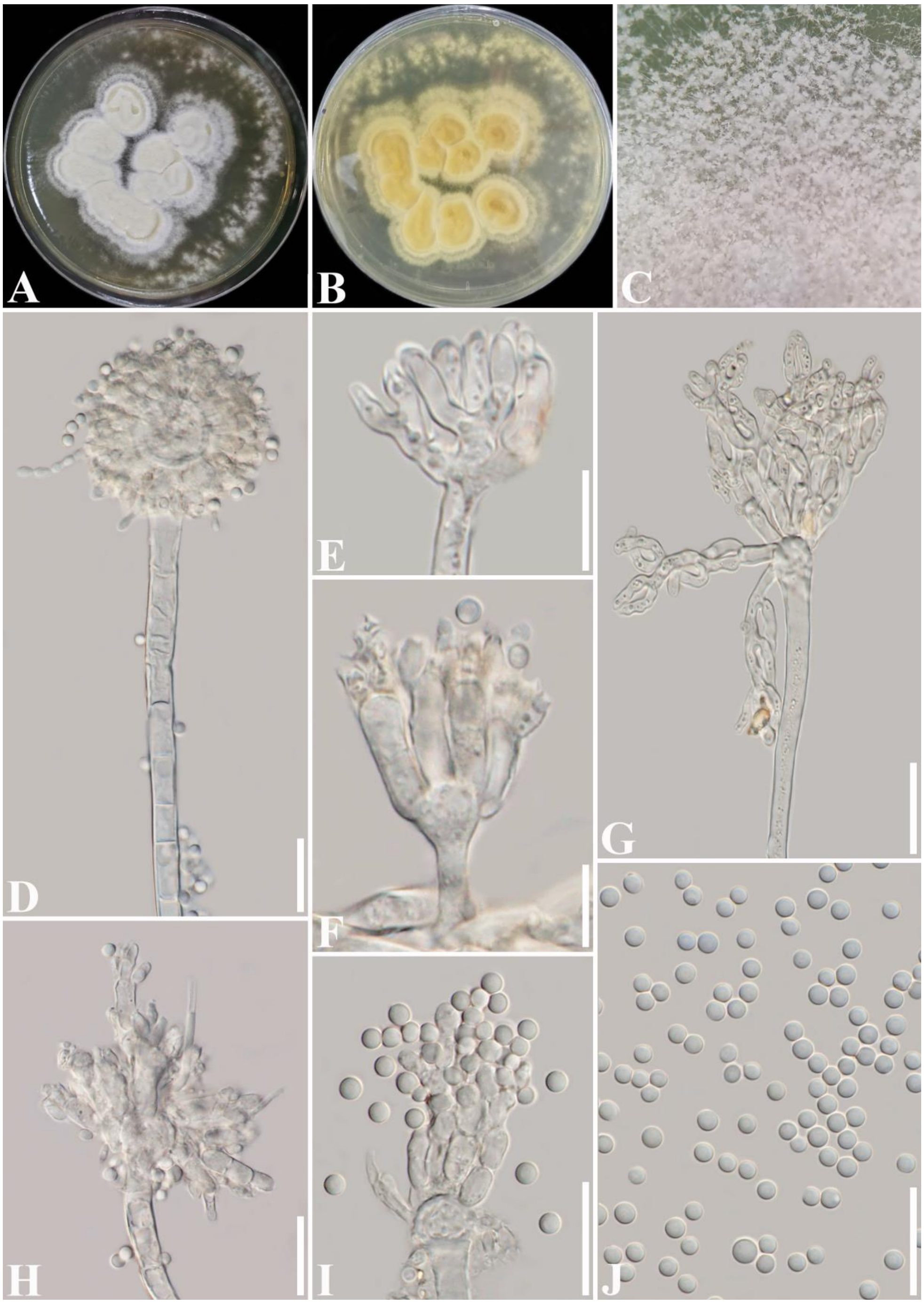

Figure 13 – *Aspergillus candidus* (KUMCC 21-0699). A, B Colony on PDA (above and below). C Close-up of colonies on PDA (80 days old culture). D Conidiophore with conidium head. E–I Conidial heads and conidia. J Conidia. Scale bars: D, G–J = 20 µm, E, F = 10 µm.

Aspergillus creber Jurjević, S.W. Peterson & B.W. Horn, IMA Fungus 3 (1): 69 (2012).

Fig. 14

MycoBank number: MB 800598; Facesoffungi number: FoF 13415

Asexual morph on PDA: Conidial heads radiate, splitting into 3 or more columns. *Conidiophores* uniseriate, sparsely branched. *Stipes* 260–740 × 4–10 µm, hyaline, septate, smooth. *Vesicles* 14–28 µm wide, globose to spathulate, metulae/phialides cover 100 % of head. *Metulae* 3–9 × 2–6 µm (x̄ = 5.67 × 3.59 µm, n = 100), uniseriate, hyaline to pale brown. *Phialides* 4–14 × 1–5 µm (x̄ = 8.27 × 2.57 µm, n = 100), ampulliform, with minute collarette. *Conidia* 2–5 × 2–4 µm (x̄ = 3.25 × 2.95 µm, n = 100), broadly ellipsoid to globose, rough at surface, hyaline to pale brown, arranged in chains. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 20–40 mm after 20 days at room temperature (20–25 °C), colonies surface rough at surface, floccose, wrinkled, mycelial areas white to cream, greenish grey to yellowish grey; reverse yellowish orange to brown black. Sporulation moderately dense on PDA after 80 days.

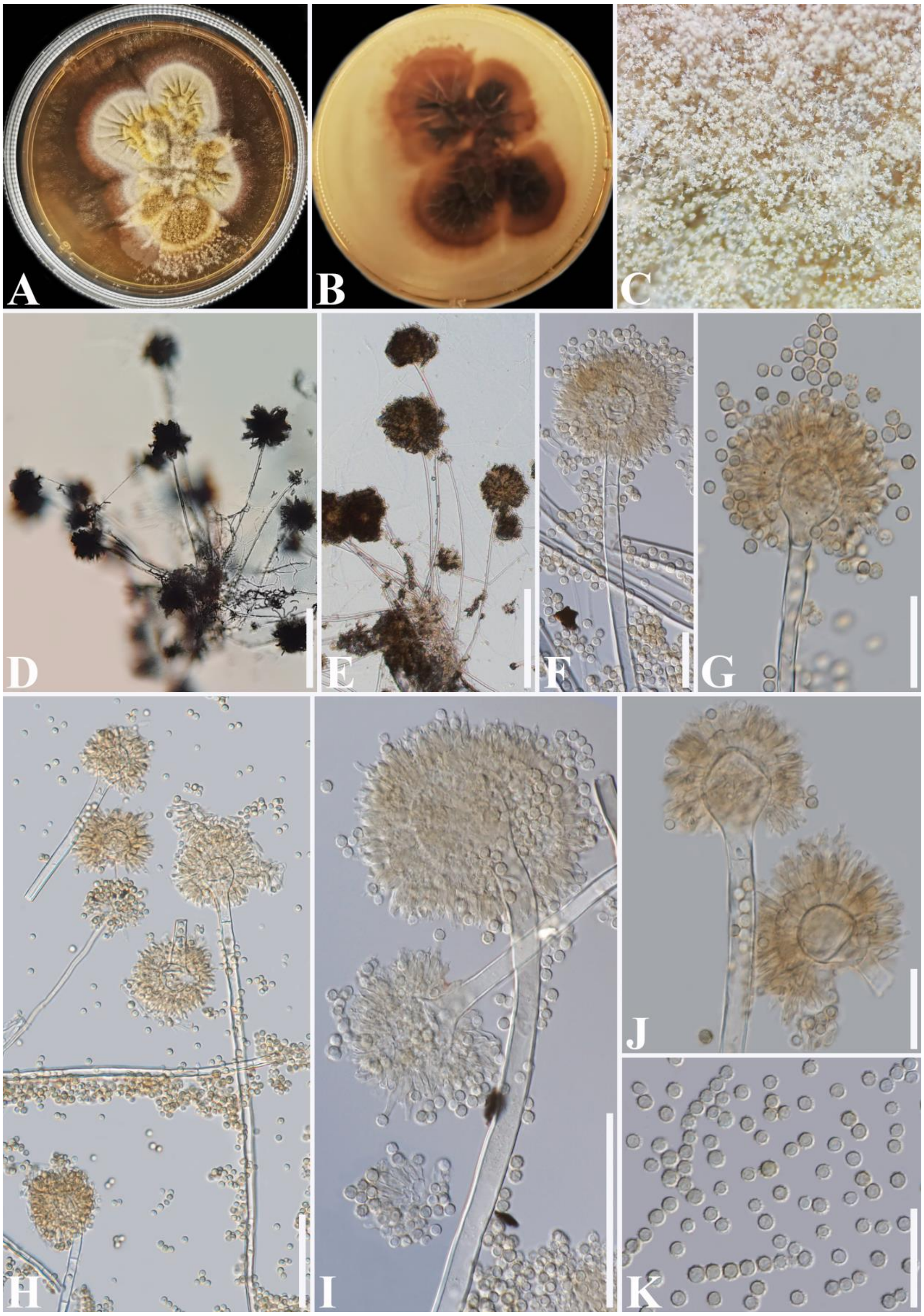

Figure 14 – *Aspergillus creber* (KUMCC 21-0819). A, B Colony characters on PDA (above and below). C–E Close-up of colonies on PDA (80 days old culture). F–J Conidiophores and conidial heads. K Conidia. Scale bars: D, E = 200 µm, F, G, J, K = 20 µm, H, I = 50 µm.

Substrata – air, bat guano, bronchus, bronchoalveolar lavage, clinical material, clinical sample – eye, dead hardwood branch, dead marten, dried *Lentinula edodes*, cave sediment, coffee berry, cystic fibrosis patient, endotracheal secret of man, fermented crop, fruit peel, guanocontaminated cave sediment, Honey of *Melipona scutellaris*, hot pepper from pepper field, house dust, human nail, ice sample, lung tissue, maize meal, moldy oil, moldy shoe, moon cake, mouse excrements in seed store, *Mytilus galloprovinciales*, paraffin, polyethylene foil, rhizosphere of pepper plants, seawater, settle plates, shoe, soil salterns, soybean, soy sauce, sputum, sunflower, surface of archive material, swab, toxic dairy cattle feed, tattoo paint, tomb of dogs, and wheat.

Distribution – Austria, Belgium, Botswana, Brazil, Canada, China, Colombia, Czech Republic, Denmark, Egypt, France, Germany, Greenland, India, Japan, Mexico, Netherlands, New Zealand, Romania, Russia, Slovakia, Slovenia, Spain, South Africa, South Korea, Türkiye, UK, Uruguay and USA.

Material examined – China, Yunnan Province, Yuxi, Yimen County, Pubei Village, Shiliansi, *Rhinolophus affinis* collected from the wing surfaces, 101.282404 E, 21.907599 N, 25 May 2021, Alice Hughes, YM-24-W6 (HKAS122855), living culture KUMCC 21-0819; *ibid*., YM-24-W6-2, living culture KUMCC 21-0820.

GenBank numbers – KUMCC 21-0819 = ITS: OP425807, *BenA*: OQ927581, *CaM*: OR022044, *RPB2*: OR022029; KUMCC 21-0820 = ITS: OP425808, *BenA*: OQ927582, *CaM*: OR022045, *RPB2*: OR022030.

Notes – *Aspergillus creber* was introduced by Jurjevic et al. (2012) from the air in the USA. Based on multi-locus phylogenetic analyses, our isolates clustered together with *As. creber*. Morphologically, the new isolates are similar to the *As. creber* by having rough surface conidia (Jurjevic et al. 2012). Sklenář et al. (2022) named *As. creber* lineage to accommodate *As. creber*, *As. cvjetkovicii* Jurjević, S.W. Peterson & B.W. Horn, *As. jensenii*, *As. puulaauensis* Jurjević, S.W. Peterson & B.W. Horn, *As. tennesseensis* Jurjević, S.W. Peterson & B.W. Horn, and *As. venenatus* Jurjević, S.W. Peterson & B.W. Horn. Based on both phylogeny and morphology, our new isolates are identified as *As. creber,* and this is the first report of *As. creber* isolated from bats in China.

Penicillium Link

Penicillium (*Pe.*) was introduced by Link (1809) with *Penicillium crustaceum* (L.) Fr. as the type species. *Penicillium* is one of the most economically important genera in the family *Aspergillaceae* (Houbraken et al. 2014). Since the discovery of penicillin from *Penicillium crustaceum* by Alexander Fleming in 1832, this genus has been intensively studied for its ability to produce a variety of secondary metabolites, many of which have biotechnological and pharmaceutical applications (Guzmán-Chávez et al. 2018). It has been over 200 years since Johann Heinrich Friedrich Link introduced the generic name *Penicillium*. To date, 1385 species epithets of *Penicillium* are available in Index Fungorum (2023). *Penicillium* is usually found in the air and indoor environments, and is also associated with food spoilage worldwide (Visagie et al. 2014). The colonies of *Penicillium* are initially white and become blue-green, grey-green, olive-grey, yellow or pinkish with time; multicellular hyphae are septate. Conidia are produced in dry chains from the tips of the phialides, with the youngest spore at the base of the chain, and are nearly always green (https://wineserver.ucdavis.edu/). The majority of *Penicillium* species are saprobic and commonly occur in soil, but some species exist as endophytes in many plant species (Chen et al. 2013a, Jeewon et al. 2013, Rashmi et al. 2019, Liang et al. 2021). *Penicillium* species are known for their positive or negative effects on humans as well (Chen et al. 2013a, Houbraken et al. 2014). We report a new record of *Penicillium brevicompactum* in this study.

Penicillium brevicompactum Dierckx, Ann. Soc. Sci. Bruxelles 25: 88 (1901). Fig. 15

MycoBank number*:* MB 149773; Facesoffungi number: FoF 13416

Asexual morph on PDA: Sporulating on PDA after 80 days. *Conidiophores* mostly biverticillate, sometimes tri-verticillate; *stipes* smooth, 150–350 × 3–11 µm; branches/rami two when present, 11–27 × 3–10 µm; *metulae* divergent, 2–6 per stipe/branch, 6–21 × 3–9 µm, vesicle 3.2–9.2 µm; *phialides* ampulliform, 5–17 × 1–6 µm, with minute collarette; average length phialide/metula 0.72. *Conidia* finely rough to rough-walled, moderately, globose, 2–5 × 2–4 µm ($\bar{x}$ = 3.46 × 3.00 µm, n = 200), often in chains. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 25–40 mm after 21 days at room temperature (20–25 ℃), rough, floccose at surface, mycelial areas cream, greenish grey to yellowish grey; reverse pigmentation brown, sometimes greyish yellow to greyish orange to brownish orange; Sporulation moderately dense, conidial mass greyish green to green after 80 days.

Substrata – decaying mushroom, grape fruit, *Grifola frondosa*, paprika, soil, and wood decay fungus.

Distribution – Algeria, Antarctica, Argentina, Australia, Belgium, Bolivia, Brazil, Cameroon, Canada, Chile, China, Colombia, Czech Republic, Denmark, Estonia, Ethiopia, Finland, France, Georgia, Germany, Guatemala, Guiana, Hungary, India, Iran, Iraq, Isle of Man, Italy, Japan, Kenya, Kyrgyzstan, Latvia, Lithuania, Mexico, Malaysia, Morocco, Netherlands, New Zealand, Norway, Pakistan, Panama, Papua New Guinea, Poland, Portugal, Russia, Slovakia, Slovenia, South Africa, South Korea, Spain, Sweden, Switzerland, Tanzania, Thailand, Türkiye, Uganda, UK, Ukraine and USA.

Material examined – China, Yunnan Province, Yuxi, Yimen County, Pubei Village, Shiliansi, *Rhinolophus siamensis*, 102.1633 E, 24.61746 N, 21 September 2020, Alice Hughes, YM-18-L (HKAS122849), living culture KUMCC 21-0766; *ibid*., YM-45-L, living culture KUMCC 21-0768; *ibid*., YM-45-W1, living culture KUMCC 21-0762; *ibid*., *Rhinolophus sinicus*, YM-52-B1, living culture KUMCC 21-0767; *ibid*., *Rhinolophus rex*, YM-17-B2, living culture KUMCC 21-0763; *ibid*., YM-30-L, living culture KUMCC 21-0765; *ibid*. YM-30-W2, living culture KUMCC 21-0769; *ibid. Rhinolophus affinis*, YM-24-W3, living culture KUMCC 21-0764.

GenBank numbers – KUMCC 21-0766 = ITS: ON426870, *BenA*: OQ927583, *CaM*: OR022046, *RPB2*: OR022031; KUMCC 21-0768 = ITS: ON426873, *BenA*: OQ927584, *CaM*: OR022047, *RPB2*: OR022032; KUMCC 21-0762 = ITS: ON426874, *BenA*: OQ927585, *CaM*: OR022048, *RPB2*: OR022033; KUMCC 21-0767 = ITS: ON426875, *BenA*: OQ927586, *CaM*: OR022049, *RPB2*: OR022034; KUMCC 21-0763 = ITS: ON426869, *BenA*: OQ927587, *CaM*: OR022050, *RPB2*: OR022035; KUMCC 21-0765 = ITS: ON426872, *BenA*: OQ927588, *CaM*: OR022051, *RPB2*: OR022036; KUMCC 21-0769 = ITS: ON426878, *BenA*: OQ927589, *CaM*: OR022052, *RPB2*: OR022037; KUMCC 21-0764 = ITS: ON426871, *BenA*: OQ927590, *CaM*: OR022053, *RPB2*: OR022038.

Notes – *Penicillium brevicompactum* was introduced by Dierckx (1901). Based on multi-gene phylogenetic analyses, our isolates clustered together with *Pe. brevicompactum* strains (AS3 15323 and CBS 257.29 (type)) in section *Brevicompacta* and close to *Pe. neocrassum* R. Serra & S.W. Peterson, *Pe. bialowiezense* K.W. Zaleski and *Pe. fennelliae* Stolk. Morphologically, the new isolates are similar to the *Pe. brevicompactum* by having rough surface conidia, penicilli compact terverticillate (Dierckx 1901). *Penicillium brevicompactum* different from *Pe. neocrassum* by the latter having smaller conidia (2–5 × 2–4 µm vs 2.5–3.5 × 2–2.5 µm) with smooth or finely roughened surface, and smaller metulae with less stipe/branch (6–21 × 3–9 µm vs 9–12 × 3.5–4 µm) (Serra & Peterson 2007). *Penicillium brevicompactum* differs from *Pe. bialowiezense* by the latter having smaller conidia (2–5 × 2–4 µm vs 2.5–3.5 × 2–3 µm), smaller cylindrical phialides (5–17 × 1–6 µm vs 6.5–9 × 2.5–3 µm) and apically inflated metulaes (Zaleski 1927). *Penicillium brevicompactum* differs from *Pe. fennelliae* by the latter having cylindrical or elliptical conidia with truncate base and smaller metulae (6–21 × 3–9 µm vs 10–16 × 2.5–4 µm) (Stolk 1969). Based on both phylogeny and morphology, the new isolates are identified as *Pe. brevicompactum*. This is the first report of *Pe. brevicompactum* isolated from bats in China.

Class ***Sordariomycetes*** O.E. Erikss. & Winka
Amphisphaeriales D. Hawksw. & O.E. Erikss.
Apiosporaceae K.D. Hyde et al.

Apiosporaceae was introduced by Hyde et al. (1998), with *Apiospora* as the type genus. *Apiosporaceae* is closely related to *Amphisphaeriaceae* within *Amphisphaeriales* (Crous & Groenewald 2013). Five genera were included in *Apiosporaceae*, *viz*., *Apiospora*, *Appendicospora* K.D. Hyde, *Arthrinium*, *Dictyoarthrinium* S. Hughes and *Nigrospora* (Wijayawardene et al. 2022).

A subsequent study by Jiang et al. (2022) introduced the new genus *Neoarthrinium* Ning Jiang within *Apiosporaceae*, thus, currently, the family comprises six genera.

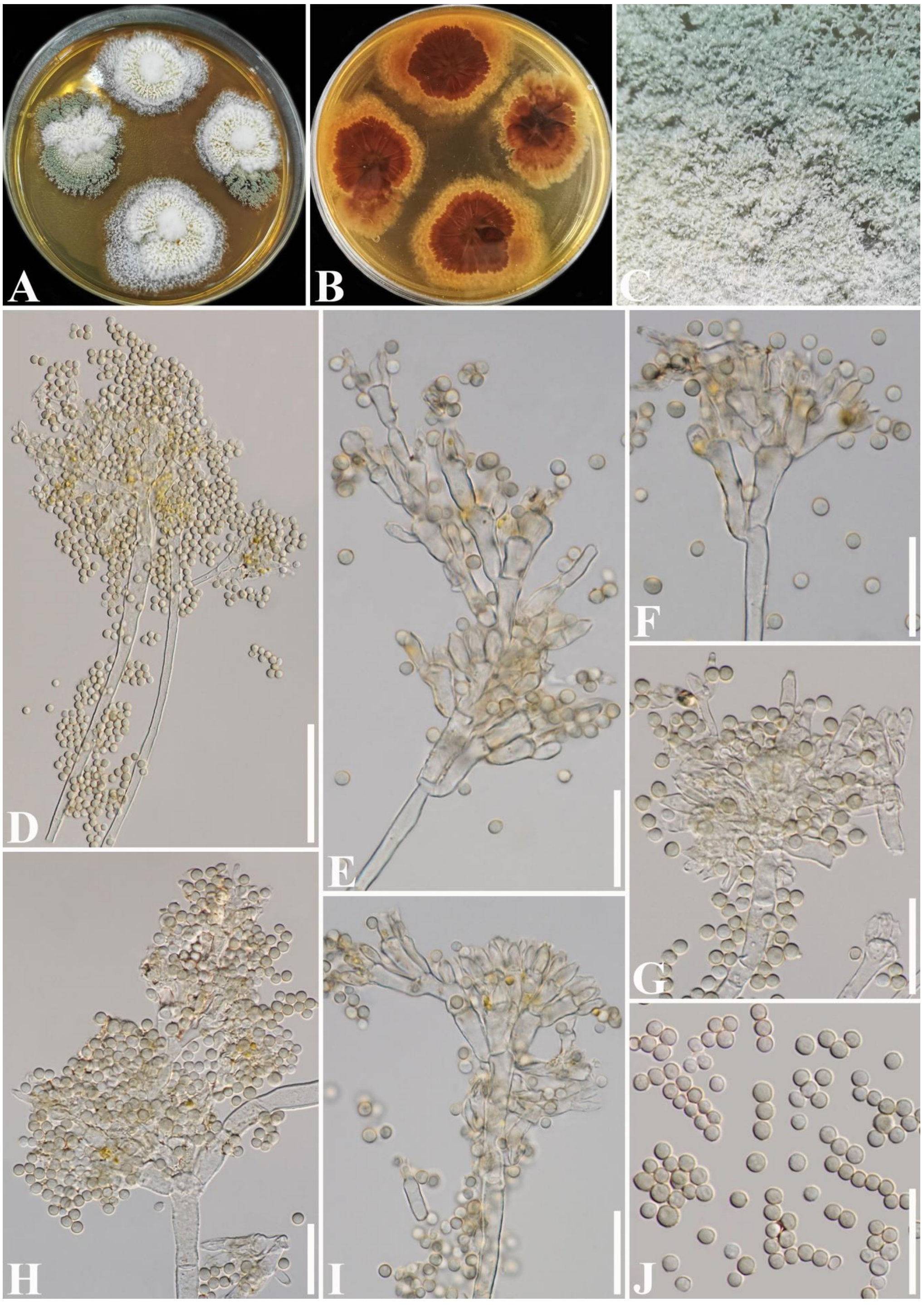

Figure 15 – *Penicillium brevicompactum* (KUMCC 21-0766). A, B Colonies on PDA (above and below). C Colony texture on PDA (30 days old culture). D–G Conidiophores, conidial heads and conidia. J Conidia. Scale bars: D = 50 µm, E–H = 20 µm.

Apiospora Sacc.

Apiospora (*Ap.*) was erected by Saccardo (1875) with *Apiospora montagnei* Sacc. as the type species. The genus is characterized by multi-locular perithecial stromata, hyaline ascospores surrounded by a thick gelatinous sheath and pale brown to brown, globose to subglobose conidia that are usually lenticular in the side view (Kunze 1817, Hyde et al. 1998, 2020, Dai et al. 2016, 2017, Pintos & Alvarado 2021, Tian et al. 2021). *Apiospora* was previously synonymized with *Arthrinium* by Crous & Groenewald (2013), but Pintos et al. (2019) showed that the clade is not monophyletic with *Apiospora*. Pintos & Alvarado (2021) reevaluated the placements of these two genera and transferred 55 species to *Apiospora* based on molecular phylogenetic analyses (Tian et al. 2021). *Apiospora* is similar to *Arthrinium* in morphology but is difficult to distinguish without phylogenetic data (Tian et al. 2021). This study introduces three new species, a new host record and a new country record.

Apiospora arundinis (Corda) Pintos & P. Alvarado, in Pintos & Alvarado, Fungal Systematics and Evolution 7: 205 (2021). Fig. 16

MycoBank number: MB 837742; Facesoffungi number: FoF 13417

Asexual morph on PDA: *Mycelium* consisting of branched, septate, hyaline to brown, smooth to asperulate, thin-walled, 1–6 µm wide hyphae. *Conidiophores* macronematous, pale brown to hyaline, flexuous, smooth, subcylindrical, transversely septate, branched. *Conidiogenous cells* 5–40 × 1–5 µm ($\bar{x}$ = 18.00 × 2.58 µm, n = 20), basauxic, aggregated in clusters or free on hyphae, hyaline to pale brown, smooth, subcylindrical to doliiform. *Conidia* 8–26 × 3–12 µm ($\bar{x}$ = 10.95 × 8.19 µm, n = 60), light brown to blackish brown, globose to subglobose, clavate to straight or flexuous, smooth or roughened at surface, sometimes lenticular inside view, occasionally with a hyaline, thin, longitudinal band, sometimes suspended with conidiogenous hyphae. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 50–60 mm after 18 days at room temperature (20–25 °C), initially compact and round, becoming widely effused, aerial mycelium with an undulated edge, white, sparse on surface; reverse pale yellow. Sporulate on PDA after 65 days.

Substrata – *Arundo donax*, *Arundo micrantha*, *Aspergillus flavus* sclerotium buried in sandy field, beach sand, *Cinnamomum camphora*, culm of cultivated *Sasa*, dead culms of *Phragmites australis*, dung, human toenail, leaf of *Hordeum vulgare*, living leaves of *Fagus sylvatica*, *Sambucus racemosa*, soil, stem of cultivated bamboo, and *Theobroma cacao.*

Distribution – Algeria, Balearic Islands, Belgium, Canada, China, Czech Republic, Estonia, Finland, France, Germany, Greece, India, Iran, Italy, Japan, Morocco, Netherlands, Philippines, Portugal, Puerto Rico, Sierra Leone, Slovakia, Spain, South Africa, Sweden, Switzerland, UK, Uruguay and USA.

Material examined – China, Yunnan Province, Kunming, Xishan District, Long cave, on *Miniopterus schreibersii*, 24º50.332' N, 102º36.027' E, 24 September 2020, Alice Hughes, Foot samples XS-5-L2 (HKAS122797), living culture KUMCC 21-0697; *ibid*., on *Myotis pilosus* foot, XS-142-L, living culture KUMCC 21-0698.

GenBank numbers – KUMCC 21-0697 = LSU: OP363250, ITS: ON426831, *TEF 1-α*: OR025963, *TUB*: OR025924; KUMCC 21-0698 = LSU: OP363251, ITS: ON426830, *TEF 1-α*: OR025964, *TUB*: OR025925.

Notes – *Apiospora arundinis* was first described as *Gymnosporium arundinis* Corda by Corda (1838). Pintos & Alvarado (2021) transferred *G. arundinis* to *Apiospora* based on the phylogenetic analyses and synonymized it as *Apiospora arundinis*. In this study, our new isolates (KUMCC 21-0697 and KUMCC 21-0698) clustered together with the strains of *Ap. arundinis* (CBS 133509 and CBS 449.92) with 100% ML and 1.00 BYPP statistical support (Fig. 5). Our strains are morphologically similar to *Ap. arundinis*. *Apiospora arundinis* has been reported as a plant pathogen causing kernel blight in barley and leaf blight of tea and a human pathogen causing nail infections (Dylag et al. 2017, Vettorato et al. 2020). This is the first report of *Ap. arundinis* from animals (bats) and also the first report in China.

Apiospora marii (Larrondo & Calvo) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 206 (2021). Fig. 17

MycoBank number: MB 837685; Facesoffungi number: FoF 14083

Asexual morph on PDA: *Hypha* 0.5–8 µm wide, hyaline to brown, branched, septate, smooth to asperulate, thin-walled. *Conidiophores* hyaline to pale brown, smooth-walled, subcylindrical, with refractive transverse septa, branched. *Conidiogenous cells* 4–28 × 1–8 µm (x̄ = 14.99 × 2.74 µm, n = 20), basauxic, aggregated in clusters, hyaline, smooth, subcylindrical to doliiform, arising from conidiophores or directly from vegetative hyphae. *Conidia* 5–13 × 5–10 µm (x̄ = 8.17 × 7.50 µm, n = 60), pale brown to blackish brown, globose to subglobose, clavate to irregular, straight or flexuous, lenticular from side view, smooth or rough-walled, occasionally with a longitudinal, hyaline, thin-walled, band. Sexual morph: Undetermined.

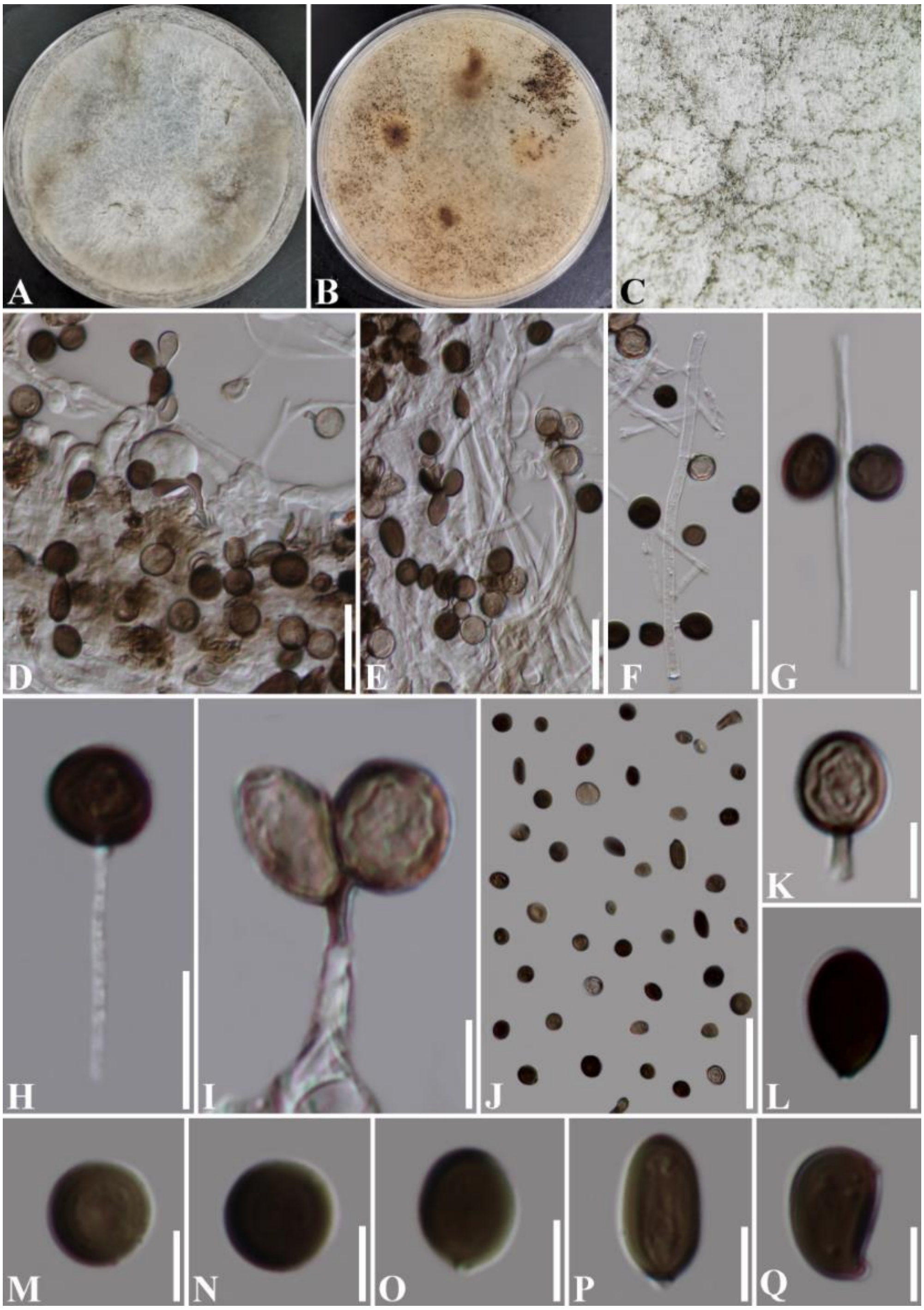

Figure 16 – *Apiospora arundinis* (KUMCC 21-0697). A–B Colony on PDA (above and below). C Conidia mass forming on PDA (65 days old culture). D, E Hyphae and conidia. F–I, K Conidiophore and conidiogenous cells. J, L–Q Conidia. Scale bars: D–F = 15 µm, G, H = 10 µm, J = 30 µm, I, K–Q = 5 µm.

Culture characteristics – Colonies on PDA attaining 45–60 mm after 14 days at room temperature (20–25 °C), initially compact and round, becoming widely effused, aerial mycelium with an undulated edge, white, sparse on surface; reverse pale yellow. Sporulate on PDA after 80 days.

Substrata – Air, *Ampelodesmos mauritanicus*, *Arundo donax*, beach sand, culm of *Arundinaria hindsi*, leaf of *Beta vulgaris*, oats, Oleaeuropaea, seaweed, and stems of *Phragmites australis*.

Distribution – Austria, Chile, China, India, Indonesia, Iran, Italy, Netherlands, Portugal, South Korea, Spain, Sweden and Tunisia.

Material examined – China, Yunnan Province, Yuxi, Yimen County, Pubei Village, Shiliansi, *Rhinolophus sinicus*, 102.1633 E, 24.61746 N, 21 September 2021, Alice Hughes, from the wing surfaces YM-56-W4 (HKAS122848), living culture KUMCC 21-0693; *ibid*., YM-56-W4-2, living culture KUMCC 21-0694.

GenBank numbers – KUMCC 21-0693 = LSU: OP363252, ITS: ON426828, *TEF 1-α*: OR025965, *TUB*: OR025926; KUMCC 21-0694 = LSU: OP363253, ITS: ON426829, *TEF 1-α*: OR025966, *TUB*: OR025927.

Notes – The National Center for Biotechnology Information (NCBI) BLAST results of our new isolate (KUMCC 21-0693) showed high similarities with *Apiospora marii* (99.22% of ITS (CBS 497.90), 99.78% of LSU (CBS 113535), 100.00% of *TEF1-α* (CBS 113535), and 99.59% of TUB (CBS 200.57)). In this study, our new isolates (KUMCC 21-0693 and KUMCC 21-0694) clustered together with the strains of *Ap. marii* (CBS 113535 and CBS 114803) with 100% ML and 1.00 BYPP statistical support (Fig. 5). Our strains are morphologically similar to *Ap. marii*. Hence, the two new isolates are identified as *Ap. marii*.

Apiospora marii was first described as *Arthrinium mari* Larrondo & Calvo by Larrondo & Calvo (1990). Pintos & Alvarado (2021) transferred *Ar. marii* to *Apiospora* based on the phylogenetic analyses and synonymized it as *Ap. marii*. *Apiospora marii* is genetically close to *Ap. piptatheri* (Pintos & P. Alvarado) Pintos & P. Alvarado, *Ap. sacchari* (Speg.) Pintos & P. Alvarado, *Ap. guizhouensis* (M. Wang & L. Cai) Pintos & P. Alvarado, *Ap. hispanica* (Larrondo & Calvo) Pintos & P. Alvarado, *Ap. mediterranea* (Larrondo & Calvo) Pintos & P. Alvarado, and *A. longistromum* D.Q. Dai & K.D. Hyde (Pintos et al. 2019). Pintos et al. (2019) believe that these apparently related species represent a single taxon, belonging to *Ap. marii*, however, the incomplete data from the type specimens of *Ap. hispanica* and *Ap. mediterranea* do not allow for a definitive answer. *Arthrinium marii* was proposed by Larrondo & Calvo (1990) who described the asexual morph, and Pintos et al. (2019) described its sexual morph collected from dead culms of *Phragmites australis*. *Apiospora marii* was isolated from the atmosphere, medicinal excipients, household dust, beach sand, various plants, as well as animal skin (Larrondo & Calvo 1990, Crous 2013, Pintos et al. 2019). This is the first report of *Ap. marii* from animals (bats) and also the first report in China.

Apiospora vietnamensis (Hol.-Jech.) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021). Fig. 18

MycoBank number: MB 837737; Facesoffungi number: FoF 14084

Asexual morph on PDA: *Hyphae* 1–6 μm wide, hyaline to brown, branched, septate, smooth to asperulate, thin-walled. *Conidiophores* macronematous, pale brown to hyaline, smooth-walled, subcylindrical, with refractive transverse septa, branched. *Conidiogenous cells* 2–11 × 1–6 µm ($\bar{x}$ = 6.60 × 3.09 μm, n = 40), basuaxic, aggregated into clusters, hyaline, smooth, subcylindrical to doliiform, arising from conidiophores or directly from vegetative hyphae. *Conidia* 2–15 × 2–7 µm ($\bar{x}$ = 5.30 × 4.69 μm, n = 90), hyaline to blackish brown, globose to subglobose, clavate to irregular, straight or flexuous, smooth or roughened-walled, lenticular lateral view, occasionally with a longitudinal, hyaline, thin-walled, band. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 50–60 mm after 15 days at room temperature (20–25 °C), initially compact and round, becoming widely effused, aerial mycelium with an undulated edge, white, sparse on surface; reverse pale yellow. Sporulate on PDA after 80 days.

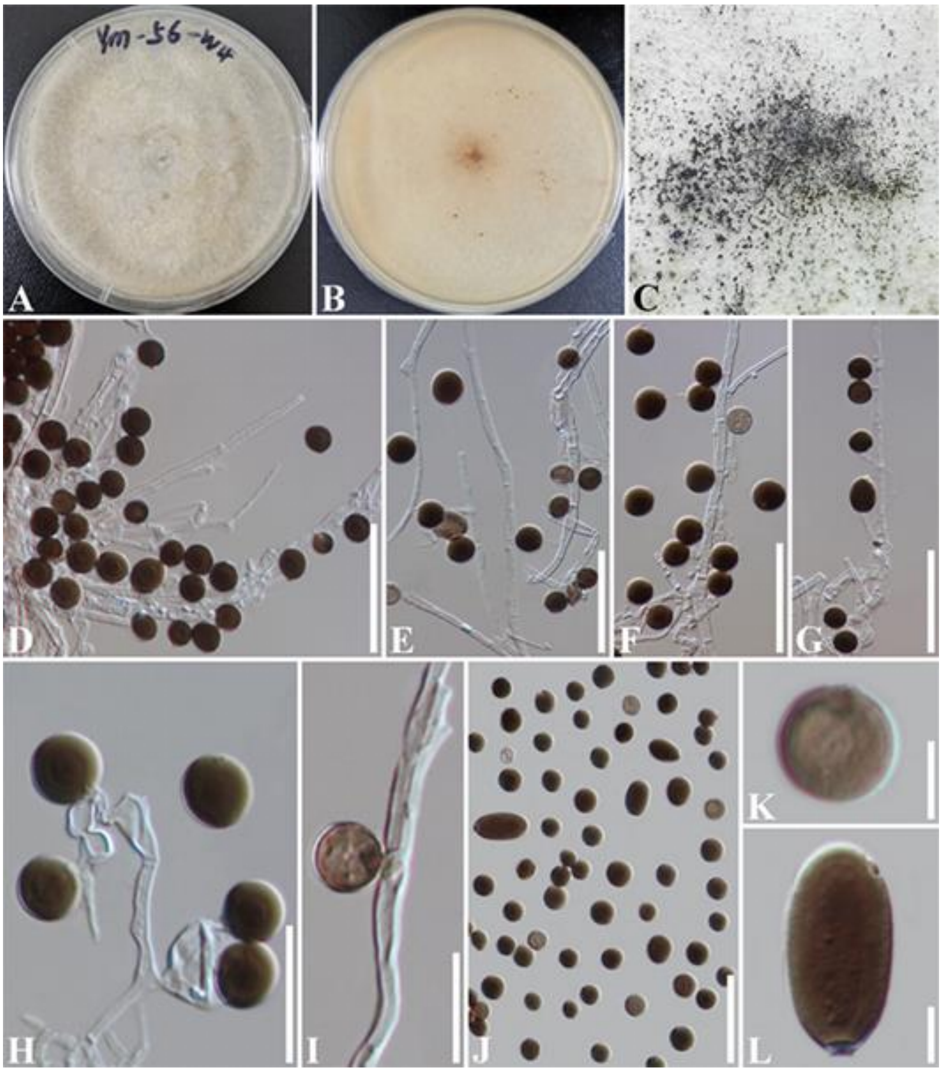

Figure 17 – *Apiospora marii* (KUMCC 21-0693). A, B Colony on PDA (above and below). C Conidia mass forming on PDA (80 days old culture). D–I Conidiophore and conidiogenous cells. J, K Conidia. L Clavate conidium. Scale bars: D–G, J = 30 µm, H, I = 15 µm, K, L = 5 µm.

Substratum – *Citrus sinensis.*

Distribution – Vietnam.

Material examined – China, Yunnan Province, Yuxi, Yimen County, Pubei Village, Shiliansi, *Hipposideros pomona*, 102.1633 E, 24.61746 N, 21 September 2021, Alice Hughes, wing surfaces YM-66-B4 (HKAS122259), living culture KUMCC 21-0428; *ibid*., YM-66-B4-2, living culture KUMCC 21-0429.

GenBank numbers – KUMCC 21-0428 = LSU: OP363254, ITS: ON426826, *TEF 1-α*: OR025967, *TUB*: OR025928; KUMCC 21-0429 = LSU: OP363255, ITS: ON426827, *TEF 1-α*: OR025968, *TUB*: OR025929.

Notes – *Apiospora vietnamensis* is controversial. *Apiospora vietnamensis* was first described as *Nigrospora vietnamensis* Hol.-Jech. by Jechová (1963). Wang et al. (2017) showed that *Ni. vietnamensis* and *Arthrinium malaysianum* Crous are conspecific, and transferred *Ni. vietnamensis* to *Arthrinium* and appeared conspecific to *Ar. malaysianum* Crous based on LSU and ITS analysis and morphology. Pintos & Alvarado (2021) transferred *Ar. malaysianum* to *Apiospora* based on the phylogenetic analyses and synonymized it as *Ap. malaysiana* (Crous) Pintos & P. Alvarado, and introduced *Ap. vietnamensis* basionymized with *Ni. vietnamensis*. In this study, our new isolates (KUMCC 21-0428 and KUMCC 21-0429) clustered together with the strains of *Ap. vietnamensis* (IMI 99670, type) (Fig. 5). Based on nucleotide comparisons, our strain (KUMCC 21-0428) is similar to *Ap. vietnamensis* (IMI 99670, type) in 0% (0/630 bp) of the ITS, 0% (0/908 bp) of the LSU, 0.61% (3/493 bp) of *TUB* and 2/610 bp (0.32%) of *TEF1-α*. Morphologically, the new isolate (KUMCC 21-0428) is similar to the holotype of *Ap. vietnamensis* (IMI 99670, type), in having aggregated, hyaline to blackish brown, globose to subglobose conidia borne as bunches, and intercalary and terminal, pale brown to hyaline, branched conidiophores (Jechová 1963, Wang et al. 2017). Based on both phylogeny and morphology, the new isolates (KUMCC 21-0428 and KUMCC 21-0429) are identified as *Ap. vietnamensis*. This is the first report of *Ap. vietnamensis* from a bat and also the first report in China.

Apiospora xishuangbannaensis Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 19

MycoBank number: MB 845342; Facesoffungi number: FoF 13263

Etymology – Named after the location Xishuangbanna, where the holotype was collected.

Holotype – HKAS122798.

Asexual morph on PDA: *Hyphae* 1–6 μm wide, hyaline to brown, branched, septate, smooth to asperulate, thin-walled. *Conidiophores* simple, macronematous, flexuous, hyaline to pale brown, smooth-walled, subcylindrical, with refractive transverse septa, branched. *Conidiogenous cells* 6–37 × 1–5 μm (x̄ = 18 × 2.58 μm, n = 20), basauxic, sometimes in clusters, hyaline, smooth, subcylindrical to doliiform, arising from conidiophores or directly from vegetative hyphae. *Conidia* 7–12 × 3–12 μm (x̄ = 10.22 × 8.19 μm, n = 60), pale brown to blackish brown, variable in shape; globose to subglobose, clavate to irregular, straight or flexuous, lenticular from side view, smooth or rough-walled, occasionally with a longitudinal, hyaline, thin-walled, guttule; conidia sometimes 11–26 × 3–9 μm, elongated, allantoid, clavate to irregular, straight to curved, brown, mixed among conidia. *Sterile cells* not observed. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 55–60 mm after 20 days at room temperature (20–25 °C), initially compact and round, becoming widely effused, aerial mycelium with undulated edge, white, sparse on surface; reverse pale yellow. Sporulate on PDA after 80 days.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, *Rhinolophus pusillus* collected from the wing surfaces in limestone forest, 101.282404 E, 21.907599 N, 25 May 2021, Alice Hughes, 25 (**holotype,** HKAS122798), ex-type KUMCC 21-0695; *ibid.*, 25-B, ex-isotype KUMCC 21-0696.

GenBank numbers – KUMCC 21-0695 = LSU: OP363248, ITS: ON426832, *TEF 1-α*: OR025969, *TUB*: OR025930; KUMCC 21-0696 = LSU: OP363249, ITS: ON426833, *TEF 1-α*: OR025970, *TUB*: OR025931.

Notes – In the phylogenetic analyses (Fig. 5), *Apiospora xishuangbannaensis* formed a distinct clade separated from *Ap. septata*, *Ap. gelatinosa* and *Ap. biserialis*. Although *Ap. xishuangbannaensis* has similar morphology to *Ap. septata* and *Ap. biserialis*, but conidiogenous cells and conidia sizes of *Ap. xishuangbannaensis* are significantly different (Feng et al. 2021) (Supplementary Table 3). *Apiospora xishuangbannaensis* differs from *A. septata* by larger conidiogenous cells (6–37 × 1–5 μm vs 4.0–18.0 × 1.5–4.0 μm), smaller conidia (7–26 × 3–12 μm vs 9–13 μm long) variable in shape, and absence of sterile cells (Feng et al. 2021). *Apiospora xishuangbannaensis* differs from *Ap. biserialis* by the latter having shorter conidiogenous cells (6–37 × 1–5 μm vs 5.0–22.0 × 2.5–5.0 μm), and smaller conidia (7–26 × 3–12 μm vs 7–11 μm long) (Feng et al. 2021) (Supplementary Table 3). Unfortunately, we were unable to compare the morphology of our isolates with *A. gelatinosa* as this species has been reported only from the sexual morph isolated from dead bamboo (Feng et al. 2021) (Supplementary Table 3). Based on the nucleotide comparisons, *Ap. hipposiderocola* (KUMCC 21-0428) is different from *Ap. septata* (CGMCC 3.20134, type), *Ap. gelatinosa* (HKAS 111962, type) and *Ap. biserialis* (CGMCC 3.20135, type) (Supplementary Table 4). The PHI test (Fig. 20) was carried out to confirm there was no recombination in the new species, compared with the closely related taxa. Based on the phylogeny and morphology, *Ap. xishuangbannaensis* is described as a distinct new species.

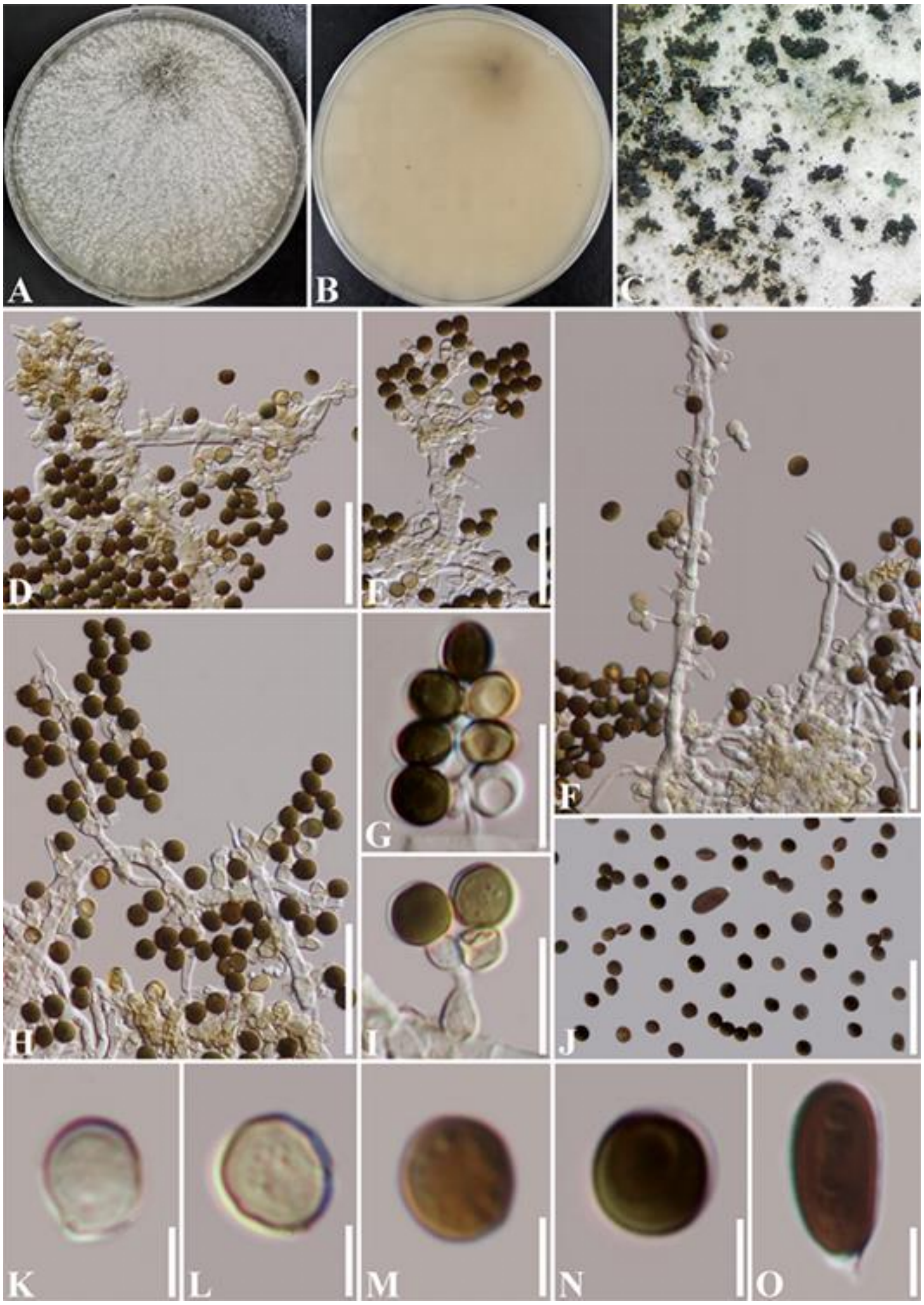

Figure 18 – *Apiospora vietnamensis* (KUMCC 21-0428). A–B Colony on PDA (above and below). C Conidia mass forming on PDA (80 days old culture). D–I Conidiophore and conidiogenous cells. J–N Conidia. O Clavate conidium. Scale bars: D–G, J = 30 µm, H, I = 15 µm, K–N = 3 µm, O = 5 µm.

Sporocadaceae Corda

Sporocadaceae was introduced by Corda (1842) and typified with *Sporocadus* Corda. *Sporocadaceae* species are typically appendage-bearing coelomycetes that can be saprobic or pathogenic on plants (branches, fruits, leaves and twigs) and endophytic or parasitic on humans and animals (Hyde et al. 2020). *Sporocadaceae* has been subjected to several taxonomic reclassifications, while Jaklitsch et al. (2016) re-validated this family, and four other families, *viz*., *Bartaliniaceae* Wijayaw. Et al., *Discosiaceae* Maharachch. & K.D. Hyde, *Pestalotiopsidaceae* Maharachch. & K.D. Hyde and *Robillardaceae* Crous, were treated as synonyms of *Sporocadaceae* (Nag Raj 1993, Crous et al. 2015, Senanayake et al. 2015, Maharachchikumbura et al. 2016, Liu et al. 2019, Hyde et al. 2020). Currently, the family comprises 35 genera (Wijayawardene et al. 2022), and we introduce one new species and one host record species belonging to *Neopestalotiopsis*.

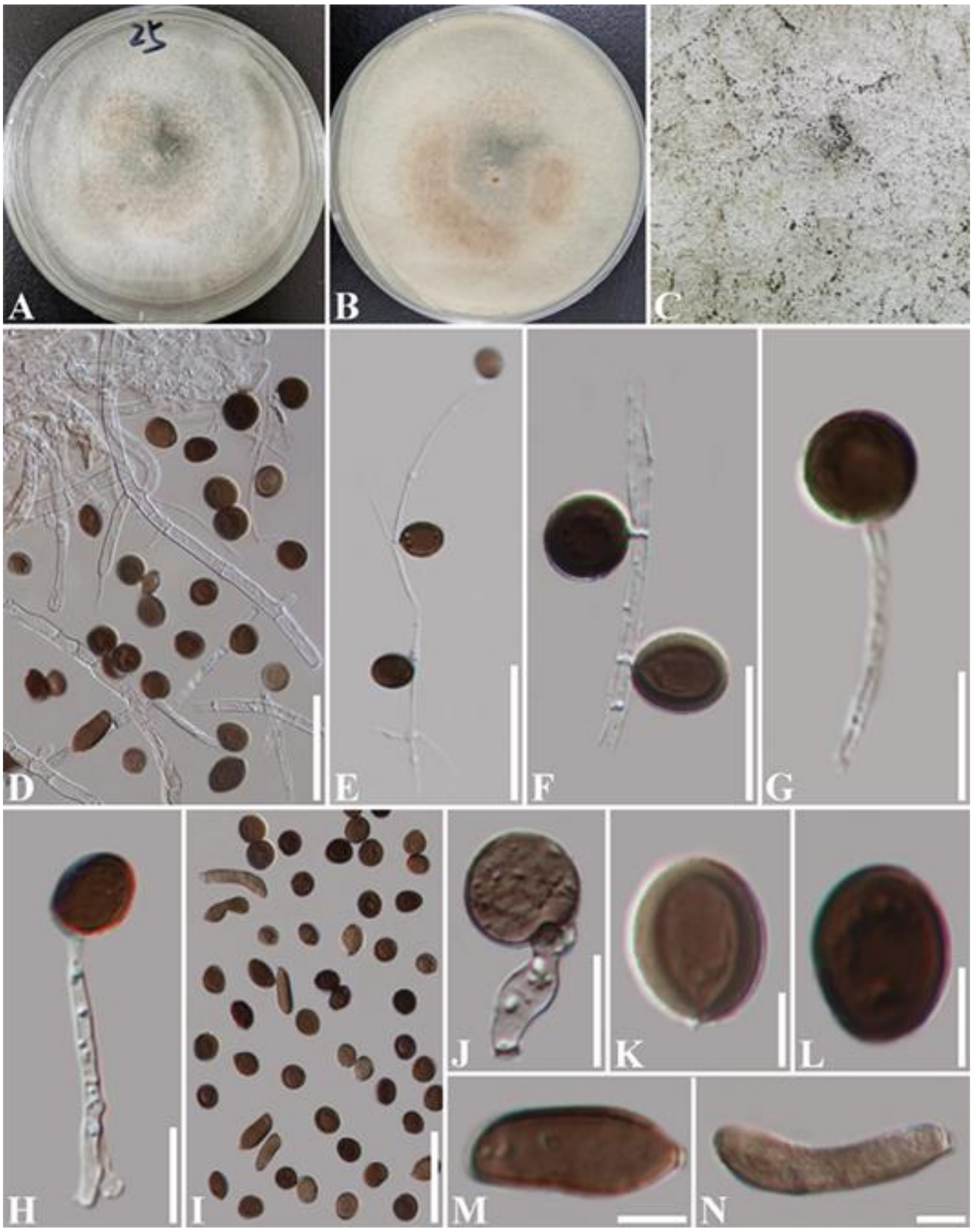

Figure 19 – *Apiospora xishuangbannaensis* (KUMCC 21-0695). A, B Colony on PDA (above and below). C Conidial mass forming on PDA (80 days old culture). D Hyphae and conidia. E–H, J Conidiophores, conidiogenous cells and conidia. I, K–N Conidia. Scale bars: D, E, I = 30 µm, F = 15 µm, G, H, J = 10 µm, K–N = 5 µm.

Neopestalotiopsis Maharachch., K.D. Hyde & Crous

Neopestalotiopsis (*N.*) was introduced by Maharachchikumbura et al. (2014) and typified with *N. Protearum* (Crous & L. Swart) Maharachch. et al. *Neopestalotiopsis* and its sister genus *Pseudopestalotiopsis* Maharachch. et al. Are distinguished from *Pestalotiopsis* based on multi-gene analyses of ITS, *TUB* and *TEF1-α* (Maharachchikumbura et al. 2014, Liu et al. 2021). However, they are very similar in morphology by having 4-septate conidia, with one to many filiform or attenuated tubular apical appendages and a single basal, tubular appendage. Furthermore, the morphological differences of *Neopestalotiopsis* that distinguish it from others include versicolourous median cells and indistinct conidiophores, which are often reduced to conidiogenous cells (Maharachchikumbura et al. 2014, Jayawardena et al. 2016, Liu et al. 2021). *Neopestalotiopsis* are found as saprobes or pathogens on plants, and the sexual morph remains unknown (Maharachchikumbura et al. 2013a, b, 2014, 2016, Gerardo-Lugo et al. 2020, Hyde et al. 2020, Liu et al. 2021). In this study, we introduce one new species, *Neopestalotiopsis xishuangbannaensis* and a new host record of *N. paeoniae-suffruticosae.*

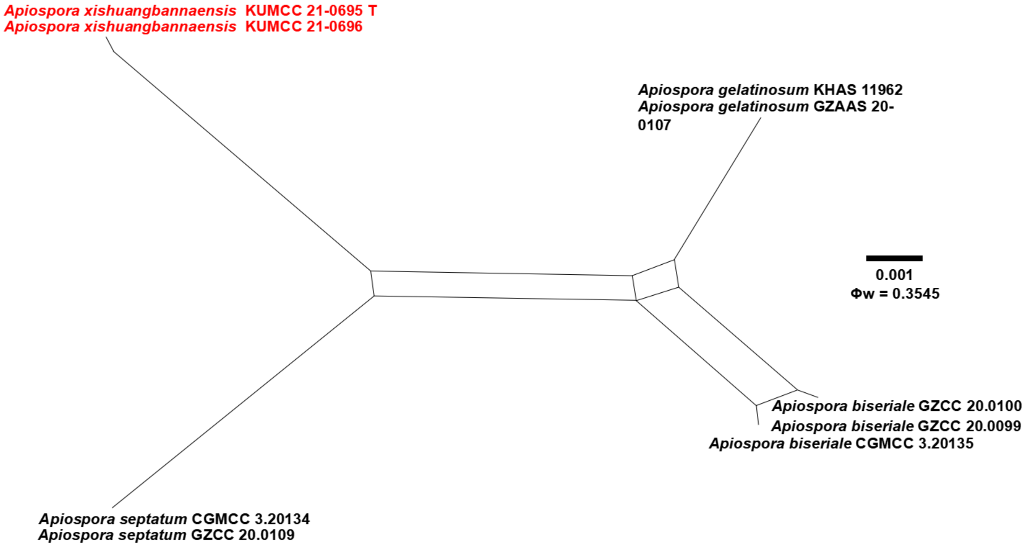

Figure 20 – The results of the pairwise homoplasy index (PHI) test of closely related species using both LogDet transformation and splits decomposition. PHI test results Φw ≤ 0.05 indicate that there is significant recombination within the dataset. The new taxon is in red bold type.

Neopestalotiopsis paeoniae-suffruticosae W.L. Li & Jian K. Liu, in Li, Dissanayake, Zhang, Maharachchikumbura & Liu, Journal of Fungi 8 (11, no. 1175): 12 (2022). Fig. 21

MycoBank number: MB 845407; Facesoffungi number: FoF 12747

Asexual morph on PDA: *Vegetative hyphae* 1–5 µm wide, hyaline, septate, branched, thin-walled aerial mycelia abundant. *Conidiomata* pycnidial on PDA after 60 days, semi-immersed or bulging on mycelial surface, globose to subglobose, scattered or aggregated, soft, black, up to 200 µm diam; exuding dark brown to black conidia in slimy masses. *Conidiophores* up to 35 µm long, septate, simple or rarely branched at base, subcylindrical, hyaline to subhyaline. *Conidiogenous cells* 5–16 × 1–4 µm (x̄ = 7.82 × 2.47 µm, n = 30), discrete, holoblastic, cylindrical, hyaline to pale brown, smooth-walled. *Conidia* 15–30 × 5–10 µm (x̄ = 22.89 × 8.25 µm, n = 30), fusiform, ellipsoid, straight to slightly curved, 4-septate, constricted at septum, granulate; basal cell conic to obconic with a truncate base, hyaline, thin-walled, 2–6 µm long (x̄ = 3.83 µm, n = 30); three median cells doliiform, 12–17 µm long (x̄ = 14.86 µm, n = 30), smooth-walled, yellow-brown to brown, septa darker than the rest of cell (second cell from the base pale brown, 3–7 µm long; third cell yellow-brown, 3–7 µm long; fourth cell brown, 3–7 µm long); apical cell 1–6 µm long (x̄ = 3.27 µm, n = 30), hyaline, subcylindrical, rugose, thin- and smooth-walled; with 2–4 tubular apical appendages (mostly 3, rarely 2 and 4), arising from the apical crest, unbranched, filiform, 5–26 µm (x̄ = 15.22 µm, n = 50); basal appendage single, filiform, tubular, unbranched, centric, 2–8 µm long (x̄ = 5.05 µm). Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 50–60 mm after 15 days at room temperature (20–25 °C), with undulated edge, white, with sparse aerial mycelium on the surface; reverse pale yellow. Sporulating conidiomata on PDA with black conidial mass after 60 days.

Substratum – *Paeonia suffruticosa.*

Distribution – China.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, wing surface, *Rhinolophus stheno* in limestone forest, 101.282404 E, 21.907599 N, 15 July 2021, Alice Hughes, 70 (HKAS122247), living culture KUMCC 21-0426; *ibid*., 70-B, living culture KUMCC 21-0427.

GenBank numbers – KUMCC 21-0426 = ITS: ON426867, *TEF 1-α*: OR025971, *TUB*: OR025932; KUMCC 21-0427 = ITS: ON426868, *TEF 1-α*: OR025972, *TUB*: OR025933.

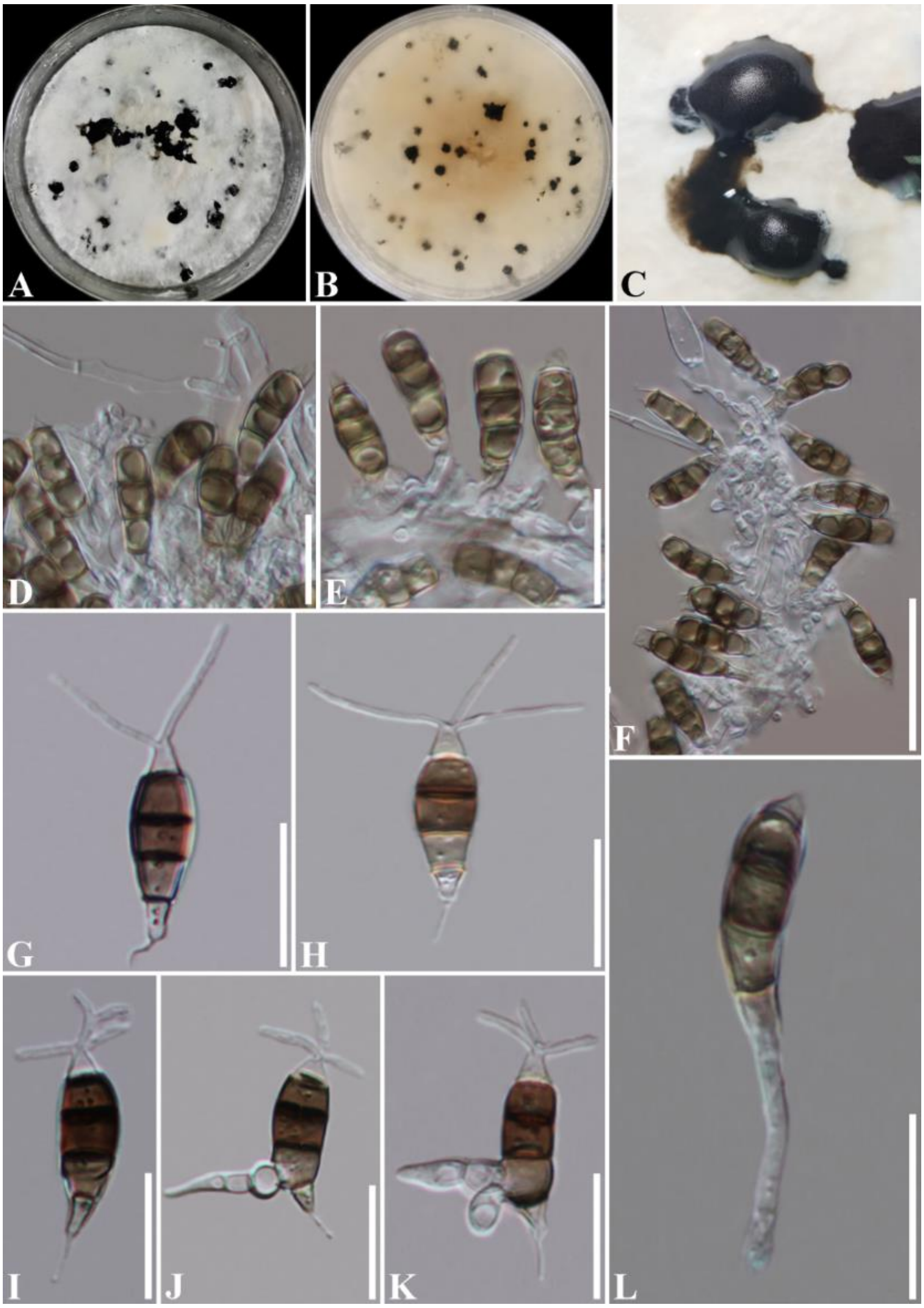

Figure 21 – *Neopestalotiopsis paeoniae-suffruticosae* (KUMCC 21-0426). A, B Colony on PDA (above and below). C Sporulating conidiomata on PDA (70 days old culture). D–F, L Conidiogenous cells with conidia. G–I Conidia. J, K Germinating conidia. Scale bars: D, E, G–L = 15 μm, F = 30 μm.

Notes – *Neopestalotiopsis paeoniae-suffruticosae* was isolated from a diseased branch of *Paeonia suffruticosa*, and introduced by Li et al. (2022). Based on multi-locus phylogenetic analyses of ITS, *TEF1-α* and *TUB*, our isolates clustered together with *N. paeoniae-suffruticosae* (CGMCC 3.23554 (type) and UESTCC 22.0007), and is closely related to *N. mianyangensis* and the new species, *N. xishuangbannaensis* (Fig. 6). In the sequence comparisons, our isolate (KUMCC 21-0426, type) is different from *N. paeoniae-suffruticosae* (CGMCC 3.23554, type) in 0.98% (5/508 bp) of the ITS, 1.59% (7/440 bp) of the *TEF1-α*, and 0.87% (4/458 bp) of *TUB*. Morphologically, the new isolate (KUMCC 21-0426) is similar to *N. paeoniae-suffruticosae* by the ellipsoid conidia with 2–4 long apical tubular appendages (Li et al. 2022). *Neopestalotiopsis paeoniae-suffruticosae* is a pathogen causing disease on the branches of *Paeonia suffruticosa* (Li et al. 2022). Based on both phylogeny and morphology, the new isolates are identified as *N. paeonia-suffruticosa*. This is the first report of *N. paeonia-suffruticosa* isolated from bats in China.

Neopestalotiopsis xishuangbannaensis Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 22

MycoBank number: MB 844268; Facesoffungi number: FoF 13265

Etymology – Named after the location Xishuangbanna, where the holotype was first discovered.

Holotype – HKAS122245.

Asexual morph on PDA: *Vegetative hyphae* 1–5 µm wide, hyaline, septate, branched, thin-walled aerial mycelia abundant. *Conidiomata* pycnidial on PDA after 60 days, semi-immersed or bulging on mycelial surface, globose to subglobose, scattered or aggregated, soft, black, up to 90 µm diam; exuding dark brown to black conidial slimy masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–17 × 1–5 µm (x̄ = 6.82 × 2.77 µm, n = 30), holoblastic, discrete, cylindrical, hyaline to pale brown, smooth-walled. *Conidia* 13–30 × 5–10 µm (x̄ = 21.88 × 8.25 µm, n = 30), fusiform, ellipsoid, straight to slightly curved, 4-septate, constricted at the septum, granulate; basal cell conic to obconic with a truncate base, hyaline, thin-walled, 2–6 µm long (x̄ = 3.93 µm, n = 30); three median cells doliiform, 10–20 µm long (x̄ = 14.76 µm, n = 30), smooth-walled, yellow-brown to brown, septa darker than the rest of the cell (second cell from the base pale brown, 3–7 µm long; third cell yellow-brown, 4–7 µm long; fourth cell brown, 3–7 µm long); apical cell 1–6 µm long (x̄ = 3.27 µm, n = 30), hyaline, subcylindrical, rugose, thin- and smooth-walled; with 2–4 tubular apical appendages (mostly 3, rarely 2 and 4), arising from the apical crest, unbranched, filiform, 6–30 µm (x̄ = 15.22 µm, n = 50); basal appendage single, filiform, tubular, unbranched, centric, 2–8 µm long (x̄ = 5.05 µm). Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 50–60 mm after 17 days at room temperature (20–25 °C), with an undulated edge, white, with sparse aerial mycelium on the surface; reverse pale yellow. Sporulating conidiomata on PDA with black conidial mass after 60 days.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, wing surface, *Kerivoula hardwickii* in limestone forest, 101.282404 E, 21.907599 N, 15 July 2021, Alice Hughes, 45 (**holotype**, HKAS12245), ex-type KUMCC 21-0424; *ibid*. 45-B, ex-isotype KUMCC 21-0425.

GenBank numbers – KUMCC 21-0424 = ITS: ON426865, *TEF 1-α*: OR025973, *TUB*: OR025934; KUMCC 21-0425 = ITS: ON426866, *TEF 1-α*: OR025974, *TUB*: OR025935.

Notes – *Neopestalotiopsis xishuangbannaensis* is phylogenetically closely related to *N. mianyangensis* and *N. paeoniae-suffruticosae*. *Neopestalotiopsis xishuangbannaensis* is different from *N. mianyangensis* by the latter having smaller conidiogenous cells (5–17 × 1–5 µm vs 3–5 × 2.1–2.5 µm) and shorter conidia (13–30 × 5–10 µm vs 19–23 × 5.5–7 µm) with three apical tubular appendages and is pathogenic on diseased branches of *Paeonia suffruticosa* (Supplementary Table 3) (Li et al. 2022). *Neopestalotiopsis xishuangbannaensis* differs from *N. paeoniae-suffruticosae* by the latter having smaller conidiogenous cells (5–17 × 1–5 µm vs 5–6.5 × 2.5–3 µm) and smaller conidia (13–30 × 5–10 µm vs 20–23 × 9–11 µm) with three apical tubular appendages (Supplementary Table 3) (Li et al. 2022). Based on the megablast search in the GenBank, the closest hits of the ITS, TEF1-α, and *TUB* sequences had the highest similarity to *N. saprophytica*

(ITS GenBank, MT576586, Identities = 574/580 (99%), 6/580 (1%); *TEF1-α* GenBank, MT706635, Identities = 867/887 (98%), 1/887 (0%); *TUB* GenBank, MT706634, Identities = 461/465 (99%), 2/465 (0%)), and *N. clavispora* (ITS GenBank, KY319134, Identities = 574/580 (99%), 6/580 (1%); *TEF1-α* GenBank, MG571262.1, Identities = 877/899 (98%), 3/899 (0%); *TUB* GenBank, MN626481, Identities = 453/456 (99%), 1/456 (0%)). *Neopestalotiopsis xishuangbannaensis* is different from *N. saprophytica* by slightly smaller and stout conidia (13–30 × 5–10 µm vs 22–30 × 5–6 µm) with 2–3 tubular and shorter (6–30 µm vs 23–35 µm) apical appendages (Supplementary Table 3) (Maharachchikumbura et al. 2012, 2014, Liu et al. 2021). *Neopestalotiopsis xishuangbannaensis* is different from *N. clavispora* by the latter having smaller conidia (13–30 × 5–10 µm vs 18–26 ×6. 5–8.5 µm) with 2–3 tubular and longer conidiogenous cells (5–17 × 1–5 µm vs 4–10 long) (Supplementary Table 3) (Maharachchikumbura et al. 2012, 2014, Liu et al. 2021). The base pair differences of *N. xishuangbannaensis* (KUMCC 21-0424, type) compared with *N. mianyangensis* (CGMCC 3.23555, type) and *N. paeonia-suffruticosa* (CGMCC 3.23554, type) are shown in Supplementary Table 4. Based on the phylogenetic analyses and morphological characteristics, *N. xishuangbannaensis* is introduced as a new species.

Hypocreales Lindau

Bionectriaceae Samuels & Rossman

The family *Bionectriaceae* was introduced by Rossman et al. (1999) and typified by *Clonostachys tonduzii* (Speg.) and accepted 26 genera, including five cleistothecial genera. In subsequent studies, Rossman et al. (2001) reported that *Bionectriaceae* is monophyletic within *Hypocreales* and accepted four cleistothecial genera (*Bulbithecium* Udagawa & T. Muroi, *Hydropisphaera* Dumort, *Leucosphaerina* Arx and *Nigrosabulum* Malloch & Cain) based on phylogenetic analyses of the LSU gene regions. *Bionectriaceae* species mostly occur in terrestrial or freshwater habitats but less in marine habitats as coprophilous, corticolous, fungicolous, herbicolous or lichenicolous taxa (Hyde et al. 2020). Wijayawardene et al. (2022) listed 47 genera in the family.

Clonostachys Corda

Clonostachys (*C.*) was introduced by Corda in 1839 and typified by *Clonostachys araucaria* Corda (Hyde et al. 2020). The genus *Clonostachys* contains 78 accepted species in the latest outline of fungi updated by Wijayawardene et al. (2022). *Bionectria* Speg. is the former sexual morph genus of *Clonostachys* (Rossman et al. 2013, Lechat et al. 2020). The species of *Clonostachys* are commonly isolated in soils, as well as in plants as endophytes, epiphytes or saprotrophs, and some have even been reported as mycoparasites of nematodes and insects (Schroers et al. 2001, Toledo et al. 2006, Zhang et al. 2008, Moreira et al. 2016, Torcato et al. 2020). *Clonostachys* is typically characterized by an asexual morph with a distinctive penicillate, frequently sporodochial conidiophores, while the sexual morph is mainly characterized by white, yellow to orange or brown, usually crowded and roughened ascomata, that do not change colour in KOH (Rossman et al. 1999, 2013, Schroers 2001, Lechat et al. 2020, Torcato et al. 2020). In this study, a new species, *Clonostachys rhinolophicola*, is described.

Clonostachys rhinolophicola Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 23

MycoBank number: MB 844274; Facesoffungi number: FoF 13266

Etymology – Refers to the host genus *Rhinolophus* (*Chiroptera*).

Holotype – HKAS122257.

Asexual morph on PDA: *Vegetative hyphae* hyaline, septate, branched, thin-walled forming abundant aerial mycelia, 1–7 µm wide, with dark brown to black slimy conidial masses. *Conidiophores* up to 500 µm long, septate, simple or branched at base, subcylindrical, hyaline to subhyaline, thick-walled, smooth, straight or slightly flexuous, terminally penicillus. *Penicilli* solitary to gregarious, not sporodochial, bi- or quater-verticillate; branches of the penicillus divergent, each branch terminating in metulae and adpressed phialides. *Phialides* 7–22 × 1–8 µm ($\bar{x}$

= 14.15 × 3.23 µm, n = 30), solitary or whorls of 2–4, mostly in 2 levels, narrowly flask-shaped, slightly tapering toward apex, with periclinal thickening, with inconspicuous collarettes, hyaline, smooth-walled. *Conidia* 3–9 × 2–5 µm (x̄ = 5.16 × 3.75 µm, n = 60), broadly ellipsoidal to oblong, rarely minutely curved, broadly rounded at ends, aseptate, straight, bi-guttulate, hilum laterally displaced, almost median or invisible, hyaline, smooth and thin-walled, without slime. Sexual morph: Undetermined.

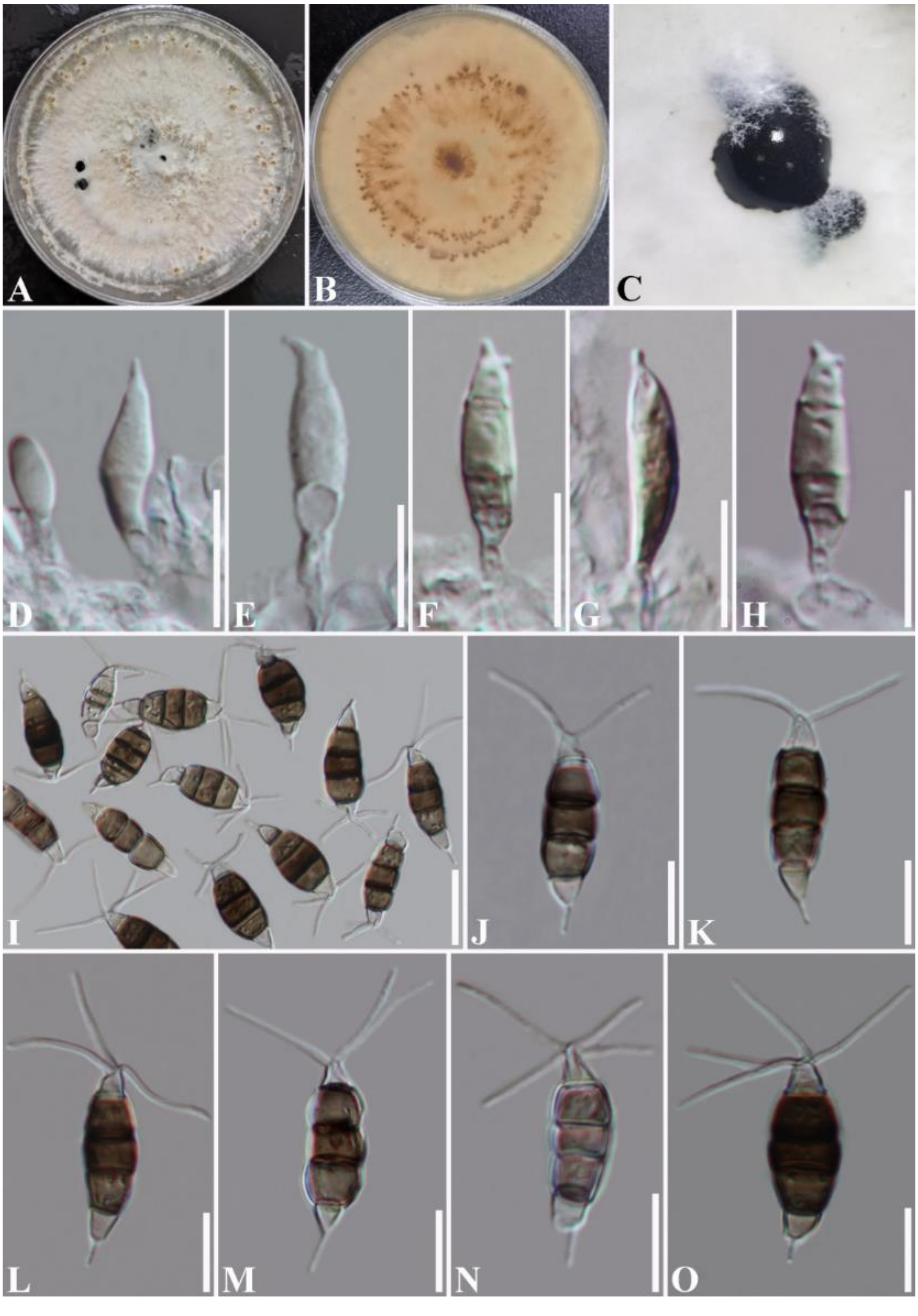

Figure 22 – *Neopestalotiopsis xishuangbannaensis* (KUMCC 21-0424). A, B Colony on PDA (above and below). C Sporulating conidiomata on PDA (70 days old culture). D–H Conidiogenous cells with conidia. I–O Conidia. Scale bars: D, I = 15 µm, E–H, J–O = 10 µm.

Culture characteristics – Colonies on PDA attaining 40–55 mm after 20 days at room temperature (20–25 °C), with an undulated edge, white, with sparse aerial mycelium on the surface; reverse pale yellow. The black conidial mass covers the stromatic colonies after 80 days.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, wing surfaces from *Rhinolophus stheno* in limestone forest, 101.282404 E, 21.907599 N, 15 July 2021, Alice Hughes, 56-F (**Holotype**, HKAS122257), ex-type KUMCC 21-0439; *ibid.* on *Hipposideros larvatus,* 62, ex-paratype KUMCC 21-0438.

GenBank numbers – KUMCC 21-0439 = ITS: ON426840, *TUB*: OR025937; KUMCC 21-0438 = ITS: ON426841, *TUB*: OR025936.

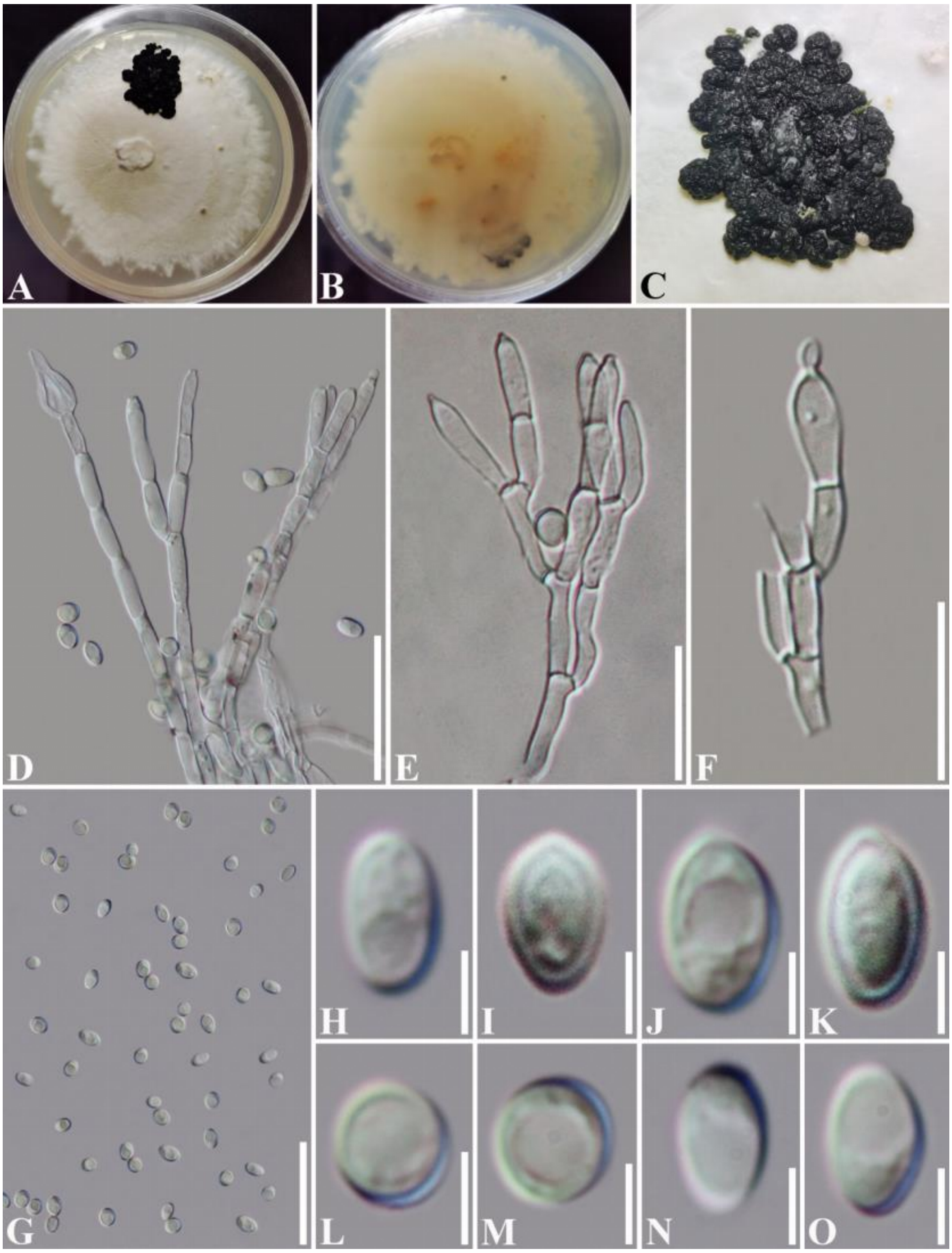

Figure 23 – *Clonostachys rhinolophicola* (KUMCC 21-0439). A, B Colony on PDA (above and below). C Conidiophores dimorphic with conidia mass formed all over the colony (90 days old culture). D–F Conidiogenous cells and conidia. G–O Conidia. Scale bars: D, G = 30 µm, E = 15 µm, F = 10 µm, H–O = 3 µm.

Notes – *Clonostachys rhinolophicola* is phylogenetically closely related to *C. pityrodes* (CBS 102033, type) (Fig. 7). Nucleotide comparison of ITS and *TUB* of the new isolate and the type strain of *C. pityrodes* showed 14/604 bp differences in ITS and 34/589 bp differences in *TUB* (Supplementary Table 4). *Clonostachys rhinolophicola* differs from *C. pityrodes* by the latter having olive green to dark green conidial mass, comparatively smaller greenish hyaline to pale green conidia (3–9 × 2–5 µm vs (4.8–)5.8–7.2(–9) × (2.4–)2.8–3.4(–4) µm) and larger 2–5 levels longer phialides (7–22 × 1–8 µm vs (5.8–)13–16.4(–19.6) × (1.6–)2.2–2.4(–3) µm) (Supplementary Table 3) (Schroers et al. 2001). We were unable to compare the asexual morphology of our isolates with genetically closely related *C. pityrodes* (*Bionectria pityrodes* (Mont.) Schroers) as this species has only been reported the sexual morph from dead wood, vine and other pyrenomycetes (Schroers et al. 2001). Based on the phylogenetic analyses and morphological characteristics, *C. rhinolophicola* is introduced as a distinct new species.

Cordycipitaceae Kreisel

Cordycipitaceae was introduced by Kreisel (1969) and typified by *Cordyceps militaris* (L.) Fr. After its initial introduction as *Cordycipitaceae*, Wehmeyer (1976) referred to it as *Cordycipitoideae*, a subfamily in *Clavicipitaceae* Rogerson, based on the type genus *Cordyceps*. Sung et al. (2007) validly segregated *Cordycipitaceae* from *Clavicipitacea* based on morphological and multi-gene phylogenetic analyses. Kepler et al. (2017) synonymized *Isaria* Pers. and *Microhilum* H.Y. Yip & A.C. Rath under *Cordyceps* Fr., and *Granulomanus* de Hoog & Samso as a synonym of *Gibellula* Cavara. *Cordycipitaceae* are found predominantly as saprobes in leaf litter and upper soil layers, parasites or pathogens of scale insects or mosses, and mostly as entomopathogens (Hyde et al. 2020).

Amphichorda Fr.

Amphichorda (*Am.*) was established by Fries (1825) with *Am. felina* (DC.) Fr. as the type. The genus is morphologically similar to *Beauveria* except for its regular conidiogenous cells without elongated, denticulate rachis, and is phylogenetically similar to *Beauveria* and *Cordyceps*. *Amphichorda* is very similar to *Beauveria* in morphology, and the new species is phylogenetically closely related to *Beauveria* in ITS, while *Beauveri*a is differentiated from *Amphichorda* by its elongate conidiogenous cells with apical denticulate rachis (Rehner et al. 2006, 2011, Chen et al. 2013b, Zhang et al. 2017). The phylogeny based on combined sequences (ITS+*RPB1*+*RPB2*+*TEF1-α*) showed that species of *Amphichorda* clustered in a well-distinct clade distant from *Beauveria*. In addition, the new species is phylogenetically distinct from the closely related genera and formed a well-supported clade in the phylogenetic analyses (100% ML/ 1.00 BYPP, Fig. 8). Currently, three species have been reported in *Amphichorda* (Zhang et al. 2017, 2020, Xu et al. 2018). In this study, we introduce *Amphichorda yunnanensis* sp. nov. on bats (Fig. 24).

Amphichorda yunnanensis Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 24

MycoBank number: MB 844275; Facesoffungi number: FoF 13267

Etymology – Refers to the Yunnan Province where the holotype was collected.

Holotype – HKAS122258.

Asexual morph on PDA: *Synnemata* arising in the centre and the edge of the colony, up to 70 mm high and 1–2 mm wide, white, cylindrical, tomentose, branched at the apex. *Vegetative hyphae* 1–2 µm wide, septate, branched, hyaline, smooth-walled. *Conidiophores* arising laterally from hyphae, cylindrical, straight or slightly curved, branched, hyaline. *Conidiogenous cells* 4–12 × 1–4 µm ($\bar{x}$ = 6.73 × 2.55 µm, n = 100), holoblastic, mono- to polyblastic, ampulliform to flask-shaped, producing conidia sympodially on divergent denticles. *Conidia* 2–5 × 2–4 µm ($\bar{x}$ = 3.71 × 2.92 µm, n = 100), globose to oval, slightly ellipsoid, hyaline, aseptate, smooth and thin-walled. Sexual morph: Undetermined.

Culture characteristics – Colony growth on PDA attaining 15–38 mm after 15 days at room temperature (20–25 °C), with undulated edge, white, sparse at aerial mycelium on the surface, with the synnemata arising in the center, cylindrical with apical apex, asymmetrically branching, tomentose, white, 2.5–6 cm long; reverse pale yellow. Conidiophores arising from the colony, white after 50 days.

Material examined – China, Yunnan Province, Yuxi, Yimen County, Pubei Village, Shiliansi, *Rhinolophus affinis*, from the wing surfaces 24.61746 N, 102.1633 E, 21 September 2020, Alice Hughes, YM-24-W4 (**Holotype**, HKAS122258), ex-type KUMCC 21-0416; *ibid*., YM-24-W1, ex-isotype KUMCC 21-0415; *ibid*., *Rhinolophus siamensis* from the wing surfaces, 24.61746 N 102.1633 E, 21 September 2020, Alice Hughes, YM-18-W6, ex-paratype KUMCC 21-0414.

GenBank numbers – KUMCC 21-0416 = ITS: ON426825, *RPB1*: OR022014, *RPB2*: OR022039, *TEF 1-α*: OR025975; KUMCC 21-0415 = ITS: ON426824, *RPB1*: OR022015, *RPB2*: OR022040, *TEF 1-α*: OR025976; KUMCC 21-0414 = ITS: ON426823, *RPB1*: OR022016, *RPB2*: OR022041, *TEF 1-α*: OR02597.

Notes – The new species was identified morphologically and phylogenetically belonging to *Amphichorda* (Fig. 8). *Amphichorda yunnanensis* is phylogenetically and morphologically closely related to *Am. cavernicola* and *Am. guana*. *Amphichorda yunnanensis* differs from *Am. cavernicola* in the former its cylindrical synnemata with asymmetric branching, comparatively larger conidia (2–5 × 2–4 µm vs 2.5–4 × 2–3.5 µm), longer conidiogenous cells (4–12 × 1–4 µm vs 4.5–8 × 2–3 µm), and the habitat (living bats vs bird faeces, bat guano, animal faeces and soil) (Supplementary Table 3) (Zhang et al. 2020). In addition, the sequence similarities of (80% similarity, 101 base pair (bp) differences in 505 bp of ITS; 98.13% similarity, 17 bp differences in 911 bp of *TEF1-α*) were observed between *Am. yunnanensis* and *Am. cavernicola* (Supplementary Table 4). *Amphichorda yunnanensis* differs from *Am. guana* by the latter having unbranched synnemata with over tomentose, larger conidia (2–5 × 2–4 µm vs 4.5–5.5 × 3.5–5 µm), smaller conidiogenous cells (4–12 × 1–4 µm vs 7–10 × 2–3 µm), significantly shorter synnemata of occasionally branched at the apex (up to 70 mm vs up to 15 mm), and the bat guano habitat (Supplementary Table 3) (Zhang et al. 2017). Furthermore, low sequence similarities (82.30% similarity, 94 bp differences in 531 bp of ITS; 96.04% similarity, 30 bp differences in 758 bp of *RPB1*; 95.97% similarity, 43 bp differences in 1068 bp of *RPB2*; and 98.91% similarity, 10 bp difference in 917 bp of *TEF1-α*) were observed among the closely related species (Supplementary Table 4). The phylogeny and morphology results show that *Am. yunnanensis* is a distinct new species.

Hypocreaceae De Not.

Hypocreaceae was introduced by De Notaris (1844) and typified by *Hypocrea* Fr. Lindau (1897) recognized *Hypocreaceae* within *Hypocreales* and divided them into six subfamilies. Kreisel (1969) accepted *Hypocreaceae* and *Nectriaceae* as two families in *Hypocreales*. Later, Rogerson (1970) recognized *Hypocreales* as the only family in Hypocreales. Rossman et al. (1999) recognized *Nectriaceae*, *Hypocreaceae* and *Bionecriaceae* as separate families within the *Hypocreales*. *Hypocreaceae* are predominantly biotrophic, hemibiotrophic, saprobic or hypersaprobic on plants, other fungi, *Myxomycetes* and lichens and distributed in aquatic and terrestrial habitats worldwide (Hyde et al. 2020).

Trichoderma Pers.

Trichoderma (*T.*) was established by Persoon (1794) and typified by *T. viride* Pers. and is one of the largest genera in the family Hypocreaceae, Hypocreales. *Trichoderma* is a highly diverse genus, frequently found in dead wood and bark, other fungi, soil, healthy plant roots, and occasionally on stems, leaves, and on bats (Vanderwolf et al. 2013b, Jaklitsch & Voglmayr 2015, Zhu et al. 2017, Holz et al. 2018, Karunarathna et al. 2020, Bustamante et al. 2021). The species of *Trichoderma* are one of the most useful groups of microbes that pose a significant impact on human welfare, serving as effective biocontrol agents and producers of enzymes, antibiotics, and heterologous proteins for food, feed, textile, and biofuel industries (Mukherjee et al. 2013, Zhu et al. 2017, Bustamante et al. 2021, Cai & Druzhinina 2021). The most outstanding features of *Trichoderma* are the beneficial effects in combating plant diseases and promoting plant health and the ability to antagonize, parasitize, kill or control other pathogenic fungi, oomycetes and even nematodes (Lorito et al. 1998, Hermosa et al. 2012, Adnan et al. 2019, Carillo et al. 2020, Sood et al. 2020, Barrera et al. 2021, Cai & Druzhinina 2021, Köhl & Ravensberg 2022). However, *Trichoderma* species have also been reported as pathogens of both pants and animals. For example, *Trichoderma* sp. can cause nosocomial mycoses in immunocompromised humans and green mold disease on mushrooms (Chouaki et al. 2002, Myoken et al. 2002, Kredics et al. 2003, 2010, Komoń-Zelazowska et al. 2007, Cai et al. 2021). This study introduces three new species viz. *Trichoderma hipposidericola*, *T. rhinolophicola*, and *T. xishuangbannaense* and two new host records (Figs 25–31).

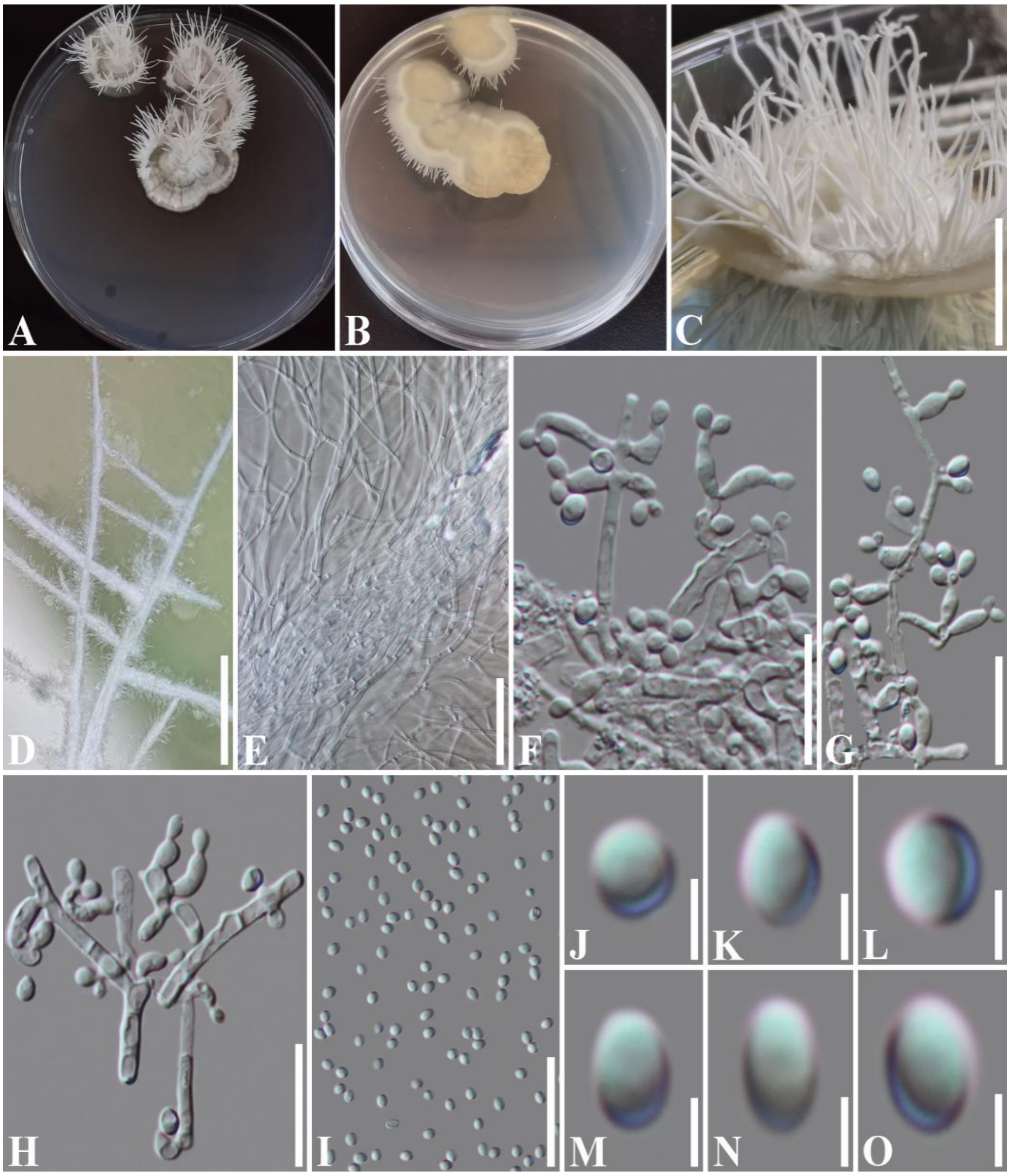

Figure 24 – *Amphichorda yunnanensis* (KUMCC 21-0416). A, B Colonies on PDA (above and below). C Conidiophores arise from the colony (50 days old culture). D Synnemata. E Hyphae. F–H Conidiogenous cells and conidia. I–O Conidia. Scale bars: C = 5 mm, D = 1 μm, E, I = 30 μm, F–H = 15 μm, J–O = 3 μm.

Trichoderma hipposiderocola Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 25

MycoBank number: MB 844277; Facesoffungi number: FoF 13268

Etymology – Refers to the host genus *Hipposideros* (*Chiroptera*).

Holotype – HKAS122850.

Asexual morph on PDA: *Vegetative hyphae* 1–5 µm wide, septate, branched, hyaline, smooth-walled. *Conidiophores* pyramidal with verticillate, paired lateral branches; *phialides* generally formed on terminal branches in divergent whorls of two to five, 3–23 × 1–5 µm (x̄ = 7.32 × 3.09 µm, n = 100); *supporting cells* 2–15 × 1–5 µm (x̄ = 8.22 × 3.25 µm, n = 100). *Conidia* ellipsoidal to ovoid, light grey to green, smooth, 1–6 × 1–5 µm (x̄ = 4.02 × 3.21 µm, n = 100). *Chlamydospores* not observed. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 50–60 mm after 10 days at room temperature (20–25 °C), white, pale yellow to green, sparse aerial mycelium on the surface; reverse white to pale yellow. The white reproductive mycelium covers the stromatic colonies after 25 days. Odor absent.

Material examined – China, Yunnan Province, Yuxi, Yimen County, Pubei Village, Shiliansi, *Hipposideros pomona* feet samples, 24.61746 N 102.1633 E, 21 September 2020, Alice Hughes, YM-66-L1 (**holotype**, HKAS122850), ex-type KUMCC 21-0801; *ibid*., YM-66-B2, ex-isotype KUMCC 21-0804; *ibid*., *Miniopterus schreibersii*, YM-62-L1, ex-paratype KUMCC 21-0805; *ibid*., *Rhinolophus affinis*, YM-88-B1, ex-paratype KUMCC 21-0803; *ibid*., YM-88-L2, ex-paratype KUMCC 21-0802.

GenBank numbers – KUMCC 21-0801 = ITS: ON426899, *RPB2*: OR025896, *TEF 1-α*: OR025978; KUMCC 21-0804 = ITS: ON426895, *RPB2*: OR025897, *TEF 1-α*: OR025979; KUMCC 21-0805 = ITS: ON426894, *RPB2*: OR025898, *TEF 1-α*: OR025980; KUMCC 21-0803 = ITS: ON426900, *RPB2*: OR025899, *TEF 1-α*: OR025981; KUMCC 21-0802 = ITS: ON426901, *RPB2*: OR025900, *TEF 1-α*: OR025982.

Notes – *Trichoderma hipposiderocola* is closely related to *T. atroviride*, *T. nordicum* Guang Zhi Zhang, *T. uncinatum* Z.F. Yu & X. Du and *T. obovatum* in the *Atroviride* clade. However, *T. hipposiderocola* differs from *T. atroviride* by possessing more phialides and larger conidia (1–6 × 1–5 µm vs 4–5 × 3–3.5 µm) (Supplementary Table 3) (Manawasinghe et al. 2021). *Trichoderma hipposiderocola* differs from *T. nordicum* by the latter having larger phialides (3–23 × 1–5 µm vs (6.2–)7.2–10.3(–12.9) × (2.6–)2.9–3.2(–3.4) µm) and curved phialides on PDA, and sometimes chlamydospores present ((8.7–)9.8 × 10.4(–12.5) µm) (Supplementary Table 3) (Zhang et al. 2022). *Trichoderma hipposiderocola* differs from *T. uncinatum* by the latter having a swollen main axis at the branch, longer supporting cells (2–15 × 1–5 µm vs 11.2–26.2 × 2.6–4.2 µm), smaller conidia (1–6 × 1–5 µm vs 3.1–4.4 × 2.7–4 µm) and smaller phialides (3–23 × 1–5 µm vs (4.3–)5.2–9.3(–10.3) × 2.3–3.9 µm) (Supplementary Table 3) (Zheng et al. 2021). *Trichoderma hipposiderocola* differs from *T. obovatum* by having larger conidia (1–6 × 1–5 µm vs 3.2–3.8 × 3–3.6 µm) and the latter having 1–4 whorls and smaller phialides (3–23 × 1–5 µm vs (4–)4.8–8.9(–10.7) × (2.3–)2.5–3.9(–4.2) µm) (Supplementary Table 3) (Zheng et al. 2021). The PHI test (Fig. 26) confirmed no recombination in the new species compared to the closely related taxa. Based on the phylogeny and morphology, *T. hipposiderocola* is introduced as a new species.

Trichoderma inconspicuum Z.F. Yu & X. Du, in Zheng, Qiao, Lv, Du, Zhang & Yu, Journal of Fungi 7 (6, no. 467): 19 (2021). Fig. 27

MycoBank number: MB 830639; Facesoffungi number: FoF 13418

Asexual morph on PDA: *Vegetative hyphae* septate, branched, hyaline, smooth-walled, 2–8 µm wide. *Conidiophores* pyramidal with verticillate, paired lateral branches; *phialides* generally formed on terminal branches, in divergent whorls of three to four, 5–17 × 1–5 µm (x̄ = 9.98 × 2.86 µm, n = 60); *supporting cells* 4–18 × 2–8 µm (x̄ = 10.12 × 4.74 µm, n = 60). *Conidia* 3–9 × 2–6 µm (x̄ = 4.31 × 3.87 µm, n = 60) globose, ellipsoidal to ovoid or minority irregular, green, smooth-walled. *Chlamydospores* 6–10 × 5–8 µm (x̄ = 8.47 × 6.71 µm, n = 10), subglobose to globous, smooth-walled, hyaline, granulate, slimy. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 50–60 mm after 14 days at room temperature (20–25 °C), white, pale yellow to green, with sparse aerial mycelium on the surface, reverse white to pale yellow. The white reproductive mycelium covers the stromatic colonies after 25 days. Odor absent.

Substratum – Living stem of *Nymphoides peltata.*

Distribution – China.

Material examined – China, Yunnan Province, Yuxi, Yimen County, Pubei Village, Shiliansi, *Miniopterus schreibersii*, 24.61746 N 102.1633 E, 21 September 2020, Alice Hughes, YM-62-B4 (HKAS122840), living culture KUMCC 21-0806.

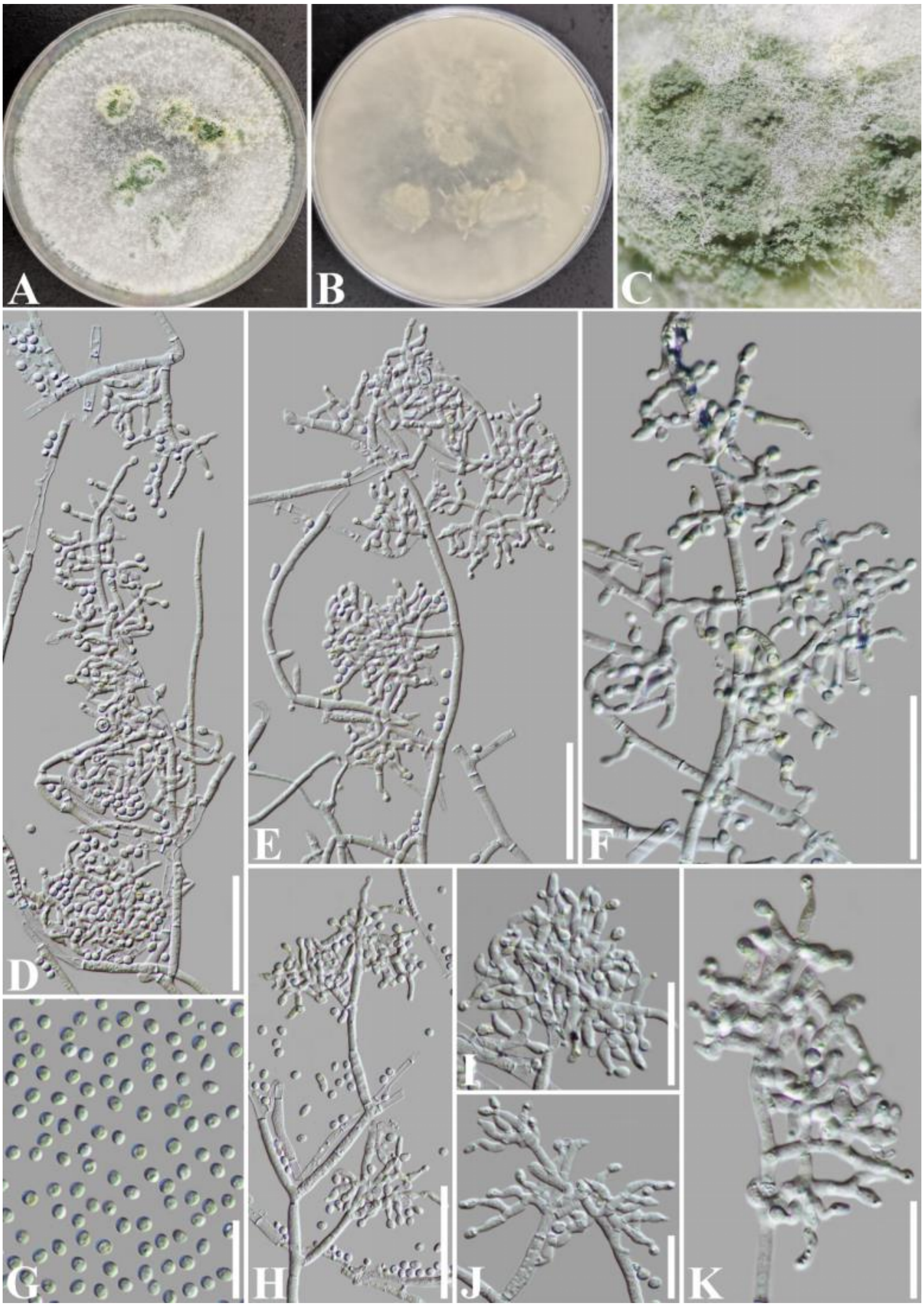

Figure 25 – *Trichoderma hipposiderocola* (KUMCC 21-0801). A, B Colony on PDA (above and below). C Sporulation on PDA (25 days old culture). D–F, H–K Conidiophores and phialides. G Conidia. Scale bars: D–F, H = 50 µm, G, I–K = 20 µm.

GenBank numbers – KUMCC 21-0806 = ITS: ON426893, *RPB2*: OR025901, *TEF 1-α*: OR025983.

Notes – *Trichoderma inconspicuum* was erected by Zheng et al. (2021) from the soil. Our isolates clustered together with *T. inconspicuum* within the *Atroviride* clade (Fig. 9). *Trichoderma inconspicuum* is phylogenetically closely related to *T. scorpioideum* Z.F. Yu & X. Du and *T. asymmetricum* Z.F. Yu & X. Du. However, *T. inconspicuum* differs from *T. scorpioideum* by having darker colonies, larger conidia (3–9 × 2–6 µm vs 3.3–4.4 × 2.4–3.8 µm), more and bigger phialides (5–17 × 1–5 µm vs (6.5–)6.8–12.7(–13.3) × 2–3.9 µm) and subglobose to globous chlamydospores (Supplementary Table 3) (Zheng et al. 2021). *Trichoderma inconspicuum* differs from *T. asymmetricum* by having larger conidia (3–9 × 2–6 µm vs 3.5–4.5(–5) × 3.2–4.1 µm), more and bigger phialides (5–17 × 1–5 µm vs (4.4–)5.9–11.8(–12.6) × 2.3–4(–4.4) µm), and subglobose to globous chlamydospores (Supplementary Table 3) (Zheng et al. 2021). This is the first report of *T. obovatum* isolated from bats in China.

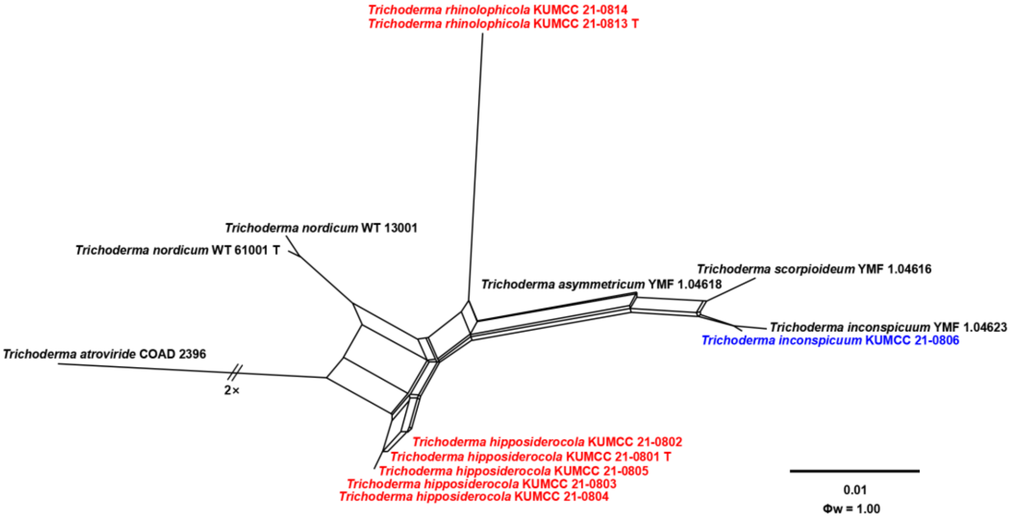

Figure 26 – The results of the pairwise homoplasy index (PHI) test of closely related species using both LogDet transformation and splits decomposition. PHI test results Φw ≤ 0.05 indicate that there is significant recombination within the dataset. The new taxon is in red, and sequences of the new strains are in blue.

Trichoderma obovatum Z.F. Yu & Y.F. Lv, in Zheng, Qiao, Lv, Du, Zhang & Yu, Journal of Fungi 7 (6, no. 467): 22 (2021). Fig. 28

MycoBank number: MB 834570; Facesoffungi number: FoF 13419

Asexual morph on PDA: *Vegetative hyphae* septate, branched, hyaline, smooth-walled, 1–5 µm wide. *Conidiophores* pyramidal with verticillate, paired lateral branches; *phialides* generally formed on terminal branches, ampulliform, in divergent whorls of two to five, 3–15 × 1–5 µm (x̄ = 7.73 × 2.95 µm, n = 100); *supporting cells* 3–17 × 1–5 µm (x̄ = 9.45 × 2.87 µm, n = 60). *Conidia* 3–8 × 2–5 µm (x̄ = 4.28 × 3.54 µm, n = 100) globose, ellipsoidal to ovoid, green, smooth-walled. Chlamydospores not observed. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 50–60 mm after 7 days at room temperature (20–25 °C), white, pale yellow to green, sparse aerial mycelium on the surface; reverse white to pale yellow. The white reproductive mycelium covers the stromatic colonies after 25 days. Odor absent.

Substratum – Soil.

Distribution – China.

Material examined – China, Yunnan Province, Yuxi, Yimen County, Pubei Village, Shiliansi, *Hipposideros pomona* feet samples, 24.61746 N 102.1633 E, 21 September 2020, Alice Hughes, YM-66-B3 (HKAS122841), living culture KUMCC 21-0809; *ibid*., YM-66-B5, living culture KUMCC 21-0810; *ibid*., YM-66-B6, living culture KUMCC 21-0811; *ibid*., *Rhinolophus rex*, YM-16-B, living culture KUMCC 21-0807; *ibid*., *Miniopterus schreibersii*, YM-62-B2, living culture KUMCC 21-0808.

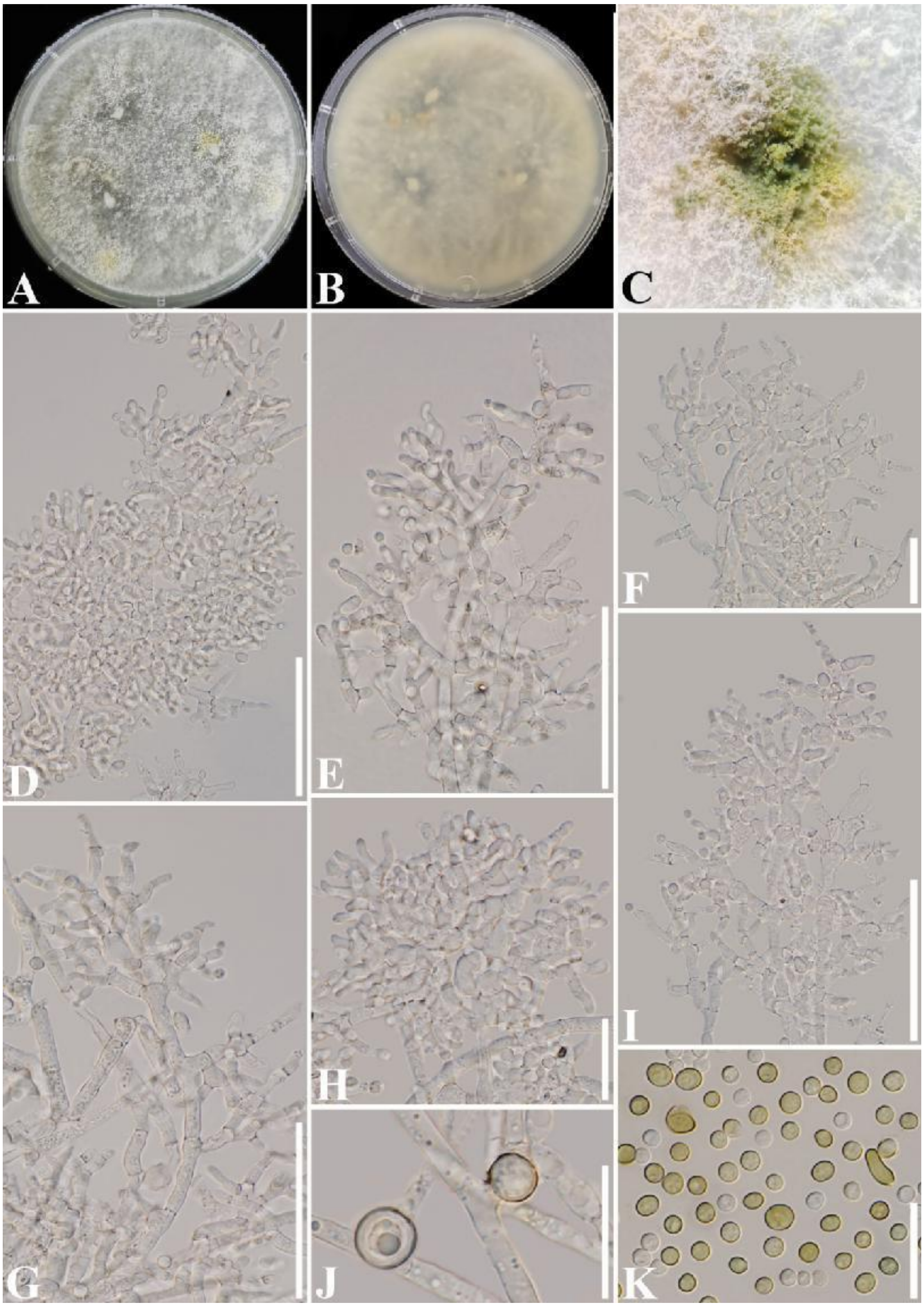

Figure 27 – *Trichoderma inconspicuum* (KUMCC 21-0806). A, B Colony on PDA (above and below). C Sporulation on PDA (15 days old culture). D–I Conidiophores and phialides. J Chlamydospores. K Conidia. Scale bars: D, E, G, I = 50 µm, F, H, J, K = 20 µm.

GenBank numbers – KUMCC 21-0807 = ITS: ON426891, *RPB2*: OR025905, *TEF 1-α*: OR025987; KUMCC 21-0808 = ITS: ON426892, *RPB2*: OR025906, *TEF 1-α*: OR025988; KUMCC 21-0809 = ITS: ON426896, *RPB2*: OR025902, *TEF 1-α*: OR025984; KUMCC 21-0810 =

ITS: ON426897, *RPB2*: OR025903, *TEF 1-α*: OR025985; KUMCC 21-0811 = ITS: ON426898, *RPB2*: OR025904, *TEF 1-α*: OR025986.

Notes – *Trichoderma obovatum* was erected by Zheng et al. (2021) and was isolated from soil in Yunnan, China. Our isolates clustered with *T. obovatum* within the *Atroviride* clade (Fig. 9). *Trichoderma obovatum* is phylogenetically closely related to *T. uncinatum* Z.F. Yu & X. Du. However, *T. obovatum* differs from *T. uncinatum* by having larger conidia (3–8 × 2–5 µm vs 3.1–4.4 × 2.7–4 µm) and bigger phialides (3–15 × 1–5 µm vs (4.3–)5.2–9.3(–10.3) × 2.3–3.9 µm) (Supplementary Table 3) (Zheng et al. 2021). This is the first report of *T. obovatum* on bats.

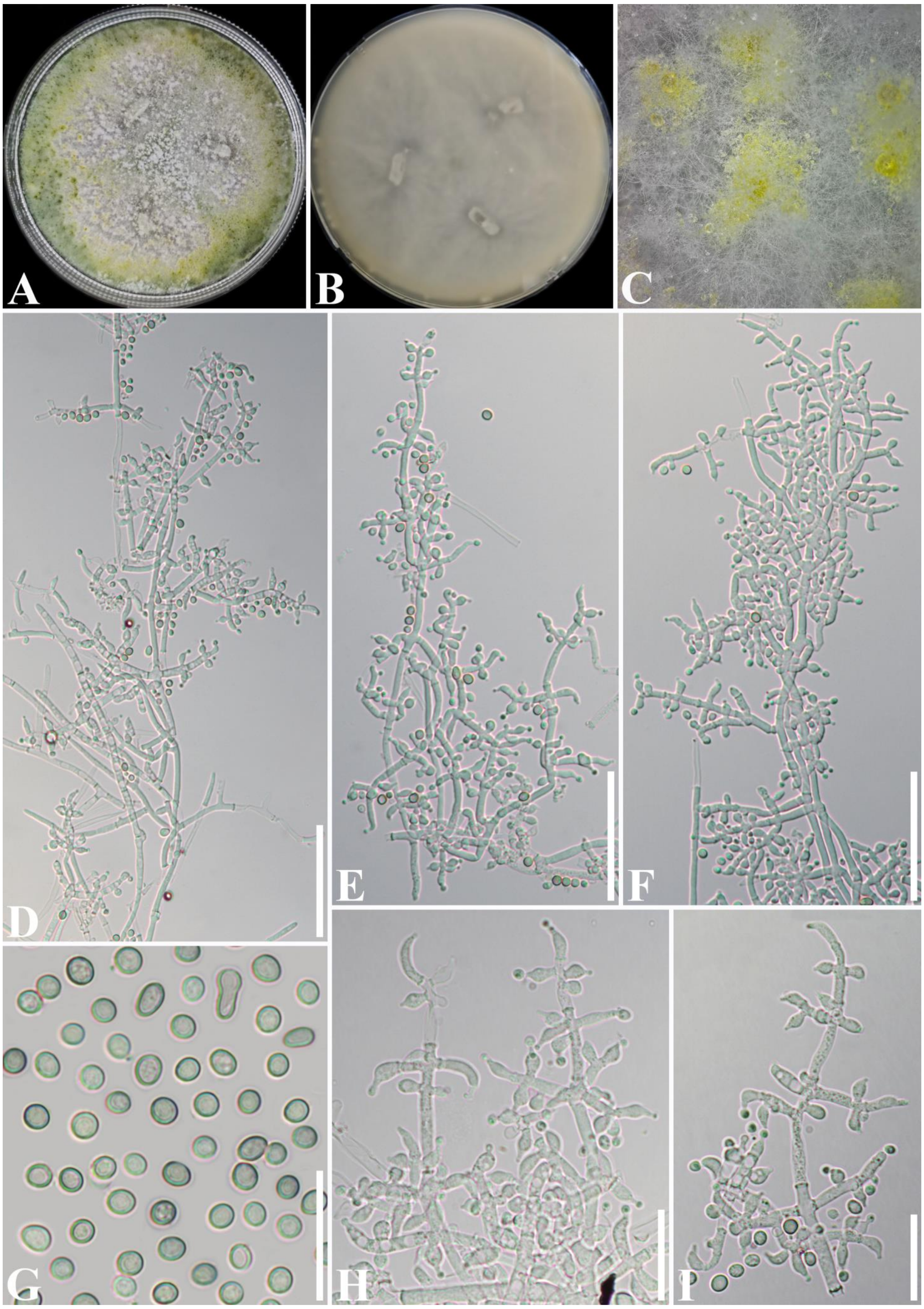

Figure 28 – *Trichoderma obovatum* (KUMCC 21-0809). A, B Colony on PDA (above and below). C Sporulation on PDA (15 days old culture). D–F, H, I Conidiophores and phialides. G Conidia. Scale bars: D–F = 50 µm, G–I = 20 µm.

Trichoderma rhinolophicola Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 29

MycoBank number: MB 844276; Facesoffungi number: FoF 13269

Etymology – Refers to the host genus *Rhinolophus* (*Chiroptera*).

Holotype – HKAS123189.

Asexual morph on PDA: *Vegetative hyphae* septate, branched, hyaline, smooth-walled, 1–6 µm wide. Septa thick, refractive. *Conidiophores* pyramidal with verticillate, paired lateral branches; *phialides* generally formed on terminal branches, in divergent whorls of one to three, 3–17 × 1–5 µm (x̄ = 7.02 × 2.99 µm, n = 100); *supporting cells* 4–16 × 2–6 µm (x̄ = 8.33 × 3.36 µm, n = 6). *Conidia* 2–12 × 2–5 µm (x̄ = 4.95 × 3.69 µm, n = 100), ellipsoidal to ovoid, subhyaline to green, smooth-walled. *Chlamydospores* 7–13 × 3–11 µm (x̄ = 9.93 × 8.25 µm, n = 15), subglobose to globose, smooth-walled, hyaline, granulate. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 55–60 mm after 10 days at room temperature (20–25 °C), white to pale green, with sparse aerial mycelium on the surface; reverse white to pale yellow. The white reproductive mycelium covers the stromatic colonies after 25 days. Odor absent.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, wing surfaces from *Rhinolophus malayanus* in limestone forest, 101.282404 E, 21.907599 N, 15 July 2021, Alice Hughes, 55-F (**holotype**, HKAS122829), ex-type KUMCC 21-0813; *ibid*., 55-F2, ex-isotype KUMCC 21-0814.

GenBank numbers – KUMCC 21-0813 = ITS: OP425803, *TEF 1-α*: OR025989; KUMCC 21-0814 = ITS: OP425804, *TEF 1-α*: OR025990.

Notes – In the phylogenetic tree, *Trichoderma rhinolophicola* formed a separate branch but was slightly closely related to *T. atroviride* in the *Atroviride* clade (Fig. 9). Based on the megablast searching GenBank, the closest hits using the ITS sequences had the highest similarity to *T. atroviride* (GenBank, KM822752.1, Identities = 629/638 (99%), Gaps = 5/638 (0%)), and *T. koningii* Oudem. (GenBank, MH588231.1, Identities = 629/638 (99%), Gaps = 5/638 (0%)); the closest hits using the *TEF1-α* sequences had the highest similarity to *T. subviride* W.T. Qin & W.Y. Zhuang (GenBank, KU529132.1, Identities = 1223/1305 (94%), Gaps = 25/1305 (1%)), and *T. paratroviride* Jaklitsch & Voglmayr (GenBank, ON258615.1, Identities = 1205/1281 (94%), Gaps = 23/1281 (1%)). Based on the sequence comparisons, *T. rhinolophicola* is different from *T. atroviride* in 40/1311bp (3.05%) of *TEF1-α* (Supplementary Table 4). Morphologically, *T. rhinolophicola* is different from *T. atroviride* in having larger conidia (2–12 × 2–5 µm vs 4–5 × 3–3.5 µm) and subglobose to globous chlamydospores (Supplementary Table 3) (Manawasinghe et al. 2021). *Trichoderma rhinolophicola* is different from *T. koningii* by the latter having smaller phialides (3–17 × 1–5 µm vs 7.5–8.2 × 2.5–3 µm) in whorls of 3–4, smaller broadly ellipsoidal conidia (2–12 × 2–5 µm vs 3–5 × 2–3 µm), and smaller chlamydospores (7–13 × 3–11 µm vs up to 12 µm wide) (Supplementary Table 3) (Oudemans & Koning 1902). *Trichoderma rhinolophicola* is different from *T. subviride* by the latter having a distinct coconut-like odor, pale yellow to yellow-green colonies, smaller phialides (3–17 × 1–5 µm vs 4.5–)5–6.5(–7)×2–3 µm) contracted at the base in whorls of 2–4(–6), smaller conidia (2–12 × 2–5 µm vs (2–)2.5–3.8(–4.5) × (2–)2.5–3.2 µm), and variously shaped chlamydospores (77–13 × 3–11 µm vs 5–8.5(–9.5) × (4–)5–7.5(–8.5) um) (Supplementary Table 3) (Qin & Zhuang 2016). *Trichoderma rhinolophicola* is different from *T. paratroviride* by the latter having pale yellow to light green colonies with 2–3 concentric zones, smaller phialides (3–17 × 1–5 µm vs (5.2–)6.2–11(–14) × (2–)2.5–3.2(–3.5) µm) in whorls of 2–4, and thick-walled conidia with 1–2 large guttules (Supplementary Table 3) (Jaklitsch & Voglmayr 2015). In addition, the PHI results also show that our strains represent a distinct new species (Fig. 26). Based on the phylogenetic analyses and morphological characteristics, *T. rhinolophicola* is described as a new species.

Trichoderma xishuangbannaense Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 30

MycoBank number: MB 845345; Facesoffungi number: FoF 13270

Etymology – Named after the location Xishuangbanna, where the fungus was first discovered.

Holotype – HKAS122850.

Asexual morph on PDA: *Vegetative hyphae* septate, branched, hyaline, smooth-walled, 1–5 µm wide. *Conidiophores* pyramidal with verticillate, paired lateral branches; *phialides* generally formed on terminal branches, in divergent whorls of two to five, 4–14 × 1–5 µm ($\bar{x}$ = 8.26 × 2.98 µm, n = 100); *supporting cells* 3–22 × 1–5 µm ($\bar{x}$ = 10.16 × 3.21 µm, n = 100). *Conidia* 3–13 × 2–6 µm ($\bar{x}$ = 4.67 × 3.67 µm, n = 100), ellipsoidal to ovoid, green, smooth. *Chlamydospores* 7–12 × 5–10 µm ($\bar{x}$ = 9.95 × 7.68 µm, n = 10), subglobose to globous, smooth, terminal. Sexual morph: Undetermined.

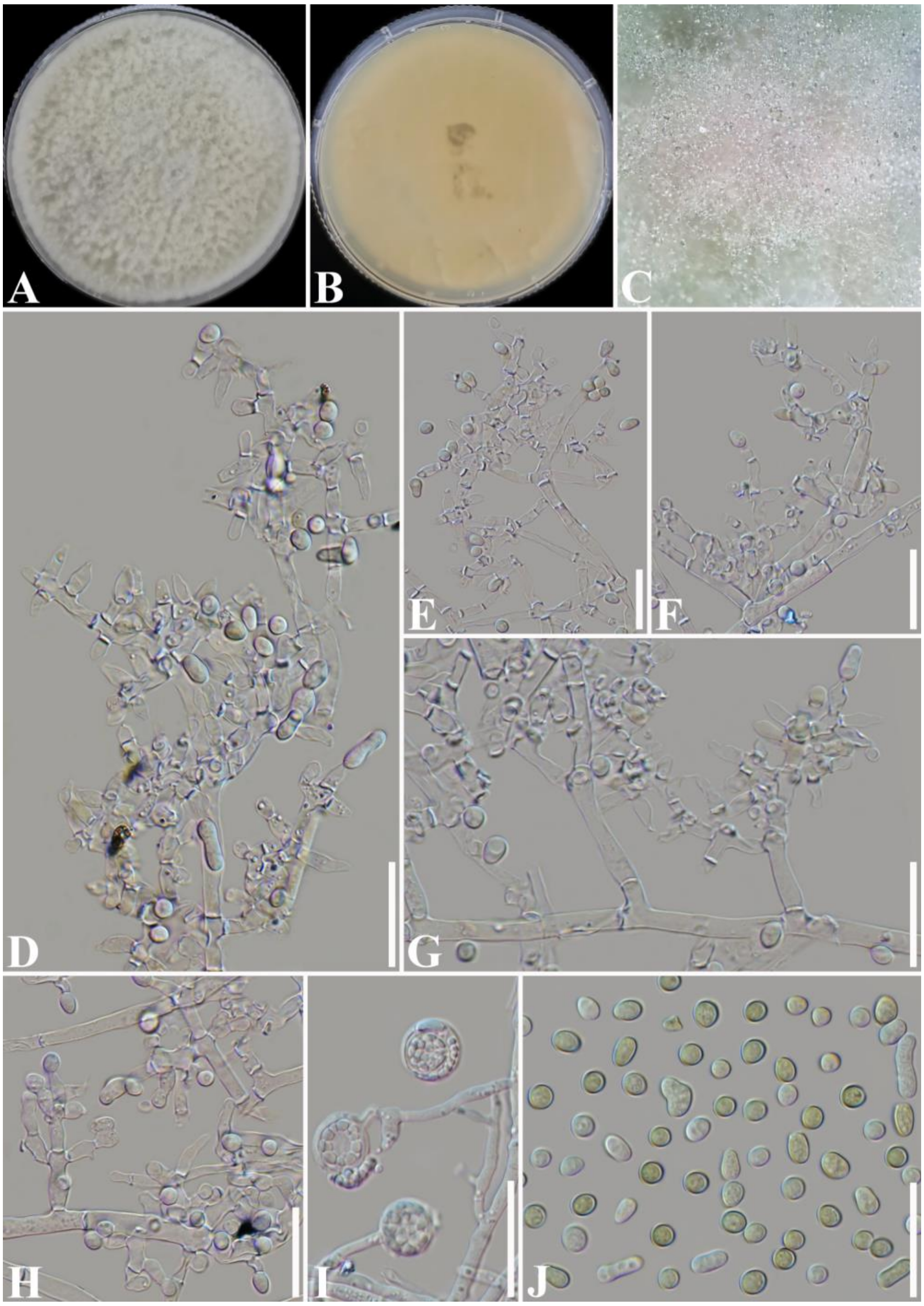

Figure 29 – *Trichoderma rhinolophicola* (KUMCC 21-0813). A, B Colony on PDA (above and below). C Mycelium on PDA (25 days old culture). D–H Conidiophores and phialides. I Chlamydospores. J Conidia. Scale bars: D–J = 20 µm.

Culture characteristics – Colonies on PDA attaining 50–60 mm after 14 days at room temperature (20–25 °C), white, pale yellow to green, sparse aerial mycelium on the surface; reverse white to pale yellow. The white reproductive mycelium covers the stromatic colonies after 30 days. Odor absent.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, wing surfaces from *Rhinolophus malayanus* in limestone forest, 101.282404 E, 21.907599 N, 15 July 2021, Alice Hughes, 73-D (**holotype**, HKAS123191), ex-type KUMCC 21-0815; *ibid*., 73-D2, ex-isotype KUMCC 21-0816.

GenBank numbers – KUMCC 21-0815 = ITS: OP425805, *RPB2*: OR025907, *TEF 1-α*: OR025991; KUMCC 21-0816 = ITS: OP425806, *RPB2*: OR025908, *TEF 1-α*: OR025992.

Notes – Phylogenetically, *Trichoderma xishuangbannaense* formed a separate branch with high statistical support (100% ML/ 1.00 BYPP, Fig. 9) basal to the *Longibrachiatum* clade and closely related to *T. awajun* M.S. Calderon, D.E. Bustamante & S. Leiva and *T. andinense* (Samuels & Petrini) Samuels, Jaklitsch & Voglmayr. Based on a megablast search in GenBank, the closest hits in the *RPB2* and *TEF1-α* sequences had the highest similarity to *T. britdaniae* (Jaklitsch & Voglmayr) Jaklitsch & Voglmayr (RPB2: GenBank, KJ634741.1, Identities = 648/712(91%), Gaps = 0/712(0%); *TEF1-α*: GenBank, KJ634774.1, Identities = 1141/1265(90%), Gaps = 23/1265(1%)). Based on the sequence comparisons, *T. xishuangbannaense* (KUMCC 21-0815, type) is different from *T. atroviride* (CHAXC CP24-7, type), *T. andinense* (COAD 2431), and *T. pluripenicillatum* (YMF 1.06198, type) (Supplementary Table 4). Morphologically, *T. xishuangbannaense* is different from *T. awajun* by the latter having green to dark green colonies, bigger phialides (4–14 × 1–5 µm vs 3.1–10 × 6.4–9.6 µm), smaller green conidia (3–13 × 2–6 µm vs 1.5–3 × 1.3–2.6 µm) and globose to subglobose chlamydospores (Supplementary Table 3) (Bustamante et al. 2021). *Trichoderma xishuangbannaense* is different from *T. andinense* by having larger conidia (3–13 × 2–6 µm vs 4.5 ± 0.3 × 3 ± 0.2 µm) (Supplementary Table 3) (Samuels et al. 2012, Jaklitsch & Voglmayr 2014). The PHI test (Fig. 31) confirmed no recombination in *T. xishuangbannaense* compared with the closely related taxa. Based on the phylogeny and morphology, *T. xishuangbannaense* is described as a distinct new species.

Nectriaceae Tul. & C. Tul.

Nectriaceae was introduced by Tulasne & Tulasne (1865) and typified by *Nectria cinnabarina* (Tode) Fr. (= *Sphaeria cinnabarina* Tode). Seaver (1909) divided *Hypocreales* into two families, *Nectriaceae* and *Hypocreaceae*, based on stromatic and perithecial characteristics. Petch (1938) also accepted Nectriaceae as a family in *Hypocreales*. However, Munk (1957) and Dennis (1960) placed *Nectriaceae* in *Sphaeriales*. Subsequently, Kreisel (1969) and Rossman et al. (1999) accepted *Nectriaceae* and *Hypocreaceae* as separate families in *Hypocreales*. Members of the *Nectriaceae* are facultative and sometimes toxic plant pathogens that cause serious problems for crops and are usually encountered as asexual variants, e.g., *Albonectria rigidiuscula* (Berk. & Broome) Rossman & Samuels, *Fusarium sambucinum* Fuckel, *F. oxysporum* Schltdl., and *Ne. liriodendri* Halleen, Rego & Crous that cause galls, cankers, root rots and wilt diseases (Ray & Hammerschmidt 1998, Rossman et al. 1999, Halleen et al. 2006, Wharton et al. 2006, Ploetz 2007, Chaverri et al. 2011, Pérez et al. 2012, Hyde et al. 2014, Chittem et al. 2015, McGovern 2015, Yang et al. 2018, Hyde et al. 2020). Some species of *Nectriaceae* are beneficial, e.g., *Fusarium moniliforme* produces gibberellic acid (Panchal & Desai 2016, Puyam et al. 2017). Nectriaceae are predominantly endophytic, pathogenic or saprobic on plants, some are entomogenous, a few are human pathogens that live in terrestrial and aquatic habitats worldwide, and have higher diversity in warm temperate and tropical regions (Rossman et al. 1999, Rossman 2000, Chaverri et al. 2011, Schroers et al. 2011, Hyde et al. 2014, Lombard et al. 2015, Hyde et al. 2020).

Fusarium Link

Fusarium (*F.*) was established by Link (1809) and typified by *F. roseum* Link. The genus *Fusarium* encompasses many important plant and human pathogens, as well as many industrially and commercially important species that produce bioactive secondary metabolites (Kvas et al. 2009, Proctor et al. 2013, Wang et al. 2019). In addition, these fungi are also found widely as endophytes of native and cultivated plants, especially grasses (Leslie & Summerell 2006, Kvas et al. 2009). Jain et al. (2011) showed that *Fusarium* species are more prevalent in clinical settings, causing a variety of diseases and infections in humans and animals for which clinical treatments are limited. *Fusarium* species complex has been extensively studied over the years because of their ability to cause plant infections, produce mycotoxins (e.g., beauvericin, fumonisins, moniliformin) and cause human infections (Nirenberg & O'Donnell 1998, Munkvold 2017, Al-Hatmi et al. 2019). Throughout the years, researchers have been working on morphological validation of the genus *Fusarium* and Link (1809) determined the primary morphological characteristics of *Fusarium* to be the distinctive canoe- or banana-shaped conidia. Nelson et al. (1983) provided a detailed morphological identification manual for *Fusarium.* However, identification of *Fusarium* based on only morphology is still confusing because of the variable phenotypes in culture, intricate or too vague descriptions of species among different studies, and the historically complicated subspecies level ranks (Gordon 1959, 1960, Leslie & Summerell 2006, Lombard et al. 2019, Wang et al. 2022). This study describes five new species as *Fusarium hipposidericola*, *F. menglaense*, *F. rhinolophicola*, *F. yunnanense* and *F. xishuangbannaense* from bats in China.

Fusarium hipposidericola Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 32

MycoBank number: MB 845349; Facesoffungi number: FoF 13271

Etymology – Refers to the host genus *Hipposideros* (*Chiroptera*).

Holotype – HKAS122803.

Asexual morph on PDA: *Vegetative hyphae* septate, branched, hyaline, smooth-walled, 1–8 μm wide, often compacted laterally into rope-like filaments. *Conidiophores* sparse on aerial mycelium, straight or flexuous, erect or prostrate, septate, smooth- and thin-walled, branched to unbranched, or reduced to conidiogenous cells borne laterally on hyphae; *Conidiogenous cells* mono- to polyphialidic, phialidic to subcylindrical, geniculate or irregularly bent, smooth- and thin-walled, 3–34 × 1–5 μm, without periclinal thickening. *Microconidia*, 3–31 × 1–6 μm (x̄ =12.05 ×3.44 μm, n = 100), falcate, oblong, reniform to lunate, or contracted at one end, hyaline, 0-1-septate, granulate, walls smooth and thin. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 40–50 mm after 7 days at room temperature (20–25 °C), with undulate edge, white, sparse aerial mycelium on the surface; reverse white to pale yellow. The white reproductive mycelium covers the stromatic colonies after 50 days. Odor absent.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, *Rhinolophus malayanus* wing surface in a limestone forest, 101.271563 E, 21.918897 N, 15 July 2020, Alice Hughes, 36-D1, (**holotype**, HKAS122830), ex-type KUMCC 21-0724; *ibid*., *Rhinolophus stheno*, 40-C, ex-paratype KUMCC 21-0725; *ibid*. 40-E, ex-paratype KUMCC 21-0726; *ibid*., *Rhinolophus malayanus*, 65-C, ex-paratype KUMCC 21-0727; *ibid*., 65-D, ex-paratype KUMCC 21-0728.

GenBank numbers – KUMCC 21-0724 = ITS: ON426846, *CAM*: OR022054, *RPB2*: OR025909, *TUB*: OR025938, *TEF 1-α*: OR025993; KUMCC 21-0725 = ITS: ON426854, *CAM*: OR022055, *RPB2*: OR025910, *TUB*: OR025939, *TEF 1-α*: OR025994; KUMCC 21-0726 = ITS: ON426855, *CAM*: OR022056, *RPB2*: OR025911, *TUB*: OR025940, *TEF 1-α*: OR025995; KUMCC 21-0727 = ITS: ON426863, *CAM*: OR022057, *RPB2*: OR025912, *TUB*: OR025941, *TEF 1-α*: OR025996; KUMCC 21-0728 = ITS: ON426864, *CAM*: OR022058, *RPB2*: OR025913, *TUB*: OR025942, *TEF 1-α*: OR025997.

Notes – Phylogenetically, *Fusarium hipposidericola* clustered in a well-separated clade with *F. fujikuroi* species complex (Fig. 10) (Sandoval-Denis et al. 2018, Wang et al. 2020). *Fusarium hipposidericola* is sister to *F. mangiferae* Britz, M.J. Wingf. & Marasas. The new species (KUMCC 21-0724, type)) is different from *F. mangiferae* (CBS 120994, type)) in 16/692 bp of the *CAM*, >100/1803 bp of *RPB2*, 24/643 bp of *TEF1-α* and 12/568 bp of *TUB* (Supplementary Table

4). Based on a megablast search in GenBank, the closest hits of the ITS, LSU, *TEF1-α* and *TUB* sequences had the highest similarity to *F. proliferatum* (Matsush.) Nirenberg ex Gerlach & Nirenberg, *F. fujikuroi* Nirenberg and *F. annulatum* Bugnic (Supplementary Table 4).

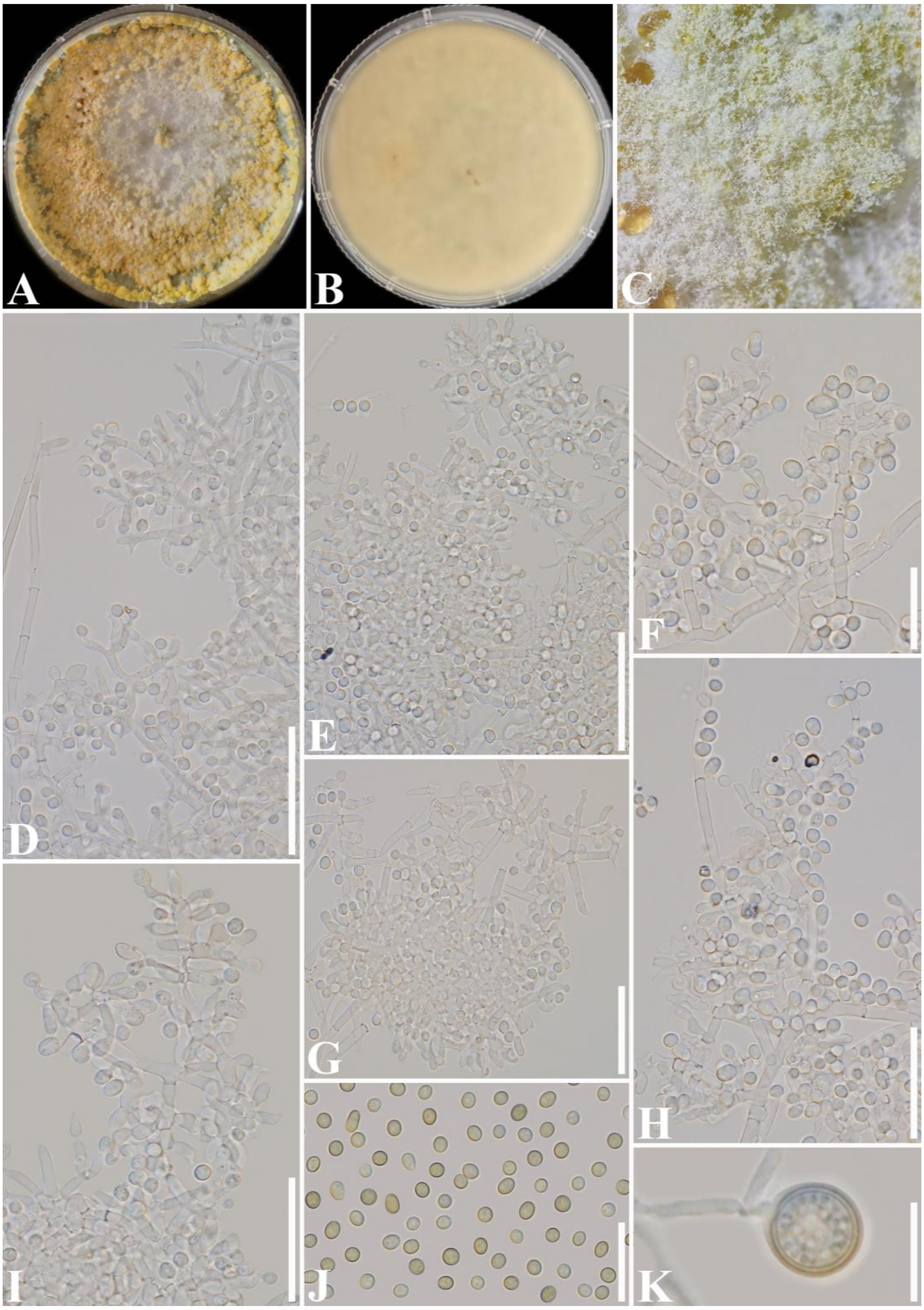

Figure 30 – *Trichoderma xishuangbannaense* (KUMCC 21-0815). A, B Colony on PDA (above and below). C Sporulation on PDA (20 days old culture). D–I Conidiophores, phialides and conidia. J Conidia. K Chlamydospores. Scale bars: D, E = 40 µm, G–I = 30 µm, F, J = 20 µm, K = 10 µm.

Morphologically, *Fusarium hipposidericola* can easily be distinguished from *F. mangiferae* by the latter having rose to dark purple colonies, conidiogenous cells and significantly different sizes of microconidia (Supplementary Table 3) (Britz et al. 2002). *Fusarium hipposidericola* can be distinguished from *F. proliferatum* by the latter having a smaller truncated base and aseptate microconidia (3–31 × 1–6 µm vs 5–11 × 2–4 µm) (Supplementary Table 3) (Matsushima 1971, Gerlach & Nirenberg 1982). *Fusarium hipposidericola* differs from *F. fujikuroi* by the latter having rosy buff to vinaceous colonies and smaller microconidia (3–31 × 1–6 µm vs 5–12 × 1.5–2.5 µm) formed in chains (Supplementary Table 3) (Wollenweber 1931). *Fusarium hipposidericola* differs from *F. annulatum* by the latter having clavate microconidia with truncate bases grouped in chains, straight, sporodochial conidia, and straight to strongly curved macroconidia (Supplementary Table 3) (Yilmaz et al. 2021). Based on the phylogeny and morphology, *F. hipposidericola* is introduced here as a distinct new species.

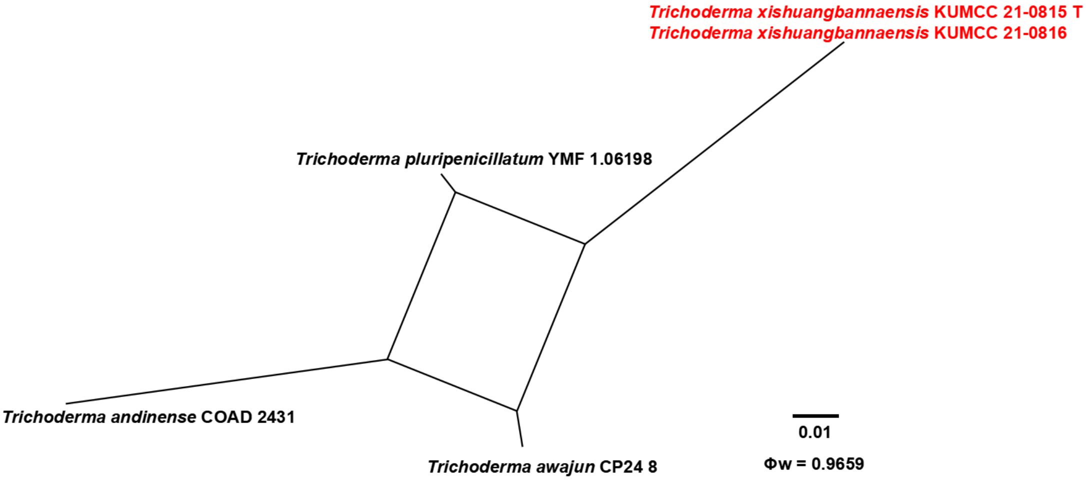

Figure 31 – The results of the pairwise homoplasy index (PHI) test of closely related species using both LogDet transformation and splits decomposition. PHI test results Φw ≤ 0.05 indicate that there is significant recombination within the dataset. The new taxon is in red bold type.

Fusarium luffae M.M. Wang, Qian Chen & L. Cai, in Wang, Chen, Diao, Duan & Cai, Persoonia 43: 85 (2019). Fig. 33

MycoBank number: MB 829540; Facesoffungi number: FoF 13420

Asexual morph on PDA: *Vegetative hyphae* septate, branched, hyaline, smooth-walled, 1–7 µm wide. *Conidiophores* sparse on aerial mycelium, straight or flexuous, erect or prostrate, smooth- and thin-walled, branched to unbranched, or reduced to conidiogenous cells borne laterally on hyphae; *Conidiogenous cells* mono- and polyphialidic, monophialides subulate to subcylindrical, smooth- and thin-walled, hyaline, 7–25 × 1–7 µm, without periclinal thickening. *Conidia* 6–30 × 1–8 µm ($\bar{x}$ = 9.56 × 3.61 µm, n = 100), falcate, oblong, reniform to lunate, straight to slightly curved, hyaline, 0–2-septate, granulate, walls smooth and thin. *Chlamydospores* 5–14 × 3–9 µm ($\bar{x}$ = 8.61 × 5.83 µm, n = 100), intercalary or terminal, ellipsoid, globose to cylindrical, smooth to slightly rough, thick-walled, hyaline. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 50–6 mm after 7 days at room temperature (20–25 °C), with undulate edge, white, sparse aerial mycelium on the surface; reverse white, pale yellow to violet color. The white reproductive mycelium covers the stromatic colonies after 60 days. Odor absent.

Substrata – Human diabetic cellulitis, Human sputum, *Humulus scandens* leaf, and *Luffa aegyptiaca.*

Distribution – Brazil, China and USA.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, *Rhinolophus malayanus* wing surface in Rainforest, 101.271563

E, 21.918897 N, 15 July 2020, Alice Hughes, 49-A (HKAS122813), living culture KUMCC 21-0734.

GenBank numbers – KUMCC 21-0734 = ITS: ON426858, *RPB1*: OR022017, *RPB2*: OR025914, *TUB*: OR025943, *TEF 1-α*: OR025998.

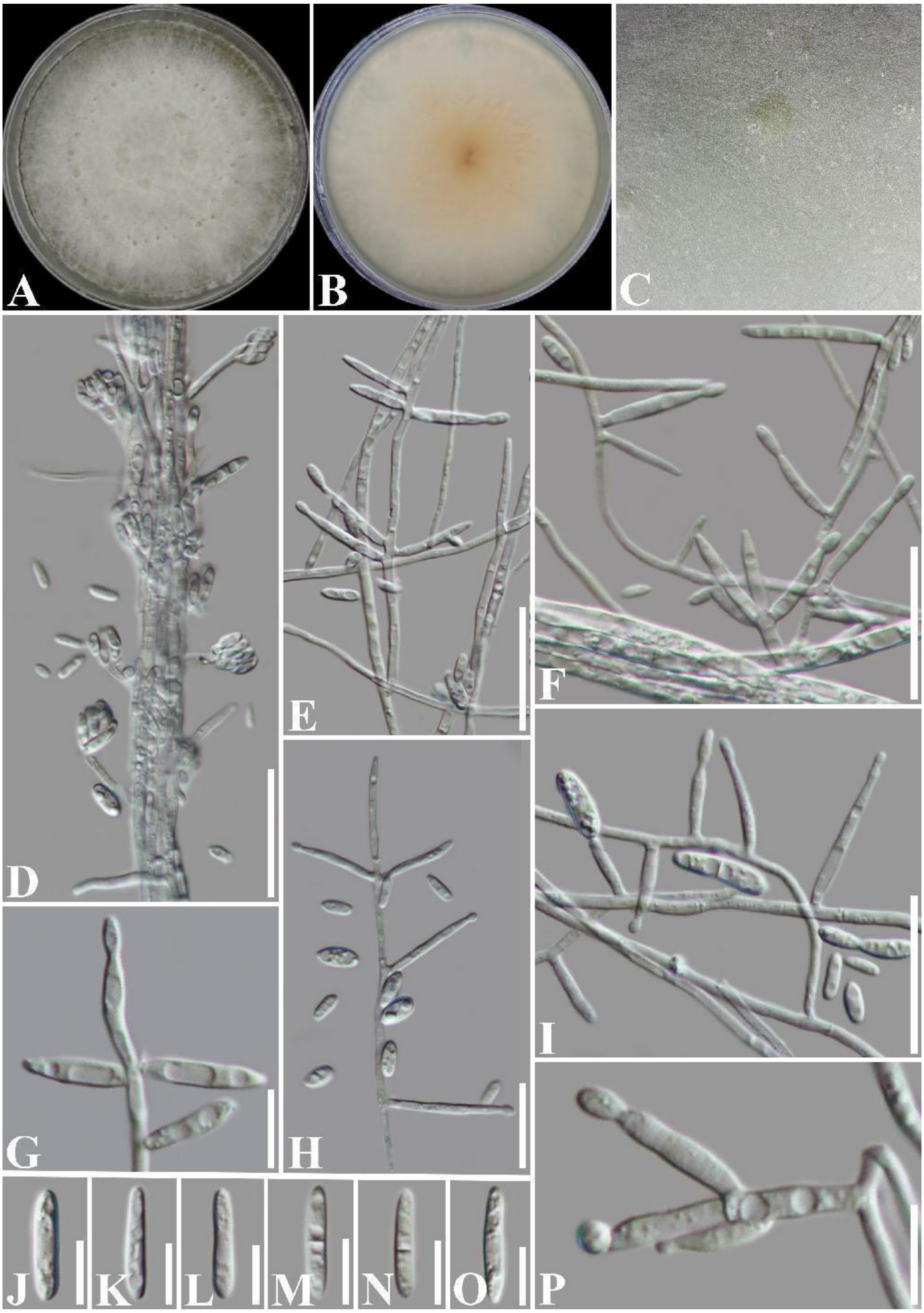

Figure 32 – *Fusarium hipposidericola* (KUMCC 21-0724). A, B Colony on PDA (above and below). C Mycelium on PDA (30 days old culture). D–I, P Hyphae, conidiogenous cells and conidia. J–O Microconidia. Scale bars: D, E = 30 µm, F, H, I = 20 µm, G, J–P = 10 µm.

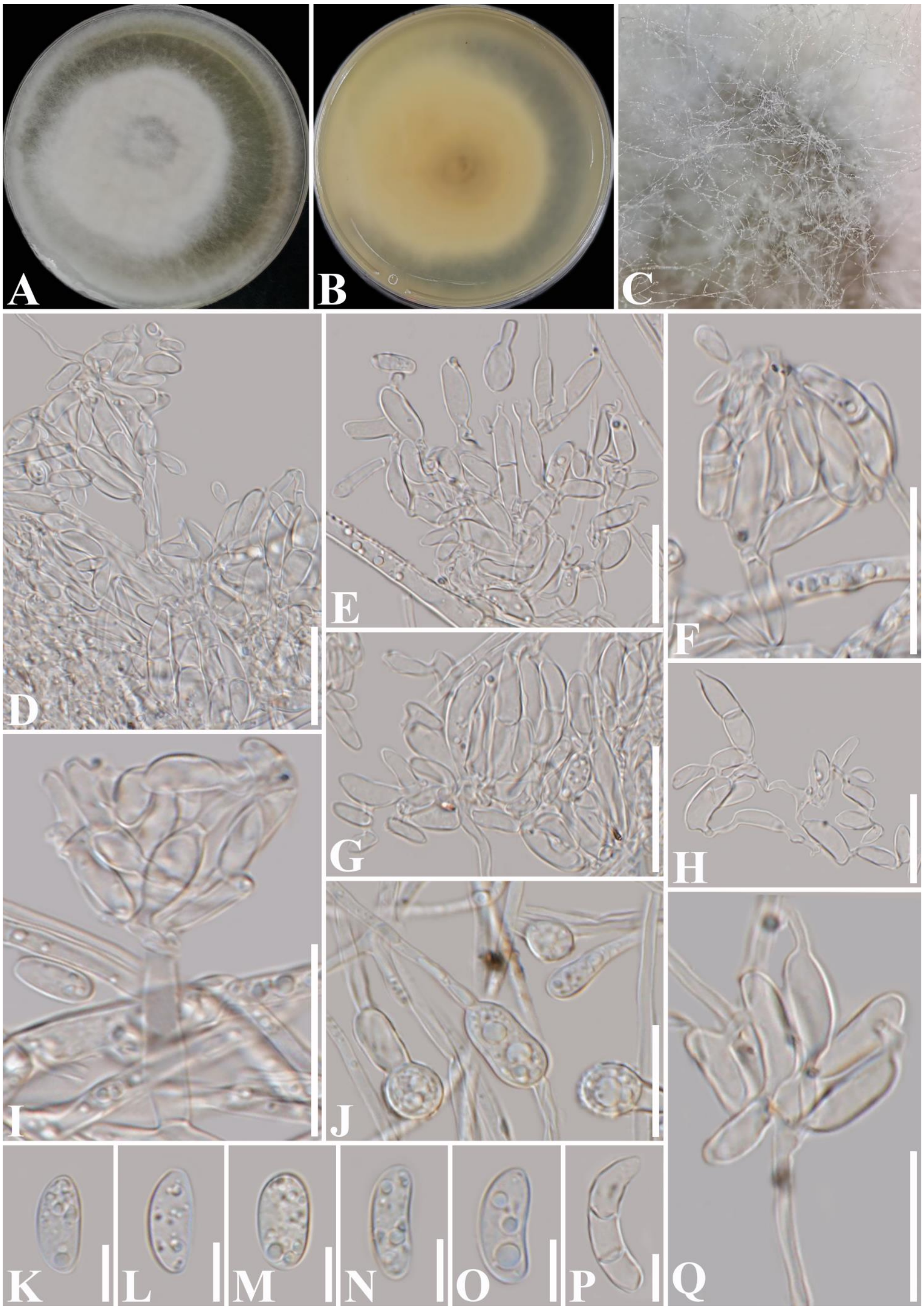

Figure 33 – *Fusarium luffae* (KUMCC 21-0734). A, B Colony on PDA (above and below). C Mycelium on PDA (60 days old culture). D–I, Q Conidiogenous cells and conidia. J Chlamydospores. K–P Microconidia. Scale bars: D–I, Q = 20 µm, J = 10 µm, K–P = 5 µm.

Notes – *Fusarium luffae* was introduced from a leaf of *Humulus scandens* in China by Wang et al. (2019) based on morphology and phylogenetic analyses. Based on multi-gene phylogenetic analyses, our isolate clustered with *F. luffae* (CQ1038) and close to *F. irregulare* M.M. Wang, Qian Chen & L. Cai and *F. arcuatisporum* M.M. Wang, Qian Chen & L. Cai. In the sequence comparisons, our isolate (KUMCC 21-0734) differs from *F. luffae* (CQ1038) in 0/572 bp (0%) of the ITS, 44/1607 bp (2.73%) of the *RPB1*, 6/1203 bp (0.50%) of *RPB2* and 19/636 bp (2.99%) of *TEF1-α*; compared to *F. irregulare* (LC12146) in 1/572 bp (0.17%) of the ITS, 20/1607 bp (1.24%)

of the *RPB1*, 11/1203 bp (0.91%) of *RPB2* and 16/635 bp (2.52%) of *TEF1-α*; and compared to *F. arcuatisporum* (LC12147) in 2/572 bp (0.35%) of the ITS, 21/1607 bp (1.31%) of the *RPB1*, 25/1203 bp (2.08%) of *RPB2* and 57/629 bp (9.06%) of *TEF1-α*. Morphologically, the new isolate (KUMCC 21-0734) is similar to the *F. luffae* by having similar conidia that are falcate, straight to slightly curved, slightly rough, hyaline and monophialides, subulate to subcylindrical conidiophores, differed from *F. irregulare* by having smaller, 3–5-septate conidia and conidiophores with 3–5 conidiogenous loci, and differed from *F. arcuatisporum* by the latter having conidiophores with 1–3 conidiogenous loci, bigger conidiogenous cells, and 0–2-septate chlamydospores (Supplementary Table 3) (Wang et al. 2019). In this study, we observed globose to cylindrical, smooth to slightly rough chlamydospores. Based on phylogeny and morphology, the new isolate (KUMCC 21-0734) is identified as *F. luffae*. This is the first report of *F. luffae* isolated from bats in China.

Fusarium menglaense Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 34

MycoBank number: MB 845347; Facesoffungi number: FoF 13272

Etymology – Named after the location Mengla, where the fungus was first discovered.

Holotype – HKAS122803.

Asexual morph on PDA: *Vegetative hyphae* septate, branched, hyaline, smooth-walled, 1–8 µm wide. *Conidiophores* sparse on aerial mycelium, straight or flexuous, erect or prostrate, smooth- and thin-walled, branched to unbranched, or reduced to conidiogenous cells borne laterally on hyphae; *Conidiogenous cells* mono- and polyphialidic, phialidic to subcylindrical, geniculate or irregularly bent, smooth- and thin-walled, 3–34 × 1–5 µm, without periclinal thickening. *Microconidia*, 3–32 × 1–6 µm ($\bar{x}$ = 12.05 ×3.44 µm, n = 60), falcate, oblong, reniform to lunate, or contracted at one end, hyaline, aseptate, granulate, walls smooth and thin. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 50–60 mm after 7 days at room temperature (20–25 ℃), with undulate edge, white, sparse aerial mycelium on the surface; reverse pale yellow. The white reproductive mycelium covers the stromatic colonies after 50 days. Odor absent.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, *Rhinolophus malayanus* wing surface in limestone forest, 101.271563 E, 21.918897 N, 15 July 2020, Alice Hughes, 39 (**holotype**, HKAS122803), ex-type KUMCC 21-0717; *ibid*., 39-B, ex-isotype KUMCC 21-0718.

GenBank numbers – KUMCC 21-0717 = ITS: ON426850, *CAM*: OR022059, *RPB1*: OR022018, *RPB2*: OR025915, *TUB*: OR025944, *TEF 1-α*: OR025999; KUMCC 21-0718 = ITS: ON426852, *CAM*: OR022060, *RPB1*: OR022019, *RPB2*: OR025916, *TUB*: OR025945, *TEF 1-α*: OR02600.

Notes – In our phylogenetic analyses, *Fusarium menglaense* clustered in the *F. fujikuroi* species complex (Sandoval-Denis et al. 2018, Wang et al. 2020) and is closely related to *F. cugenangense* Maryani, L. Lombard, Kema & Crous, *F. inflexum* R. Schneid., *F. curvatum* L. Lombard & Crous and *F. nirenbergiae* L. Lombard & Crous. Morphologically, *F. menglaense* differs from *F. cugenangense* by the latter having dark purple to white colony surface, smaller microconidia (3–32 × 1–6 µm vs (7–)8–11(–24) × (2–)7(–12) µm), and globose to subglobose chlamydospores formed terminally (Supplementary Table 3) (Maryani et al. 2019). Based on the sequence comparisons, *F. menglaense* (KUMCC 21-0717) is different from *F. inflexum* (CBS 716.74), *F. cugenangense* (CBS 130308), *F. curvatum* (NRRL 22902), and *F. nirenbergiae* (CBS 744.97) (Supplementary Table 4). Morphologically, *Fusarium menglaense* differs from *F. inflexum* by the latter having smaller conidiogenous cells (3–34 × 1–5 µm vs 7–15 × 3–5 µm) and a large number of chlamydospores (Supplementary Table 3) (Schneider & Dalchow 1975). *Fusarium menglaense* differs from *F. curvatum* by the latter having strongly curved, 3-septate macroconidia and pale vinaceous to rosy vinaceous colony surface (Supplementary Table 3) (Lombard et al. 2019). *Fusarium menglaense* differs from *F. nirenbergiae* by the latter having pale vinaceous to vinaceous colonies surface, smaller microconidia (3–32 × 1–6 µm vs 5–14 × 2–4 µm), smaller conidiogenous cells (3–34 × 1–5 µm vs 8–24 × 2–4 µm) with a small false head on the tips, and globose to subglobose chlamydospores (Supplementary Table 3) (Lombard et al. 2019). Based on the phylogenetic analyses and morphological characteristics, *F. menglaense* is described as a distinct new species.

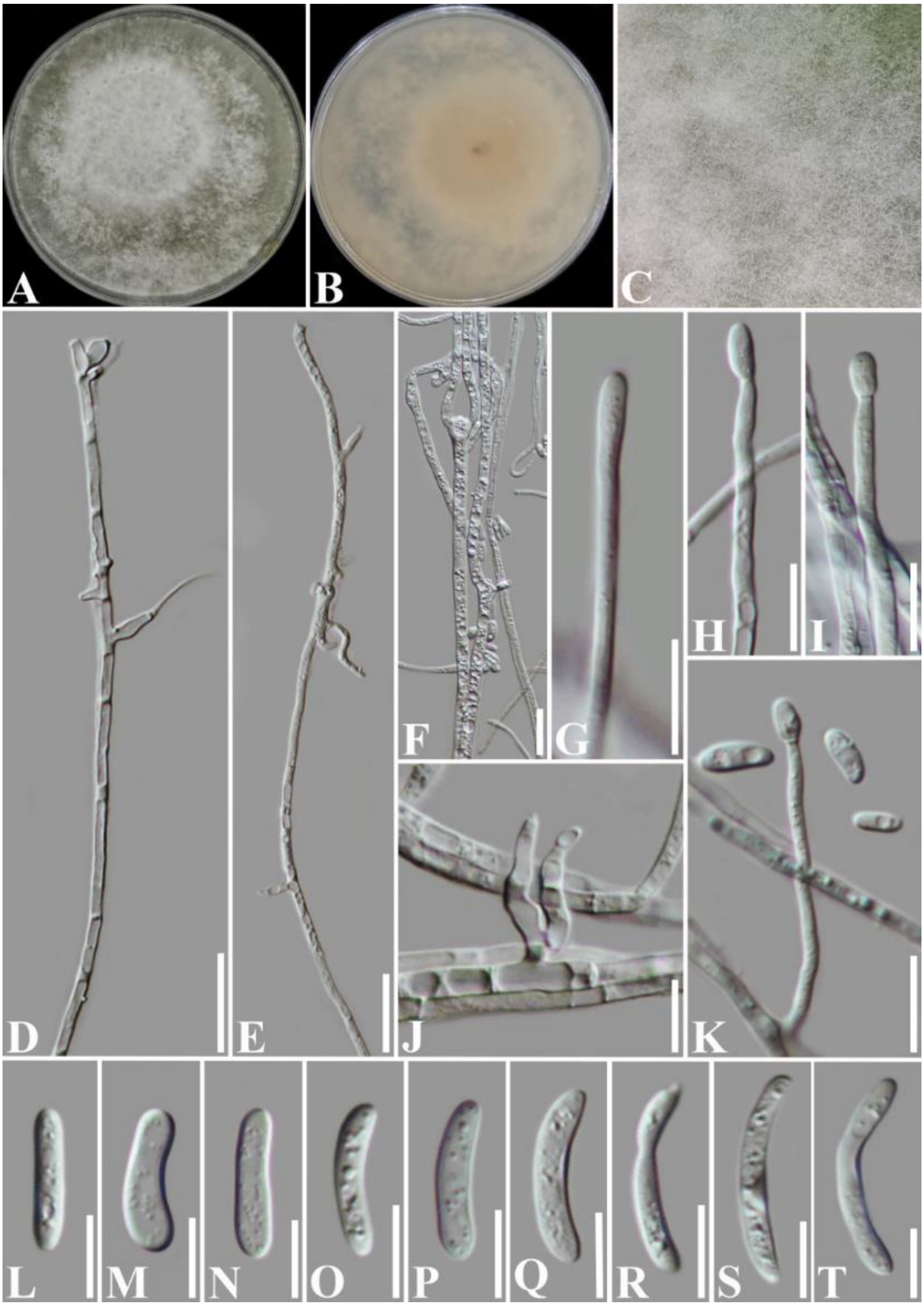

Figure 34 – *Fusarium menglaense* (KUMCC 21-0717). A, B Colony on PDA (above and below). C Mycelium on PDA (50 days old culture). D–F Hyphae, conidiogenous cells. G–I, K Conidiogenous cells and Conidia. J Conidiogenous cells. L–T Conidia. Scale bars: D–F = 20 µm, G–T = 10 µm.

Fusarium rhinolophicola Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 35

MycoBank number: MB 844278; Facesoffungi number: FoF 13273

Etymology – Refers to the host genus *Rhinolophus* (*Chiroptera*).

Holotype – HKAS122253.

Asexual morph on PDA: *Vegetative hyphae* septate, branched, hyaline, smooth-walled, 1–12 µm wide. *Conidiophores* sparse on aerial mycelium, straight or flexuous, erect or prostrate, smooth- and thin-walled, branched to unbranched, or reduced to conidiogenous cells borne laterally on hyphae; *Conidiogenous cells* mono- and polyphialidic, phialidic to subcylindrical, geniculate or irregularly bent, smooth- and thin-walled, 5–65 × 1–7 µm, without periclinal thickening. *Microconidia* 2–31 × 2–10 µm ($\bar{x}$ =10.85 × 3.55 µm, n = 60), oblong, reniform to lunate, or contracted at one end, hyaline, aseptate, granulate, walls smooth and thin. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 45–60 mm after 17 days at room temperature (20–25 °C), with undulate edge, white, sparse aerial mycelium on the surface; reverse pale yellow. The white reproductive mycelium covers the stromatic colonies after 50 days. Odor absent.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, *Rhinolophus malayanus* wing surface in limestone forest, 101.271563 E, 21.918897 N, 15 July 2020, Alice Hughes, 38-B, (holotype, HKAS122253), ex-type KUMCC 21-0449; *ibid*., 38, ex-isotype KUMCC 21-0448; *ibid*., 38-C, ex-isotype KUMCC 21-0450.

GenBank numbers – KUMCC 21-0449 = ITS: ON426848, *CAM*: OR022061, *RPB1*: OR022020, *RPB2*: OR025917, *TUB*: OR025946, *TEF 1-α*: OR026001; KUMCC 21-0448 = ITS: ON426847, *CAM*: OR022062, *RPB1*: OR022021, *RPB2*: OR025918, *TUB*: OR025947, *TEF 1-α*: OR026002; KUMCC 21-0450 = ITS: ON426849, *CAM*: OR022063, *RPB1*: OR022022, *RPB2*: OR025919, *TUB*: OR025948, *TEF 1-α*: OR026003.

Notes – In our phylogenetic analyses, *Fusarium rhinolophicola* clusters sister to *F. hainanense* M.M. Wang, Qian Chen & L. Cai with 78% ML and 1.00 BYPP statistical support (Fig. 10). In the phylogenetic analyses based on the five-loci combined dataset (ITS, *TEF-1α*, *CAM*, *RPB1* and *RPB2*), the new species clustered within the *F. incarnatum-equiseti* species complex (Sandoval-Denis et al. 2018, Wang et al. 2019, Crous et al. 2021). However, the sequences of the new species (KUMCC 21-0449, type) are different compared with *F. hainanense* (LC11638, type) in 3/572 bp of ITS, 1/647 bp of the *CAM*, 28/1201 bp of *RPB2*, 40/1607 bp of *RPB1*, and 16/636 bp of *TEF1-α* (Supplementary Table 4). Morphologically, *F. rhinolophicola* differs from *F. hainanense* by having oblong, reniform to lunate microconidia, while the latter has falcate to fusiform macroconidia (Supplementary Table 3) (Wang et al. 2019). Based on the phylogeny and morphology, *F. rhinolophicola* is described here as a distinct new species.

Fusarium xishuangbannaense Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 36

MycoBank number: MB 845351; Facesoffungi number: FoF 13274

Etymology – Named after the location Xishuangbanna, where the holotype was collected.

Holotype – HKAS122815.

Asexual morph on PDA: *Vegetative hyphae* septate, branched, hyaline, smooth-walled, 1–3 µm wide. *Conidiophores* with holoblastic to phialidic, solitary or occurring in dense lateral clusters, subsphaerical at base, 3–6 µm wide; *Conidiogenous cells* sympodially branched, tapering at the neck into a long, slender, denticulate rachis, geniculate or irregularly bent, 12–36 × 1–4 µm. *Microconidia*, 2–36 × 1–3 µm ($\bar{x}$ =2.7 ×3.6 µm, n = 30), oblong, reniform to lunate, or contracted at one end, hyaline, aseptate, granulate, smooth and thin walls. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 50–60 mm after 15 days at room temperature (20–25 °C), with undulate edge, white, sparse aerial mycelium on the surface; reverse pale yellow. The white reproductive mycelium covers the stromatic colonies after 65 days. Odor absent.

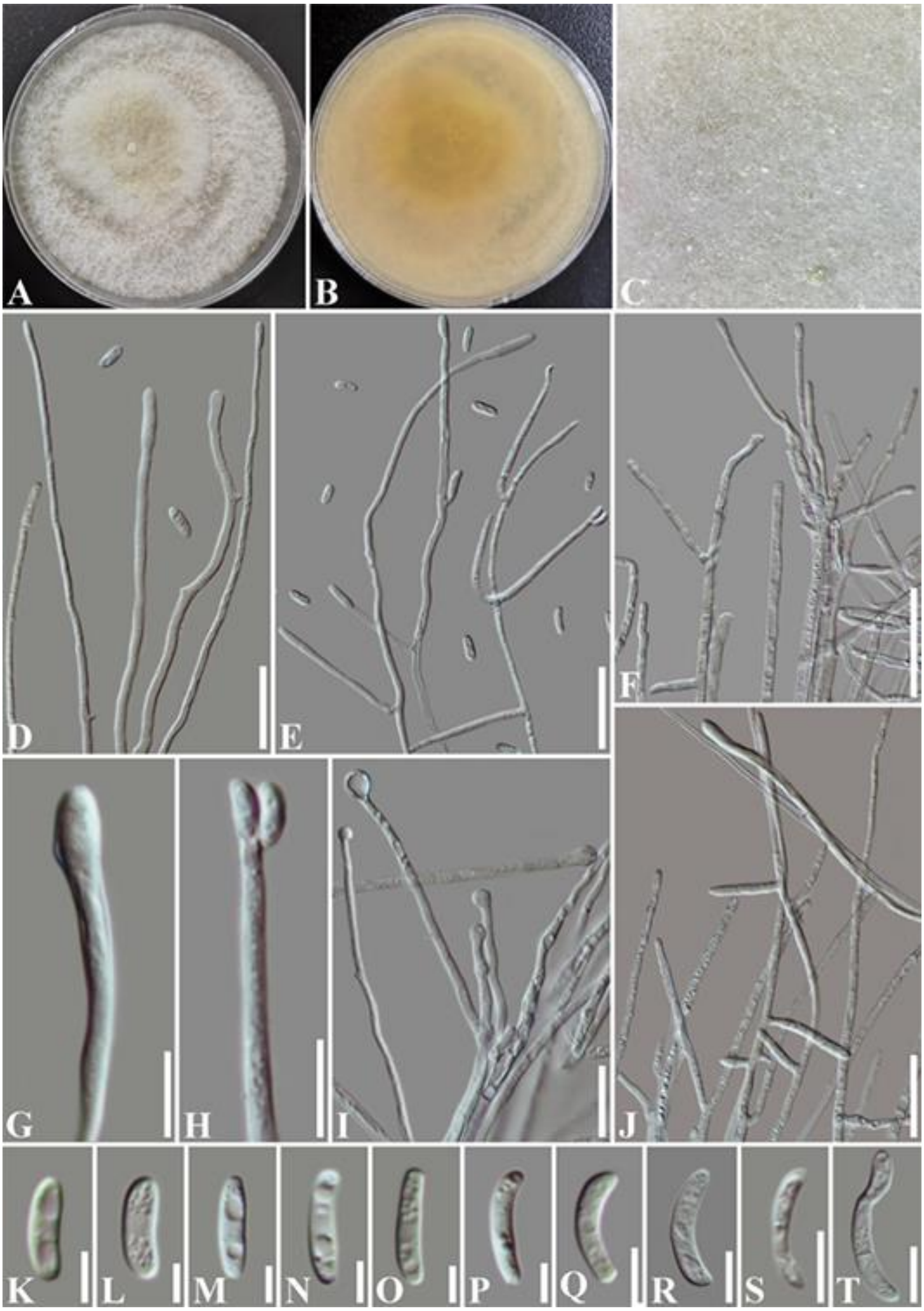

Figure 35 – *Fusarium rhinolophicola* (KUMCC 21-0449). A, B Colony on PDA (above and below). C Mycelium on PDA (50 days old culture). D–J Hyphae, conidiogenous cells and conidia. K–T Microconidia. Scale bars: D = 50 μm, E = 30 μm, F = 15 μm, G–J, P–T = 10 μm, K–O = 5 μm.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, *Rhinolophus malayanus* wing surface, in limestone forest, 101.282404 E, 21.907599 N, 15 July 2020, Alice Hughes, 55-A, (**holotype**, HKAS122815), ex-type KUMCC 21-0432; *ibid*., 55-D, ex-isotype KUMCC 21-0731.

GenBank numbers – KUMCC 21-0432 = ITS: ON426859, *CAM*: OR022064, *RPB1*: OR022023, *RPB2*: OR025920, *TUB*: OR025949, *TEF 1-α*: OR026004; KUMCC 21-0731 = ITS: ON426860, *CAM*: OR022065, *RPB1*: OR022024, *RPB2*: OR025921, *TUB*: OR025950, *TEF 1-α*: OR026005.

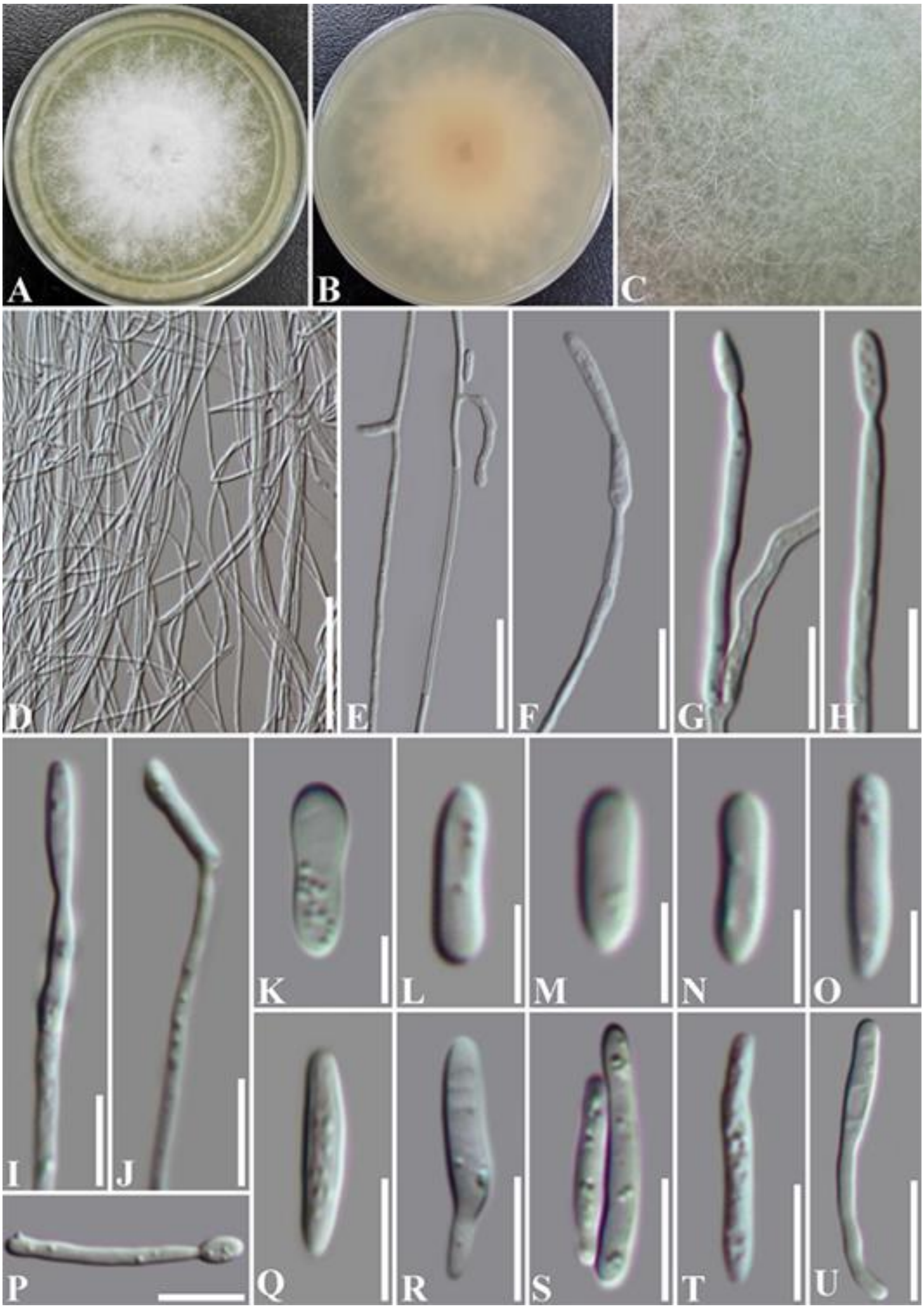

Figure 36 – *Fusarium xishuangbannaense* (KUMCC 21-0432). A, B Colony characteristics on PDA (above and below). C Mycelium on PDA (65 days old culture). D Hyphae. E–J, P Conidiogenous cells and conidia. K–O, Q–U Microconidia. Scale bars: D = 50 µm, E = 30 µm, F, U = 15 µm, G–J, P–T = 10 µm, K–O = 5 µm.

Notes – *Fusarium xishuangbannaense* is phylogenetically closely related to *F. annulatum*, *F. fujikuroi* and *F. siculi* Sand.-Den., Guarnaccia & Polizzi in the *F. fujikuroi* species complex (Sandoval-Denis et al. 2018, Wang et al. 2019, Crous et al. 2021). Based on the sequence comparisons, *F. xishuangbannaense* (KUMCC 21-0432, type) is different from *F. annulatum* (CBS 258.54, type), *F. fujikuroi* (CBS 221.76, type), *F. globosum* (CBS 428.97, type), and *F. siculi* (CBS 142222, type) (Supplementary Table 4). *Fusarium xishuangbannaense* differs from *F. annulatum* by the latter having clavate microconidia (Yilmaz et al. 2021). *Fusarium xishuangbannaense* differs from *F. fujikuroi* by the latter having smaller aseptate microconidia (2–36 × 1–3 µm vs 5–13 × 2.1–4.7 µm) (Supplementary Table 3) (Choi et al. 2011). *Fusarium xishuangbannaense* is different from *F. globosum* by the latter having shorter, variable in shape microconidia (2–36 × 1–3 µm vs 8–20 × 2–4.5 µm) and shorter conidiogenous cells (12–36 × 1–4 µm vs 10–20 × 3–4 µm) with periclinal thickening (Supplementary Table 3) (Rheeder et al. 1996). *Fusarium xishuangbannaense* is different from *F. siculi* by the latter having peach to pale rose colony, smaller subulate to subcylindrical conidiogenous cells (12–36 × 1–4 µm vs 16.5–33.5 × 2–4 µm) and smaller microconidia (2–36 × 1–3 µm vs (5.3–)8.5–12.3(–16.8) × (2.3–)2.9–3.5(–3.8) µm) (Supplementary Table 3) (Sandoval-Denis et al. 2018). Based on the phylogeny and morphology, *F. xishuangbannaense* is described as a new species.

Fusarium yunnanense Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 37

MycoBank number: MB 845352; Facesoffungi number: FoF 13275

Etymology – Refers to Yunnan Province where the holotype was collected.

Holotype – HKAS122803.

Asexual morph on PDA: *Vegetative hyphae* septate, branched, hyaline, smooth-walled, 1–9 µm wide. *Conidiophores* sparse on aerial mycelium, straight or flexuous, erect or prostrate, smooth- and thin-walled, 90–210 µm, branched to unbranched, or reduced to conidiogenous cells borne laterally on hyphae; *Conidiogenous cells* mono- and polyphialidic, phialidic to subcylindrical, geniculate or irregularly bent, smooth- and thin-walled, 6–45 × 1–6 µm, without periclinal thickening. *Microconidia* 5–28 × 1–5 µm ($\bar{x}$ = 10.32 × 3.33 µm, n = 60), falcate, oblong, reniform to lunate, or contracted at one end, hyaline, 0–1-septate, granulate, walls smooth and thin. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 55–60 mm after 18 days at room temperature (20–25 °C), with undulate edge, white, sparse aerial mycelium on the surface; reverse pale yellow. The white reproductive mycelium covers the stromatic colonies after 50 days. Odor absent.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, *Rhinolophus malayanus* in limestone forest, 101.271563 E, 21.918897 N, 15 July 2020, Alice Hughes, 39-A, (**holotype**, HKAS122810), ex-type KUMCC 21-0732; *ibid*., 39-C, ex-isotype KUMCC 21-0733.

GenBank numbers – KUMCC 21-0732 = ITS: ON426851, *CAM*: OR022066, *RPB1*: OR022025, *RPB2*: OR025922, *TUB*: OR025951, *TEF 1-α*: OR026006; KUMCC 21-0733 = ITS: ON426853, *CAM*: OR022067, *RPB1*: OR022026, *RPB2*: OR025923, *TUB*: OR025952, *TEF 1-α*: OR026007.

Notes – In the multigene phylogenetic analyses, *Fusarium yunnanense* clustered in a well-separated clade with 99% ML and 1.00 BYPP statistical support (Fig. 10). Our strains formed a new species complex (*F. yunnanense* species complex) sister to *F. tricinctum* species complex, *F. sambucinum* species complex and *F. heterosporum* species complex (Sandoval-Denis et al. 2018, Wang et al. 2020). Morphologically, *F. yunnanense* is different from the type of *F. tricinctum* species complex (*F. tricinctum* (Corda) Sacc.) by the latter having a white to rose colony surface and smaller microconidia (5–28 × 1–5 µm vs 5–9.4 × 1.2–20 µm) (Supplementary Table 3) (Chen et al. 2017). *Fusarium yunnanense* differs from the type of *F. sambucinum* species complex (*F. sambucinum*) by having a white to red colony surface and chlamydospores (Supplementary Table 3) (Chehri et al. 2010, Erper et al. 2021). *Fusarium yunnanense* is different from the type of *F.*

heterosporum species complex (*F. heterosporum* Nees & T. Nees) by the latter having white to pink colony surface, smaller conidiogenous cells (6–45 × 1–6 µm vs 10–20 × 2.5–3.5 µm) and sparse chlamydospores (Supplementary Table 3) (Fungi of Great Britain and Ireland 2022). Based on the phylogeny and morphology, *F. yunnanense* is described as a distinct new species.

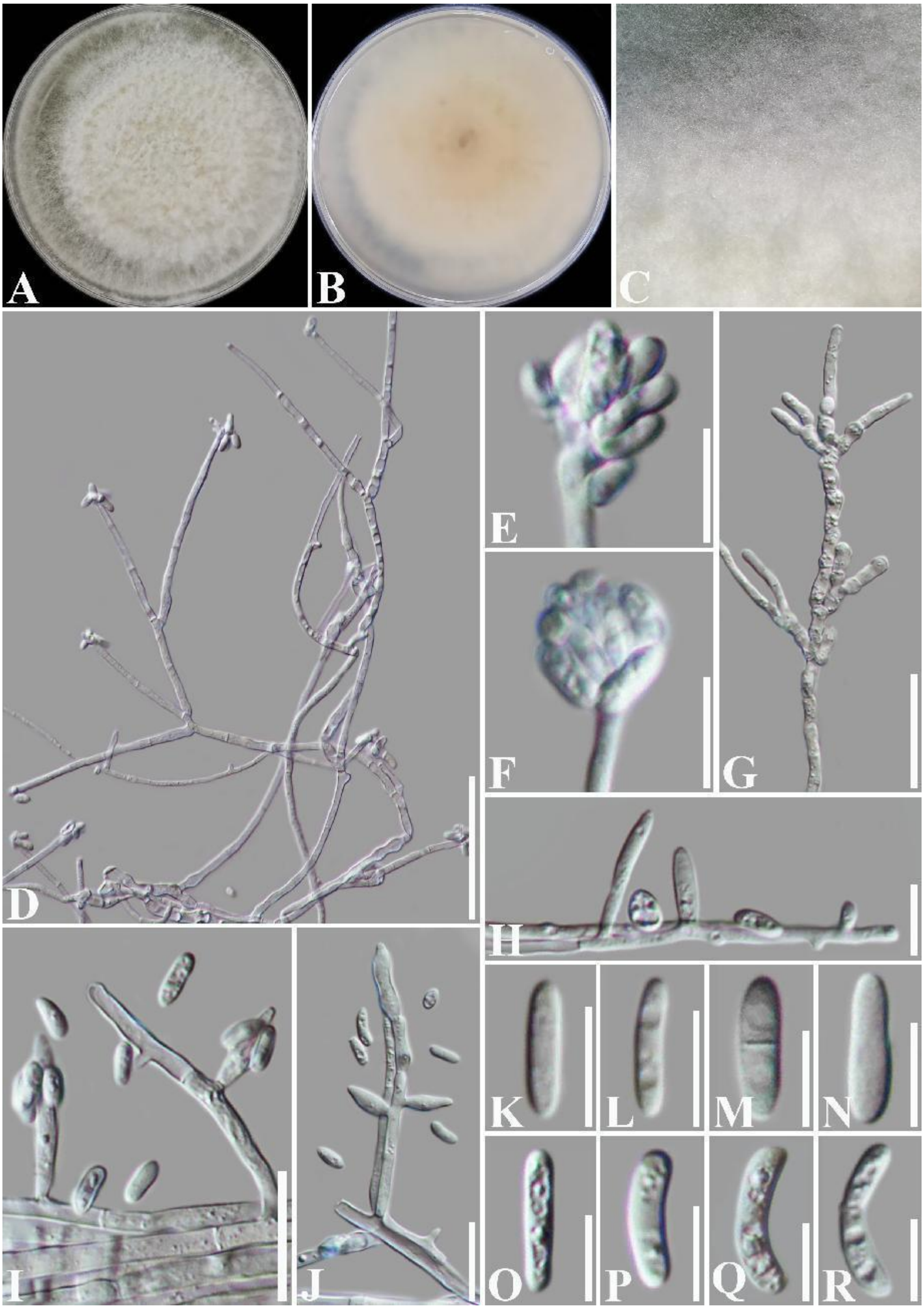

Figure 37 – *Fusarium yunnanense* (KUMCC 21-0732). A, B Colony on PDA (above and below). C Mycelium on PDA (50 days old culture). D, G Hyphae, conidiogenous cells. E, F Conidiophores.

H–J Conidiogenous cells and Microconidia. K–R Microconidia. Scale bars: D–F = 20 μm, G–T = 10 μm.

Microascales Luttr. ex Benny & R.K. Benj.

Microascaceae Luttr. ex Malloch

Microascaceae was introduced by Malloch (1970) with *Microascus* as the type genus. But this family was first circumscribed in 1951 by Luttrell to accommodate *Microasctts* Zukal in the new order *Microascales* Luttr. ex Benny & R.K. Benj. (Malloch 1970, Hyde et al. 2020). Then Malloch (1970) validated and formally proposed the new concept of the family *Microascaceae* based on past research. There are 290 species belonging to 23 genera in *Microascaceae*, according to the latest publication by Wijayawardene et al. (2022).

Scopulariopsis Bainier

Scopulariopsis (*Sco*.) was erected by Bainier (1907) with *Sco*. *brevicaulis* Bainier as the type. This genus is characterized by its globose or subglobose, annellidic conidia with a truncate base arranged in a chain and frequently branched conidiophores mostly restricted to the apical region (Pan et al. 2014). The species of *Scopulariopsis* are mostly saprogenous, widely distributed in soil, fibrous matters, air, bats, and are important for cellulose degradation and humus formation (Morton & Smith 1963, Vanderwolf et al. 2013b, Pan et al. 2014, Woudenberg et al. 2017, Ogórek et al. 2020). However, some species of *Scopulariopsis* are conditional pathogens of animals and humans, which can cause tinea unguium (Pan et al. 2014). In this study, a new record of *Scopulariopsis brevicaulis* is introduced (Fig. 38).

Scopulariopsis brevicaulis (Sacc.) Bainier, Bulletin de la Société Mycologique de France 23: 99 (1907) Fig. 38

MycoBank number: MB 154310; Facesoffungi number: FoF 09619

Asexual morph on PDA: *Vegetative hyphae* 1–7 μm wide, branched, hyaline, septate, smooth-walled. *Conidiophores* arising from substrate mycelium, simple to indistinctive. *Conidiogenous cells* annellidic, cylindrical to slight ampulliform, 9–30 × 1–6 μm, single, hyaline, smooth-walled. *Conidia* 3–9 × 3–8 μm ($\bar{x}$ = 6.53 × 5.83 μm, n = 100), globose to subglobose, with truncate base, rounded at top, hyaline to yellowish brown, spinulose on surface, thick-walled, arranged in chains, with a disjuncture between adjacent conidia. Sexual morph: Undetermined.

Culture characteristics – Colony growth on PDA, 15–38 mm diam. after 15 days at room temperature (20–25 ℃), folded, white to light yellow, margin undulate to erose to fimbriate. Conidiophores arise from the colony, yellowish brown after 50 days.

Substrata – Air biofilter, alkaline soil, archive, *Arge berberidis* pupa, bone, elephant, hat rack, human BAL, human blood, human hair, human lung mass, human nail, human skin, human spine, human sputum, human toe, human toenail, indoor, indoor air, indoor bakery, plaster, *Pteronus pini* pupa, soil, tattoo-paint and wall paper.

Distribution – Canada, Czech Republic, Denmark, France, Germany, Mexico, Netherlands, Poland, Russia, South Africa, UK and USA.

Material examined – China, Yunnan Province, Yuxi, Yimen County, Pubei Village, Shiliansi, *Rhinolophus siamensis* wing surface, in limestone forest, 24.61746 N, 102.1633 E, 21 September 2020, Alice Hughes, YM-18-W2 (HKAS122262), living culture KUMCC 21-0444; *ibid*., YM-18-W2-2, living culture KUMCC 21-0445; *ibid*., YM-18-W5, living culture KUMCC 21-0446; *ibid*., YM-18-W5-2, living culture KUMCC 21-0447.

GenBank numbers – KUMCC 21-0444 = ITS: ON426887, LSU: OP363284, *TUB*: OR025953, *TEF 1-α*: OR026008; KUMCC 21-0445 = TS: ON426888, LSU: OP363285, *TUB*: OR025954, *TEF 1-α*: OR026009; KUMCC 21-0446 = ITS: ON426889, LSU: OP363286, *TUB*: OR025955, *TEF 1-α*: OR026010; KUMCC 21-0447 = ITS: ON426890, LSU: OP363287, *TUB*: OR025956, *TEF 1-α*: OR026011.

Notes – *Scopulariopsis brevicaulis* was introduced by Bainier (1907) as the type species of *Scopulariopsis*. Based on multi-gene phylogenetic analyses, our isolates clustered with *Sco. brevicaulis* and close to *Sco. alboflavescens* Zach and *Sco. albida* Woudenb. & Samson. Morphologically, the new isolates are similar to the *Sco. brevicaulis* by having similar powdery to floccose, cream-coloured to brownish colonies, slightly long cylindrical conidiogenous cells, spherical to obovoidal or bullet-shaped, rough-walled conidia, with truncate base, arranged in chains (Bainier 1907, Pan et al. 2014). *Scopulariopsis brevicaulis* differed from *Sco. alboflavescens* by the latter having smooth-walled conidia (Jagielski et al. 2016). *Scopulariopsis brevicaulis* differed from *Sco. albida* by longer conidiogenous cells (9–30 × 1–6 µm vs (6–)8.5–19.5(–29.5) × (2.5–) 3–5(5.5) µm) and slightly bigger conidia (3–9 × 3–8 µm vs (5–)6.5–8(–8.5) × (6–)6.5–7.5(–8) µm) (Supplementary Table 3) (Woudenberg et al. 2017). Based on phylogeny and morphology, the new isolates are identified as *Sco. brevicaulis*. This is the first report of *Sco. brevicaulis* isolated from bats in China.

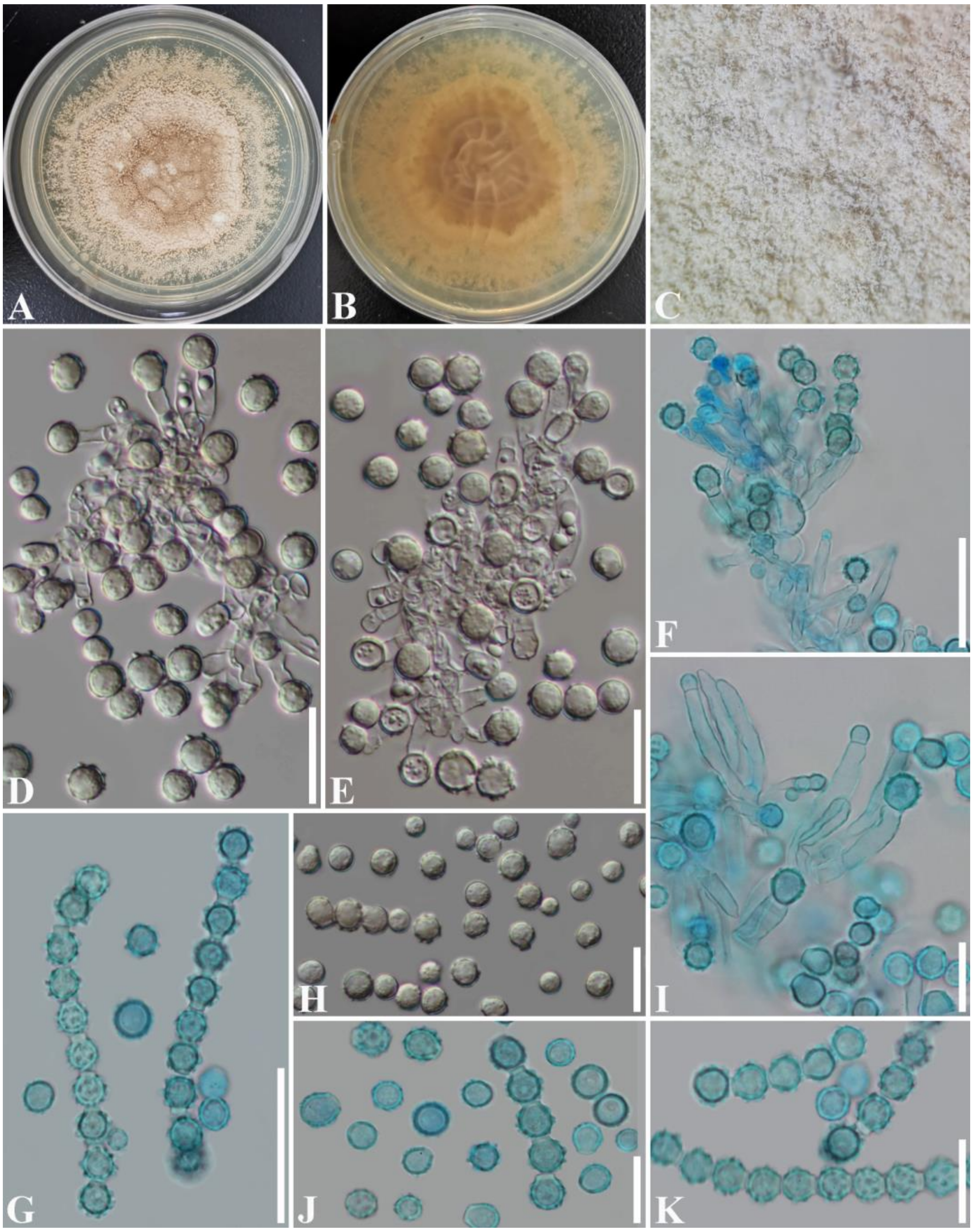

Figure 38 – *Scopulariopsis brevicaulis* (KUMCC 21-0444). A, B Colony on PDA (above and below). C Conidiophores arise from the colony (60 days old culture). D–F, I Conidiophores,

annellides and conidia. G, H, J, K Conidia (F, G, I–K strained with cotton blue reagent). Scale bars D, E, H = 20 µm, F, G = 30 µm, I–K = 10 µm.

Sordariomycetes genera *incertae sedis*

Phialemoniopsis Perdomo, Dania García, Gené, Cano & Guarro

Phialemoniopsis (*Ph.*) was erected by Perdomo et al. (2013) with *Ph. ocularis* (Gené & Guarro) Perdomo, Dania García, Gené & Guarro as the type species. The genus currently includes seven species, viz., *Phialemoniopsis cornearis* Perdomo et al., *Ph. curvata* (W. Gams & W.B. Cooke) Perdomo, Dania García, Gené, Cano & Guarro, *Ph. endophytica* Lei Su & Y.C. Niu, *Ph. hongkongensis* C.C.C. Tsang et al., *Ph. limonesiae* A. Riat, L.W. Hou & Crous, *Ph. ocularis* and *Ph. pluriloculosa* Perdomo et al. (Perdomo et al. 2013, Tsang et al. 2014, Su et al. 2016, Martinez et al. 2021). The asexual morph of *Phialemoniopsis* is characterized by vegetative hyphae hyaline to brown, smooth- to rough-walled; conidiogenesis enteroblastic; conidiophores simple or slightly branched, hyaline or pale brown; conidiogenous cells monophialidic, discrete, terminal or lateral, cylindrical to flask-shaped, straight to slightly flexuose, or intercalary with a cylindrical lateral projection; pycnidium-like conidiomata superficial or semi-immersed, uni- or multilocular, globose, subglobose, ellipsoidal or pyriform, surrounded by a thin wall of several layers; walls of *textura intricata* or *textura epidermoidea* or both with irregular dehiscence; usually have setae; conidia one-celled, ellipsoidal, allantoid to obovoid, and slightly apiculate at the base, hyaline to subhyaline, smooth-walled, aggregated in slimy heads; and the sexual morph unknown (Perdomo et al. 2013, Tsang et al. 2014, Su et al. 2016, Martinez et al. 2021). Since the *Phialemoniopsis* was introduced in 2013, seven species have been reported, six of which have been isolated from human fluids, forearm, nails or skin, and only *Ph. endophytica* was isolated from plants (Perdomo et al. 2013, Tsang et al. 2014, Su et al. 2016, Martinez et al. 2021). We describe *Phialemoniopsis hipposiderocola* sp. nov. and *Ph. xishuangbannaensis* sp. nov. in this study (Figs 39, 40).

Phialemoniopsis hipposidericola Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 39

MycoBank number: MB 845357; Facesoffungi number: FoF 13276

Etymology – Refers to the host genus *Hipposideros* (*Chiroptera*).

Holotype – HKAS122833.

Asexual morph on PDA: Aerial mycelium floccose. *Vegetative hyphae* septate, branched, hyaline, smooth-walled, 1–5 µm wide. *Conidiophores* arising from submerged or superficial hyphae, erect or suberect, simple or branched, bearing 1–3 levels with 1–2 phialides per node, lateral or terminal, 4–16 µm long, 1–4 µm wide at the base, hyaline, smooth-walled, with cell walls usually slight thicker than those of the vegetative hyphae. *Conidiogenous cells* 4–15 × 1–5 µm (x̄ = 7.95 ×2.81 µm, n = 30), terminal or lateral, straight to slightly flexuose, cylindrical, with a distinct periclinal thickening at the conidiogenous locus, hyaline, smooth-walled. *Conidia* 2–8 × 1–5 µm (x̄ = 5.07 ×2.59 µm, n = 60), ellipsoidal to cylindrical, or reniform, 0–1-septate, hyaline, smooth-walled, not arranged in long chains, guttulate. *Chlamydospores* not observed. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 15–40 mm after 20 days at room temperature (20–25 °C), with undulate edge, white, sparse aerial mycelium on the surface; reverse pale yellow. The white reproductive mycelium covers the stromatic colonies after 65 days. Aerial mycelium floccose. Odor present.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, *Hipposideros larvatus* in limestone forest, 101.282404 E, 21.907599 N, 15 July 2020, Alice Hughes, 62-D, (**holotype**, HKAS122833), ex-type KUMCC 21-0778; *ibid*., 62-D2, ex-isotype KUMCC 21-0779.

GenBank numbers – KUMCC 21-0778 = ITS: ON426882, LSU: OP363279, *Act*: OQ930298, *TUB*: OR025957; KUMCC 21-0779 = ITS: ON426886, LSU: OP363283, *Act*: OQ930299, *TUB*: OR025958.

Notes – *Phialemoniopsis hipposidericola* formed a separate clade in the phylogenetic analyses with 93% ML and 1.00 BYPP statistical support and is closely related to *Ph. pluriloculosa*, *Ph. endophytica* and *Ph. xishuangbannaensis*. Based on sequence comparisons, *Ph. hipposidericola* differs from *Ph. pluriloculosa*, *Ph. endophytica* and *Ph. xishuangbannaensis* (Supplementary Table 4). Morphologically, *Ph. pluriloculosa* is distinct from *Ph. hipposidericola* by having multilocular, globose to subglobose, pycnidium-like conidiomata with marginal setae, smaller, ellipsoidal conidia (2–3 × 1–1.5 µm vs 2–8 × 1–5 µm), and subglobose, oval to pyriform chlamydospores in chains (Supplementary Table 3) (Perdomo et al. 2013). *Phialemoniopsis endophytica* is distinct from *Ph. hipposidericola* by having globose to subglobose or ovoid, pycnidium-like conidiomata, smaller conidia (2–3.5 × 1–2 µm vs 2–8 × 1–5 µm) and ellipsoidal to ovoid chlamydospores (Supplementary Table 3) (Su et al. 2016). This is the first report of *Phialemoniopsis* species from bats in China. *Phialemoniopsis xishuangbannaensis* is distinct from *Ph. hipposidericola* by the latter having white colonies, smaller conidiogenous cells (5–46 × 1–8 µm vs 4–15 × 1–5 µm) and bigger conidia (3.1–5.8 × 1.3–3.4 µm vs 2–8 × 1–5 µm) (Supplementary Table 3). Both *Ph. xishuangbannaensis* and *Ph. hipposidericola* were isolated from bats (*Hipposideros larvatus*). The phylogeny and morphology results support *Ph. hipposidericola* as a distinct new species.

Phialemoniopsis xishuangbannaensis Karun., Tibpromma & X.F. Liu, sp. nov. Fig. 40

MycoBank number: MB 845358; Facesoffungi number: FoF 13277

Etymology – Named after the location Xishuangbanna, where the holotype was collected.

Holotype – HKAS122832.

Asexual morph on PDA: *Vegetative hyphae* septate, branched, hyaline to brown, smooth-walled, 1–11 µm wide. *Conidiophores* arising from submerged or superficial hyphae, erect or suberect, simple or branched, bearing 1–4 levels with 1–3 phialides per node, lateral or terminal, 40–150 µm long, 1–9 µm wide at the base, hyaline, smooth-walled, with cell walls usually slight thicker than those of the vegetative hyphae. *Conidiogenous cells* 5–46 × 1–8 µm (x̄ =7.95 ×2.81 µm, n = 30), terminal or lateral, straight to slightly flexuose, cylindrical, phialidic, with a distinct periclinal thickening at the conidiogenous locus, 1–2- guttulate, hyaline, smooth-walled. *Conidia* one-celled, 3–6 × 1–4 µm (x̄ = 4.33 ×2.33 µm, n = 100), ellipsoidal to cylindrical, or reniform with distinct connectives on both ends, hyaline, smooth. *Chlamydospores* present, unicellular, ellipsoidal to ovoid, or irregular, 2–16 × 1–11 µm (x̄ = 5.72 × 4.29 µm, n = 60). Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 15–38 mm after 6 days at room temperature (20–25 °C), with undulate edge, white to brown/black, sparse aerial mycelium on the surface; reverse black pale yellow. Aerial mycelium floccose. The white to brown reproductive mycelium covers the stromatic colonies after 30 days. Odor present.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, *Hipposideros larvatus* in limestone forest, 101.282404 E, 21.907599 N, 15 July 2020, Alice Hughes, 62-C, (**holotype**, HKAS122827), ex-type KUMCC 21-0774; *ibid*., 62-G, ex-isotype KUMCC 21-0775; *ibid*., 62-G1, ex-isotype KUMCC 21-0776; *ibid*., 62-E, ex-isotype KUMCC 21-0777.

GenBank numbers – KUMCC 21-0774 = ITS: ON426881, LSU: OP363278, *Act*: OQ930300, *TUB*: OR025959; KUMCC 21-0775 = ITS: ON426884, LSU: OP363281, *Act*: OQ930301, *TUB*: OR025960; KUMCC 21-0776 = ITS: ON426885, LSU: OP363282, *Act*: OQ930302, *TUB*: OR025961; KUMCC 21-0777 = ITS: ON426883, LSU: OP363280, *Act*: OQ930303, *TUB*: OR025962

Notes – *Phialemoniopsis xishuangbannaensis* formed a distinct clade, closely related to *Ph. pluriloculosa* and *Ph. hipposidericola* in the phylogeny. Based on the sequence comparisons, *Ph. xishuangbannaensis* is different from *Ph. pluriloculosa* in 0.42% (2/471 bp) of ITS, 0.19% (1/536 bp) of LSU, 0.85% (6/705 bp) of *Act* and 0.33% (5/375 bp) of *TUB* (Supplementary Table 4). *Phialemoniopsis xishuangbannaensis* is different from *Ph. hipposiderocola* in 1.94% (11/568 bp) of ITS, 2.09% (19/909 bp) of LSU, 4.26% (24/564 bp) of *TUB* (Supplementary Table 4).

Morphologically, *Ph. xishuangbannaensis* is distinct from *Ph. pluriloculosa* by the latter having multilocular, pycnidium-like conidiomata, subglobose, smaller, subcylindrical phialides (5–46 × 1–8 µm vs 6–12 × 1–1.5 µm), smaller conidia (3–6 × 1–4 µm vs 2–3 × 1–1.5 µm), and oval to pyriform chlamydospores (2–16 × 1–11 µm vs 5–9 × 4–6 µm) (Supplementary Table 3) (Perdomo et al. 2013). *Phialemoniopsis pluriloculosa* has been reported as a pathogen from human toenails and synovial fluid (Perdomo et al. 2013). Based on the phylogenetic analyses and morphological characteristics, *Ph. xishuangbannaensis* is described as a distinct new species.

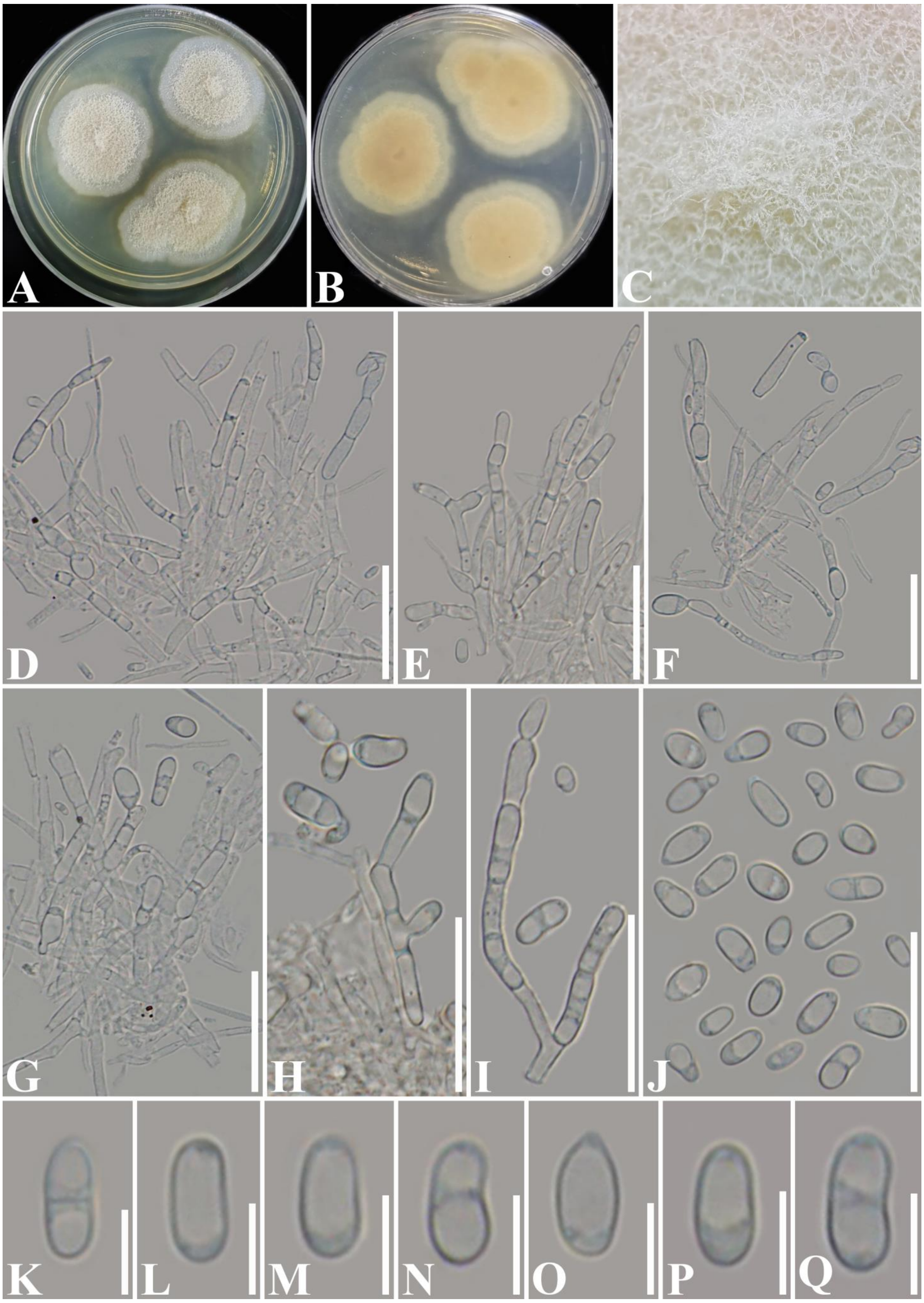

Figure 39 – *Phialemoniopsis hipposidericola* (KUMCC 21-0778). A, B Colonies on PDA (above and below). C Mycelium on PDA (90 days old culture). D–I Conidiophores. J–Q Conidia. Scale bars: D–J = 20 µm, K–Q = 5 µm.

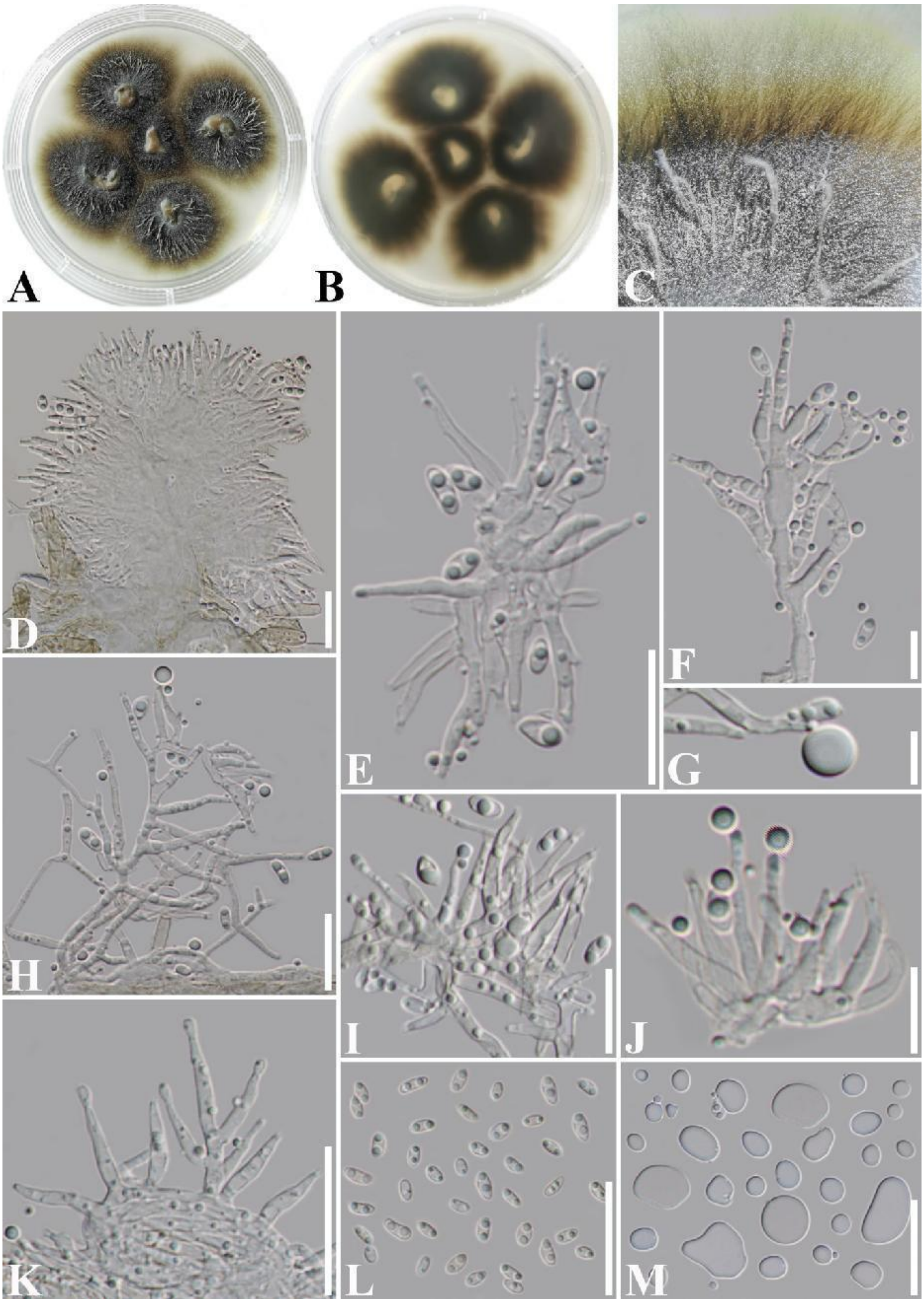

Figure 40 – *Phialemoniopsis xishuangbannaensis* (KUMCC 21-0774). A, B Colonies on PDA (above and below). C Mycelium on PDA (40 days old culture). D–F, H–K Conidiophores. L Conidia. G, M Chlamydospores. Scale bars: D–F, H, K–M = 20 µm, G = 5 µm, I, J = 10 µm.

Discussion

In recent years, bats have received extensive and special attention due to the human pathogenic viruses they carry, but fungi associated with bats have been poorly studied (Cunha et al. 2020, Karunarathna et al. 2020). Bat-associated fungi mainly originate from bat roosting areas and cave environments, due to bat foraging behavior, and bat migration routes. Stable mild temperatures, high humidity and abundant sources of organic matter make bat roosts and cave environments ideal for fungal growth (Zhang et al. 2017, 2020). In addition, bats constantly move between caves, forests, farmland and human settlements during their daily and seasonal activities, which provide opportunities for exposure and transmission of fungi (Cleveland et al. 2006, Muscarella & Fleming 2007, Jiang et al. 2020).

There are 370 fungal and five fungus-like organisms recorded from live bats and 33 species from dead bats, with data coming from 18 countries, 13 studies and 34 bat species (Fig. 41, Supplementary Table 5) (Voyron et al. 2011, Nováková et al. 2012, 2018, Vanderwolf et al. 2013a, b, 2016, Holz et al. 2018, Lorch et al. 2018, Cunha et al. 2020, Karunarathna et al. 2020, Ogórek et al. 2020, Kim et al. 2023). Australia and Canada have the highest number of recorded fungal species associated with bats, followed by Brazil, Slovakia, USA, Italy and China. However, these numbers are more strongly associated with the number of studies conducted in the respective regions, and not necessarily on the diversity of fungi. The dominant fungal groups associated with bats in these studies were *Aspergillus* and *Penicillium*, both of which comprise pathogenic as well as saprophytic fungal groups. Given that over 1400 bat species have been described, and as much as over 40% remain undescribed in some groups (Chornelia et al. 2022), we estimate that around 97% of bat species have had no study on the fungal diversity that they potentially host. In this study, we documented 164 fungal strains representing 25 culturable fungal species, of which 14 are new to science, while 11 are new host records. We found up to eight fungal taxa on a single bat species and an average of three fungal species per bat sampled. It is worth mentioning that these are only the species of fungi that are culturable and fast-growing, and assumed that the fungal species count would be far higher if unculturable and slow growing species were to be included. The high individual load and diversity also demonstrate the potential role played by bats as the host and disperse a diverse range of fungi.

Including the 25 species obtained in our study, we can now report 423 fungal species from five phyla isolated from bats and bat carcasses (Figs 41, 42, Supplementary Table 5). The fungal genera most frequently reported from studies on cave mycology are *Aspergillus* (28), *Penicillium* (27), *Fusarium* (15), *Mortierella* Coem. (13), *Mucor* Fresen. (10), *Cladosporium* Link (9), *Candida* Berkhout (7), *Cryptococcus* Vuill. (7), *Trichosporon* Behrend (7), *Trichoderma* (7), *Oidiodendron* Robak (7), *Chrysosporium* Corda (6) and *Acremonium* Link (5) (Fig. 43, Supplementary Table 5). In previous reports (Voyron et al. 2011, Nováková et al. 2012, 2018, Vanderwolf et al. 2013a, b, 2016, Holz et al. 2018, Lorch et al. 2018, Cunha et al. 2020, Ogórek et al. 2020), *Aspergillus* and *Penicillium* were the most common genera similar to our study, as we found species belonging to *Penicillium* to be the most common fungi. Furthermore, four bat-specific fungal genera were isolated in this study, viz., *Amphichorda*, *Clonostachys*, *Neopestalotiopsis* and *Phialemoniopsis*.

There are approximately 50 pathogens among the 423 known fungi directly associated with bats, many of which are exclusively associated with diseases in animals and humans, some of which have led to death in immunodeficient patients (Voyron et al. 2011, Nováková et al. 2012, 2018, Vanderwolf et al. 2013a, b, 2016, Holz et al. 2018, Lorch et al. 2018, Cunha et al. 2020, Karunarathna et al. 2020, 2023, Ogórek et al. 2020, Kim et al. 2023). Given the wide distribution of bats, we must assess the risk these pathogens pose to human and domestic animal safety and food security (Fisher et al. 2012, Jiang et al. 2020). Limiting human activities in natural landscapes with large numbers of roosting or breeding bats will likely help reduce exposure to potential vectors (Jiang et al. 2020).

Research on bat-associated fungi has mainly been concentrated in Australia, Brazil, Canada, Italy, Poland, Slovakia, the USA and China (Fig. 41, Supplementary Table 5) (Voyron et al. 2011, Nováková et al. 2012, 2018, Vanderwolf et al. 2013a, b, 2016, Holz et al. 2018, Lorch et al. 2018, Cunha et al. 2020, Karunarathna et al. 2020, Ogórek et al. 2020, Kim et al. 2023). Bat-associated fungi were included as a part of cave habitat fungi in previous reports; however, our current study is the first comprehensive taxonomic study conducted using both morphological and phylogenetic analyses of bat-associated fungi, and the study partially fills a gap in bat-associated fungal research, we hope this work will act as a catalyst in driving further research along these lines. The results of our study highlight the hidden diversity of fungi associated with bats and call for enhanced efforts to study these fungi better, as many species likely remain to be described. In addition, we note that many of the fungi we retrieved from the bats during the course of our work could in fact be found as airborne fungi within these environments. Whilst this is the most extensive study conducted on the culturable fungi living on bats to date, we hope to see an expanding focus on these topics whilst also noting that further work will be needed to assess species of fungi living on bats which cannot be cultured, and thus remain unknown at present.

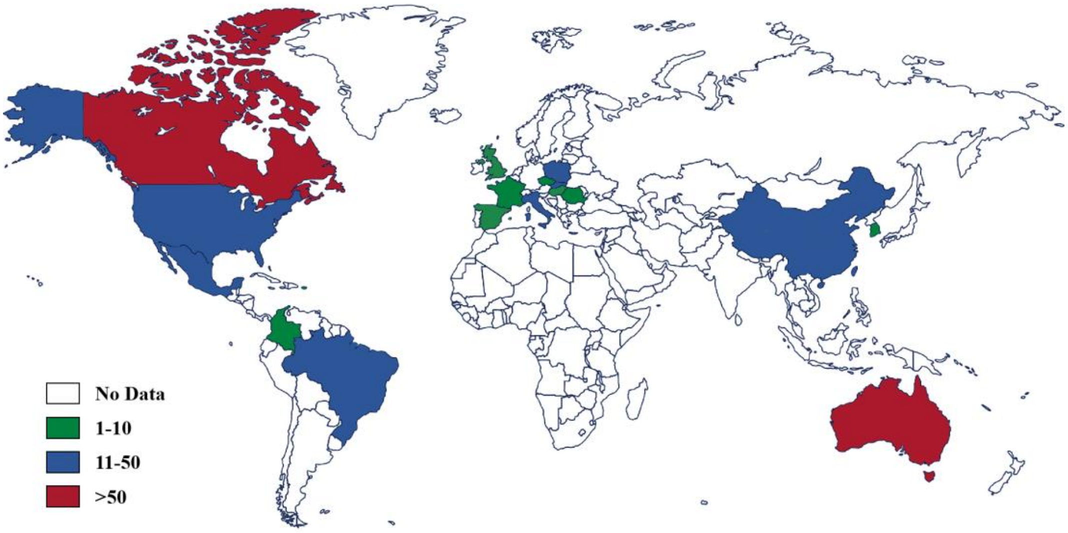

Figure 41 – The distribution of fungal species isolated from bats. Each location was categorized into either: > 50 species, 11–50 species, 1–10 species, or no species data. Source*:* The original map was extracted from the World Map Vector Outline: http://getdrawings.com/world-map-vector-outline

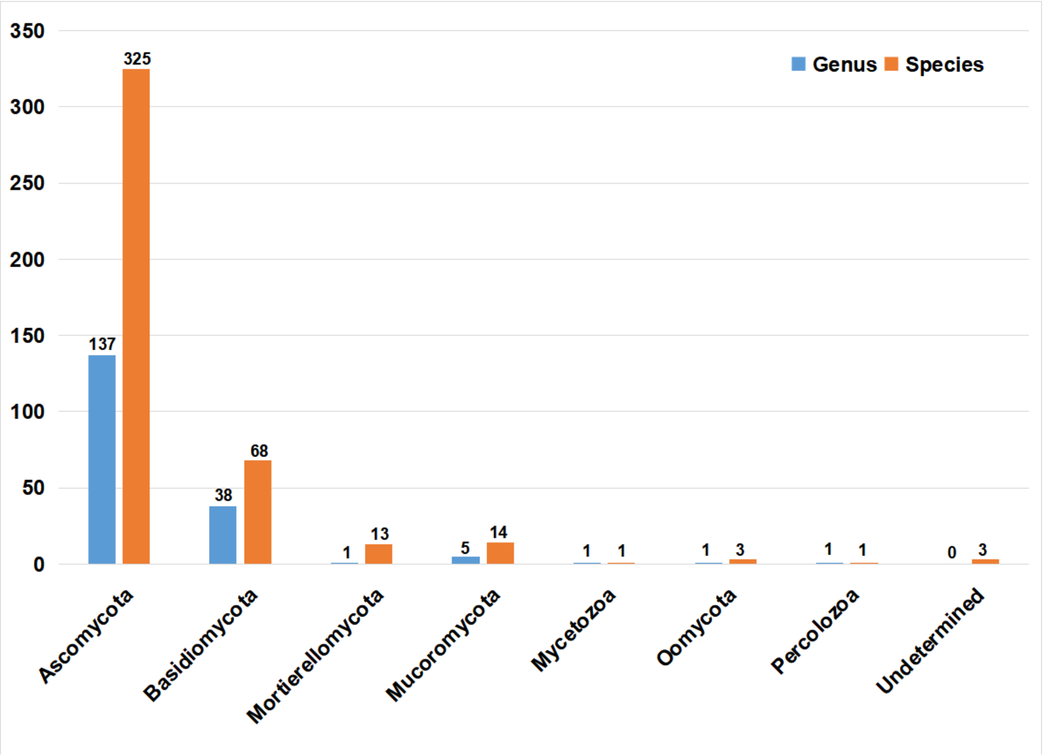

Figure 42 – The number of bat-associated fungal and fungus-like genera and species reported globally.

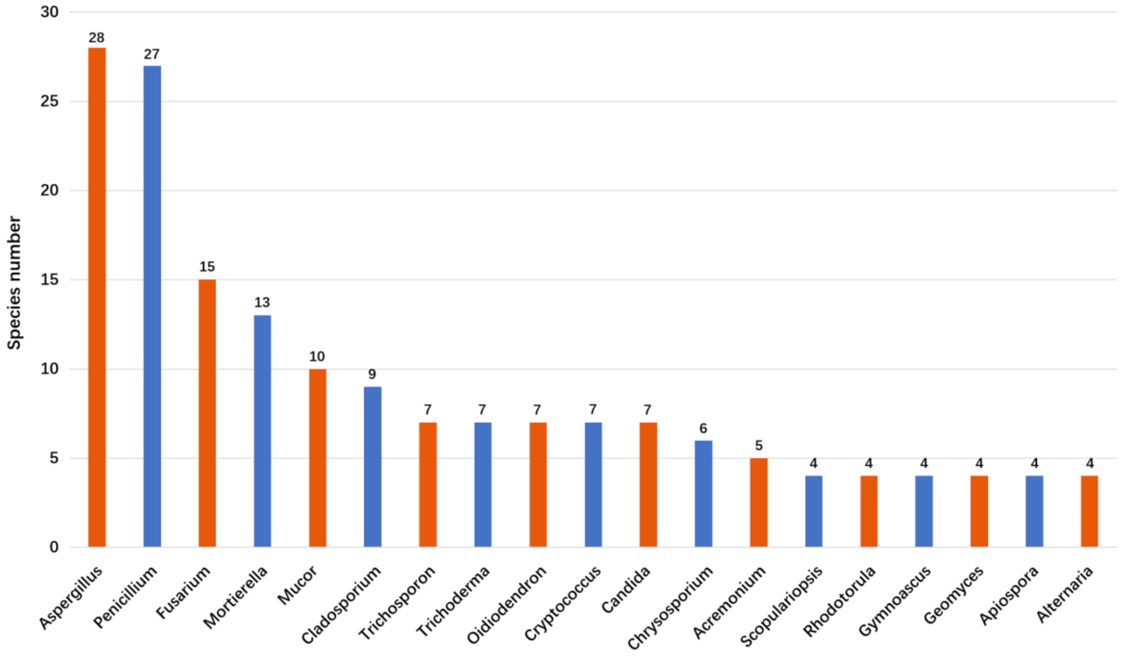

Figure 43 – The most abundant bat associated fungal genera reported worldwide (≥ 4 species).

There remain a number of challenges to be met and questions that need to be addressed in future studies on the topic of bat-associated fungi. Logistical issues in accessing many of the environments where bats are found will remain a challenge to scientists. Being able to distinguish between fungi that are simply transported by bats (such as spores within the fur of bats) and fungi that are hosted by bats (growing on the bats) will be an important topic for future work. We are yet to determine if there are phylogenetic relationships between the fungi associated with, or hosted by, bats; and if fungi found growing on bats or being transported by bats have evolved morphological adaptions to aid these processes. Addressing these knowledge gaps will ensure that we are better able to understand the ecological implications of the fungi associated with bats.

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Conflict of interest

The authors declare that there is no conflict of interest.

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Supplementary materials

Supplementary Table 1 The information of species in this study.

Fungal species	**Bat species**	**Bat microhabitats of sample collected**	**Locations**	**Host records of same bat**
Amphichorda yunnanensis	*Rhinolophus affinis*	Wing surfaces	Yunnan province, Yuxi, Yimen county, Pubei vallige, Shiliansi	New
Amphichorda yunnanensis	*Rhinolophus siamensi*	Wing surfaces	Yunnan province, Yuxi, Yimen county, Pubei vallige, Shiliansi	New
Apiospora arundinis	*Miniopterus schreibersii*	Foot	Yunnan Province, Kunming, Xishan district, Long Cave	New
Apiospora arundinis	*Myotis pilosus*	Foot	Yunnan Province, Kunming, Xishan district, Long Cave	New
Apiospora hipposiderocola	*Hipposideros pomona*	Wing surfaces	Yunnan province, Yuxi, Yimen county, Pubei vallige, Shiliansi	New
Apiospora rhinolophicola	*Rhinolophus sinicus*	Wing surfaces	Yunnan province, Yuxi, Yimen county, Pubei vallige, Shiliansi	New
Apiospora xishuangbannaensis	*Rhinolophus pusillus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Aspergillus creber	*Rhinolophus affinis*	Wing surfaces	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Aspergillus creber	*Rhinolophus affinis*	Wing surfaces	Yunnan province, Kunming, Xishan district, Long Cave	New
Aspergillus candidus	*Hipposideros armiger*	Wing surfaces	Yunnan province, Kunming, Xishan district, Long Cave	New
Aspergillus candidus	*Hipposideros armiger*	Wing surfaces	Yunnan province, Kunming, Xishan district, Long Cave	New
Clonostachys rhinolophicola	*Hipposideros larvatus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Clonostachys rhinolophicola	*Rhinolophus stheno*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Fusarium hipposidericola	*Rhinolophus malayanus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Fusarium hipposidericola	*Rhinolophus stheno*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Fusarium luffa	*Rhinolophus malayanus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Fusarium menglaense	*Rhinolophus malayanus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Fusarium rhinolophicola	*Rhinolophus malayanus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Fusarium xishuangbannaense	*Rhinolophus malayanus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Fusarium yunnanense	*Rhinolophus malayanus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Neopestalotiopsis paeoniae-suffruticosae	*Rhinolophus stheno*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New

Supplementary Table 1 Continued.

Fungal species	Bat species	Bat microhabitats of sample collected	Locations	Host records of same bat
Neopestalotiopsis xishuangbannaensis	*Kerivoula hardwickii*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Penicillium rhinolophicola	*Rhinolophus sinicus*	Wing surfaces	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Penicillium brevicompactum	*Rhinolophus affinis*	Wing surfaces	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Penicillium brevicompactum	*Rhinolophus rex*	Wing surfaces	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Penicillium brevicompactum	*Rhinolophus siamensis*	Wing surfaces	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Penicillium brevicompactum	*Rhinolophus sinicus*	Wing surfaces	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Penicillium brevicompactum	*Rhinolophus sinicus*	Wing surfaces	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Phialemoniopsis hipposiderocola	*Hipposideros larvatus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Phialemoniopsis xishuangbannaensis	*Hipposideros larvatus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Scopulariopsis brevicaulis	*Rhinolophus siamensis*	Wing surfaces	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Scopulariopsis brevicaulis	*Hipposideros pomona*	Foot	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Scopulariopsis brevicaulis	*Rhinolophus siamensis*	Wing surfaces	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Trichoderma hipposiderocola	*Hipposideros pomona*	Foot	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Trichoderma hipposiderocola	*Miniopterus schreibersii*	Foot	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Trichoderma hipposiderocola	*Rhinolophus affinis*	Foot	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Trichoderma inconspicuum	*Miniopterus schreibersii*	Wing surfaces	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Trichoderma obovatum	*Miniopterus schreibersii*	Foot	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Trichoderma obovatum	*Rhinolophus rex*	Foot	Yunnan Province, Yuxi, Yimen County, Pubei village, Shiliansi	New
Trichoderma rhinolophicola	*Rhinolophus malayanus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New
Trichoderma xishuangbannaense	*Rhinolophus malayanus*	Wing surfaces	Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town	New

Supplementary Table 2 Details of the fungal strains included in the phylogenetic analyses.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Amphichorda cavernicola	LC12448 T	MK329058	–	MK335999	–	–	–	–	–	–
Amphichorda cavernicola	LC12553	MK329059	–	MK336000	–	–	–	–	–	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Amphichorda cavernicola	LC12560	MK329061	–	MK336002	–	–	–	–	–	–
Amphichorda felina	MTCC 2499	JQ266096	–	JQ990899	–	–	JQ990855	JQ990877	–	–
Amphichorda guana	CGMCC3.17908 T	KU746665	–	KX855211	–	–	KY883228	KY883202	–	–
Amphichorda guana	CGMCC3.17909	KU746666	–	KX855212	–	–	–	KY883203	–	–
Amphichorda yunnanensis	**KUMCC 21-0414**	**ON426823**	–	**OR02597**	**–**	**–**	**OR022041**	**OR022016**	–	–
Amphichorda yunnanensis	**KUMCC 21-0415**	**ON426824**	–	**OR025976**	**–**	**–**	**OR022040**	**OR022015**	–	–
Amphichorda yunnanensis	**KUMCC 21-0416 T**	**ON426825**	–	**OR025975**	**–**	**–**	**OR022039**	**OR022014**	–	–
Apiospora acutiapica	KUMCC 20-0210	MT946343	MT946339	MT947360	MT947366	–	–	–	–	–
Apiospora agari	KUC21333	MH498520	–	MH544663	MH498478	–	–	–	–	–
Apiospora agari	KUC21361	MH498519	–	MN868914	MH498477	–	–	–	–	–
Apiospora aquaticum	S-642	MK828608	MK835806	–	–	–	–	–	–	–
Apiospora arctoscopi	KUC21331 T	MH498529	–	MN868918	MH498487	–	–	–	–	–
Apiospora arctoscopi	KUC21344	MH498528	–	MN868919	MH498486	–	–	–	–	–
Apiospora arundinis	CBS 133509	KF144886	KF144930	KF145018	KF144976	–	–	–	–	–
Apiospora arundinis	CBS 449.92	KF144887	KF144931	KF145019	KF144977	–	–	–	–	–
Apiospora arundinis	**KUMCC 21-0697**	**ON426831**	**OP363250**	**OR025963**	**OR025924**	–	–	–	–	–
Apiospora arundinis	**KUMCC 21-0698**	**ON426830**	**OP363251**	**OR025964**	**OR025924**	–	–	–	–	–
Apiospora aurea	CBS 244.83 T	AB220251	KF144935	KF145023	KF144981	–	–	–	–	–
Apiospora balearica	CBS 145129 T	MK014869	MK014836	MK017946	MK017975	–	–	–	–	–
Apiospora bambusae	CBS 145133	MK014875	MK014842	MK017952	MK017981	–	–	–	–	–
Apiospora bambusae	ICPM 6889 T	MK014874	MK014841	MK017951	MK017980	–	–	–	–	–
Apiospora bambusicola	MFLUCC20-0144 T	MW173030	MW173087	MW183262	–	–	–	–	–	–
Apiospora biserialis	CGMCC 3.20135 T	MW481708	MW478885	MW522938	MW522955	–	–	–	–	–
Apiospora biserialis	GZCC 20_0099	MW481709	MW478886	MW522939	MW522956	–	–	–	–	–
Apiospora biserialis	GZCC 20_0100	MW481710	MW478887	MW522940	MW522957	–	–	–	–	–
Apiospora camelliae-sinensis	LC 5007 T	KY494704	KY494780	KY705103	KY705173	–	–	–	–	–
Apiospora camelliae-sinensis	LC 8181	KY494761	KY494837	KY705157	KY705229	–	–	–	–	–
Apiospora chiangraiense	MFLUCC21-0053 T	MZ542520	MZ542524	–	MZ546409	–	–	–	–	–
Apiospora chromolaenae	MFLUCC 17-1505 T	MT214342	MT214436	MT235802	–	–	–	–	–	–
Apiospora cordylinae	GUCC 10026	MT040105	–	MT040126	MT040147	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Apiospora cyclobalanopsidis	CGMCC 3.20136 T	MW481713	MW478892	MW522945	MW522962	–	–	–	–	–
Apiospora cyclobalanopsidis	GZCC 20_0103	MW481714	MW478893	MW522946	MW522963	–	–	–	–	–
Apiospora descalsii	CBS 145130 T	MK014870	MK014837	MK017947	MK017976	–	–	–	–	–
Apiospora dichotomanthi	LC 4950 T	KY494697	KY494773	KY705096	KY705167	–	–	–	–	–
Apiospora dichotomanthi	LC 8175	KY494755	KY494831	KY705151	KY705223	–	–	–	–	–
Apiospora esporlensis	CBS 145136 T	MK014878	MK014845	MK017954	MK017983	–	–	–	–	–
Apiospora euphorbiae	IMI 285638b	AB220241	AB220335	–	AB220288	–	–	–	–	–
Apiospora fermenti	KUC21288 T	MF615230	–	MH544668	MF615235	–	–	–	–	–
Apiospora fermenti	KUC21289	MF615226	–	MH544667	MF615231	–	–	–	–	–
Apiospora gaoyouensis	CFCC 52301 T	MH197124	–	MH236793	MH236789	–	–	–	–	–
Apiospora gaoyouensis	CFCC 52302	MH197125	–	MH236794	MH236790	–	–	–	–	–
Apiospora garethjonesii	KUMCC 16-0202 T	KY356086	KY356091	–	–	–	–	–	–	–
Apiospora gelatinosa	GZAAS 20_0107	MW481707	MW478889	MW522942	MW522959	–	–	–	–	–
Apiospora gelatinosa	KHAS 11962 T	MW481706	MW478888	MW522941	MW522958	–	–	–	–	–
Apiospora guiyangensis	MFLU 19-2113 T	NR_175678	MW240577	MW759535	MW775604	–	–	–	–	–
Apiospora guizhouensis	LC 5318	KY494708	KY494784	KY705107	KY705177	–	–	–	–	–
Apiospora guizhouensis	LC 5322 T	KY494709	KY494785	KY705108	KY705178	–	–	–	–	–
Apiospora hispanica	IMI 326877 T	AB220242	AB220336	–	AB220289	–	–	–	–	–
Apiospora hydei	CBS 114990 T	KF144890	KF144936	KF145024	KF144982	–	–	–	–	–
Apiospora hydei	KUMCC 16-0204	KY356087	KY356092	–	–	–	–	–	–	–
Apiospora hyphopodii	KUMCC 16-0201	KY356088	KY356093	–	–	–	–	–	–	–
Apiospora hyphopodii	MFLUCC 15-0003 T	KR069110	–	–	–	–	–	–	–	–
Apiospora iberica	CBS 145137 T	MK014879	MK014846	MK017955	MK017984	–	–	–	–	–
Apiospora intestini	CBS 135835 T	KR011352	MH877577	KR011351	KR011350	–	–	–	–	–
Apiospora intestini	MFLUCC 21-0052	MZ542521	MZ542525	MZ546406	MZ546410	–	–	–	–	–
Apiospora italica	CBS 145138 T	MK014880	MK014847	MK017956	MK017985	–	–	–	–	–
Apiospora italica	CBS 145139	MK014881	MK014848	–	MK017986	–	–	–	–	–
Apiospora jatrophae	AMH-9556	HE981191	–	–	–	–	–	–	–	–
Apiospora jatrophae	AMH-9557 T	JQ246355	–	–	–	–	–	–	–	–
Apiospora jiangxiensis	LC 4494	KY494690	KY494766	KY705089	KY705160	–	–	–	–	–
Apiospora jiangxiensis	LC 4577 T	KY494693	KY494769	KY705092	KY705163	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Apiospora kogelbergensis	CBS 113332	KF144891	KF144937	KF145025	KF144983	–	–	–	–	–
Apiospora kogelbergensis	CBS 113333 T	KF144892	KF144938	KF145026	KF144984	–	–	–	–	–
Apiospora koreana	KUC21332	MH498524	–	MH544664	MH498482	–	–	–	–	–
Apiospora koreana	KUC21348	MH498523	–	MN868927	MH498481	–	–	–	–	–
Apiospora locuta-pollinis	LC 11683 T	MF939595	–	MF939616	MF939622	–	–	–	–	–
Apiospora locuta-pollinis	LC 11688	MF939596	–	MF939618	MF939623	–	–	–	–	–
Apiospora locuta-pollinis	GUCC 10228	MT040124	–	MT040145	MT040166	–	–	–	–	–
Apiospora longistroma	MFLUCC 11-0479 T	KU940142	KU863130	–	–	–	–	–	–	–
Apiospora longistroma	MFLUCC 11-0481	KU940141	KU863129	–	–	–	–	–	–	–
Apiospora magnispora	ZHKUCC 22-0001 T	OM728647	OM486971	OM543543	OM543544	–	–	–	–	–
Apiospora malaysiana	CBS 102053 T	KF144896	KF144942	KF145030	KF144988	–	–	–	–	–
Apiospora marianiae	AP18219	ON692406	ON692422	ON677180	ON677186	–	–	–	–	–
Apiospora marii	**KUMCC 21-0693**	**ON426828**	**OP363252**	**OR025965**	**OR025926**	–	–	–	–	–
Apiospora marii	**KUMCC 21-0694**	**ON426829**	**OP363253**	**OR025966**	**OR025927**	–	–	–	–	–
Apiospora marii	CBS 200.57	KF144900	KF144946	KF145034	KF144992	–	–	–	–	–
Apiospora marii	CBS 497.90 T	AB220252	KF144947	KF145035	KF144993	–	–	–	–	–
Apiospora marii	CBS 113535	KF144898	KF144944	KF145032	KF144990	–	–	–	–	–
Apiospora marii	CBS 114803	KF144899	KF144945	KF145033	KF144991	–	–	–	–	–
Apiospora marii	CPC 18904	KF144902	KF144949	KF145036	KF144994	–	–	–	–	–
Apiospora marii	CBS 114803	KF144899	KF144945	KF145033	KF144991	–	–	–	–	–
Apiospora marii	DiSSPA_A1	MK602320	–	MK645472	MK614695	–	–	–	–	–
Apiospora marina	KUC21328 T	MH498538	–	MH544669	MH498496	–	–	–	–	–
Apiospora marina	KUC21353	MH498537	–	MN868923	MH498495	–	–	–	–	–
Apiospora mediterranea	IMI 326875 T	AB220243	AB220337	–	AB220290	–	–	–	–	–
Apiospora minutispora	1.70E-41	LC517882	–	LC518889	LC518888	–	–	–	–	–
Apiospora mori	NCYUCC 19-0340	MW114314	MW114394	–	–	–	–	–	–	–
Apiospora mori	MFLUCC 20-0181 T	MW114313	MW114393	–	–	–	–	–	–	–
Apiospora mytilomorpha	DAOM 214595 T	KY494685	–	–	–	–	–	–	–	–
Apiospora neobambusae	LC 7106 T	KY494718	KY494794	KY806204	KY705186	–	–	–	–	–
Apiospora neobambusae	LC 7124	KY494727	KY494803	KY806206	KY705195	–	–	–	–	–
Apiospora neochinensis	CFCC 53036 T	MK819291	–	MK818545	MK818547	–	–	–	–	–
Apiospora neochinensis	CFCC 53037	MK819292	–	MK818546	MK818548	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Apiospora neogarethjonesii	DQD 2019a T	MK070897	MK070898	–	–	–	–	–	–	–
Apiospora neosubglobosa	JHB 006	KY356089	KY356094	–	–	–	–	–	–	–
Apiospora neosubglobosa	KUMCC 16-0203 T	KY356090	KY356095	–	–	–	–	–	–	–
Apiospora obovata	LC 4940 T	KY494696	KY494772	KY705095	KY705166	–	–	–	–	–
Apiospora obovata	LC 8177	KY494757	KY494833	KY705153	KY705225	–	–	–	–	–
Apiospora ovata	CBS 115042 T	KF144903	KF144950	KF145037	KF144995	–	–	–	–	–
Apiospora paraphaeosperma	MFLUCC 13-0644 T	KX822128	KX822124	–	–	–	–	–	–	–
Apiospora phragmitis	CPC 18900 T	KF144909	KF144956	KF145043	KF145001	–	–	–	–	–
Apiospora phyllostachydis	MFLUCC 18-1101	MK351842	MH368077	MK340918	MK291949	–	–	–	–	–
Apiospora piptatheri	CBS 145149 T	MK014893	MK014860	MK017969	–	–	–	–	–	–
Apiospora pseudoparenchymatica	LC 7234 T	KY494743	KY494819	KY705139	KY705211	–	–	–	–	–
Apiospora pseudoparenchymatica	LC 8173	KY494753	KY494829	KY705149	KY705221	–	–	–	–	–
Apiospora pseudorasikravindrae	KUMCC 20-0208 T	MT946344	–	MT947361	MT947367	–	–	–	–	–
Apiospora pseudosinensis	CPC 21546 T	KF144910	KF144957	KF145044	–	–	–	–	–	–
Apiospora pseudospegazzinii	CBS 102052 T	KF144911	KF144958	KF145045	KF145002	–	–	–	–	–
Apiospora pterosperma	CBS 123185	KF144912	KF144959	–	KF145003	–	–	–	–	–
Apiospora pterosperma	CPC 20193 T	KF144913	KF144960	KF145046	KF145004	–	–	–	–	–
Apiospora pusillisperma	KUC21357	MH498532	–	MN868931	MH498490	–	–	–	–	–
Apiospora pusillisperma	KUC21321 T	MH498533	–	MN868930	MH498491	–	–	–	–	–
Apiospora qinlingensis	CFCC 52303 T	MH197120	–	MH236795	MH236791	–	–	–	–	–
Apiospora qinlingensis	CFCC 52304	MH197121	–	MH236796	MH236792	–	–	–	–	–
Apiospora rasikravindrae	LC 8179	KY494759	KY494835	KY705155	KY705227	–	–	–	–	–
Apiospora rasikravindrae	MFLUCC 21-0051	MZ542523	MZ542527	MZ546408	MZ546412	–	–	–	–	–
Apiospora rasikravindrae	MFLUCC 21-0054	MZ542522	MZ542526	MZ546407	MZ546411	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Apiospora rasikravindrae	NFCCI 2144 T	JF326454	–	–	–	–	–	–	–	–
Apiospora sacchari	CBS 372.67	KF144918	KF144964	KF145049	KF145007	–	–	–	–	–
Apiospora sacchari	CBS 664.74	KF144919	KF144965	KF145050	KF145008	–	–	–	–	–
Apiospora saccharicola	CBS 191.73	KF144920	KF144966	KF145051	KF145009	–	–	–	–	–
Apiospora saccharicola	CBS 831.71	KF144922	KF144969	KF145054	KF145012	–	–	–	–	–
Apiospora sargassi	KUC21228 T	KT207746	–	MH544677	KT207644	–	–	–	–	–
Apiospora sargassi	KUC21232	KT207750	–	MH544676	KT207648	–	–	–	–	–
Apiospora septatum	CGMCC 3.20134 T	MW481711	MW478890	MW522943	MW522960	–	–	–	–	–
Apiospora septatum	GZCC 20_0109	MW481712	MW478891	MW522944	MW522961	–	–	–	–	–
Apiospora serenensis	IMI 326869 T	AB220250	AB220344	–	AB220297	–	–	–	–	–
Apiospora setariae	MT492005	MT492005	–	MW118457	MT497467	–	–	–	–	–
Apiospora setostroma	KUMCC 19-0217 T	MN528012	MN528011	MN527357	–	–	–	–	–	–
Apiospora sichuanensis	HKAS 107008 T	MW240648	MW240578	MW759536	MW775605	–	–	–	–	–
Apiospora sorghi	RVO-2019a T	MK371706	–	–	MK348526	–	–	–	–	–
Apiospora subglobosa	MFLUCC 11-0397 T	KR069112	KR069113	–	–	–	–	–	–	–
Apiospora subrosea	LC 7291	KY494751	KY494827	KY705147	KY705219	–	–	–	–	–
Apiospora subrosea	LC 7292 T	KY494752	KY494828	KY705148	KY705220	–	–	–	–	–
Apiospora taeanensis	KUC21359	MH498513	–	MN868935	MH498471	–	–	–	–	–
Apiospora taeanensis	KUC21322 T	MH498515	–	MH544662	MH498473	–	–	–	–	–
Apiospora thailandica	MFLUCC 15-0199	KU940146	KU863134	–	–	–	–	–	–	–
Apiospora thailandica	MFLUCC 15-0202 T	KU940145	KU863133	–	–	–	–	–	–	–
Apiospora tropica	MFLU 21-0084 T	OK491657	OK491653	–	OK560922	–	–	–	–	–
Apiospora vietnamensis	**KUMCC 21-0428**	**ON426826**	**OP363254**	**OR025967**	**OR025928**	–	–	–	–	–
Apiospora vietnamensis	**KUMCC 21-0429**	**ON426827**	**OP363255**	**OR025968**	**OR025929**	–	–	–	–	–
Apiospora vietnamensis	IMI 99670 T	KX986096	KX986111	–	KY019466	–	–	–	–	–
Apiospora xenocordella	CBS 478.86 T	KF144925	KF144970	KF145055	KF145013	–	–	–	–	–
Apiospora xenocordella	CBS 595.66	KF144926	KF144971	–	–	–	–	–	–	–
Apiospora xishuangbannaensis	**KUMCC 21-0695 T**	**ON426832**	**OP363248**	**OR025969**	**OR025930**	–	–	–	–	–
Apiospora xishuangbannaensis	**KUMCC 21-0696**	**ON426833**	**OP363249**	**OR025970**	**OR025931**	–	–	–	–	–
Apiospora yunnana	DDQ 00281	KU940148	KU863136	–	–	–	–	–	–	–
Apiospora yunnana	MFLUCC 15-1002 T	KU940147	KU863135	–	–	–	–	–	–	–
Arachnocrea scabrida	BEO 0201	–	–	DQ834457	–	–	DQ834458	–	–	–
Arachnocrea stipata	TFC 9743	–	–	–	–	–	EU710770	–	–	–
Arthrinium austriacum	GZU 345004	MW208928	–	–	–	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Arthrinium austriacum	GZU 345006	MW208929	MW208860	–	–	–	–	–	–	–
Arthrinium caricicola	CBS 145127	MK014871	MK014838	MK017948	MK017977	–	–	–	–	–
Arthrinium cf. *sporophleoides*	GZU 345102	MW208944	MW208866	–	–	–	–	–	–	–
Arthrinium crenatum	AG 19066	MW208931	MW208861	–	–	–	–	–	–	–
Arthrinium curvatum	AP 25418	MK014872	MK014839	MK017949	MK017978	–	–	–	–	–
Arthrinium japonicum	IFO 30500	AB220262	AB220356	–	AB220309	–	–	–	–	–
Arthrinium japonicum	IFO 31098	AB220264	AB220358	–	AB220311	–	–	–	–	–
Arthrinium luzulae	AP7619-3	MW208937	MW208863	–	–	–	–	–	–	–
Arthrinium morthieri	GZU 345043	MW208938	MW208864	–	–	–	–	–	–	–
Arthrinium phaeospermum	CBS 114317	KF144906	KF144953	KF145040	KF144998	–	–	–	–	–
Arthrinium phaeospermum	CBS 114318	KF144907	KF144954	KF145041	KF144999	–	–	–	–	–
Arthrinium puccinioides	CBS 549.86	AB220253	AB220347	–	AB220300	–	–	–	–	–
Arthrinium sphaerospermum	AP25619/CBS 146355	MW208943	MW208865	–	–	–	–	–	–	–
Arthrinium sporophleum	CBS 145154	MK014898	MK014865	MK017973	MK018001	–	–	–	–	–
Arthrinium trachycarpum	CFCC 53038	MK301098	–	MK303396	MK303394	–	–	–	–	–
Arthrinium urticae	IMI 326344	AB220245	AB220339	–	AB220292	–	–	–	–	–
Arthriniumtrachycarpum	CFCC 53039	MK301099	–	MK303397	MK303395	–	–	–	–	–
Aspergillus flavipes	NRRL302 T	EF669591	–	–	EU014085	–	EF669633	–	EF669549	–
Aspergillus iizukae	CBS541.69 T	EF669597	–	–	EU014086	–	EF669639	–	EF669555	–
Aspergillus pseudodeflectus	CBS 756.74 T	EF652507	–	–	EF652331	–	EF652243	–	EF652419	–
Aspergillus acanthosporus	CBS558.71T	EU078625	–	–	EU076322	–	EF669779	–	EU078676	–
Aspergillus aeneus	CBS 128.54	EF652474	–	–	EF652298	–	EF652210	–	EF652386	–
Aspergillus aflatoxiformans	CBS143679T	MG662388	–	–	MG517706	–	MG517897	–	MG518076	–
Aspergillus alabamensis	CBS125693 T	KP987071	–	–	KP987049	–	KP987018	–	EU147583	–
Aspergillus alboluteus	CBS 145854	MW448664	–	–	MW478498	–	MW478533	–	MW478512	–
Aspergillus alboluteus	CBS 145855 T	MW448663	–	–	MW478497	–	MW478532	–	MW478511	–
Aspergillus alboluteus	CBS 147421	MW480880	–	–	MW480788	–	MW480790	–	MW480706	–
Aspergillus alboviridis	CBS 142665 T	LT798909	–	–	LT798936	–	LT798938	–	LT798937	–
Aspergillus allahabadii	CBS164.63 T	EF669601	–	–	EF669531	–	EF669643	–	EF669559	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Aspergillus alliaceus	CBS536.65T	EF661551	–	–	EF661465	–	MG517825	–	EF661534	–
Aspergillus amethystinus	NRRL 4178 T	EF652462	–	–	EF652286	–	EF652198	–	EF652374	–
Aspergillus amoenus	NRRL4838T	EF652480	–	–	JN853946	–	JN853824	–	JN854035	–
Aspergillus angustatus	CBS 273.65 T	EU448283	–	–	AY339993	–	KU867013	–	EU443984	–
Aspergillus arcoverdensis	CBS139187T	KY808748	–	–	AB818845	–	KY808940	–	AB818856	–
Aspergillus ardalensis	CCF4031 T	FR733808	–	–	HG916683	–	HG916704	–	HG916725	–
Aspergillus arizonicus	CCF 5341 T	OK322364	–	–	OK334128	–	OK334129	–	OK334127	–
Aspergillus askiburgiensis	CBS134374T	LN873939	–	–	LN873952	–	LN873984	–	LN873965	–
Aspergillus aspearensis	CBS143672T	MG662398	–	–	MG517669	–	MG517857	–	MG518040	–
Aspergillus asperescens	CBS110.51T	EF652475	–	–	EF652299	–	EF652211	–	EF652387	–
Aspergillus astellatus	CBS 135.55	EU448273	–	–	AY339994	–	KU866936	–	EU443975	–
Aspergillus astellatus	CBS 261.93 T	EF652446	–	–	EF652270	–	EF652182	–	EF652358	–
Aspergillus atacamensis	CBS 142046 T	KX900619	–	–	–	–	–	–	–	–
Aspergillus atacamensis	EXF 6659	KX900618	–	–	–	–	–	–	–	–
Aspergillus aurantiobrunneus	CBS465.65T	EF652465	–	–	EF652289	–	EF652201	–	EF652377	–
Aspergillus aureolus	CBS105.55T	EF669950	–	–	EF669808	–	EF669738	–	HG426051	–
Aspergillus aureoterreus	CBS503.65 T	EF669580	–	–	EF669524	–	EF669622	–	EF669538	–
Aspergillus avenaceus	CBS109.46T	AF104446	–	–	FJ491481	–	JN121424	–	FJ491496	–
Aspergillus baarnensis	DAOMC 251735	KY980623	–	–	KY980551	–	KY980448	–	KY980587	–
Aspergillus baarnensis	DAOMC 251736	KY980624	–	–	KY980552	–	KY980449	–	KY980588	–
Aspergillus banksianus	FRR 6047 T	MH280013	–	–	MT184780	–	MT184792	–	MT184786	–
Aspergillus bicolor	CBS 425.77 T	EF652511	–	–	EF652335	–	EF652247	–	EF652423	–
Aspergillus burnettii	MST FP2249 T	MK429758	–	–	MT211761	–	MT211763	–	MT211762	–
Aspergillus calidoustus	CBS121601 T	HE616558	–	–	FJ624456	–	–	–	HE616559	–
Aspergillus candidus	CCF 4659	HG915889	–	–	HG916672	–	LT626998	–	HG916681	–
Aspergillus candidus	DTO 223-E5	LT626955	–	–	LT627011	–	LT627013	–	LT627012	–
Aspergillus candidus	**KUMCC 21-0699**	**OQ928957**	–	–	**OQ927579**	–	**OR022027**	**–**	**OR022042**	–
Aspergillus candidus	**KUMCC 21-0700**	**OQ928958**	–	–	**OQ927580**	–	**OR022028**	**–**	**OR022043**	–
Aspergillus candidus	CBS566.65T	EF669592	–	–	EU014089	–	EF669634	–	EF669550	–
Aspergillus caninus	CBS 128032 T	KY980618	–	–	KY980546	–	JN121445	–	KY980582	–
Aspergillus capensis	CBS138188 T	KJ775550	–	–	KJ775072	–	KP987020	–	KJ775279	–
Aspergillus carlsbadensis	CBS123894 T	FJ531151	–	–	FJ531179	–	KU866973	–	FJ531126	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Aspergillus carneus	CBS494.65 T	EF669611	–	–	EF669529	–	EF669653	–	EF669569	–
Aspergillus cf *alabamensis*	CBS142981	LT798912	–	–	LT798945	–	LT798947	–	LT798946	–
Aspergillus chaetosartoryae	CBS 265.73 T	EF652144	–	–	EF652117	–	EF652099	–	EF652129	–
Aspergillus chlamydosporus	CBS 109945 T	KY980617	–	–	KY980545	–	KY980444	–	KY980581	–
Aspergillus citrinoterreus	CBS 138921 T	KP175260	–	–	LN680657	–	–	–	LN680685	–
Aspergillus citrinoterreus	NRRL1913	EF669579	–	–	EF669518	–	EF669621	–	EF669537	–
Aspergillus clavatus	CBS513.65T	EF669942	–	–	EF669802	–	EF669730	–	EF669871	–
Aspergillus coloradensis	CCF 6118 T	MK713539	–	–	MK695646	–	MK695668	–	MK695657	–
Aspergillus contaminans	CBS142451 T	LT594451	–	–	LT594443	–	LT594434	–	LT594425	–
Aspergillus creber	**KUMCC 21-0819**	**OP425807**	–	–	**OQ927581**	–	**OR022029**	**–**	**OR022044**	–
Aspergillus creber	**KUMCC 21-0820**	**OP4258078**	–	–	**OQ927582**	–	**OR022030**	**–**	**OR022045**	–
Aspergillus creber	NRRL 25627	–	–	–	JN853982		JN853821		JN854032	
Aspergillus creber	NRRL 58592 T	JQ301889	–	–	JN853980	–	JN853832	–	JN854043	–
Aspergillus creber	NRRL 58597	–	–	–	JN853986		JN853834		JN854045	
Aspergillus creber	NRRL 58673	–	–	–	JN853993		JN853845		JN854056	
Aspergillus croceiaffinis	CCF 6035 T	MK713538	–	–	MK695645	–	MK695667	–	MK695656	–
Aspergillus croceiaffinis	CCF 6036	MK713537	–	–	MK695644	–	MK695666	–	MK695655	–
Aspergillus croceus	CBS 134396T	LN873931	–	–	LN873944	–	LN873976	–	LN873957	–
Aspergillus crustosus	CBS 478.65 T	EF652489	–	–	EF652313	–	EF652225	–	EF652401	–
Aspergillus curvatus	AUMC 11038 T	MN006961	–	–	–	–	–	–	–	–
Aspergillus dipodomyus	NRRL 66273 T	MK713535	–	–	MK695642	–	MK695664	–	MK695653	–
Aspergillus discophorus	CBS 469.88 T	EU448272	–	–	AY339999	–	KX423661	–	EU443970	–
Aspergillus dobrogensis	CCF4651T	LT626959	–	–	LT627027	–	LT627028	–	LT558722	–
Aspergillus dromiae	CBS 140633 T	KU866580	–	–	KU866885	–	KU866958	–	KU866703	–
Aspergillus dromiae	CBS 140639	KU866672	–	–	KU866909	–	KU867057	–	KU866792	–
Aspergillus elsenburgensis	PPRI 2994 T	MK450651	–	–	MK451215	–	MK450804	–	MK451513	–
Aspergillus falconensis	CBS 271.91 T	KU866575	–	–	KU866815	–	KU866697	–	KU866697	–
Aspergillus falconensis	CBS 989.72	KU866576	–	–	KU866816	–	KU866953	–	KU866698	–
Aspergillus fennelliae	CBS598.74 T	EF669994	–	–	AF057320	–	EF669781	–	EF669920	–
Aspergillus fischeri	CBS544.65T	EF669936	–	–	EF669796	–	EF669724	–	EF669865	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Aspergillus flavus	CBS569.65T	AF027863	–	–	EF661485	–	EF661440	–	EF661508	–
Aspergillus flavus	NRRL3751	EF661554	–	–	EF661488	–	EF661443	–	EF661511	–
Aspergillus floccosus	CBS116.37 T	FJ531205	–	–	FJ491714	–	–	–	FJ531219	–
Aspergillus foeniculicola	CBS 156.80 T	EU448274	–	–	EU443990	–	KU867027	–	EU443968	–
Aspergillus fruticulosus	CBS 486.65 T	EF652483	–	–	EF652307	–	EF652219	–	EF652395	–
Aspergillus fumigatiaffinis	PPRI13089	MK450636	–	–	MK450913	–	–	–	MK451390	–
Aspergillus fumigatus	CBS 133.61T	EF669931	–	–	EF669791	–	EF669719	–	EF669860	–
Aspergillus fumigatus	KUMCC 18-0197	MT152331	–	–	MT161678	–	MT384369	–	MT178246	–
Aspergillus fumigatus	NRRL 5587	EF669996	–	–	EF669851	–	EF669783	–	EF669922	–
Aspergillus fuscicans	BAFCcult4564 T	–	–	–	KY853416	–	–	–	KY853415	–
Aspergillus gaarensis	AUMC 11046 T	MN648408	–	–	–	–	–	–	–	–
Aspergillus germanicus	CBS123887 T	FJ531146	–	–	FJ531172	–	KU866944	–	FJ531141	–
Aspergillus griseoaurantiacus	CBS138191 T	KJ775553	–	–	KJ775086	–	KU866988	–	KJ775357	–
Aspergillus heldtiae	PPRI 4229 T	MK450656	–	–	MK450981	–	MK450809	–	MK451518	–
Aspergillus hongkongensis	HKU49T	AB987907	–	–	LC000552	–	LC000578	–	LC000565	–
Aspergillus hortai	CBS 124230 T	FJ531192	–	–	FJ491706	–	–	–	FJ531242	–
Aspergillus hortai	IBT26384	FJ531209	–	–	EU147701	–	–	–	EU147515	–
Aspergillus hydei	KUMCC 18-0196 T	MT152332	–	–	MT161679	–	MT384370	–	MT178247	–
Aspergillus insolitus	CBS 181.90	KY980620	–	–	KY980548	–	KY980446	–	KY980584	–
Aspergillus insolitus	CBS 384.61 T	KY980622	–	–	KY980550	–	KY980447	–	KY980586	–
Aspergillus inusitatus	DTO 121-G5 T	MW448669	–	–	MW478502	–	MW478542	–	MW478517	–
Aspergillus iranicus	CBS 139561 T	KP987077	–	–	KP987045	–	KP987034	–	KP987060	–
Aspergillus israelensis	CBS 140627 T	KU866677	–	–	KU866915	–	KU867062	–	KU866797	–
Aspergillus creber	NRRL 58671	–	–	–	JN854008	–	JN853843	–	JN854054	–
Aspergillus creber	NRRL 58600 T	JQ301892	–	–	JN854007	–	JN853835	–	JN854046	–
Aspergillus kalimae	CBS 143506 T	KY980650	–	–	KY980578	–	KY980475	–	KY980614	–
Aspergillus karnatakaensis	CBS 102800 T	EU482441	–	–	EU482438	–	KU866956	–	EU482431	–
Aspergillus karnatakaensis	NRRL 4649	EF652468	–	–	EF652292	–	EF652204	–	EF652380	–
Aspergillus keratitidis	BCRC 34221 T	KY980616	–	–	KY980544	–	KY980443	–	KY980580	–
Aspergillus keratitidis	DAOMC 251750	KY980626	–	–	KY980554	–	KY980451	–	KY980590	–
Aspergillus krugeri	PPRI 8986 T	MK450655	–	–	MK451098	–	MK450808	–	MK451517	–
Aspergillus kumbius	FRR 6049 T	MT179307	–	–	MT184782	–	MT184794	–	MT184788	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Aspergillus laciniosus	CBS117721 T	AB299413	–	–	AY870756	–	–	–	AY870716	–
Aspergillus lannaensis	SDBR-CMUO8 T	MW588211	–	–	MW219783	–	MW219785	–	MW219781	–
Aspergillus lanuginosus	NRRL 4610 T	EF669604	–	–	EU014080	–	EF669646	–	EF669562	–
Aspergillus latilabiatus	CBS 426.93 T	KU866624	–	–	KU866864	–	KU867025	–	KU866762	–
Aspergillus lentulus	CBS117885 T	EF669969	–	–	EF669825	–	EF669756	–	EF669895	–
Aspergillus leporis	CBS151.66 T	AF104443	–	–	EF661499	–	EF661459	–	EF661541	–
Aspergillus limoniformis	CGMCC3.19323 T	MK329066	–	–	MK336093	–	MK335972	–	–	–
Aspergillus longistipitatus	CCF 5788 T	MK713534	–	–	MK695641	–	MK695663	–	MK695652	–
Aspergillus longistipitatus	CCF 6117	MK713533	–	–	MK695640	–	MK695662	–	MK695651	–
Aspergillus luteorubrus	FRR 5427 T	MT179305	–	–	MT184781	–	MT184793	–	MT184787	–
Aspergillus magaliesburgensis	PPRI 6165 T	MK450649	–	–	MK451116	–	MK450802	–	MK451511	–
Aspergillus malvicolor	FRR 2383 T	MT179308	–	–	MT184784	–	MT184796	–	MT184790	–
Aspergillus micronesiensis	CBS138183 T	KJ775548	–	–	KJ775085	–	KP987023	–	KJ775355	–
Aspergillus minisclerotigenes	CBS117635 T	EF409239	–	–	EF203148	–	MG517799	–	MG518009	–
Aspergillus montoensis	BRIP 64533 T	OK441076	–	–	–	–	OK509073	–	–	–
Aspergillus multiplicatus	CBS646.95 T	HE974445	–	–	DQ114129	–	HE974397	–	DQ114137	–
Aspergillus nanangensis	FRR 6048 T	MK979278	–	–	MT184783	–	MT184795	–	MT184789	–
Aspergillus neoafricanus	CBS 130.55 T	AY822633	–	–	EF669516	–	EF669627	–	EF669543	–
Aspergillus neoflavipes	CBS260.73 T	EF669614	–	–	EU014084	–	EF669656	–	EF669572	–
Aspergillus neoglaber	CBS111.55 T	EF669948	–	–	EU014107	–	EF669736	–	EU014120	–
Aspergillus neoindicus	CBS 444.75 T	EF669616	–	–	EF669532	–	EF669658	–	EF669574	–
Aspergillus niveus	CBS115.27 T	EF669615	–	–	EF669528	–	EF669657	–	EF669573	–
Aspergillus nomius	CBS260.88 T	AF027860	–	–	AF255067	–	EF661456	–	AY017588	–
Aspergillus noonimiae	CBS 143382 T	KY980641	–	–	KY980569	–	KY980466	–	KY980605	–
Aspergillus novoparasiticus	CBS126849 T	MG662397	–	–	MG517684	–	MG517875	–	MG518055	–
Aspergillus okavangoensis	CBS 147420 T	MW480881	–	–	MW480789	–	MW480791	–	MW480707	–
Aspergillus oxumiae	CCDCA 11546 T	MN431160	–	–	MN521388	–	MN521389	–	MN531842	–
Aspergillus phialiformis	CGMCC3.19314 T	MK329068	–	–	MK336095	–	MK335974	–	–	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Aspergillus phialosimplex	CGMCC3.19637 T	MK329070	–	–	MK336097	–	MK335976	–	–	–
Aspergillus phialosimplex	LC12625	MK329071	–	–	MK336098	–	MK335977	–	–	–
Aspergillus pisci	CBS 101166 T	MF362690	–	–	MF362691	–	JN121415	–	–	–
Aspergillus pluriseminatus	CBS100523T	KU866566	–	–	AY339989	–	KU866937	–	EU443988	–
Aspergillus polyporicola	NRRL32683 T	EF669595	–	–	EU014088	–	EF669637	–	EF669553	–
Aspergillus posadasensis	FMR12168 T	HG529483	–	–	HG529481	–	HF954977	–	HG529488	–
Aspergillus protuberus	CBS602.74 T	EF652460	–	–	EF652284	–	EF652196	–	EF652372	–
Aspergillus pseudocaelatus	CBS117616 T	EF409242	–	–	MG517626	–	MG517809	–	MG517995	–
Aspergillus pseudonomius	CBS119388 T	AF338643	–	–	EF661495	–	EF661454	–	EF661529	–
Aspergillus pseudoterreus	CBS123890 T	EF669598	–	–	EF669523	–	EF669640	–	EF669556	–
Aspergillus pseudoustus	CBS123904 T	FJ531147	–	–	FJ531168	–	KU866978	–	FJ531129	–
Aspergillus purpureocrustaceus	PPRI 3840 T	MK450653	–	–	MK451138	–	MK450806	–	MK451515	–
Aspergillus purpureus	CBS754.74 T	EF652506	–	–	EF652330	–	EF652242	–	EF652418	–
Aspergillus quadrilineatus	CBS591.65 T	EF652433	–	–	EF652257	–	EF652169	–	EF652345	–
Aspergillus recurvatus	CBS496.65 T	EF652482	–	–	EF652306	–	EF652218	–	EF652394	–
Aspergillus rugulosus	CBS133.60 T	EF652434	–	–	EF652258	–	EF652170	–	EF652346	–
Aspergillus salinarus	CBS 138583 T	KY980619	–	–	KY980547	–	KY980445	–	KY980583	–
Aspergillus salinarus	EXF 10245	KX900624	–	–	–	–	–	–	–	–
Aspergillus salisburgensis	CBS 142047 T	KX900623	–	–	–	–	–	–	–	–
Aspergillus salisburgensis	EXF 10244	KX900621	–	–	–	–	–	–	–	–
Aspergillus sclerotialis	CBS 366.77 T	KF267869	–	–	KY980579	–	JN121505	–	KY980615	–
Aspergillus seifertii	PPRI 3211 T	MK450647	–	–	MK451093	–	MK450800	–	MK451509	–
Aspergillus sibiricus	CBS 143307	MG587008	–	–	MG722970	–	MG710809	–	MG722971	–
Aspergillus sigurros	PPRI 15889 T	MK450650	–	–	MK451066	–	MK450803	–	MK451512	–
Aspergillus spectabilis	CBS 429.77 T	EF652510	–	–	EU482437	–	EF652246	–	EU482429	–
Aspergillus spectabilis	CCF 5113	LS999633	–	–	LS999622	–	LS999621	–	LS999620	–
Aspergillus spelaeus	CCF 4425 T	HG915905	–	–	HG916698	–	HG916719	–	HG916741	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Aspergillus spelaeus	CCF 4886	LM999908	–	–	LM644272	–	LM644259	–	HG916748	–
Aspergillus spelunceus	CBS497.65 T	EF652490	–	–	EF652314	–	EF652226	–	EF652402	–
Aspergillus spinosus	CBS483.65 T	EF669988	–	–	EF669844	–	EF669775	–	EF669914	–
Aspergillus stella-maris	CBS 113638 T	EU448269	–	–	KU866886	–	KU866929	–	EU443978	–
Aspergillus stella-maris	CBS 113639	EU448270	–	–	EF428367	–	KU866930	–	KU866687	–
Aspergillus stellatus	CBS 598.65 T	EF652426	–	–	EF652250	–	EF652162	–	EF652338	–
Aspergillus stellatus	CBS 668.82	EU448281	–	–	AY339992	–	KU866924	–	KU866685	–
Aspergillus stelliformis	CCF 5375 T	MK713531	–	–	MK695638	–	MK695660	–	MK695649	–
Aspergillus subalbidus	CBS567.65 T	KJ866983	–	–	EU076295	–	EF669635	–	EF669551	–
Aspergillus subversicolor	NRRL58999 T	JQ301894	–	–	JN853970	–	JN853799	–	JN854010	–
Aspergillus sulphureoviridis	CBS 140626 T	KU866673	–	–	KU866911	–	KU867058	–	KU866793	–
Aspergillus sulphureoviridis	NRRL 66274	MK713530	–	–	–	–	MK695659	–	MK695648	–
Aspergillus suttoniae	CBS 143866 T	LT899487	–	–	LT899536	–	LT899644	–	LT899589	–
Aspergillus sydowii	CBS593.65 T	EF652450	–	–	EF652274	–	EF652186	–	EF652362	–
Aspergillus taichungensis	IBT19404 T	LT626957	–	–	EU076297	–	LT627016	–	EU076310	–
Aspergillus tamarii	CBS104.13 T	AF004929	–	–	EF661474	–	EU021629	–	EF661526	–
Aspergillus telluris	CGMCC3.19701 T	MN640767	–	–	MN635253	–	MN635276	–	MN635264	–
Aspergillus telluris	CGMCC3.19703	MN640769	–	–	MN635243	–	MN635278	–	MN635266	–
Aspergillus templicola	CBS 138181 T	KJ775545	–	–	KJ775092	–	KP987038	–	KJ775394	–
Aspergillus templicola	CCF 4698	HG915902	–	–	HG916695	–	HG916716	–	HG916738	–
Aspergillus terreus	CBS 594.65	–	–	–	EU147709	–	–	–	EU147523	–
Aspergillus terreus	CBS 601.65 T	EF669586	–	–	EF669519	–	EF669628	–	EF669544	–
Aspergillus thailandensis	CBS 143383 T	KY980642	–	–	KY980570	–	KY980467	–	KY980606	–
Aspergillus thailandensis	DAOMC 251756	KY980643	–	–	KY980571	–	KY980468	–	KY980607	–
Aspergillus thermomutatus	CBS208.92 T	EF669946	–	–	EF669805	–	EF669734	–	EF669874	–
Aspergillus transmontanensis	CBS130015 T	JF412774	–	–	HM803101	–	HM802980	–	HM803020	–
Aspergillus tritici	CBS266.81 T	LT626958	–	–	EU076293	–	LT627017	–	EU076305	–
Aspergillus udagawae	CBS114217 T	AB250781	–	–	AF132226	–	KY808929	–	AB748566	–
Aspergillus unguis	CBS 132.55 T	EF652443	–	–	EF652267	–	EF652179	–	EF652355	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Aspergillus unguis	DTO 017-A6	KU866567	–	–	KU866807	–	KU866939	–	KU866688	–
Aspergillus urmiensis	CBS 139557	KP987072	–	–	KP987039	–	KP987029	–	KP987055	–
Aspergillus urmiensis	CBS 139558 T	KP987073	–	–	KP987041	–	KP987030	–	KP987056	–
Aspergillus vandermerwei	CBS612.78 T	EF661567	–	–	EF661469	–	MG517838	–	EF661540	–
Aspergillus varians	CBS505.65 T	EF652479	–	–	EF652303	–	EF652215	–	EF652391	–
Aspergillus vinaceus	ITAL 47.456 T	MN575692	–	–	MN583579	–	MN583581	–	MN583580	–
Aspergillus violaceus	CBS 138.55	EF652438	–	–	EF652262	–	EF652174	–	EF652350	–
Aspergillus violaceus	CBS 293.93	EU448279	–	–	EF428374	–	KU866927	–	EU443987	–
Aspergillus viridicatenatus	CBS140629 T	KU866682	–	–	KX423621	–	KU867067	–	KU866802	–
Aspergillus waynelawii	CBS 143384 T	KY980639	–	–	KY980567	–	KY980464	–	KY980603	–
Aspergillus waynelawii	DAOMC 251752	KY980640	–	–	KY980568	–	KY980465	–	KY980604	–
Aspergillus wentii	CBS 104.07 T	EF652151	–	–	EF652106	–	EF652092	–	EF652131	–
Aspergillus whitfifieldii	CBS 143385 T	KY980645	–	–	KY980573	–	KY980470	–	KY980609	–
Aspergillus whitfifieldii	DAOMC 251761	KY980646	–	–	KY980574	–	KY980471	–	KY980610	–
Aspergillus wyomingensis	CCF4417 T	HG324081	–	–	HF933359	–	HF937378	–	HF933397	–
Beauveria acridophila	HUA 179220	JQ958600	–	JQ958614	–	–	JX003842	JX003852	–	–
Beauveria acridophila	HUA 179221 T	JQ958601	–	JQ958615	–	–	JX003843	JX003853	–	–
Beauveria amorpha	ARSEF 7542	HQ880805	–	HQ881007	–	HQ880736	HQ880949	HQ880877	–	–
Beauveria amorpha	ARSEF4149	HQ880804	–	HQ881006	–	HQ880735	HQ880948	HQ880876	–	–
Beauveria asiatica	BCC24977	MN401633	–	MN401459	–	MN401513	–	MN401557	–	–
Beauveria asiatica	BCC24980	MN401632	–	MN401458	–	MN401512	–	MN401556	–	–
Beauveria australis	ARSEF 4580	HQ880788	–	HQ880994	–	HQ880719	HQ880932	HQ880860	–	–
Beauveria australis	ARSEF 4622	HQ880790	–	HQ880996	–	HQ880721	HQ880934	HQ880862	–	–
Beauveria baoshanensis	BUB205 T	–	–	MG642897	–	–	MG642867	MG642854	–	–
Beauveria baoshanensis	BUB283	–	–	MG642898	–	–	MG642868	MG642855	–	–
Beauveria bassiana	BCC14481	MN401659	–	MN401487	–	–	MN401609	MN401585	–	–
Beauveria bassiana	BCC14482	MN401666	–	MN401494	–	–	MN401614	MN401592	–	–
Beauveria brongniartii	ARSEF 6214	HQ880774	–	HQ880984	–	HQ880705	HQ880918	HQ880846	–	–
Beauveria brongniartii	ARSEF 6215	HQ880781	–	HQ880990	–	HQ880712	HQ880925	HQ880853	–	–
Beauveria caledonica	ARSEF 1567	AY531986	–	AY531894	–	HQ880747	HQ880960	HQ880888	–	–
Beauveria caledonica	ARSEF 2567	AY532006	–	AY531915	–	HQ880748	HQ880961	HQ880889	–	–
Beauveria diapheromeriphila	QCNE 186272 T	JQ958599	–	JQ958610	–	–	–	JX003848	–	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Beauveria diapheromeriphila	QCNE 186714	JQ958603	–	JQ958611	–	–	–	JX003850	–	–
Beauveria gryllotalpidicola	BCC76572	MN401624	–	MN401450	–	–	–	MN401548	–	–
Beauveria gryllotalpidicola	BCC81472	MK632053	–	MK632068	–	MN401506	MK632151	MK632178	–	–
Beauveria hoplocheli	Bt121	KC339687	–	KC339704	–	KM453968	KM453965	KM453956	–	–
Beauveria hoplocheli	Bt96	KC339697	–	KC339709	–	KM453974	KM453959	KM453950	–	–
Beauveria kipukae	ARSEF 7032 T	HQ880803	–	HQ881005	–	HQ880734	HQ880947	HQ880875	–	–
Beauveria lii	RCEF5500 T	JN689372	–	JN689371	–	JN689373	JN689370	JN689374	–	–
Beauveria locustiphila	HUA 179217	JQ958609	–	–	–	–	–	JX003847	–	–
Beauveria locustiphila	HUA 179218 T	JQ958606	–	JQ958619	–	–	JX003845	JX003846	–	–
Beauveria loeiensis	BCC23107 T	MN401621	–	MN401447	–	–	MN401601	MN401545	–	–
Beauveria loeiensis	BCC66202	FJ459786	–	FJ459794	–	–	MK632156	MK632183	–	–
Beauveria majiangensis	GZU12141 T	MG052642	–	MG052640	–	MG052639	–	MG052644	–	–
Beauveria majiangensis	GZU12142	MG052643	–	MG052641	–	MG052638	–	MG052645	–	–
Beauveria malawiensis	ARSEF 4755	HQ880825	–	HQ881015	–	HQ880754	HQ880967	HQ880895	–	–
Beauveria malawiensis	BCC17613	HQ880824	–	HQ881016	–	HQ880755	HQ880968	HQ880896	–	–
Beauveria mimosiformis	BCC75812 T	MN401672	–	MN401500	–	MN401542	–	MN401597	–	–
Beauveria mimosiformis	BCC75813	MN401673	–	MN401501	–	MN401543	–	MN401598	–	–
Beauveria pseudobassiana	ARSEF 1855	HQ880796	–	HQ880999	–	HQ880727	HQ880940	HQ880868	–	–
Beauveria pseudobassiana	ARSEF 3405 T	AY532022	–	AY531931	–	HQ880723	HQ880936	HQ880864	–	–
Beauveria sinensis	RCEF3903 T	HQ270152	–	HQ270151	–	–	JX524284	JX524283	–	–
Beauveria sungii	ARSEF 1685 T	AY531990	–	AY531899	–	HQ880740	HQ880953	HQ880881	–	–
Beauveria sungii	ARSEF 5689	AY532030	–	AY531939	–	HQ880741	HQ880954	HQ880882	–	–
Beauveria varroae	ARSEF 2694	HQ880802	–	HQ881004	–	HQ880733	HQ880946	HQ880874	–	–
Beauveria varroae	ARSEF 8257 T	HQ880800	–	HQ881002	–	HQ880731	HQ880944	HQ880872	–	–
Beauveria vermiconia	ARSEF 2922 T	AY532012	–	AY531920	–	HQ880753	HQ880966	HQ880894	–	–
Beauveria yunnanensis	BUB2 T	–	–	MG642901	–	–	MG642871	–	–	–
Beauveria yunnanensis	BUB347	–	–	MG642900	–	–	MG642870	MG642857	–	–
Cephalotrichum asperulum	CBS 582.71 IT	KX923818	KX924027	KX924043	–	–	–	–	–	–
Clonostachys agrawalii	CBS 533.81 T	AF358241	–	–	AF358187	–	–	–	–	–
Clonostachys ambigua	PAD S00003 T	MT554898	–	–	–	–	–	–	–	–
Clonostachys apocyni	CBS 130.87 T	AF210688	–	–	AF358168	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Clonostachys aranearum	QLS 0625 T	NR164542	–	–	KU212400	–	–	–	–	–
Clonostachys aureofulvella	CBS 195.93	AF358226	–	–	AF358181	–	–	–	–	–
Clonostachys buxi	CBS 696.93	AF210667	–	–	AF358215	–	–	–	–	–
Clonostachys byssicola	CBS 36478 T	MH861151	–	–	AF358153	–	–	–	–	–
Clonostachys chongqingensis	HMAS 290894 T	OP205475	–	–	OP205324	–	–	–	–	–
Clonostachys chloroleuca	CML 1941 T	KC806286	–	–	KF871172	–	–	–	–	–
Clonostachys candelabrum	CBS 504.67	AF210668	–	–	–	–	–	–	–	–
Clonostachys capitata	CBS 218.93 T	AF358240	–	–	AF358188	–	–	–	–	–
Clonostachys chlorina	CBS 287.90 T	NR_137651	–	–	–	–	–	–	–	–
Clonostachys coccicola	HD 2016	KU720552	–	–	–	–	–	–	–	–
Clonostachys compactiuscula	CBS 592.93	AF358247	–	–	AF358192	–	–	–	–	–
Clonostachys compactiuscula	CBS 913.97 T	AF358245	–	–	AF358194	–	–	–	–	–
Clonostachys divergens	CBS 967.73 T	NR_137532	–	–	AF358191	–	–	–	–	–
Clonostachys epichloe	CBS 101037 T	AF210675	–	–	AF358209	–	–	–	–	–
Clonostachys eriocamporesiana	MFLUCC 17-2620 T	MN699132	–	–	MN699965	–	–	–	–	–
Clonostachys eriocamporesii	MFLUCC 19-0486 T	MN699133	–	–	–	–	–	–	–	–
Clonostachys farinosa	CBS 364.78 T	MH861151	–	–	AF358153	–	–	–	–	–
Clonostachys farinosa	CBS 914.97	AF358252	–	–	AF358151	–	–	–	–	–
Clonostachys grammicospora	CBS 209.93 T	AF210678	–	–	AF358206	–	–	–	–	–
Clonostachys grammicosporopsis	CBS 102834	AF358256	–	–	–	–	–	–	–	–
Clonostachys granuligera	PAD S00011 T	MT554904	–	–	–	–	–	–	–	–
Clonostachys impariphialis	HMAS 275560	KX096609	–	–	–	–	–	–	–	–
Clonostachys indica	RKV 2015 T	KT291441	–	–	–	–	–	–	–	–
Clonostachys intermedia	CBS 508.82 T	NR_137652	–	–	AF358205	–	–	–	–	–
Clonostachys kowhai	CBS 461.95 T	NR_154748	–	–	AF358170	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Clonostachys krabiensis	MFLUCC 160254 T	NR168189	–	–	–	–	–	–	–	–
Clonostachys leptoderma	HMAS 255834 T	OP205474	–	–	OP205323	–	–	–	–	–
Clonostachys levigata	CBS 948.97	AF210680	–	–	AF358196	–	–	–	–	–
Clonostachys lucifer	CBS 100008 T	AF210683	–	–	AF358208	–	–	–	–	–
Clonostachys miodochialis	CBS 997.69 T	NR_137649	–	–	AF358210	–	–	–	–	–
Clonostachys oblongispora	CBS 100285 T	AF358248	–	–	AF358169	–	–	–	–	–
Clonostachys oligospora	HMAS 290895 T	OP205473	–	–	OP205322	–	–	–	–	–
Clonostachys pallens	PAD S00004 T	MT554899	–	–	–	–	–	–	–	–
Clonostachys phyllophila	CBS 921.97 T	NR_137531	–	–	–	–	–	–	–	–
Clonostachys pityrodes	CBS 102033 T	AF210672	–	–	AF358212	–	–	–	–	–
Clonostachys pityrodes	CBS 126394	MH864280	–	–	–	–	–	–	–	–
Clonostachys pseudochroleuca	CBS 192.94 T	AF358238	–	–	AF358171	–	–	–	–	–
Clonostachys pseudostriata	CBS 119.87	AF358251	–	–	AF358183	–	–	–	–	–
Clonostachys ralfsii	CBS 129.87	AF210676	–	–	AF358195	–	–	–	–	–
Clonostachys rhinolophicola	**KUMCC 21-0438**	**ON426841**	–	–	**OR025936**	–	–	–	–	–
Clonostachys rhinolophicola	**KUMCC 21-0439 T**	**ON426840**	–	–	**OR025937**	–	–	–	–	–
Clonostachys rhizophaga	CBS 202.37 T	AF358225	–	–	AF358156	–	–	–	–	–
Clonostachys rogersoniana	CBS 58289	AF210691	–	–	KX185047	–	–	–	–	–
Clonostachys rosea	CBS 122171	DQ674381	–	–	–	–	–	–	–	–
Clonostachys rosea	CBS 193.94	AF210686	–	–	AF358159	–	–	–	–	–
Clonostachys rosea f. *catenulata*	CBS 154.27 T	NR_165993	–	–	AF358160	–	–	–	–	–
Clonostachys rosea f. *catenulata*	CBS 221.72b	AF358234	–	–	AF358203	–	–	–	–	–
Clonostachys rossmaniae	CBS 210.93	AF358227	–	–	AF358213	–	–	–	–	–
Clonostachys samuelsii	CBS 699.97 T	AF358236	–	–	AF358190	–	–	–	–	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Clonostachys saulensis	BRFM 2782 T	MK635054	–	–	–	–	–	–	–	–
Clonostachys sesquicillii	CBS 180.88 T	AF210666	–	–	AF358214	–	–	–	–	–
Clonostachys setosa	CBS 834.91	AF210670	–	–	AF358211	–	–	–	–	–
Clonostachys solani	CBS 101924	AF358232	–	–	AF358180	–	–	–	–	–
Clonostachys sporodochialis	CBS 101921 T	AF210685	–	–	AF358149	–	–	–	–	–
Clonostachys squamuligera	PAD S00020 T	MT554908	–	–	–	–	–	–	–	–
Clonostachys squamuligera	PAD S00021	MT554909	–	–	–	–	–	–	–	–
Clonostachys subquaternata	CBS 100003 T	MT537603	–	–	–	–	–	–	–	–
Clonostachys swieteniae	MFLU 18-2770 T	MT215573	–	–	–	–	–	–	–	–
Clonostachys vesiculosa	HMAS 183151 T	NR_119828	–	–	–	–	–	–	–	–
Clonostachys viticola	CAA 944 T	MK156282	–	–	MK156290	–	–	–	–	–
Clonostachys viticola	CAA 945	MK156283	–	–	MK156291	–	–	–	–	–
Clonostachys viticola	CAA 946	MK156284	–	–	MK156292	–	–	–	–	–
Clonostachys wenpingii	HMAS 172156 T	NR_119651	–	–	–	–	–	–	–	–
Clonostachys zelandiaenovae	CBS 100979 T	AF358229	–	–	–	–	–	–	–	–
Clonostachys zelandiaenovae	CBS 232.80	AF210684	–	–	AF358185	–	–	–	–	–
Cordyceps bifusispora	EFCC 5690	–	–	EF468746	–	–	EF468909	EF468854	–	–
Cordyceps bifusispora	EFCC 8260	–	–	EF468747	–	–	EF468910	EF468855	–	–
Cordyceps blackwelliae	TBRC 7253	MF140739	–	MF140825	–	–	MF140798	MF140774	–	–
Cordyceps blackwelliae	TBRC 7254	MF140738	–	MF140824	–	–	MF140797	MF140773	–	–
Cordyceps cateniannulata	TBRC 7258	MF140753	–	MF140850	–	–	–	MF140767	–	–
Cordyceps coleopterorum	CBS 110.73	AY624177	–	JF416028	–	–	JF416006	–	–	–
Cordyceps fumosorosea	CBS 244.31	MH855200	–	MF416503	–	–	MF416454	MF416660	–	–
Cordyceps javanica	TBRC 7259	MF140745	–	MF140831	–	–	MF140804	MF140780	–	–
Cordyceps javanica	TBRC 7260	MF140744	–	MF140830	–	–	MF140803	MF140779	–	–
Cordyceps lepidopterorum	EFCC 7263 T	MF140765	–	MF140819	–	–	MF140792	MF140768	–	–
Cordyceps lepidopterorum	EFCC 7264	MF140766	–	MF140820	–	–	MF140793	MF140769	–	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Cordyceps tenuipes	TBRC 7265	MF140741	–	MF140827	–	–	MF140800	MF140776	–	–
Cordyceps tenuipes	TBRC 7266	MF140742	–	MF140828	–	–	MF140801	MF140777	–	–
Fusarium acutatum	CBS 137545	–	–	MN533987	MN534062	–	MN534228	MW402587	MN534147	–
Fusarium acutatum	CBS 402.97	NR_111142	–	–	MT011051	–	–	–	–	–
Fusarium agapanthi	NRRL 54463 T	–	–	KU900630	KU900635	–	KU900625	KU900620	KU900611	–
Fusarium agapanthi	NRRL 54464	–	–	MN193856	KU900637	–	KU900627	MW402718	KU900613	–
Fusarium akasia	CMW54735 T	MN954357	–	MT009971	–	–	MT009931	–	–	–
Fusarium ananatum	CBS 118516 T	–	–	LT996091	MN534089	–	LT996137	MW402507	MW402376	–
Fusarium ananatum	CBS 118517	–	–	MN533988	MN534090	–	MN534229	MW402508	MN534157	–
Fusarium andiyazi	CBS 119856	–	–	MN533989	MN534081	–	MN534286	MW402523	MN534174	–
Fusarium andiyazi	CBS 119857 T	–	–	MN193854	LT996113	–	LT996138	MW402524	MN534175	–
Fusarium annulatum	CBS 131573	–	–	MW402037	MW402236	–	MW402796	MW402565	MW402406	–
Fusarium annulatum	CBS 258.54 T	–	–	MT010994	MT011041	–	MT010983	MT010944	MT010908	–
Fusarium annulatum	CBS 533.95	–	–	MW402138	MW402338	–	MW402817	–	MW402470	–
Fusarium anthophilum	CBS 119859	–	–	MN533991	MN534092	–	MN534233	MW402526	MN534164	–
Fusarium anthophilum	CBS 222.76 T	–	–	MW402114	MW402312	–	MW402811	MW402641	MW402451	–
Fusarium arcuatisporum	LC11639	MK280840	–	MK289586	–	–	MK289736	MK289798	MK289658	–
Fusarium arcuatisporum	LC12147 T	MK280802	–	MK289584	–	–	MK289739	MK289799	MK289697	–
Fusarium hipposidericola	**KUMCC 21-0724 T**	**ON426846**	–	**OR025993**	**OR025938**	**–**	**OR025909**	**–**	**OR022054**	–
Fusarium hipposidericola	**KUMCC 21-0725**	**ON426854**	–	**OR025994**	**OR025939**	**–**	**OR025910**	**–**	**OR022055**	–
Fusarium hipposidericola	**KUMCC 21-0726**	**ON426855**	–	**OR025995**	**OR025940**	**–**	**OR025911**	**–**	**OR022056**	–
Fusarium hipposidericola	**KUMCC 21-0727**	**ON426863**	–	**OR025996**	**OR025941**	**–**	**OR025912**	**–**	**OR022057**	–
Fusarium hipposidericola	**KUMCC 21-0728**	**ON426864**	–	**OR025997**	**OR025942**	**–**	**OR025913**	**–**	**OR022058**	–
Fusarium awan	CMW 54719 T	MN954345	–	MT009959	–	–	MT009919	–	–	–
Fusarium awaxy	CBS 119832	–	–	MN534057	MN534106	–	MN534237	MW402514	MN534170	–
Fusarium awaxy	CBS 139380	–	–	MN534058	MN534107	–	MN534240	MW402515	MN534172	–
Fusarium bactridioides	CBS 100057 T	–	–	MN533993	MN534112	–	MN534235	MW402490	MN534173	–
Fusarium bactridioides	NRRL 20476	–	–	AF160290	U34434	–	–	–	AF158343	–
Fusarium begoniae	CBS 403.97	–	–	MN193858	U61543	–	MN193886	MW402654	MW402460	–
Fusarium begoniae	CBS 452.97 T	–	–	MN533994	MN534101	–	MN534243	MW402675	MN534163	–
Fusarium beomiforme	CBS 740.97	U61674	–	–	–	–	JX171619	JX171506	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Fusarium brevicatenulatum	CBS 100196	–	–	MN193859	–	–	MN193887	MW402492	–	–
Fusarium brevicatenulatum	CBS 404.97 T	–	–	MN533995	MN534063	–	MN534295	MW402655	–	–
Fusarium buharicum	CBS 796.70	U34581	–	–	–	–	JX171563	JX171449	–	–
Fusarium bulbicola	CBS 220.76 T	–	–	KF466415	KF466437	–	MW402767	–	MW402450	–
Fusarium chinhoyiense	NRRL 25221 T	–	–	MN534050	MN534082	–	MN534262	MW402711	MN534196	–
Fusarium chinhoyiense	NY 001B5	–	–	MN534051	MN534083	–	MN534263	MW402725	MN534197	–
Fusarium circinatum	CBS 141668	–	–	MW402081	MW402280	–	–	MW402608	MW402425	–
Fusarium circinatum	CBS 405.97 T	–	–	MN533997	MN534097	–	MN534252	MW402656	MN534199	–
Fusarium citri	LC4879	MK280820	–	MK289615	–	–	MK289768	MK289827	MK289665	–
Fusarium citri	LC6896 T	MK280803	–	MK289617	–	–	MK289771	MK289828	MK289668	–
Fusarium coicis	NRRL 66233 T	–	–	KP083251	LT996115	–	KP083274	–	LT996178	–
Fusarium compactum	NRRL 13829	–	–	–	–	–	JX171574	JX171460	–	–
Fusarium concentricum	CBS 450.97 T	–	–	AF160282	MW402334	–	JF741086	MW402674	MW402467	–
Fusarium concentricum	CBS 453.97	–	–	MN533998	MN534123	–	MN534264	MW402676	MN534216	–
Fusarium cugenangense	CBS 130308	MW827607	–	MH485011	–	–	JX171625	JX171512	–	–
Fusarium curvatum	NRRL 22902	–	–	AF160312	U34424	–	LT575065	LT996203	AF158365	–
Fusarium denticulatum	CBS 406.97	–	–	MN533999	MN534067	–	MN534273	MW402657	MN534185	–
Fusarium denticulatum	CBS 407.97 T	–	–	MN534000	MN534068	–	MN534274	MW402658	MN534186	–
Fusarium dlaminii	CBS 119860 T	–	–	MW401995	MW402195	–	KU171701	KU171681	MW402388	–
Fusarium dlaminii	CBS 175.88	–	–	MN534002	MN534138	–	MN534256	MW402623	MN534150	–
Fusarium echinatum	CBS 146496	–	–	MW834272	MW834300	–	MW834003	MW834186	MW834109	–
Fusarium echinatum	CBS 146497 T	–	–	MW834273	MW834301	–	MW834004	MW834187	MW834110	–
Fusarium equiseti	CBS 245.61	MH858038	–	–	–	–	JX171595	JX171481	–	–
Fusarium ficicrescens	CBS 125178 T	–	–	KU604452	KP662896	–	KT154002	MW402546	KU603958	–
Fusarium ficicrescens	CBS 125181	–	–	MN534007	MN534072	–	MN534282	MW402548	MN534177	–
Fusarium flocciferum	CBS 831.85	–	–	–	–	–	JX171627	JX171514	–	–
Fusarium fracticaudum	CBS 137234 T	–	–	KJ541059	KJ541051	–	LT996144	LT996196	LT996179	–
Fusarium fractiflexum	NRRL 28852 T	–	–	AF160288	AF160315	–	LT575064	–	AF158341	–
Fusarium fredkrugeri	CBS 144209 T	–	–	LT996097	LT996118	–	LT996147	LT996199	LT996181	–
Fusarium fredkrugeri	CBS 144495	–	–	LT996096	LT996117	–	LT996146	LT996198	LT996180	–
Fusarium fujikuroi	CBS 221.76 T	–	–	MN534010	MN534130	–	KU604255	MW402640	–	–
Fusarium fujikuroi	CBS 257.52	–	–	MW402119	MW402317	–	MW402812	MW402645	MW402454	–
Fusarium globosum	CBS 428.97 T	–	–	KF466417	MN534124	–	KF466406	MW402668	MN534218	–
Fusarium globosum	CBS 431.97	–	–	MW402131	MW402330	–	MW402816	MW402669	MW402465	–
Fusarium graminearum	CBS 123657	DQ459823	–	AY452957	–	–	JX171644	JX171531	–	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Fusarium guilinense	LC12160 T	MK280837	–	MK289594	–	–	MK289747	MK289831	MK289652	–
Fusarium guilinense	NRRL 13335	GQ505679	–	GQ505590	–	–	GQ505768	–	GQ505502	–
Fusarium guttiforme	CBS 409.97 T	–	–	MT010999	MT011048	–	MT010967	MT010938	MT010901	–
Fusarium guttiforme	NRRL 22945	–	–	AF160297	U34420	–	JX171618	JX171505	AF158350	–
Fusarium hainanense	LC11638 T	MK280836	–	MK289581	–	–	MK289735	MK289833	MK289657	–
Fusarium hainanense	LC12161	MK280793	–	MK289595	–	–	MK289748	MK289832	MK289648	–
Fusarium heterosporum	CBS 720.79	MW827609	–	–	–	–	JX171594	JX171480	–	–
Fusarium humuli	CQ1027	MK280843	–	MK289567	–	–	MK289721	MK289838	MK289709	–
Fusarium humuli	CQ1039 T	MK280845	–	MK289570	–	–	MK289724	MK289840	MK289712	–
Fusarium inflexum	CBS 716.74	–	–	AF008479	U34435	–	JX171583	JX171469	AF158366	–
Fusarium ipomoeae	LC12165 T	MK280832	–	MK289599	–	–	MK289752	MK289859	MK289704	–
Fusarium ipomoeae	LC12166	MK280791	–	MK289600	–	–	MK289753	MK289860	MK289706	–
Fusarium luffae	**KUMCC 21-0734**	**ON426858**	–	**OR025998**	**OR025943**	**–**	**OR025914**	**OR022017**	**–**	–
Fusarium irregulare	LC12146	MK280831	–	MK289583	–	–	MK289738	MK289865	MK289682	–
Fusarium irregulare	LC7188 T	MK280829	–	MK289629	–	–	MK289783	MK289863	MK289680	–
Fusarium konzum	CBS 119849 T	–	–	LT996098	MN534095	–	MW402733	MW402519	LT996182	–
Fusarium konzum	CBS 139382	–	–	MW402071	MW402270	–	MW402804	MW402598	MW402418	–
Fusarium lactis	CBS 411.97 T	–	–	MN193862	MN534077	–	MN534275	MW402659	MN534178	–
Fusarium lactis	CBS 420.97	–	–	MN534015	MN534078	–	MN534296	MW402667	MN534181	–
Fusarium lateritium	NRRL 13622	–	–	–	–	–	JX171571	JX171457	–	–
Fusarium longicornicola	NRRL 52706 T	–	–	JF740788	MW402360	–	JF741114	–	MW402487	–
Fusarium longicornicola	NRRL 52712	–	–	JF740794	MW402361	–	JF741120	MW402716	MW402488	–
Fusarium longipes	NRRL 20723	–	–	–	–	–	JX171596	JX171483	–	–
Fusarium luffae	CQ1038	MK280852	–	MK289569	–	–	MK289723	MK289870	MK289711	–
Fusarium luffae	LC12167 T	MK280807	–	MK289601	–	–	MK289754	MK289869	MK289698	–
Fusarium lumajangense	InaCCF872 T	–	–	LS479441	LS479433	–	LS479850	–	–	–
Fusarium lumajangense	InaCCF993	–	–	LS479442	LS479434	–	LS479851	–	–	–
Fusarium madaense	CBS 146656	–	–	MW402097	MW402296	–	MW402763	MW402618	MW402438	–
Fusarium madaense	CBS 146669 T	–	–	MW402098	MW402297	–	MW402764	MW402619	MW402439	–
Fusarium mangiferae	CBS 119853	–	–	MN534016	MN534140	–	MN534270	MW402522	MN534225	–
Fusarium mangiferae	CBS 120994 T	–	–	MN534017	MN534128	–	MN534271	MW402530	MN534224	–
Fusarium mekan	CMW 54714 T	MN954342	–	MT009956	–	–	MT009916	–	–	–
Fusarium melanochlorum	CBS 202.65	MH858541	–	–	–	–	JX171649	JX171537	–	–
Fusarium menglaense	**KUMCC 21-0717 T**	**ON426850**	–	**OR025999**	**OR025944**	**–**	**OR025915**	**OR022018**	**OR022059**	–
Fusarium menglaense	**KUMCC 21-0718**	**ON426852**	–	**OR02600**	**OR025945**	**–**	**OR025916**	**OR022019**	**OR022060**	–
Fusarium mexicanum	NRRL 53147 T	–	–	GU737282	GU737494	–	MN724973	MG838088	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Fusarium mexicanum	NRRL 53580	–	–	GU737421	GU737313	–	–	–	GU737394	–
Fusarium mundagurra	RGB5717 T	–	–	KP083256	MN534146	–	KP083276	–	MN534214	–
Fusarium musae	CBS 624.87 T	–	–	FN552086	FN545368	–	MW402772	MW402689	MW402474	–
Fusarium musae	NRRL 28893	–	–	FN552092	FN545374	–	FN552114	–	FN552070	–
Fusarium nanum	LC12168 T	MK280794	–	MK289602	–	–	MK289755	MK289871	MK289651	–
Fusarium nanum	LC1384	MK280842	–	MK289611	–	–	MK289764	MK289872	MK289661	–
Fusarium napiforme	CBS 135139	–	–	MN534019	MN534084	–	MN534290	MW402572	MN534183	–
Fusarium napiforme	CBS 748.97 T	–	–	MN193863	MN534085	–	MN534291	MW402701	MN534192	–
Fusarium nirenbergiae	CBS 744.97	–	–	AF160312	U34424	–	LT575065	–	AF158365	–
Fusarium nurragi	CBS 392.96	MW827610	–	–	–	–	JX171650	JX171538	–	–
Fusarium nygamai	CBS 413.97 T	–	–	MW402127	MW402325	–	MW402815	MW402660	MW402462	–
Fusarium nygamai	CBS 749.97 T	–	–	MW402151	MW402151	–	EF470114	MW402703	MW402479	–
Fusarium ophioides	CBS 118512 T	–	–	MN534022	MN534118	–	MN534303	–	MN534209	–
Fusarium ophioides	CBS 118513	–	–	MN534023	MN534119	–	MN534300	–	MN534202	–
Fusarium parvisorum	CMW 25267 T	–	–	KJ541060	KJ541055	–	–	–	–	–
Fusarium phyllophilum	CBS 216.76 T	–	–	MN193864	KF466443	–	KF466410	MW402637	KF466333	–
Fusarium phyllophilum	CBS 246.61	–	–	MW402118	MW402316	–	–	MW402644	MW402453	–
Fusarium pilosicola	NRRL 29123	–	–	MN534054	MN534098	–	MN534247	–	MN534165	–
Fusarium pilosicola	NRRL 29124 T	–	–	MN534055	MN534099	–	MN534248	–	MN534159	–
Fusarium poae	NRRL 13714	–	–	–	–	–	JX171572	JX171458	–	–
Fusarium prieskaense	CBS 146498T	–	–	MW834275	MW834303	–	MW834007	MW834190	MW834112	–
Fusarium prieskaense	CPC 30825	–	–	MW834274	MW834302	–	MW834006	MW834189	MW834111	–
Fusarium proliferatum	CBS 480.96 T	–	–	MN534059	MN534129	–	MN534272	–	MN534217	–
Fusarium pseudoanthophilum	CBS 414.97 T	–	–	MW402128	MW402326	–	–	MW402661	MW402463	–
Fusarium pseudoanthophilum	CBS 745.97	–	–	MW402148	MW402349	–	MW402820	MW402697	MW402476	–
Fusarium pseudocircinatum	CBS 449.97 T	–	–	AF160271	MN534069	–	MN534277	MW402673	MN534190	–
Fusarium pseudocircinatum	CBS 455.97	–	–	MN534029	MN534070	–	MN534276	–	MN534184	–
Fusarium pseudograminearum	CBS 109956	DQ459871	–	AF212468	–	–	JX171637	JX171524	–	–
Fusarium pseudonygamai	CBS 417.97 T	–	–	AF160263	MN534066	–	MN534285	MW402664	AF158316	–
Fusarium pseudonygamai	CBS 484.94	–	–	MN534031	MN534065	–	MN534284	MW402681	MN534195	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Fusarium ramigenum	CBS 418.97 T	–	–	KF466423	MN534145	–	KF466412	MW402665	MN534187	–
Fusarium ramigenum	CBS 526.97	–	–	MN534032	MN534086	–	MN534292	MW402682	MN534188	–
Fusarium redolens	CBS 743.97	U34565	–	MT409452	–	–	JX171616	JX171503	–	–
Fusarium rhinolophicola	**KUMCC 21-0448**	**ON426847**	–	**OR026002**	**OR025947**	**–**	**OR025918**	**OR022021**	**OR022062**	–
Fusarium rhinolophicola	**KUMCC 21-0449 T**	**ON426848**	–	**OR026001**	**OR025946**	**–**	**OR025917**	**OR022020**	**OR022061**	–
Fusarium rhinolophicola	**KUMCC 21-0450**	**ON426849**	–	**OR026003**	**OR025948**	**–**	**OR025919**	**OR022022**	**OR022063**	–
Fusarium sacchari	CBS 135143	–	–	MW402047	MW402246	–	MW402799	–	MW402409	–
Fusarium sacchari	CBS 139376	–	–	MW402069	MW402268	–	MW402803	MW402596	–	–
Fusarium sambucinum	CBS 146.95	–	–	MW834277	–	–	JX171606	JX171493	–	–
Fusarium sarcochroum	CBS 745.79	MW827611	–	MW834278	–	–	JX171586	JX171472	–	–
Fusarium scirpi	NRRL 13402	GQ505681	–	GQ505592	–	–	JX171566	JX171452	–	–
Fusarium secorum	NRRL 62593 T	–	–	KJ189225	–	–	–	–	KJ189235	–
Fusarium secorum	NRRL 62594	–	–	KJ189228	–	–	–	–	KJ189238	–
Fusarium siculi	CBS 142222 T	–	–	LT746214	LT746346	–	LT746327	–	LT746189	–
Fusarium siculi	CPC 27189	–	–	LT746215	LT746347	–	LT746328	–	LT746190	–
Fusarium sororula	CBS 137242 T	–	–	KJ541067	KJ541057	–	LT996153	LT996206	LT996184	–
Fusarium sterilihyposum	NRRL 25623 T	–	–	MN193869	AF160316	–	MN193897	MW402713	AF158353	–
Fusarium sterilihyposum	NRRL 53991	–	–	GU737413	GU737305	–	–	–	GU737386	–
Fusarium stilboides	NRRL 20429	–	–	–	–	–	JX171582	JX171468	–	–
Fusarium subglutinans	CBS 215.76	–	–	MN534061	MN534109	–	MN534241	MW402636	MN534171	–
Fusarium subglutinans	CBS 536.95	–	–	MW402139	MW402339	–	MW402836	MW402685	MW402471	–
Fusarium sublunatum	CBS 189.34 T	HQ897830	–	–	–	–	JX171565	JX171451	–	–
Fusarium succisae	CBS 187.34	–	–	MW402109	MW402307	–	MW402810	–	MW402448	–
Fusarium succisae	CBS 219.76 T	–	–	AF160291	U34419	–	MW402766	MW402639	AF158344	–
Fusarium sudanense	CBS 454.97 T	–	–	MN534037	MN534073	–	MN534278	MW402677	MN534179	–
Fusarium sudanense	CBS 675.94	–	–	MN534038	MN534074	–	MN534279	MW402693	MN534182	–
Fusarium temperatum	CBS 135538	–	–	MN534039	MN534111	–	MN534239	MW402575	MN534168	–
Fusarium temperatum	CBS 135539	–	–	MN534040	MN534110	–	MN534242	MW402576	MN534169	–
Fusarium terricola	CBS 119850	–	–	MN534041	MN534075	–	MN534280	MW402520	MN534180	–
Fusarium terricola	CBS 483.94 T	–	–	MN534042	MN534076	–	LT996156	MW402680	MN534189	–
Fusarium thapsinum	CBS 100312	–	–	MW401961	MW402162	–	MW402780	MW402494	MW402365	–
Fusarium thapsinum	CBS 100313	–	–	MW401962	MW402163	–	MW402781	MW402495	MW402366	–
Fusarium tjaetaba	NRRL 66243T	–	–	KP083263	GU737296	–	KP083275	–	LT996187	–
Fusarium torreyae	CBS 133858 T	HM068344	–	HM068337	–	–	JX171660	JX171548	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Fusarium tricinctum	CBS 393.93 T	HM068317	–	AB674263	–	–	JX171629	JX171516	–	–
Fusarium tupiense	CML345	–	–	DQ452861	DQ445783	–	–	–	–	–
Fusarium tupiense	NRRL 53996	–	–	DQ452860	DQ445782	–	–	–	–	–
Fusarium udum	CBS 178.32	–	–	AF160275	U34433	–	LT996172	MW402624	MW402442	–
Fusarium udum	CBS 747.79 T	–	–	MN193872	MN534141	–	MN534258	MW402699	MN534154	–
Fusarium variasi	CMW 53734	MN954356	–	MT009953	–	–	MT009913	–	–	–
Fusarium venenatum	NRRL 22196	–	–	–	–	–	JX171607	JX171494	–	–
Fusarium verticillioides	CBS 141.59	–	–	MW402080	MW402279	–	–	MW402607	MW402424	–
Fusarium verticillioides	CBS 218.76 T	–	–	MW402113	MW402311	–	–	MW402638	MW402449	–
Fusarium volatile	CBS 143874 T	–	–	LR596007	LR596008	–	LR596006	–	MK984595	–
Fusarium volatile	NRRL 25615	–	–	AF160304	AF160320	–	–	–	AF158357	–
Fusarium warna	CMW 54720	MN954346	–	MT009960	–	–	MT009920	–	–	–
Fusarium werrikimbe	CBS 125535 T	–	–	–	MN534104	–	MN534304	–	MN534203	–
Fusarium xishuangbannaensee	**KUMCC 21-0432 T**	**ON426859**	–	**OR026004**	**OR025949**	**–**	**OR025920**	**OR022023**	**OR022064**	–
Fusarium xishuangbannaensee	**KUMCC 21-0731**	**ON426860**	–	**OR026005**	**OR025950**	**–**	**OR025921**	**OR022024**	**OR022065**	–
Fusarium xylarioides	CBS 258.52 T	–	–	MN193874	AY707118	–	HM068355	MW402646	MW402455	–
Fusarium xylarioides	CBS 749.79	–	–	MN534049	MN534143	–	MN534259	MW402702	AF158326	–
Fusarium xyrophilum	NRRL 62721 T	–	–	MN193877	–	–	MN193905	MW402721	–	–
Fusarium xyrophilum	NRRL 66890	–	–	MN193876	–	–	MN193904	MW402724	–	–
Fusarium yunnanense	**KUMCC 21-0732 T**	**ON426851**	–	**OR026006**	**OR025951**	**–**	**OR025922**	**OR022025**	**OR022066**	–
Fusarium yunnanense	**KUMCC 21-0733**	**ON426853**	–	**OR026007**	**OR025952**	**–**	**OR025923**	**OR022026**	**OR022067**	–
Hevansia arachnophila	NHJ 10469 T	–	–	EU369008	–	–	–	EU369047	–	–
Hevansia arachnophila	NHJ2633	MH532899	–	MH521916	–	–	–	–	–	–
Hevansia cinerea	BCC47914	–	–	MH521888	–	–	MH521851	MH521821	–	–
Hevansia cinerea	NHJ 3510 T	–	–	EU369009	–	–	EU369070	EU369048	–	–
Hevansia nelumboides	BCC 2093	–	–	MF416473	–	–	MF416437	–	–	–
Hevansia nelumboides	TNS 16306 T	–	–	MF416475	–	–	MF416438	–	–	–
Hevansia novoguineensis	NHJ 11923	–	–	EU369013	–	–	EU369072	EU369052	–	–
Hevansia novoguineensis	NHJ 4314	–	–	EU369012	–	–	EU369071	EU369051	–	–
Hypomyces dactylarioides	CBS 14178 T	NR_111430	–	HF911722	–	–	FN868683	–	–	–
Hypomyces lactifluorum	TAAM 170476	FN859432	–	FN868751	–	–	EU710773	–	–	–
Hypomyces odoratus	GAm 329	FN859434	–	FN868753	–	–	FN868688	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Hypomyces rosellus	TFC 201071	FN859443	–	HF911779	–	–	FN868697	–	–	–
Hypomyces samuelsii	TFC 2007-23	FN859451	–	FN868769	–	–	FN868705	–	–	–
Lecythophora lignicola	CBS 267.33	HE610335	FR691986	–	HE610353	–	–	–	–	HE610345
Microascus alveolaris	CBS 139501 T	KX923829	KX924029	KX924053	KX924263	–	–	–	–	–
Microascus atrogriseus	CBS 295.52 T	LM652433	KX924030	KX924056	KX924265	–	–	–	–	–
Microascus brunneosporus	CBS 138276 T	KX923834	HG380497	HG380420	KX924269	–	–	–	–	–
Microascus chartarus	CBS 294.52 T	LM652393	HG380463	HG380386	LM652607	–	–	–	–	–
Microascus chinensis	CBS 139628 T	LN850760	LN850809	LN850906	LN850858	–	–	–	–	–
Microascus cinereus	CBS 138709 NT	KX923837	KX924031	KX924063	KX924272	–	–	–	–	–
Microascus cirrosus	CBS 217.31 T	KX923838	KX924032	KX924064	KX924273	–	–	–	–	–
Microascus cleistocarpus	CBS 134638 T	KX923851	KX924033	KX924076	KX924286	–	–	–	–	–
Microascus croci	CBS 158.44 T	KX923852	LM652508	KX924077	KX924287	–	–	–	–	–
Microascus expansus	CBS 138127 T	KX923859	HG380492	KX924084	KX924294	–	–	–	–	–
Microascus fusisporus	CBS 896.68 T	LM652432	LN850825	HG380372	LM652645	–	–	–	–	–
Microascus gracilis	CBS 369.70 T	KX923861	HG380467	KX924086	KX924297	–	–	–	–	–
Microascus hollandicus	CBS 141582 T	KX923869	KX924034	KX924094	KX924304	–	–	–	–	–
Microascus hyalinus	CBS 766.70 T	KX923870	LM652513	LM652564	KX924305	–	–	–	–	–
Microascus intricatus	CBS 138128 T	KX923872	HG380496	HG380419	KX924307	–	–	–	–	–
Microascus longicollis	CBS 752.97	KX923874	KX924035	KX924097	KX924309	–	–	–	–	–
Microascus longirostris	CBS 196.61T	LM652421	LM652515	LM652566	LM652634	–	–	–	–	HE610345
Microascus macrosporus	CBS 662.71	LM652423	LM652517	LM652568	LM652636	–	–	–	–	–
Microascus melanosporus	CBS 272.60 T	KX923876	KX924036	LM652572	KX924311	–	–	–	–	–
Microascus micronesiensis	CBS 141523 T	KX923905	KX924037	KX924128	KX924340	–	–	–	–	–
Microascus murinus	CBS 830.70 T	KX923908	HG380481	KX924131	KX924342	–	–	–	–	–
Microascus onychoides	CBS 139629 T	LN850774	LN850823	LN850920	LN850871	–	–	–	–	–
Microascus paisii	CBS 213.27 T	LM652434	LM652518	KX924133	KX924343	–	–	–	–	–
Microascus pseudolongirostris	CBS 462.97 T	LN850782	LN850831	KX924147	LN850879	–	–	–	–	–
Microascus pseudopaisii	CBS 141581 T	KX923923	KX924038	KX924148	KX924358	–	–	–	–	–
Microascus pyramidus	CBS 212.65 T	KX923925	HG380435	KX924150	KX924360	–	–	–	–	–
Microascus restrictus	CBS 138277 T	KX923928	HG380494	KX924152	KX924362	–	–	–	–	–
Microascus senegalensis	CBS 277.74 T	KX923929	LM652523	KX924153	KX924363	–	–	–	–	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Microascus senegalensis	CBS 594.78T	LN850781	LN850830	KX924055	LN850878	–	–	–	–	–
Microascus terreus	CBS 601.67 T	LN850783	LN850832	LN850928	LN850880	–	–	–	–	–
Microascus trautmannii	CBS 141583 T	KX923942	KX924039	KX924166	KX924376	–	–	–	–	–
Microascus trigonosporus	CBS 139501 T	KX923829	KX924029	KX924053	KX924263	–	–	–	–	–
Microascus verrucosus	CBS 138278 T	KX923950	HG380493	HG380416	LM652658	–	–	–	–	–
Microcera coccophila	CBS 310.34	MH855540	–	–	–	–	JX171576	JX171462	–	–
Microcera diploa	CBS 735.79	MW827623	–	–	–	–	JX171577	JX171463	–	–
Nectria cinnabarina	CBS 279.48	AF163025	–	–	HM484802	–	–	–	–	–
Nectria eustromatica	CBS 125578	HM534897	–	HM534876	–	–	HM534887	–	–	–
Neopestalotiopsis acrostichi	MFLUCC 17-1754 T	MK764272	–	MK764316	MK764338	–	–	–	–	–
Neopestalotiopsis acrostichi	MFLUCC 17-1755	MK764273	–	MK764317	MK764339	–	–	–	–	–
Neopestalotiopsis alpapicalis	MFLUCC 17-2544 T	MK357772	–	MK463547	MK463545	–	–	–	–	–
Neopestalotiopsis alpapicalis	MFLUCC 17-2545	MK357773	–	MK463548	MK463546	–	–	–	–	–
Neopestalotiopsis aotearoa	CBS 367.54 T	KM199369	–	KM199526	KM199454	–	–	–	–	–
Neopestalotiopsis asiatica	MFLUCC 12-0286 T	JX398983	–	JX399049	JX399018	–	–	–	–	–
Neopestalotiopsis australis	CBS 114159 T	KM199348	–	KM199537	KM199432	–	–	–	–	–
Neopestalotiopsis brasiliensis	COAD 2166 T	MG686469	–	MG692402	MG692400	–	–	–	–	–
Neopestalotiopsis camelliae-oleiferae	CSUFTCC81 T	OK493585	–	OK507955	OK562360	–	–	–	–	–
Neopestalotiopsis camelliae-oleiferae	CSUFTCC82	OK493586	–	OK507956	OK562361	–	–	–	–	–
Neopestalotiopsis cavernicola	KUMCC 20-0269 T	MW545802	–	MW550735	MW557596	–	–	–	–	–
Neopestalotiopsis cavernicola	KUMCC 20-0332	MW581238	–	MW590327	MW590328	–	–	–	–	–
Neopestalotiopsis chiangmaiensis	MFLUCC 18-0113 T	–	–	MH388404	MH412725	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Neopestalotiopsis chrysea	MFLUCC 12-0261 T	JX398985	–	JX399051	JX399020	–	–	–	–	–
Neopestalotiopsis chrysea	MFLUCC 12-0262	JX398986	–	JX399052	JX399021	–	–	–	–	–
Neopestalotiopsis clavispora	MFLUCC 12-0280	JX398978	–	JX399044	JX399013	–	–	–	–	–
Neopestalotiopsis clavispora	MFLUCC 12-0281 T	JX398979	–	JX399045	JX399014	–	–	–	–	–
Neopestalotiopsis cocoës	MFLUCC 15-0152 T	KX789687	–	KX789689	—	–	–	–	–	–
Neopestalotiopsis coffeae-arabicae	HGUP4015	KF412647	–	KF412644	KF412641	–	–	–	–	–
Neopestalotiopsis coffeae-arabicae	HGUP4019 T	KF412649	–	KF412646	KF412643	–	–	–	–	–
Neopestalotiopsis cubana	CBS 600.96 T	KM199347	–	KM199521	KM199438	–	–	–	–	–
Neopestalotiopsis dendrobii	MFLUCC 14-0099	MK993570	–	MK975828	MK975834	–	–	–	–	–
Neopestalotiopsis dendrobii	MFLUCC 14-0106 T	MK993571	–	MK975829	MK975835	–	–	–	–	–
Neopestalotiopsis drenthii	BRIP 72263a	MZ303786	–	MZ344171	MZ312679	–	–	–	–	–
Neopestalotiopsis drenthii	BRIP 72264a T	MZ303787	–	MZ344172	MZ312680	–	–	–	–	–
Neopestalotiopsis egyptiaca	CBS 22294 T	KP943747	–	KP943748	KP943746	–	–	–	–	–
Neopestalotiopsis ellipsospora	MFLUCC 12-0283 T	JX398980	–	JX399047	JX399016	–	–	–	–	–
Neopestalotiopsis eucalypticola	CBS 264.37 T	KM199376	–	KM199551	KM199431	–	–	–	–	–
Neopestalotiopsis eucalyptorum	MEAN 1308 T	MW794108	–	MW805397	MW802841	–	–	–	–	–
Neopestalotiopsis eucalyptorum	MEAN 1309	MW794098	–	MW805398	MW802831	–	–	–	–	–
Neopestalotiopsis foedans	CGMCC 3.9123 T	JX398987	–	JX399053	JX399022	–	–	–	–	–
Neopestalotiopsis foedans	CGMCC 3.9178	JX398989	–	JX399055	JX399024	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Neopestalotiopsis formicarum	CBS 115.83	KM199344	–	KM199519	KM199444	–	–	–	–	–
Neopestalotiopsis formicarum	CBS 362.72 T	KM199358	–	KM199517	KM199455	–	–	–	–	–
Neopestalotiopsis guajavae	FMB0026 T	MF783085	–	MH460868	MH460871	–	–	–	–	–
Neopestalotiopsis guajavae	FMB0027	MF783084	–	MH460869	MH460872	–	–	–	–	–
Neopestalotiopsis guajavicola	FMB0129 T	MH209245	–	MH460870	MH460873	–	–	–	–	–
Neopestalotiopsis hispanica	MEAN 1310 T	MW794107	–	MW805399	MW802840	–	–	–	–	–
Neopestalotiopsis hispanica	MEAN 1311	MW794106	–	MW805400	MW802839	–	–	–	–	–
Neopestalotiopsis honoluluana	CBS 111535	KM199363	–	KM199546	KM199461	–	–	–	–	–
Neopestalotiopsis honoluluana	CBS 114495 T	KM199364	–	KM199548	KM199457	–	–	–	–	–
Neopestalotiopsis hydeana	MFLUCC 20–0132T	MW266069	–	MW251129	MW251119	–	–	–	–	–
Neopestalotiopsis iberica	MEAN 1313 T	MW794111	–	MW805402	MW802844	–	–	–	–	–
Neopestalotiopsis iberica	MEAN 1314	MW794114	–	MW805403	MW802847	–	–	–	–	–
Neopestalotiopsis iranensis	CBS 137767	KM074045	–	KM074053	KM074056	–	–	–	–	–
Neopestalotiopsis iranensis	CBS 137768T	KM074048	–	KM074051	KM074057	–	–	–	–	–
Neopestalotiopsis javaensis	CBS 257.31 T	KM199357	–	KM199543	KM199437	–	–	–	–	–
Neopestalotiopsis keteleeria	MFLUCC 13–0915 T	KJ023087	–	KJ023089	KJ023088	–	–	–	–	–
Neopestalotiopsis longiappendiculata	MEAN 1315 T	MW794112	–	MW805404	MW802845	–	–	–	–	–
Neopestalotiopsis longiappendiculata	MEAN 1316	MW794103	–	MW805405	MW802836	–	–	–	–	–
Neopestalotiopsis lusitanica	MEAN 1317 T	MW794110	–	MW805406	MW802843	–	–	–	–	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Neopestalotiopsis lusitanica	MEAN 1320	MW794097	–	MW805409	MW802830	–	–	–	–	–
Neopestalotiopsis lusitanica	MEAN 132	MW794101	–	MW805410	MW802834	–	–	–	–	–
Neopestalotiopsis macadamiae	BRIP 63737c T	KX186604	–	KX186627	KX186654	–	–	–	–	–
Neopestalotiopsis macadamiae	BRIP 63742a	KX186599	–	KX186629	KX186657	–	–	–	–	–
Neopestalotiopsis maddoxii	BRIP 72262a	MZ303781	–	MZ344166	MZ312674	–	–	–	–	–
Neopestalotiopsis maddoxii	BRIP 72266a T	MZ303782	–	MZ344167	MZ312675	–	–	–	–	–
Neopestalotiopsis magna	MFLUCC 12-652 T	KF582795	–	KF582791	KF582793	–	–	–	–	–
Neopestalotiopsis mesopotamica	CBS 299.74	KM199361	–	KM199541	KM199435	–	–	–	–	–
Neopestalotiopsis mesopotamica	CBS 336.86 T	KM199362	–	KM199555	KM199441	–	–	–	–	–
Neopestalotiopsis mianyangensis	CGMCC 3.23555 T	OP546681	–	OP723490	OP672161	–	–	–	–	–
Neopestalotiopsis mianyangensis	UESTCC 22.0006	OP082291	–	OP204793	OP235979	–	–	–	–	–
Neopestalotiopsis natalensis	CBS 138.41 T	KM199377	–	KM199552	KM199466	–	–	–	–	–
Neopestalotiopsis nebuloides	BRIP 66617 T	MK966338	–	MK977633	MK977632	–	–	–	–	–
Neopestalotiopsis olumideae	BRIP 72273a T	MZ303790	–	MZ344175	MZ312683	–	–	–	–	–
Neopestalotiopsis olumideae	BRIP 72283a	MZ303791	–	MZ344176	MZ312684	–	–	–	–	–
Neopestalotiopsis paeoniae-suffruticosae	CGMCC 3.23554 T	OP082292	–	OP204794	OP235980	–	–	–	–	–
Neopestalotiopsis paeoniae-suffruticosae	UESTCC 22.0007	OP082293	–	OP204795	OP235981	–	–	–	–	–
Neopestalotiopsis paeoniae-suffruticosae	**KUMCC 21-0426**	**ON426867**	–	**OR025971**	**OR025932**	–	–	–	–	–
Neopestalotiopsis paeoniae-suffruticosae	**KUMCC 21-0427**	**ON426868**	–	**OR025972**	**OR025933**	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Neopestalotiopsis pandanicola	KUMCC 17-0175	–	–	MH388389	MH412720	–	–	–	–	–
Neopestalotiopsis pernambucana	RV02	KJ792467	–	KU306740	–	–	–	–	–	–
Neopestalotiopsis pernambucana	URM7148 T	KJ792466	–	KU306739	–	–	–	–	–	–
Neopestalotiopsis perukae	FMB0127 T	MH209077	–	MH523647	MH460876	–	–	–	–	–
Neopestalotiopsis perukae	FMB0128	MH209246	–	MH523646	MH460875	–	–	–	–	–
Neopestalotiopsis petila	MFLUCC 17-1737 T	MK764275	–	MK764319	MK764341	–	–	–	–	–
Neopestalotiopsis petila	MFLUCC 17-1738	MK764276	–	MK764320	MK764342	–	–	–	–	–
Neopestalotiopsis phangngaensis	MFLUCC 18-0119 T	MH388354	–	MH388390	MH412721	–	–	–	–	–
Neopestalotiopsis piceana	CBS 254.32	KM199372	–	KM199529	KM199452	–	–	–	–	–
Neopestalotiopsis piceana	CBS 394.48 T	KM199368	–	KM199527	KM199453	–	–	–	–	–
Neopestalotiopsis protearum	CBS 114178 T	JN712498	–	LT853201	KM199463	–	–	–	–	–
Neopestalotiopsis psidii	FMB0028 T	MF783082	–	MH460874	MH477870	–	–	–	–	–
Neopestalotiopsis rhapidis	GUCC 21501 T	MW931620	–	MW980442	MW980441	–	–	–	–	–
Neopestalotiopsis rhizophorae	MFLUCC 17-1550 T	MK764277	–	MK764321	MK764343	–	–	–	–	–
Neopestalotiopsis rhizophorae	MFLUCC 17-1551	MK764278	–	MK764322	MK764344	–	–	–	–	–
Neopestalotiopsis rhododendri	GUCC 21504 T	MW979577	–	MW980444	MW980443	–	–	–	–	–
Neopestalotiopsis rhododendri	GUCC 21505	MW979576	–	MW980446	MW980445	–	–	–	–	–
Neopestalotiopsis rosae	CBS 101057 T	KM199359	–	KM199523	KM199429	–	–	–	–	–
Neopestalotiopsis rosae	CBS 124745	KM199360	–	KM199524	KM199430	–	–	–	–	–
Neopestalotiopsis rosicola	CFCC 51992 T	KY885239	–	KY885243	KY885245	–	–	–	–	–
Neopestalotiopsis rosicola	CFCC 51993	KY885240	–	KY885244	KY885246	–	–	–	–	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Neopestalotiopsis samarangensis	CBS 115451 T	KM199365	–	KM199556	KM199447	–	–	–	–	–
Neopestalotiopsis samarangensis	SS010	JQ968609	–	JQ968611	JQ968610	–	–	–	–	–
Neopestalotiopsis saprophytica	CBS 115452	KM199345	–	KM199538	KM199433	–	–	–	–	–
Neopestalotiopsis saprophytica	MFLUCC 12-0282 T	JX398982	–	JX399048	JX399017	–	–	–	–	–
Neopestalotiopsis saprophytica	RP	MW405888	–	MW423612	MW423614	–	–	–	–	–
Neopestalotiopsis saprophytica	RP1	MW405889	–	MW423613	MW423615	–	–	–	–	–
Neopestalotiopsis saprophytica	YLWB-FBR01	MT913525	–	MT706635	MT706634	–	–	–	–	–
Neopestalotiopsis scalabiensis	CAA1029 T	MW969748	–	MW959100	MW934611	–	–	–	–	–
Neopestalotiopsis scalabiensis	CFCC 54338	MW166231	–	–	–	–	–	–	–	–
Neopestalotiopsis scalabiensis	SM15-1C	MW166232	–	–	–	–	–	–	–	–
Neopestalotiopsis sichuanensis	CFCC 54338 T	MW166231	–	MW199750	MW218524	–	–	–	–	–
Neopestalotiopsis sichuanensis	SM15-1C	MW166232	–	MW199751	MW218525	–	–	–	–	–
Neopestalotiopsis sonneratae	MFLUCC 17-1744	MK764279	–	MK764323	MK764345	–	–	–	–	–
Neopestalotiopsis sonneratae	MFLUCC 17-1745 T	MK764280	–	MK764324	MK764346	–	–	–	–	–
Neopestalotiopsis sp.	CSUFTCC61	OK493590	–	OK507960	OK562365	–	–	–	–	–
Neopestalotiopsis sp.	CSUFTCC62	OK493591	–	OK507961	OK562366	–	–	–	–	–
Neopestalotiopsis sp.	CSUFTCC63	OK493592	–	OK507962	OK562367	–	–	–	–	–
Neopestalotiopsis sp. 1	CFCC 54337	MW166233	–	MW199752	MW218526	–	–	–	–	–
Neopestalotiopsis sp. 1	ZX12-1	MW166234	–	MW199753	MW218527	–	–	–	–	–
Neopestalotiopsis sp. 2	CFCC 54340	MW166235	–	MW199754	MW218528	–	–	–	–	–
Neopestalotiopsis sp. 2	ZX22B	MW166236	–	MW199755	MW218529	–	–	–	–	–
Neopestalotiopsis steyaertii	IMI 192475 T	KF582796	–	KF582792	KF582794	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Neopestalotiopsis surinamensis	CBS 450.74 T	KM199351	–	KM199518	KM199465	–	–	–	–	–
Neopestalotiopsis terricola	CGMCC 3.23553 T	OP082294	–	OP204796	OP235982	–	–	–	–	–
Neopestalotiopsis terricola	UESTCC 22.0008	OP082295	–	OP204797	OP235983	–	–	–	–	–
Neopestalotiopsis thailandica	MFLUCC 17-1730 T	MK764281	–	MK764325	MK764347	–	–	–	–	–
Neopestalotiopsis thailandica	MFLUCC 17-1731	MK764282	–	MK764326	MK764348	–	–	–	–	–
Neopestalotiopsis umbrinospora	MFLUCC 12-0285 T	JX398984	–	JX399050	JX399019	–	–	–	–	–
Neopestalotiopsis vaccinii	CAA1021	MW969745	–	MW934608	MW959097	–	–	–	–	–
Neopestalotiopsis vaccinii	CAA1027	MW969746	–	MW934609	MW959098	–	–	–	–	–
Neopestalotiopsis vaccinii	CAA1059 T	MW969747	–	MW934610	MW959099	–	–	–	–	–
Neopestalotiopsis vacciniicola	CAA1053	MW969749	–	MW959101	MW934612	–	–	–	–	–
Neopestalotiopsis vacciniicola	CAA1054	MW969750	–	MW959102	MW934613	–	–	–	–	–
Neopestalotiopsis vheenae	BRIP 72293a T	MZ303792	–	MZ344177	MZ312685	–	–	–	–	–
Neopestalotiopsis vitis	MFLUCC 15-1265 T	KU140694	–	KU140676	KU140685	–	–	–	–	–
Neopestalotiopsis vitis	MFLUCC 15-1270	KU140699	–	KU140681	KU140690	–	–	–	–	–
Neopestalotiopsis xishuangbannaensis	**KUMCC 21-0424 T**	**ON426865**	–	**OR025973**	**OR025934**	–	–	–	–	–
Neopestalotiopsis xishuangbannaensis	**KUMCC 21-0425**	**ON426866**	–	**OR025974**	**OR025935**	–	–	–	–	–
Neopestalotiopsis zakeelii	BRIP 72271a	MZ303788	–	MZ344173	MZ312681	–	–	–	–	–
Neopestalotiopsis zakeelii	BRIP 72282a T	MZ303789	–	MZ344174	MZ312682	–	–	–	–	–
Neopestalotiopsis zimbabwana	CBS 111495 T	JX556231	–	KM199545	KM199456	–	–	–	–	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Neopestalotiopsis zimbabwana	MEAN 1329	MW794095	–	MW805418	MW802828	–	–	–	–	–
Neopestalotiopsis zimbabwana	MEAN 1330	MW794109	–	MW805419	MW802842	–	–	–	–	–
Neopestalotiopsis brachiata	MFLUCC 17–555 T	MK764274	–	MK764318	MK764340	–	–	–	–	–
Neopestalotiopsis musae	MFLUCC 15-0776 T	KX789683	–	KX789685	KX789686	–	–	–	–	–
Nigrospora aurantiaca	CGMCC 3.18130 T	KX986064	KX986098	KY019295	KY019465	–	–	–	–	–
Nigrospora camelliae-sinensis	CGMCC 3.18125 T	KX985986	KX986103	KY019293	KY019460	–	–	–	–	–
Nigrospora chinensis	CGMCC 3.18127 T	KX986023	KX986107	KY019422	KY019462	–	–	–	–	–
Nigrospora gorlenkoana	CBS 480.73	KX986048	KX986109	KY019420	KY019456	–	–	–	–	–
Nigrospora guilinensis	CGMCC 3.18124 T	KX985983	KX986113	KY019292	KY019459	–	–	–	–	–
Nigrospora hainanensis	CGMCC 3.18129 T	KX986091	KX986112	KY019415	KY019464	–	–	–	–	–
Nigrospora lacticolonia	CGMCC 3.18123 T	KX985978	KX986105	KY019291	KY019458	–	–	–	–	–
Nigrospora musae	CBS 319.34	MH855545	KX986110	KY019419	KY019455	–	–	–	–	–
Nigrospora oryzae	LC2693	KX985944	KX986101	KY019299	KY019471	–	–	–	–	–
Nigrospora osmanthi	CGMCC 3.18126 T	KX986010	KX986106	KY019421	KY019461	–	–	–	–	–
Nigrospora pyriformis	CGMCC 3.18122 T	KX985940	KX986100	KY019290	KY019457	–	–	–	–	–
Nigrospora rubi	LC2698/CGMCC 3.18326 T	KX985948	KX986102	KY019302	KY019475	–	–	–	–	–
Nigrospora sphaerica	LC7298	KX985937	KX986097	KY019401	KY019606	–	–	–	–	–
Nigrospora vesicularis	CGMCC 3.18128 T	KX986088	KX986099	KY019294	KY019463	–	–	–	–	–
Penicillium allsoppiae	CN086C6	MW364385	–	–	MW357820	–	MW357840	–	MW357831	–
Penicillium allsoppiae	CN086C7	MW364386	–	–	MW357821	–	MW357841	–	MW357832	–
Penicillium annulatum	CBS 135126 T	JX091426	–	–	JX091514	–	KF296410	–	JX141545	–
Penicillium antarcticum	CBS 116938	KP016845	–	–	KP016925	–	KP016848	–	KP016827	–
Penicillium antarcticum	CBS 116939	KP016829	–	–	KP016921	–	KP016849	–	JX157255	–
Penicillium arizonense	IBT:12289 T	MH492021	–	–	MH492019	–	MH492022	–	MH492020	–
Penicillium astrolabium	NRRL 35656	DQ658168	–	–	DQ658166	–	JN406634	–	DQ658167	–
Penicillium atramentosum	CBS 291.48 T	MH856347	–	–	–	–	JN406584	–	KU896821	–
Penicillium atrovenetum	CBS 241.56 T	AF033492	–	–	JX140944	–	JN121467	–	KJ867004	–
Penicillium atrovenetum	CBS 243.56	KP016835	–	–	JX140945	–	KP016854	–	MN969241	–
Penicillium ausonanum	FMR 16948 T	LR655808	–	–	LR655809	–	LR655811	–	LR655810	–
Penicillium austrosinense	CBS 144505 T	KY495017	–	–	KY495126	–	KY495070	–	MN969328	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Penicillium barbosae	URM 7705 T	MW191494	–	–	MG452818	–	LR898886	–	MW183245	–
Penicillium barbosae	URM 7824	MW191495	–	–	MG452819	–	LR898887	–	MW183246	–
Penicillium bialowiezense	CBS 227.28 T	MH854996	–	–	–	–	JN406604	–	–	–
Penicillium bissettii	NN071640	KY494999	–	–	KY495108	–	KY495055	–	KY494939	–
Penicillium bissettii	NN071814	KY495002	–	–	KY495111	–	KY495058	–	KY494942	–
Penicillium brasilianum	CBS 253.55 T	GU981577	–	–	GU981629	–	KF296420	–	AB667857	–
Penicillium brefeldianum	NRRL 710 T	AF033435	–	–	GU981623	–	EU021658	–	AB667857	–
Penicillium brevicompactum	AS3.15323	KC427185	–	–	KC427165	–	–	–	KC427145	–
Penicillium brevicompactum	CBS 257.29 T	KF465776	–	–	KF499573	–	JN406594	–	AY484813	–
Penicillium brevicompactum	**KUMCC 21-0762**	**ON426874**	–	–	**OQ927585**	–	**OR022033**	**–**	**OR022048**	–
Penicillium brevicompactum	**KUMCC 21-0763**	**ON426869**	–	–	**OQ927587**	–	**OR022035**	**–**	**OR022050**	–
Penicillium brevicompactum	**KUMCC 21-0764**	**ON426871**	–	–	**OQ927590**	–	**OR022038**	**–**	**OR022053**	–
Penicillium brevicompactum	**KUMCC 21-0765**	**ON426872**	–	–	**OQ927588**	–	**OR022036**	**–**	**OR022051**	–
Penicillium brevicompactum	**KUMCC 21-0766**	**ON426870**	–	–	**OQ927583**	–	**OR022031**	**–**	**OR022046**	–
Penicillium brevicompactum	**KUMCC 21-0767**	**ON426875**	–	–	**OQ927586**	–	**OR022034**	**–**	**OR022049**	–
Penicillium brevicompactum	**KUMCC 21-0768**	**ON426873**	–	–	**OQ927584**	–	**OR022032**	**–**	**OR022047**	–
Penicillium brevicompactum	**KUMCC 21-0769**	**ON426878**	–	–	**OQ927589**	–	**OR022037**	**–**	**OR022052**	–
Penicillium buchwaldii	CBS 117181 T	JX313164	–	–	JX313182	–	JN406637	–	JX313148	–
Penicillium camponotum	NN058252	KY494996	–	–	KY495105	–	KY495054	–	KY494936	–
Penicillium camponotum	NN072443	KY495026	–	–	KY495135	–	KY495077	–	KY494966	–
Penicillium canescens	CBS 300.48 T	AF033493	–	–	JX140946	–	JN121485	–	KJ867009	–
Penicillium canescens	IMI:149218	KP016841	–	–	JX140951	–	KP016917	–	KP027409	–
Penicillium cf. *murcianum*	CN086C9	MW364388	–	–	MW357823	–	MW357843	–	MW357833	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Penicillium cf. *murcianum*	CN086D1	MW364389	–	–	MW357824	–	MW357844	–	MW357834	–
Penicillium chrysogenum	CBS 306.48 T	MH856357	–	–	AY495981	–	JN121487	–	JF909973	–
Penicillium coprophilum	CBS 110760 T	MH860442	–	–	AY674421	–	JN406645	–	KU896831	–
Penicillium coprophilum	CMV005G5	MK450685	–	–	MK451056	–	–	–	MK451606	–
Penicillium coprophilum	CN001B6	MW504354	–	–	MW480801	–	–	–	MW480821	–
Penicillium coralligerum	CBS 114.69	KP016836	–	–	KJ866970	–	KP016847	–	KJ866991	–
Penicillium coralligerum	CBS 123.65 T	JN617667	–	–	MN969378	–	JN406632	–	MN969248	–
Penicillium corvianum	CN086D3	MW364391	–	–	MW357826	–	MW357846	–	MW357836	–
Penicillium corvianum	CN086D5	MW364393	–	–	MW357828	–	MW357848	–	MW357838	–
Penicillium corylophilum	CBS 330.79	JN617701	–	–	GU944557	–	JN606591	–	GU944607	–
Penicillium doidgeae	CBS 138947 T	JX140804	–	–	JX141006	–	KP016915	–	JX157413	–
Penicillium doidgeae	CBS 138948	JX140805	–	–	JX141007	–	KP016916	–	JX157414	–
Penicillium donggangicum	AS3.15900 T	MW946996	–	–	MZ004914	–	MW979253	–	MZ004918	–
Penicillium dunedinense	CBS 138218 T	KJ775678	–	–	KJ775171	–	MN969116	–	KJ775405	–
Penicillium ehrlichii	CBS 324.48 T	AF033432	–	–	KF296464	–	KF296428	–	KF296395	–
Penicillium eickeri	CBS 138939 T	JX140824	–	–	JX140979	–	KP016876	–	JX157365	–
Penicillium eickeri	CBS 138940	JX140825	–	–	JX140980	–	KP016877	–	JX157366	–
Penicillium elizabethiae	NRRL 917 T	KP016840	–	–	KJ866964	–	KP016918	–	KJ867021	–
Penicillium estinogenum	CBS 329.59 T	MN431388	–	–	MN969381	–	–	–	MN969255	–
Penicillium fennelliae	CBS 711.68	JX313169	–	–	MN969382	–	JN406536	–	JX313151	–
Penicillium ferraniaense	CBS 147594	MW694952	–	–	MW689337	–	MW689341	–	MW689339	–
Penicillium ferraniaense	CBS H-24757	MW694951	–	–	MW689336	–	MW689340	–	MW689338	–
Penicillium geumsanense	CNUFC-GEU2229-1 T	–	–	–	MK481059	–	MK481055	–	MK481062	–
Penicillium glabrum	CBS 125543 T	MH863551	–	–	GU981619	–	JF417447	–	–	–
Penicillium glabrum	DAOM 239074	MW862782	–	–	MZ393464	–	–	–	MZ393462	–
Penicillium glabrum	DTO 076-G8	KM189530	–	–	KM088767	–	KM089539	–	KM089152	–
Penicillium glandicola	CBS 498.75 T	MH860946	–	–	KU896814	–	JN406527	–	KU896838	–
Penicillium granulatum	CBS 333.48 T	MH856371	–	–	MT478038	–	MT253109	–	MT478036	–
Penicillium griseoazureum	CBS 162.42 T	KC411679	–	–	KP016919	–	KP016852	–	KP016823	–
Penicillium griseofulvum	CBS 185.27 T	MH854925	–	–	JF909942	–	JN121449	–	JX996966	–
Penicillium guaibinense	KUMCC 18-0199 T	MT152336	–	–	MT161680	–	MT384371	–	MT178248	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Penicillium guarroi	FMR 17747 T	LR814139	–	–	LR814134	–	LR814145	–	LR814140	–
Penicillium hepuense	AS3.16039 T	MW946994	–	–	MZ004912	–	MW979254	–	MZ004916	–
Penicillium hepuense	AS3.16040	MW946995	–	–	MZ004913	–	MW979255	–	MZ004917	–
Penicillium heteromorphum	CBS 226.89 T	KC411702	–	–	KJ834455	–	JN406605	–	KP016786	–
Penicillium irregulare	FMR 17859 T	LR814181	–	–	LR814144	–	LR814182	–	LR814151	–
Penicillium janczewskii	CBS 166.81	KC411682	–	–	KJ866967	–	KP016853	–	KJ866998	–
Penicillium janczewskii	CBS 221.28 T	AY157487	–	–	MN969386	–	JN406612	–	MN969267	–
Penicillium jensenii	CBS 216.28	JN617693	–	–	KJ866963	–	JN606629	–	KJ867000	–
Penicillium jensenii	CBS 327.59 T	AY443470	–	–	JX140954	–	JN406614	–	AY443490	–
Penicillium jiaozhouwanicum	AS3.16027	OM203537	–	–	OM220087	–	OM220089	–	OM220088	–
Penicillium jiaozhouwanicum	AS3.16038 T	MW946993	–	–	MZ004911	–	MW979252	–	MZ004915	–
Penicillium katangense	CBS 247.67 T		–	–	KJ834462	–	KP064646	–	KP016788	–
Penicillium kewense	CBS 344.61 T	MH858076	–	–	KU896816	–	JF417428	–	JX996973	–
Penicillium labradorum	UTHSCSA DI19-20 T	MK881918	–	–	MK887898	–	MK887900	–	MK887899	–
Penicillium labradorum	UTHSCSA DI19-21	MK882920	–	–	MK887901	–	MK887903	–	MK887902	–
Penicillium lanosocoeruleum	CBS 215.30 T	MH855121	–	–	KU896817	–	JX996712	–	JX996967	–
Penicillium levitum	NRRL 705 T	GU981607	–	–	GU981654	–	KF296432	–	KF296394	–
Penicillium lgoetzii	CBS 285.73 T	JX997091	–	–	KU896815	–	JX996716	–	JX996971	–
Penicillium limae	URM 7706 T	MW191493	–	–	MG452820	–	LR898888	–	MW183244	–
Penicillium linzhiense	CCTCC-M2019870 T	MT461156	–	–	MT461157	–	–	–	MT461162	–
Penicillium mdaleae	CBS 211.28 T	MH854984	–	–	GU981649	–	KF296427	–	MN969251	–
Penicillium meridianum	CBS 314.67 T	–	–	–	KJ834472	–	JN406576	–	KP016794	–
Penicillium murcianum	CBS 161.81	KP016844	–	–	MN969419	–	MN969202	–	MN969341	–
Penicillium murcianum	CBS 458.69	KP016843	–	–	KP016923	–	KP016860	–	KP016822	–
Penicillium neocrassum	NRRL 35639 T	DQ645805	–	–	DQ645794	–	JN406633	–	DQ645809	–
Penicillium nigricans	CBS 354.48 T	KC411755	–	–	KJ866965	–	KP016857	–	KJ867012	–
Penicillium novaezeelandiae	CBS 137.41 T	JN617688	–	–	MN969390	–	JN406628	–	MN969279	–
Penicillium novaezeelandiae	CBS 138936	JX140853	–	–	JX140956	–	KP016864	–	JX157352	–
Penicillium nucicola	DAOMC:250521	KT887846	–	–	KT887807	–	–	–	KT887768	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Penicillium nucicola	DAOMC:250522 T	KT887860	–	–	KT887821	–	MN969171	–	KT887782	–
Penicillium ochrochloron	CBS 133150	KC346347	–	–	KC346324	–	KC346318	–	KC346341	–
Penicillium ochrochloron	CBS 357.48 T	GU981604	–	–	GU981672	–	KF296445	–	KF296378	–
Penicillium olsonii	CBS 232.60 NT	MH857964	–	–	AY674445	–	JN121464	–	DQ658165	–
Penicillium parvum	CBS 359.48 T	MH856390	–	–	–	–	JN406559	–	–	–
Penicillium persicinum	CBS 111235 T	MH862874	–	–	JF909951	–	JN406644	–	JX996954	–
Penicillium piscarium	CBS 220.30	KC346342	–	–	KC346319	–	KC346309	–	KC346333	–
Penicillium piscarium	CBS 362.48 T	GU981600	–	–	GU981668	–	KF296451	–	KF296379	–
Penicillium pole-evansii	CBS 138946 T	JX140831	–	–	JX141005	–	KP016911	–	JX157412	–
Penicillium pulvillorum	CBS 275.83	AF178513	–	–	KF296463	–	KC346310	–	KF296376	–
Penicillium pulvillorum	CBS 280.39 T	AF178517	–	–	GU981670	–	KC346310	–	KF296377	–
Penicillium radiatolobatum	CBS 340.79 T	KC411745	–	–	MN969413	–	MN969168	–	MT066183	–
Penicillium radiatolobatum	IBT:31958	JX140832	–	–	JX140948	–	KP016871	–	JX157359	–
Penicillium restrictum	CBS 367.48 T	MH856396	–	–	KJ834486	–	JN121506	–	KP016803	–
Penicillium reticulisporum	NRRL 3447 T	AF033437	–	–	GU981665	–	KF296454	–	KF296391	–
Penicillium robsamsonii	CBS 140573 T	KU904339	–	–	–	–	–	–	–	–
Penicillium rolfsii	NRRL 1078 T	JN617705	–	–	GU981667	–	KC346314	–	KF296375	–
Penicillium rotoruae	43A T	MN315103	–	–	MN315104	–	MT240842	–	MN315102	–
Penicillium rubidurum	CBS 609.73 T	–	–	–	–	–	–	–	–	–
Penicillium saanichanum	DAOMC251850 T	KY469059	–	–	KY469096	–	MN795070	–	KY469020	–
Penicillium sacculum	CBS 231.61	KC411707	–	–	KJ834488	–	JN121462	–	KU896849	–
Penicillium sanguifluum	CBS 127032 T	JN617681	–	–	JN606819	–	–	–	JN606555	–
Penicillium sanguifluum	FMR 17617	LR861779	–	–	LR861778	–	–	–	LR861781	–
Penicillium sanjayi	NFCCI5017 T	MZ571358	–	–	MZ558484	–	MZ558482	–	MZ558492	–
Penicillium sanjayi	NFCCI5018	MZ571359	–	–	MZ558485	–	MZ558483	–	MZ558493	–
Penicillium scottii	CBS 138935	JX140823	–	–	JX140977	–	KP016863	–	JX157351	–
Penicillium scottii	CBS 138937	JX140826	–	–	JX140978	–	KP016867	–	JX157355	–
Penicillium sicoris	FMR 18076 T	LR884497	–	–	LR884494	–	LR884495	–	LR884496	–
Penicillium simplicissimum	CBS 372.48 T	GU981588	–	–	GU981632	–	JN121507	–	KF296368	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Penicillium sinaicum	CBS 279.82 T	MH861498	–	–	KU896818	–	JN406587	–	JX996970	–
Penicillium skrjabinii	NRRL 13055 T	GU981576	–	–	GU981626	–	EU427252	–	KF296370	–
Penicillium soli	KUMCC 18-0202 T	MT152337	–	–	MT161681	–	MT384372	–	MT178249	–
Penicillium spathulatum	CBS 117192 T	JX313165	–	–	JX313183	–	JN406636	–	JX313149	–
Penicillium submersum	FMR 17140 T	LR814194	–	–	LR814187	–	LR814195	–	LR814188	–
Penicillium subrubescens	CBS 129543	KC797635	–	–	KC797610	–	KC797600	–	KC797590	–
Penicillium subrubescens	CBS 132785 T	KC346350	–	–	KC346327	–	KC346306	–	KC346330	–
Penicillium svalbardense	CBS 122416 T	GU981603	–	–	KC346325	–	KF296457	–	KC346338	–
Penicillium svalbardense	DTO 11716	KC346348	–	–	KC346325	–	KC346311	–	KC346335	–
Penicillium tardochrysogenum	CBS 132200 T	JX997028	–	–	JX996898	–	JX996634	–	JX996239	–
Penicillium taurinense	CBS 145672 T	MF595981	–	–	MF595977	–	MT253108	–	MF595979	–
Penicillium thomii	CBS 347.59	MH857887	–	–	GQ367510	–	JN121501	–	GQ367535	–
Penicillium tularense	CBS 430.69 T	JX313166	–	–	KC427175	–	JN121516	–	JX313135	–
Penicillium ulleungdoense	KACC 48990 T	MN640087	–	–	MN737487	–	MN756007	–	MN745074	–
Penicillium ulleungdoense	KACC 48991	MN640088	–	–	MN737488	–	MN756008	–	MN745075	–
Penicillium uttarakhandense	AMH 10225 T	MN967315	–	–	MN972443	–	MN972447	–	MN972445	–
Penicillium uttarakhandense	NFCCI 4809	MN967316	–	–	MN972444	–	MN972448	–	MN972446	–
Penicillium vaccaeorum	CBS 148.83 T	MH861558	–	–	JN606846	–	–	–	JN606543	–
Penicillium vaccaeorum	FMR 17967	LR814235	–	–	LR814226	–	–	–	LR814227	–
Penicillium vasconiae	CBS 339.79 T	GU981599	–	–	GU981653	–	KF296459	–	KF296386	–
Penicillium vascosobrinhous	URM 8193 T	LR744067	–	–	LR744069	–	LR744065	–	LR744063	–
Penicillium vascosobrinhous	URM 8194	LR744068	–	–	LR744062	–	LR744066	–	LR744064	–
Penicillium yarmokense	CBS 410.69 T	KC411757	–	–	MN969407	–	JN406553	–	MN969314	–
Phialemoniopsis cornearis	UTHSC 06-1465	HE599285	HE599270	–	HE599302	–	–	–	–	HE599253

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Phialemoniopsis cornearis	UTHSC 06–1820 T	HE599284	HE599269	–	HE599301	–	–	–	–	HE599252
Phialemoniopsis curvata	CBS 490.82 T	HE599290	FR691977	–	HE599307	–	–	–	–	HE599258
Phialemoniopsis curvata	CBS 491.82	HE599289	FR691976	–	HE599306	–	–	–	–	HE599257
Phialemoniopsis curvata	UTHSC 06-4324	HE599288	HE599273	–	HE599305	–	–	–	–	HE599256
Phialemoniopsis endophytica	ACCC 38978	KT799555	KT799558	–	KT799561	–	–	–	–	KT799552
Phialemoniopsis endophytica	ACCC 38979	KT799556	KT799559	–	KT799562	–	–	–	–	KT799553
Phialemoniopsis endophytica	ACCC 38980 T	KT799557	KT799560	–	KT799563	–	–	–	–	KT799554
Phialemoniopsis hipposidericola	**KUMCC 21-0778 T**	**ON426882**	**OP363279**	–	**OR025957**	–	–	–	–	**OQ930298**
Phialemoniopsis hipposidericola	**KUMCC 21-0779**	**ON426886**	**OP363283**	–	**OR025958**	–	–	–	–	**OQ930299**
Phialemoniopsis hongkongensis	HKU39 T	KJ573442	KJ573447	–	KJ573457	–	–	–	–	KJ573452
Phialemoniopsis limonesiae	CBS 146752 T	MW050977	MW050976	–	MW048608	–	–	–	–	MW349126
Phialemoniopsis ocularis	UTHSC 05-2527	HE599281	HE599266	–	HE599298	–	–	–	–	HE599249
Phialemoniopsis ocularis	UTHSC 07-3736	HE599283	HE599268	–	HE599300	–	–	–	–	HE599251
Phialemoniopsis ocularis	UTHSC 09-2358	HE599282	HE599267	–	HE599299	–	–	–	–	HE599250
Phialemoniopsis pluriloculosa	CBS 131712	KJ573446	KJ573451	–	KJ573461	–	–	–	–	KJ573456
Phialemoniopsis pluriloculosa	UTHSC 04–7 T	HE599286	HE599271	–	HE599303	–	–	–	–	HE599254
Phialemoniopsis pluriloculosa	UTHSC 09-3589	HE599287	HE599272	–	HE599304	–	–	–	–	HE599255
Phialemoniopsis xishuangbannaensis	**KUMCC 21-0774 T**	**ON426881**	**OP363278**	–	**OR025959**	–	–	–	–	**OQ930300**
Phialemoniopsis xishuangbannaensis	**KUMCC 21-0775**	**ON426884**	**OP363281**	–	**OR025960**	–	–	–	–	**OQ930301**
Phialemoniopsis xishuangbannaensis	**KUMCC 21-0776**	**ON426885**	**OP363282**	–	**OR025961**	–	–	–	–	**OQ930302**

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	LSU	*TEF1-α*	*TUB*	*Bloc*	*RPB2*	*RPB1*	*CaM*	*Act*
Phialemoniopsis xishuangbannaensis	**KUMCC 21-0777**	**ON426883**	**OP363280**	–	**OR025962**	–	–	–	–	**OQ930303**
Phialemonium atrogriseum	CBS 306.85	HE610366	HE610466	–	HE599345	–	–	–	–	HE599326
Phialemonium atrogriseum	CBS 604.67 T	HE610367	HE610470	–	HE599346	–	–	–	–	HE599327
Phialemonium atrogriseum	CBS 774.97	HE610369	HE610472	–	HE599344	–	–	–	–	HE599325
Scopulariopsis albida	CBS 415.51	KX923955	–	KX924177	KX924389	–	–	–	–	–
Scopulariopsis alboflavescens	CBS 152.22	LN850785	–	KX924178	LN850882	–	–	–	–	–
Phialemonium globosum	UTHSC 03–3661 T	HE610358	HE610461	–	HE599349	–	–	–	–	HE599330
Phialemonium inflatum	CBS 259.39 T	HE610364	HE610464	–	HE599347	–	–	–	–	HE599328
Phialemonium inflatum	NBRC 31965	HE610371	HE610474	–	HE599348	–	–	–	–	HE599329
Phialemonium obovatum	UTHSC 01-1399	HE610354	FR745945	–	HE599337	–	–	–	–	HE599318
Phialemonium obovatum	UTHSC 01-317	HE610355	FR745951	–	HE599336	–	–	–	–	HE599317
Phialemonium obovatum	UTHSC 04-616	HE610360	FR745944	–	HE599333	–	–	–	–	HE599314
Protocrea farinosa	CBS 121551 T	MH863119	–	–	–	–	EU703935	–	–	–
Protocrea illinoensis	GJS 94-54	EU703929	–	EU703904	–	–	EU703951	–	–	–
Protocrea illinoensis	TFC 9698 T	EU703930	–	EU703905	–	–	EU703952	–	–	–
Protocrea pallida	CBS 29878 T	EU703924	–	EU703899	–	–	EU703947	–	–	–
Protocrea pallida	CBS 29978	EU703925	–	EU703900	–	–	EU703948	–	–	–
Pseudopestalotiopsis cocos	CBS 272.29 T	KM199378	–	KM199553	KM199467	–	–	–	–	–
Pseudopestalotiopsis indica	CBS 459.78 T	KM199381	–	KM199560	KM199470	–	–	–	–	–
Pseudopestalotiopsis theae	MFLUCC12-0055 T	JQ683727	–	JQ683743	JQ683711	–	–	–	–	–
Purpureocillium lilacinum	CBS 284-36	MH855800	–	EF468792	–	–	EF468941	EF468898	–	–
Purpureocillium lilacinum	CBS 431-87	HQ842812	–	EF468791	–	–	EF468940	EF468897	–	–
Scopulariopsis africana	CBS 118736 T	KX923954	KX924040	KX924176	KX924388	–	–	–	–	–
Scopulariopsis albida	CBS 119.43 T	LN850800	LN850849	LM652592	LN850897	–	–	–	–	–
Scopulariopsis alboflavescens	CBS 208.61	LN850786	–	LN850931	LN850883	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Scopulariopsis alboflavescens	CBS 399.34 T	KX923956	LM652539	KX924179	JQ434537	–	–	–	–	–
Scopulariopsis asperula	CBS 204.27 T	KX923958	–	KX924181	KX924391	–	–	–	–	–
Scopulariopsis asperula	CBS 289.38 T	KX923960	LM652538	KX924184	KX924394	–	–	–	–	–
Scopulariopsis asperula	CBS 298.67	LN850789	–	LN850934	LN850886	–	–	–	–	–
Scopulariopsis asperula	CBS 351.49	KX923961	–	KX924185	KX924395	–	–	–	–	–
Scopulariopsis asperula	CBS 401.34	LM652463	–	KX924182	KX924392	–	–	–	–	–
Scopulariopsis asperula	CBS 853.68	KX923963	MH870961	KX924188	JQ434558	–	–	–	–	–
Scopulariopsis asperula	CBS 872.68	KX923964	–	KX924189	KX924397	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 118469	KX923981	–	KX924207	KX924414	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 118472 T	KX923984	–	KX924210	KX924417	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 115540	KX923978	–	KX924204	KX924411	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 118470	KX923982	–	KX924208	KX924415	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 120.20	KX923970	–	KX924195	KX924402	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 127812 T	LM652465	HG380440	HG380363	KX924423	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 127825	KX923990	–	KX924216	KX924424	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 137632	KX923992	–	KX924218	KX924426	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 147.41	KX923974	–	KX924200	KX924407	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 334.35	LN850790	–	LN850935	LN850887	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 335.35	LM652477	–	KX924197	KX924404	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 340.39	KX923972	–	KX924198	KX924405	–	–	–	–	–
Scopulariopsis brevicaulis	CBS 341.39	KX923973	–	KX924199	KX924406	–	–	–	–	–
Scopulariopsis brevicaulis	**KUMCC 21-0444**	**ON426887**	**OP3632874**	**OR026008**	**OR025953**	–	–	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Scopulariopsis brevicaulis	**KUMCC 21-0445**	**ON426888**	**OP3632875**	**OR026009**	**OR025954**	–	–	–	–	–
Scopulariopsis brevicaulis	**KUMCC 21-0446**	**ON426889**	**OP3632876**	**OR026010**	**OR025955**	–	–	–	–	–
Scopulariopsis brevicaulis	**KUMCC 21-0447**	**ON426890**	**OP363287**	**OR026011**	**OR025956**	–	–	–	–	–
Scopulariopsis brevicaulis	DTO 012-C7	KX923993	–	KX924219	KX924427	–	–	–	–	–
Scopulariopsis brevicaulis	DTO 012-F6	KX923995	–	KX924221	KX924429	–	–	–	–	–
Scopulariopsis brevicaulis	DTO 168-A4	KX923999	–	KX924225	KX924433	–	–	–	–	–
Scopulariopsis brevicaulis	DTO 168-A5	KX924000	–	KX924226	KX924434	–	–	–	–	–
Scopulariopsis brevicaulis	DTO 168-A6	KX924001	–	KX924227	KX924435	–	–	–	–	–
Scopulariopsis brevicaulis	DTO 305-A2	KX924005	–	KX924231	KX924439	–	–	–	–	–
Scopulariopsis brevicaulis	DTO 305-A8	KX924009	–	KX924235	KX924443	–	–	–	–	–
Scopulariopsis candida	CBS 254.69	KX924013	–	KX924240	KX924448	–	–	–	–	–
Scopulariopsis caseicola	CBS 480.62 T	KX924020	KX924041	KX924247	KX924454	–	–	–	–	–
Scopulariopsis cordiae	CBS 138129 T	KX924022	HG380499	KX924249	KX924456	–	–	–	–	–
Scopulariopsis cordiae	CBS 816.73	KX924021	–	KX924248	KX924455	–	–	–	–	–
Scopulariopsis crassa	CGMCC 3.17941 T	KU746704	KU746750	KX855249	KU746795	–	–	–	–	–
Scopulariopsis crassa	CGMCC 3.17942	KU746703	KU746749	KX855250	KU746796	–	–	–	–	–
Scopulariopsis flava	CBS 207.61 T	KX924023	HG380464	HG380387	KX924457	–	–	–	–	–
Scopulariopsis gossypii	CGMCC 3.17896 T	KU523862	KU523865	KU523859	KU523868	–	–	–	–	–
Scopulariopsis gossypii	CGMCC 3.17897	KU523869	KU523866	KU523860	KU523869	–	–	–	–	–
Scopulariopsis macurae	CBS 506.66 T	LN850805	LN850854	KX924250	LN850902	–	–	–	–	–
Scopulariopsis sexualis	CBS 250.64 T	KX924024	KX924042	KX924251	KX924458	–	–	–	–	–
Scopulariopsis sexualis	CBS 332.78	KX924026	–	KX924253	KX924460	–	–	–	–	–
Scopulariopsis sexualis	CBS 667.71	KX924025	–	KX924252	KX924459	–	–	–	–	–
Scopulariopsis soppii	UAMH 9169 T	LM652495	LM652552	LM652595	LM652698	–	–	–	–	–
Sporocadus trimorphus	CBS 114203	MH553977	MH554196	MH554395	MH554636	–	–	–	–	–
Trichoderma achlamydosporum	YMF 1.06226 T	MN977791	–	MT070156	–	–	MT052180	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Trichoderma afarasin	BAFC 4355	–	–	MG755812	–	–		–	–	–
Trichoderma afarasin	Dis 314	FJ442259	–	FJ463400	–	–	FJ442778	–	–	–
Trichoderma afroharzianum	Fes1712	–	–	MW014362	–	–	MW014361	–	–	–
Trichoderma afroharzianum	NAIMCC-F-01938	KY419889	–	KY419891	–	–	KY419895	–	–	–
Trichoderma aggressivum	COAD 2432	–	–	MK044156	–	–	MK044249	–	–	–
Trichoderma amoenum	YMF 1.06209 T	MN977801	–	MT070146	–	–	MT052192	–	–	–
Trichoderma amoenum	YMF 1.06210	MN977802	–	MT070145	–	–	MT070161	–	–	–
Trichoderma anaharzianum	YMF 1.00241	MH262584	–	MH236493	–	–	MH262577	–	–	–
Trichoderma anaharzianum	YMF 1.00383 T	MH113931	–	MH183182	–	–	MH158995	–	–	–
Trichoderma andinense	COAD 2431	–	–	MK044155	–	–	MK044248	–	–	–
Trichoderma anisohamatum	YMF 1.00333 T	MH262583	–	MH236494	–	–	MH262576	–	–	–
Trichoderma anisohamatum	YMF 1.00253	MH262586	–	MH236495	–	–	MH262578	–	–	–
Trichoderma aquatica	YMF 1.04624	MH383057	–	MK775506	–	–	MK775511	–	–	–
Trichoderma aquatica	YMF 1.04625 T	MH383058	–	MK775507	–	–	MK775512	–	–	–
Trichoderma arenarium	TUCIM 10301 T	MT217123	–	MT242303	–	–	MT242310	–	–	–
Trichoderma arenarium	TUCIM 10302	–	–	MT347687	–	–	MT347691	–	–	–
Trichoderma asiaticum	YMF 1.00168	MH262582	–	MH236492	–	–	MH262575	–	–	–
Trichoderma asiaticum	YMF 1.00352 T	MH113930	–	MH183183	–	–	MH158994	–	–	–
Trichoderma asymmetricum	YMF 1.04618 T	MK795991	–	MK795983	–	–	MK795987	–	–	–
Trichoderma atroviride	COAD 2396	–	–	MK044083	–	–	MK044177	–	–	–
Trichoderma austroindianum	GJS 08-128	–	–	MH352423	–	–	–	–	–	–
Trichoderma austroindianum	VAB-T050 T	–	–	MH352421	–	–	–	–	–	–
Trichoderma awajun	CHAXC CP24-7 T	–	–	MW480138	–	–	MW480147	–	–	–
Trichoderma awajun	CHAXC CP24-8	–	–	MW480139	–	–	MW480148	–	–	–
Trichoderma azevedoi	CEN1422 T	MK714902	–	MK696660	–	–	MK696821	–	–	–
Trichoderma azevedoi	CEN1423	MK714903	–	MK696661	–	–	MK696822	–	–	–
Trichoderma botryosum	COAD 2520	–	–	MK044140	–	–	MK044233	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Trichoderma botryosum	COAD 2543	–	–	MK044141	–	–	MK044234	–	–	–
Trichoderma breve	COAD 2402	–	–	MK044089	–	–	MK044182	–	–	–
Trichoderma breve	COAD 2429	–	–	MK044150	–	–	MK044243	–	–	–
Trichoderma caeruloviride	COAD 2415 T	–	–	MK044109	–	–	MK044202	–	–	–
Trichoderma caeruloviride	COAD 2416	–	–	MK044108	–	–	MK044201	–	–	–
Trichoderma camelliae	JZBH336000 T	MW008452	–	–	–	–	–	–	–	–
Trichoderma camelliae	JZBH3360002 T	MW008451	–	–	–	–	–	–	–	–
Trichoderma camerunense	GJS 99-230 T	–	–	AF348107	–	–	–	–	–	–
Trichoderma camerunense	GJS 99-231	AY027783	–	AF348108	–	–	–	–	–	–
Trichoderma catoptron	GJS 02-76 T	AY737766	–	AY737726	–	–	AY391900	–	–	–
Trichoderma catoptron	HMAS 252533	–	–	KF923290	–	–	KF923310	–	–	–
Trichoderma ceratophylli	YMF 1.04621 T	MK327581	–	MK327579	–	–	MK327580	–	–	–
Trichoderma cinnamomeum	GJS 97-233	–	–	AY391978	–	–	AY391919	–	–	–
Trichoderma cinnamomeum	GJS 97-237	AY737759	–	AY391979	–	–	AY391920	–	–	–
Trichoderma dorothopsis	CGMCC3.19672 T	MH624140	–	MK850827	–	–	MH647795	–	–	–
Trichoderma dorothopsis	CGMCC3.19673	MH624143	–	MK850830	–	–	MH647798	–	–	–
Trichoderma endophyticum	BAFC 4372	–	–	MH371397	–	–	–	–	–	–
Trichoderma endophyticum	H1-S-97	–	–	MT821957	–	–	MT822003	–	–	–
Trichoderma gansuanum	HMAS 279687 T	MT084412	–	MT095060	–	–	MT087287	–	–	–
Trichoderma guizhouense	PARC1025	MT448971	–	MT454128	–	–	MT454144	–	–	–
Trichoderma guizhouense	PARC1026	MT448972	–	MT454129	–	–	MT454145	–	–	–
Trichoderma hailarense	WT 17803	MH606226	–	MH606229	–	–	MH606232	–	–	–
Trichoderma hailarense	WT 17901 T	MH287485	–	MH287505	–	–	MH287506	–	–	–
Trichoderma hamatum	COAD 2417	–	–	MK044110	–	–	MK044203	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Trichoderma hamatum	COAD 2418	–	–	MK044111	–	–	MK044204	–	–	–
Trichoderma harzianum	CBS 226.95	–	–	AF348101	–	–	AF545549	–	–	–
Trichoderma harzianum	CGMCC 20739	–	–	MZ603732	–	–	MZ603731	–	–	–
Trichoderma hipposidericola	**KUMCC 21-0805**	**ON426894**	–	**OR025980**	**–**	**–**	**OR025898**	–	–	–
Trichoderma hipposidericola	**KUMCC 21-0801 T**	**ON426899**	–	**OR025978**	**–**	**–**	**OR025896**	–	–	–
Trichoderma hipposidericola	**KUMCC 21-0804**	**ON426895**	–	**OR025979**	**–**	**–**	**OR025897**	–	–	–
Trichoderma hipposidericola	**KUMCC 21-0803**	**ON426900**	–	**OR025981**	**–**	**–**	**OR025899**	–	–	–
Trichoderma hipposidericola	**KUMCC 21-0802**	**ON426901**	–	**OR025982**	**–**	**–**	**OR025900**	–	–	–
Trichoderma hirsutum	HMAS 248842	KY687925	–	KY688041	–	–	KY687981	–	–	–
Trichoderma hirsutum	HMAS 248860	KY687943	–	KY688042	–	–	KY687999	–	–	–
Trichoderma hortense	DAOM 230830	AY605743	–	AY605786	–	–	KJ842180	–	–	–
Trichoderma hortense	GJS 04-70	–	–	FJ463352	–	–	FJ442711	–	–	–
Trichoderma inaequilaterale	YMF 1.06203 T	MN977795	–	MT070152	–	–	MT052186	–	–	–
Trichoderma inconspicuum	YMF 1.04623	MK795993	–	MK795985	–	–	MK795989	–	–	–
Trichoderma inconspicuum	**KUMCC 21-0806**	**ON426893**	–	**OR025983**	**–**	**–**	**OR025901**	–	–	–
Trichoderma insigne	YMF 1.00207 T	MH113925	–	MH177911	–	–	MH155271	–	–	–
Trichoderma insigne	YMF 1.00272	MH113927	–	MH177913	–	–	MH155274	–	–	–
Trichoderma jaklitschii	CP01-6	–	–	MW480144	–	–	MW480150	–	–	–
Trichoderma jaklitschii	CP61-2 T	–	–	MW480140	–	–	MW480149	–	–	–
Trichoderma koningiopsis	COAD 2405	–	–	MK044092	–	–	MK044185	–	–	–
Trichoderma koningiopsis	COAD 2502	–	–	MK044097	–	–	MK044190	–	–	–
Trichoderma lentiforme	CEN1429	MK714910	–	MK696668	–	–	MK696828	–	–	–
Trichoderma lentiforme	H1-R-96		–	MT821992	–	–	MT822037	–	–	–
Trichoderma lentinulae	CGMCC 3.19848	MN594470	–	MN605879	–	–	MN605868	–	–	–
Trichoderma lentinulae	HMAS 248256 T	MN594469	–	MN605878	–	–	MN605867	–	–	–
Trichoderma lentissimum	COAD 2399 T	–	–	MK044086	–	–	MK044179	–	–	–

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Trichoderma lixii	GJS 97-106	–	–	AF443939	–	–	FJ442771	–	–	–
Trichoderma lixii	GJS 97-96 T	NR_131264	–	AF443938	–	–	KJ665290	–	–	–
Trichoderma lycogaloides	CBS 123493 T	–	–	KF134800	–	–	KF134792	–	–	–
Trichoderma macrofasciculatum	WT 37805 T	MH287487	–	MH287509	–	–	MH287493	–	–	–
Trichoderma macrofasciculatum	WT 37810	MH287488	–	MH287510	–	–	MH287494	–	–	–
Trichoderma neotropicale	GJS 08-182	–	–	MG822718	–	–	–	–	–	–
Trichoderma neotropicale	GJS 08-183	–	–	MG822719	–	–	–	–	–	–
Trichoderma nordicum	WT 13001	MH287483	–	MH287501	–	–	MH287502	–	–	–
Trichoderma nordicum	WT 61001 T	MH287484	–	MH287503	–	–	MH287504	–	–	–
Trichoderma obovatum	**KUMCC 21-0807**	**ON426891**	**–**	**OR025987**	**–**	**–**	**OR025905**	–	–	–
Trichoderma obovatum	**KUMCC 21-0808**	**ON426892**	–	**OR025988**	**–**	**–**	**OR025906**	–	–	–
Trichoderma obovatum	**KUMCC 21-0809**	**ON426896**	–	**OR025984**	**–**	**–**	**OR025902**	–	–	–
Trichoderma obovatum	**KUMCC 21-0810**	**ON426897**	–	**OR025985**	**–**	**–**	**OR025903**	–	–	–
Trichoderma obovatum	**KUMCC 21-0811**	**ON426898**	–	**OR025986**	**–**	**–**	**OR025904**	–	–	–
Trichoderma obovatum	YMF 1.06211	MN977803	–	MT070144	–	–	MT038432	–	–	–
Trichoderma obovatum	YMF 1.06212	MN977804	–	MT070143	–	–	MT038433	–	–	–
Trichoderma panacis	SYPF 8050 T	MF565524	–	MF565523	–	–	MF565525	–	–	–
Trichoderma parareesei	COAD 2482	–	–	MK044154	–	–	MK044247	–	–	–
Trichoderma parareesei	COAD 2483	–	–	MK044153	–	–	MK044246	–	–	–
Trichoderma paraviride	YMF 1.04628 T	MK775514	–	MK775508	–	–	MK775513	–	–	–
Trichoderma peberdyi	CEN1389	MK714863	–	MK696621	–	–	MK696783	–	–	–
Trichoderma peberdyi	CEN1426 T	MK714906	–	MK696664	–	–	MK696825	–	–	–
Trichoderma peruvianum	CP15-2 T	–	–	MW480145	–	–	MW480153	–	–	–
Trichoderma peruvianum	CP15-9	–	–	MW480146	–	–	MW480154	–	–	–
Trichoderma pluripenicillatum	YMF 1.06198 T	MN977788	–	MT070159	–	–	MT070160	–	–	–
Trichoderma propepolypori	YMF 1.06199	MN977790	–	MT070157	–	–	MT052182	–	–	–
Trichoderma propepolypori	YMF 1.06224 T	MN977789	–	MT070158	–	–	MT052181	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Trichoderma pseudoasiaticum	YMF 1.06200 T	MN977792	–	MT070155	–	–	MT052183	–	–	–
Trichoderma pseudoasperelloides	YMF 1.00152	MH262581	–	MH236491	–	–	MH262574	–	–	–
Trichoderma pseudoasperelloides	YMF 1.04629 T	MH383059	–	MK775504	–	–	MK775509	–	–	–
Trichoderma pseudopyramidale	COAD 2433	–	–	MK044157	–	–	MK044250	–	–	–
Trichoderma pseudopyramidale	COAD 2434	–	–	MK044158	–	–	MK044251	–	–	–
Trichoderma rhinolophicola	**KUMCC 21-0813 T**	**OP425803**	–	**OR025989**	–	–	–	–	–	–
Trichoderma rhinolophicola	**KUMCC 21-0814**	**OP425804**	–	**OR025990**	–	–	–	–	–	–
Trichoderma rifaii	DIS 337F T	FJ442621	–	FJ463321	–	–	FJ442720	–	–	–
Trichoderma rifaii	J2-2CR	–	–	MK644113	–	–	–	–	–	–
Trichoderma scorpioideum	YMF 1.04616 T	MK795992	–	MK795984	–	–	MK795988	–	–	–
Trichoderma shangrilaense	WT 34004 T	MH287489	–	MH287495	–	–	MH287496	–	–	–
Trichoderma shangrilaense	WT 40502	MH606224	–	MH606227	–	–	MH606230	–	–	–
Trichoderma simile	YMF 1.06201 T	MN977793	–	MT070154	–	–	MT052184	–	–	–
Trichoderma simile	YMF 1.06202	MN977794	–	MT070153	–	–	MT052185	–	–	–
Trichoderma spirale	COAD 2404	–	–	MK044091	–	–	MK044184	–	–	–
Trichoderma spirale	COAD 2408	–	–	MK044096	–	–	MK044189	–	–	–
Trichoderma stramineum	GJS 02-84 T	AY737765	–	AY737746	–	–	AY391945	–	–	–
Trichoderma stramineum	TAMA 0425	AB856609	–	AB856675	–	–	AB856748	–	–	–
Trichoderma subazureum	YMF 1.06207 T	MN977799	–	MT070148	–	–	MT052190	–	–	–
Trichoderma subuliforme	YMF 1.06204	MN977796	–	MT070151	–	–	MT052187	–	–	–
Trichoderma subuliforme	YMF 1.06205	MN977797	–	MT070150	–	–	MT052188	–	–	–

Supplementary Table 2 Continued.

Species	**Strains**	**GenBank accession numbers**								
		ITS	**LSU**	***TEF1-α***	***TUB***	***Bloc***	***RPB2***	***RPB1***	***CaM***	***Act***
Trichoderma sulawesense	GJS85-228 T	AY737753	–	AY737730	–	–	AY391954	–	–	–
Trichoderma supraverticillatum	YMF 1.06208 T	MN977800	–	MT070147	–	–	MT052191	–	–	–
Trichoderma syagri	BAFC 4357 T	–	–	MG822711	–	–	–	–	–	–
Trichoderma syagri	BAFC 4371	–	–	MG822710	–	–	–	–	–	–
Trichoderma theobromicola	COAD 2406	–	–	MK044093	–	–	MK044186	–	–	–
Trichoderma theobromicola	COAD 2407	–	–	MK044094	–	–	MK044187	–	–	–
Trichoderma tibetica	YMF 1.05583 T	MK779177	–	MK779179	–	–	MK779178	–	–	–
Trichoderma uncinatum	YMF 1.04622	MK795994	–	MK795986	–	–	MK795990	–	–	–
Trichoderma vadicola	WT 10708 T	MH287491	–	MH287499	–	–	MH287511	–	–	–
Trichoderma vadicola	WT 32801	MH606225	–	MH606228	–	–	MH606231	–	–	–
Trichoderma vermifimicola	CGMCC 3.19850	MN594472	–	MN605881	–	–	MN605870	–	–	–
Trichoderma vermifimicola	HMAS 248255 T	MN594473	–	MN605882	–	–	MN605871	–	–	–
Trichoderma virens	COAD 2400		–	MK044087	–	–	MK044180	–	–	–
Trichoderma virens	GJS 01-287	DQ083023	–	AY750894	–	–	EU341804	–	–	–
Trichoderma virens	V-1	KF144616	–	KF668098	–	–	KF574111	–	–	–
Trichoderma virens	V-2	KF144617	–	KF668099	–	–	KF574108	–	–	–
Trichoderma xixiacum	CGMCC 3.19698	MN594477	–	MN605886	–	–	MN605875	–	–	–
Trichoderma xixiacum	HMAS 248253 T	MN594476	–	MN605885	–	–	MN605874	–	–	–
Trichoderma xishuangbannaense	**KUMCC 21-0815 T**	**OP425805**	**–**	**OR025991**	**–**	**–**	**OR025907**	–	–	–
Trichoderma xishuangbannaense	**KUMCC 21-0816**	**OP425806**	–	**OR025992**	**–**	**–**	**OR025908**	–	–	–
Trichoderma zelobreve	CGMCC 3.19696	MN594475	–	MN605884	–	–	MN605873	–	–	–
Trichoderma zelobreve	HMAS 248254 T	MN594474	–	MN605883	–	–	MN605872	–	–	–
Yunnania carbonaria	CBS 205.61 T	KX923820	HG380462	KX924044	KX924254	–	–	–	–	–
Yunnania penicillata	CBS 130296 T	JN831361	KY659809	KY659808	KY659807	–	–	–	–	–
Yunnania smithii	CBS 855.68 T	KX923822	KX924028	KX924046	KX924256	–	–	–	–	–

T indicates the ex-type; – data unavailable; Newly generated sequences are in bold.

Supplementary Table 3 The information of new species and the closely related species reported in this study.

Taxa	Country	Host/Substrate	Life model	Conidia	Conidiogenous cells	References
Amphichorda						
Am. cavernicola	China	Bat guano, bird faeces, soil	Saprobes	2.5–4 × 2–4 µm	4.5–8 × 2–3 µm	Zhang et al. (2020)
Am. guana	China	Bat guano	Saprobes	4.5–5.5 × 3.5–5 µm	7–10 × 2–3 µm	Zhang et al. (2017)
Am. yunnanensis	China	*Rhinolophus affinis* (Bat), *Rhinolophus siamensis* (Bat)	Associated with bats	2–5 × 2–4 µm	4–12 × 1–4 µm	This study
Apiospora						
Ap. biserialis	China	Dead bamboo	Saprobes	7–11 µm long	5–22 × 2.5–5 µm	Feng et al. (2021), Tian et al. (2021)
Ap. chromolaenae	Thailand	*Chromolaena odorata*	Saprobes	4–6 × 4.5–6.5 µm	6.5–12 × 1–2 µm	Mapook et al. (2020), Pintos & Alvarado (2021)
Ap. euphorbiae	Zambia	*Euphorabia*	Saprobes	4–5.5 × 3–4 µm	4–5 × 3.5–5 µm	Ellis (1965), Tian et al. (2021)
Ap. gaoyouensis	China	*Phragmites australis*	Saprobes	5–8 × 4–8 µm	1–2 × 2–3 µm	Jiang & Tian (2018)
Ap. gelatinosa	China	Dead bamboo	Saprobes	–	–	Feng et al. (2021), Tian et al. (2021)
Ap. locuta-pollinis	China	*Aristolochia debilis*, *Brassica campestris*, *Cordyline fruticosa*, *Disporopsis pernyi*, *Epimedium acuminatum*, *Hosta ventricosa*, *Pachysandra terminalis*	Associated with hosts	5.5–9 × 4.5–8 µm	3–7.5 × 3–6 µm	Zhao et al. (2018), Chen et al. (2021), Tian et al. (2021)
Ap. malaysiana	Malaysia	*Cinnamomum camphora*, *Macaranga hullettii*	Saprobes	5–6 × 3–4 µm	4–7 × 3–5 µm	Crous & Groenewald (2013), Wang et al. (2017), Pintos & Alvarado (2021)
Ap. marii	China, Italy, Netherlands, Spain and Sweden	*Ammophila arenaria*, *Avena sativa*, *Beta vulgaris*, *Olea europaea*, *Phragmites australis*	Saprobes	7.2–7.5 × 6.1–6.5 µm	–	Larrondo & Calvo (1990), Pintos & Alvarado (2021), Farr & Rossman (2022)
Ap. phyllostachydis	China	*Phyllostachys heteroclada*	Saprobes	5–6 × 4–6 µm	20–55 × 1.5–2.5 µm	Yang et al. (2019), Pintos & Alvarado (2021)
Ap. septata	China	Dead bamboo	Saprobes	9–13 µm long	4–18.0 × 1.5–4 µm	Feng et al. (2021), Tian et al. (2021)
Ap. vietnamensis	Vietnam	*Citrus sinensis*	Saprobes	5–6 × 3–4 µm	4–7 × 3–5 µm	Crous & Groenewald (2013), Wang et al. (2017), Pintos & Alvarado (2021)
Ap. Xishuangbannaensis	China	*Rhinolophus pusillus* (Bat)	Associated with bats	7–12 × 3–12 µm	6–37 × 1–5 µm	This study

Supplementary Table 3 Continued.

Taxa	Country	Host/Substrate	Life model	Conidia	Conidiogenous cells	References
Clonostachys						
C. rhinolophicola	China	*Hipposideros larvatus* (Bat), *Rhinolophus stheno* (Bat)	Associated with bats	3–9 × 2–5 µm	7–22 × 1–8 µm	This study
C. pityrodes	Brazil, Guiana, Indonesia, Mauritius, Mexico, Panama, Spain, USA, Venezuela	Wood	Saprobes	(4.8–)5.8–7.2(–9) × (2.4–)2.8–3.4(–4) µm	(5.8–)13–16.4(–19.6) × (1.6–)2.2–2.4(–3) µm	Schroers et al. (2001)
Fusarium						
F. annulatum	New Caledonia	*Oryza sativa*	Saprobes			Yilmaz et al. (2021)
F. cugenangense	Indonesia, Java	*Musa* spp.	Pathogens	(7–)8–11(–24) × (2–)7(–12) µm	(5–)12–31(–45) × (3–)5–7(–8) µm	Maryani et al. (2019)
F. curvatum	Germany, Netherlands	*Beaucarnia* sp., *Hedera helix*, *Matthiola incana*	Saprobes	(4–)5–13 × 2–4 µm	3–30 × 2–5 µm	Lombard et al. (2019)
F. fujikuroi	Australia, Bangladesh, Brazil, China, India, Indonesia, Italy, Japan, Korea, Laos, Malaysia, Nepal, Philippines, Sri Lanka, Turkey, USA, Vietnam	*Acacia koa*, *Actinidia chinensis*, *Ananas comosus*, *Barnyard grass*, *Canna edulis*, *Conyza canadensis*, *Dalbergia odorifera*, *Glycine max*, *Macleaya cordata*, *Mangifera indica*, *Oryza sativa*, *Panax ginseng*, *Reineckea carnea*, *Triticum aestivum*, *Zea mays*	Saprobes	5–12 × 1.5–2.5 µm	–	Wollenweber (1931), Choi et al. (2011), Farr & Rossman (2022)
F. globosum	South Africa	*Zea mays*	Pathogen	8–20 × 2–4.5 µm	10–20 × 3–4 µm	Rheeder et al. (1996), Sandoval-Denis et al. (2018)
F. hainanense	China	*Musa nana*, *Oryza* sp.	Endophytes	18–22.5 × 3–4 µm	20–22.5 × 2–3 µm	Wang et al. (2019)
F. heterosporum	Brazil, Canada, China, Thiopia, Dominican Republic, Libya, New Zealand, Poland, Tanzania, Uganda, USA, Zimbabwe	*Andropogon sorghum* var. *Sudanensis*, *Brachiaria brizantha*, *Cenchrus ciliaris*, *Panicum maximum*, *Paspalum* sp., *Pinus monticola*, *Zea mays*	Saprobes	(15–) 25–35 (–50) × 2.5–4 µm	10–20 × 2.5–3.5 µm	Farr & Rossman (2022), Fungi of Great Britain and Ireland (2022)

Supplementary Table 3 Continued.

Taxa	**Country**	**Host/Substrate**	**Life model**	**Conidia**	**Conidiogenous cells**	**References**
F. hipposidericola	China	*Rhinolophus malayanus* (Bat), *Rhinolophus stheno* (Bat)	Associated with bats	3–31 × 1–6 µm	3–34 × 1–5 µm	This study
F. inflexum	Germany	*Viciae fahae*	Saprobes	10.6–34.2 × 2.9–4.6 µm	7–15 × 3–5 µm	Schneider & Dalchow (1975)
F. irregulare	China	Bamboo	Saprobes	16–38.5 × 3–5 µm	13.5–22.5 × 2–4 µm	Wang et al. (2019)
F. luffae	China	*Luffa aegyptiaca*, *Humulus scandens*	Associated with bats, saprobes	6–30 × 1–8 µm	7–25 × 1–7 µm	Wang et al. (2019), This study
F. mangiferae	Israel, Malaysia, South Africa, USA	*Mangifera indica*	Saprobes	4.3–9–18.4 × 1.7–2.4–3.3 µm	–	Britz et al. (2002)
F. menglaense	China	*Rhinolophus malayanus* (Bat)	Associated with bats	3–32 × 1–6 µm	3–34 × 1–5 µm	This study
F. nirenbergiae	Brazil, Italy, Netherlands, South Africa, Unknown locality, USA	*Agathosma Betulina*, *Bouvardia longiflora*, *Chrysanthemum* sp., *Dianthus caryophyllus*, *Musa* sp., *Passiflora edulis*, *Secale cereale*, *Solanum lycopersicum*, *Solanum tuberosum*	Saprobes	5–14 × 2–4 µm	8–24 × 2–4 µm	Lombard et al. (2019)
F. proliferatum	Papua New Guinea	*Cephalosporium proliferatum*	Saprobes	5–11 × 2–4 µm	–	Matsushima (1971), Gerlach & Nirenberg (1982)
F. rhinolophicola	China	*Rhinolophus malayanus* (Bat)	Associated with bats	2–31 × 2–10 µm	5–65 × 1–7 µm	This study
F. sambucinum	Argentina, Australia, Bahrain, Brazil, Bulgaria, Canada, Chile, China, Czechoslovakia, Egypt, England, Estonia, Finland, France, Germany, India, Iran, Italy, Japan, Kenya, Korea, Libya, Malaysia, Montenegro, Netherlands,	*Acer negundo*, *Aegopodium podagraria*, *Albizia lebbeck*, *Amaranthus hybridus*, *Ammi majus*, *Andropogon gerardii*, *Arachis hypogaea*, *Avena sativa*, *Beta vulgaris*, *Brassica oleracea*, *Buddleja* sp., *Calluna vulgaris*, *Carex acutiformis*, *Chenopodium album*, *Citrus limetta*, *Citrus nobilis*, *Citrus reticulata*, *Citrus sinensis*, *Clianthus puniceus*, *Cocos nucifera*, *Cornus macrophylla*, *Cucumis melo*, *Cucurbita maxima*, *Cucurbita* sp.,	Pathogen	–	–	Farr & Rossman (2022)

Supplementary Table 3 Continued.

Taxa	Country	Host/Substrate	Life model	Conidia	Conidiogenous cells	References
	New Zealand, Norway, Pakistan, Poland, Russia, Sierra Leone, Singapore, Spain, South Africa, Switzerland, Tanzania, Trinidad and Tobago, Virginia, Turkey, UK, Ukraine, USA	*Cuminum cyminum*, *Cupressus lusitanica*, *Cytisus scoparius*, *Dactylis glomerata*, *Datura stramonium*, *Elaeis guineensis*, *Eleocharis palustris*, *Eucalyptus fastigata*, *Fagopyrum esculentum*, *Fraxinus excelsior*, *Glycine max*, *Hordeum vulgare*, *Humulus lupulus*, *Hypolixus haerens*, *Ixora parviflora*, *Juglans regia*, *Lablab purpureus*, *Linum usitatissimum*, *Lycopersicon esculentum*, *Medicago sativa*, *Melilotus parviflorus*, *Melinis minutiflora*, *Musa* sp., *Oryza sativa*, *Passiflora edulis*, *Persea americana*, *Phaseolus vulgaris*, *Phoenix canariensis*, *Phragmites australis*, *Phyllanthus emblica*, *Pinus elliottii*, *Pisum sativum*, *Pueraria phaseoloides*, *Sabal glabra*, *Salvadora oleoides*, *Sambucus racemosa*, *Solanum* spp., *Solanum tuberosum*, *Sporobolus poiretii*, *Syringa vulgaris*, *Taraxacum kok-saghyz*, *Tectona grandis*, *Theobroma cacao*, *Trifolium* spp., *Trifolium subterraneum*, *Trigonella* spp., *Triticum aestivum*, *Triticum spelta*, *Ulex europaeus*, *Urtica* sp., *Vicia faba*, *Vitis vinifera*, *Zea* spp., *Zinnia elegans*				
F. siculi	Italy	*Citrus sinensis*	Saprobes	16.5–33.5 × 2–4 µm	(5.3–)8.5–12.3(–16.8) × (2.3–)2.9–3.5(–3.8) µm	Sandoval-Denis et al. (2018)

Supplementary Table 3 Continued.

Taxa	Country	Host/Substrate	Life model	Conidia	Conidiogenous cells	References
F. tricinctum	Argentina, Brazil, Canada, China, Denmark, Finland, France, Germany, Hungary, Italy, Japan, Netherlands, New Zealand, Norway, Poland, Scotland, Serbia, South Africa, South Korea, Syria, Turkey, USA	*Allium cepa*, *Allium sativum*, *Ammi visnaga*, *Arachis hypogaea*, *Artemisia* sp., *Astragalus canadensis*, *Avena sativa*, *Beta vulgaris*, *Brassica oleracea var*. *italica*, *Castanea crenata*, *Cucurbita moschata*, *Dactylis glomerata*, *Daucus carota*, *Dianthus* sp., *Fritillaria przewalskii*, *Glycine max*, *Hordeum* sp., *Hordeum vulgare*, *Hosta fortunei*, *Lens culinaris*, *Lilium davidii var*. *unicolor*, *Lilium* sp., *Linum usitatissimum*, *Lycium barbarum*, *Lythrum salicaria*, *Malus domestica*, *Malus sieversii*, *Medicago sativa*, *Medicago truncatula*, *Musa* sp., *Nelumbo nucifera*, *Nicotiana tabacum*, *Oryza sativa*, *Passiflora edulis*, *Phaseolus vulgaris*, *Pinus banksiana*, *Pisum sativum*, *Pisum sativum* subsp. *sativum*, *Quercus brantii*, *Secale cereale*, *Sophora japonica*, *Sorghum vulgare*, *Trachycarpus fortunei*, *Trifolium incarnatum*, *Triticum aestivum*, *Triticum* sp., *Triticum spelta*, *Urena lobata*, *Vicia faba*, *Zea mays*	Pathogen	5–9.4 × 1.2–20 µm	–	Chen et al. (2017), Farr & Rossman (2022)
F. xishuangbannaensee	China	*Rhinolophus malayanus* (Bat)	Associated with bats	2–36 × 1–3 µm	12–36 × 1–4 µm	This study
F. yunnanense	China	*Rhinolophus malayanus* (Bat)	Associated with bats	5–28 × 1–5 µm	6–45 × 1–6 µm	This study

Supplementary Table 3 Continued.

Taxa	**Country**	**Host/Substrate**	**Life model**	**Conidia**	**Conidiogenous cells**	**References**
Neopestalotiopsis						
N. clavispora	Alabama, Argentina, Australia, China, Cuba, India, Iran, Italy, South Korea, Spain, Sri Lanka, Uruguay, USA	*Magnolia* sp., *Quercus rubra*	Saprobes	18–26 ×6. 5–8.5 µm	4–10 µm long	Maharachchikumbura et al. (2012, 2014b), Farr & Rossman (2022)
N. chiangmaiensis	Thailand	*Pandanus* sp.	Saprobes	18–22 × 8–11 µm	–	Tibpromma et al. (2018)
N. dendrobii	Thailand	*Dendrobium cariniferum*	Endophytes	(19–) 20.5–23 (–24.5) × (6–) 6.5–7.5 (–8) µm	–	Ma et al. (2019)
N. mianyangensis	China	*Paeonia suffruticosa*	Pathogens	19–23 × 5.5–7 µm	3–5 × 2.1–2.5 µm	Li et al. (2022)
N. paeonia-suffruticosa	China	*Paeonia suffruticosa*, *Rhinolophus stheno* (Bat)	Pathogens	15–30 × 5–10 µm	5–16 × 1–4 µm	Li et al. (2022), This study
N. saprophytica	China	*Litsea rotundifolia*, *Magnolia* sp.	Saprobes	22–30 × 5–6 µm	–	Maharachchikumbura et al. (2012, 2014), Liu et al. (2021)
N. xishuangbannaensis	China	*Kerivoula hardwickii* (Bat)	Associated with bats	13– 30 × 5–10 µm	5–17 × 1–5 µm	This study
Phialemoniopsis						
Ph. endophytica	China	*Luffa cylindrica*	Endophytes	2–3.5 × 1–2 µm	6.5–15 × 1.5–3 µm	Su et al. (2016)
Ph. hipposidericola	China	*Hipposideros larvatus* (Bat)	Associated with bats	2–8 × 1–5 µm	4–15 × 1–5 µm	This study
Ph. pluriloculosa	USA	Human toe nai and synovial fluidl	Pathogen	2–3 × 1–1.5 µm	6–12 × 1–1.5 µm	Perdomo et al. (2013)
Ph. xishuangbannaensis	China	*Hipposideros larvatus* (Bat)	Associated with bats	3–6 × 1–4 µm	5–46 × 1–8 µm	This study
Trichoderma						
T. andinense				4.5 ± 0.3 × 3 ± 0.2 µm		Samuels et al. (2012), Jaklitsch & Voglmayr (2014)
T. asymmetricum	China	*Hippuris vulgaris*	Endophytes	3.5–4.5(–5) × 3.2–4.1 µm	(4.4–)5.9–11.8(–12.6) × 2.3–4(–4.4) µm	Zheng et al. (2021)
T. atroviride	China	*Camellia sinensis*	Saprobes	4–5 × 3–3.5 µm	–	Manawasinghe et al. (2021)
T. awajun	Peru	Soil	Saprobes	1.5–3 × 1.3–2.6 µm	3.1–10 × 6.4–9.6 µm	Bustamante et al. (2021)
T. hipposiderocola	China	*Hipposideros pomona* (Bat), *Miniopterus schreibersii* (Bat), *Rhinolophus affinis* (Bat)	Associated with bats	1–6 × 1–5 µm	2–15 × 1–5 µm	This study

Supplementary Table 3 Continued.

Taxa	Country	Host/Substrate	Life model	Conidia	Conidiogenous cells	References
T. inconspicuum	China	*Miniopterus schreibersii* (Bat), *Nymphoides peltatum*,	Associated with bats, endophytes	2.8–4.5 × 2.6–4 µm	6.4–14.4(–16.2) × 1.9–4 µm	Zheng et al. (2021)
T. koningii	Australia, Canada, China, Italy, Japan, Malaysia, New Zealand, Poland, Papua New Guinea, Russia, South Africa, Thailand, USA, Venezuela	*Abies alba*, *Betula pendula*, *Brassica oleracea*, *Cocos nucifera*, *Ipomoea batatas*, *Leucadendron* sp., *Nothofagus truncata*, *Pinus caribaea*, *Vitis* sp., *Zea mays*	Saprobes	3–5 × 2–3 µm	7.5–8.2 × 2.5–3 µm	Oudemans & Koning (1902), Lee et al. (2004), Farr & Rossman (2022)
T. obovatum	China	*Hipposideros pomona* (Bat), *Miniopterus schreibersii* (Bat), *Rhinolophus rex* (Bat), Soil	Associated with bats, saprobes	3–8 × 2–5 µm	3–15 × 1–5 µm	Zheng et al. (2021), This study
T. paratroviride	Spain	*Phillyrea angustifolia*, *Teline linifolia*	Saprobes	(3–)3.3–3.7(–4) × (3–)3.2–3.5(–3.7) µm	5.2–)6.2–11(–14) × (2–)2.5–3.2(–3.5) µm	Jaklitsch & Voglmayr (2015)
T. rhinolophicola	China	*Rhinolophus malayanus* (Bat)	Associated with bats	2–12 × 2–5 µm	3–17 × 1–5 µm	This study
T. scorpioideum	China	*Hippuris vulgaris*	Endophytes	3.3–4.4 × 2.4–3.8 µm	(6.5–)6.8–12.7(–13.3) × 2–3.9 µm	Zheng et al. (2021)
T. subviride	China	Wood	Saprobes	(2–)2.5–3.8(–4.5)× (2–)2.5–3.2 µm	4.5–)5–6.5(–7)×2–3 µm	Qin & Zhuang (2016)
T. uncinatum	China	*Potamogeton malaianus*	Endophytes	3.1–4.4 × 2.7–4 µm	(4.3–)5.2–9.3(–10.3) × 2.3–3.9 µm	Zheng et al. (2021)
T. xishuangbannaense	China	*Rhinolophus malayanus* (Bat)	Associated with bats	3–13 × 2–6 µm	4–14 × 1–5 µm	This study

– = Data not available.

Supplementary Table 4 The base pair comparison of sequences generated in this study and closely related sequences.

Taxa	Locus	The sequences comparison result
Apiospora xishuangbannaensis KUMCC 21-0695	ITS (ITS5/ITS4)	0.95% (6/630 bp) different to *Ap. septata* (CGMCC 3.20134); 1.01% (6/595 bp) different to *Ap. gelatinosa* (HKAS 111962); 1.08% (7/648 bp) different to *Ap. biserialis* (CGMCC 3.20135)
	LSU (LR0R/LR5)	0.24% (2/850 bp) different to *Ap. septata* (CGMCC 3.20134); 0.80% (7/876 bp) different to *Ap. gelatinosa* (HKAS 111962); 0.24% (2/844 bp) different to *Ap. biserialis* (CGMCC 3.20135)

Supplementary Table 4 Continued.

Taxa	Locus	The sequences comparison result
	TUB (Bt2a/Bt2b)	3.13% (15/479 bp) different to *Ap. septata* (CGMCC 3.20134); 3.97% (19/479 bp) different to *Ap. gelatinosa* (HKAS 111962); 4.59% (22/479 bp) different to *Ap. biserialis* (CGMCC 3.20135)
	TEF1-α (EF1-728F/EF-2)	1.58% (7/443 bp) different to *Ap. septata* (CGMCC 3.20134); 3.04% (13/427 bp) different to *Ap. gelatinosa* (HKAS 111962); 3.38% (15/444 bp) different to *Ap. biserialis* (CGMCC 3.20135)
N. xishuangbannaensis KUMCC 21-0424	ITS (ITS5/ITS4)	0.39% (2/508 bp) different to *N. paeonia-suffruticosa* (CGMCC 3.23554); 0.20% (1/499 bp) different to *N. mianyangensis* (CGMCC 3.23555); 0.21% (1/484 bp) different to *N. saprophytica* (CBS 115452);
	TUB (Bt2a/Bt2b)	1.08% (5/465 bp) different to *N. paeonia-suffruticosa* (CGMCC 3.23554); 1.08% (5/465 bp) different to *N. mianyangensis* (CGMCC 3.23555); 0.88% (4/452 bp) different to *N. saprophytica* (CBS 115452);
	TEF1-α (EF1-728F/EF1-1567R)	3.41% (15/440 bp) different to *N. paeonia-suffruticosa* (CGMCC 3.23554); 0.92% (4/436 bp) different to *N. mianyangensis* (CGMCC 3.23555); 2.45% (22/899 bp) different to *N. saprophytica* (CBS 115452);
Clonostachys rhinolophicola KUMCC 21-0439	ITS (ITS1/ITS4)	2.32% (14/604 bp) different to *C. pityrodes* (CBS 102033)
	TUB (T1/T22)	5.78% (34/589 bp) different to *C. pityrodes* (CBS 102033)
Amphichorda yunnanensis KUMCC 21-0416	ITS (ITS5/ITS4)	20.00% (105/505 bp) different to *Am. cavernicola* (LC12448); 17.70% (94/531 bp) different to *Am. guana* (CGMCC3.17908)
	RPB1 (RPB1A/RPB1B-G2R)	3.96% (30/758 bp) different to *Am. guana* (CGMCC3.17908)
	RPB2 (RPB2-5f/RPB2-7cR)	4.02% (43/1068 bp) different to *Am. guana* (CGMCC3.17908)
	TEF1-α (EF1-983F/EF1-2218R)	1.87% (17/911 bp) different to *Am. cavernicola* (LC12448); 1.09% (10/917 bp) different to *Am. guana* (CGMCC3.17908)
Trichoderma hipposiderocola KUMCC 21-0801	ITS (ITS1/ITS4)	2.20% (13/592 bp) different to *T. nordicum* (WT 61001); 1.69% (10/592 bp) different to *T. uncinatum* (YMF 1.04622); 0.17% (1/572 bp) different to *T. obovatum* (YMF 1.06211)
	RPB2 (RPB2-5f/RPB2-7cR)	2.51% (10/398 bp) different to *T. atroviride* (COAD 2396); 3.15% (37/1176 bp) different to *T. nordicum* (WT 61001); 1.86% (16/858 bp) different to *T. uncinatum* (YMF 1.04622); 2.34% (25/1068 bp) different to *T. obovatum* (YMF 1.06211)
	TEF1-α (EF1-728F/TEF1LLErev)	20.83% (>100/480 bp) different to *T. atroviride* (COAD 2396); 2.74% (23/840 bp) different to *T. nordicum* (WT 61001); 2.38% (20/840 bp) different to *T. uncinatum* (YMF 1.04622); 2.86% (24/840 bp) different to *T. obovatum* (YMF 1.06211)

Supplementary Table 4 Continued.

Taxa	**Locus**	**The sequences comparison result**
Trichoderma rhinolophicola	*TEF1-α* (EF1-728F/TEF1LLErev)	3.05% (40/1311 bp) different to *T. atroviride* (COAD 2396)
KUMCC 21-0813		
Trichoderma xishuangbannaense	ITS (ITS1/ITS4)	3.37% (20/593 bp) different to *T. pluripenicillatum* (YMF 1.06198)
KUMCC 21-0815	*RPB2* (RPB2-5f/RPB2-7cR)	9.82% (70/713 bp) different to *T. awajun* (CHAXC CP24-7);
		10.52% (75/713 bp) different to *T. andinense* (COAD 2431);
		10.24% (83/713 bp) different to *T. pluripenicillatum* (YMF 1.06198)
	TEF1-α (EF1-728F/TEF1LLErev)	>8.35% (>100/1198 bp) different to *T. awajun* (CHAXC CP24-7);
		14.87% (94/632 bp) different to *T. andinense* (COAD 2431);
		>8.01% (>100/1248 bp) different to *T. pluripenicillatum* (YMF 1.06198)
Fusarium hipposidericola	*CaM* (CL1/CL2A)	2.31% (16/692 bp) different to *F. mangiferae* (CBS 120994)
KUMCC 21-0724	*RPB2* (RPB2-5f/RPB2-7cR)	5.55% (>100/1803 bp) different to *F. mangiferae* (CBS 120994)
	TUB (T1/T2)	2.11% (12/568 bp) different to *F. mangiferae* (CBS 120994)
	TEF1-α (EF1/EF2)	3.73% (24/643 bp) different to *F. mangiferae* (CBS 120994)
Fusarium menglaense	ITS (ITS5/ITS4)	0.20% (1/510 bp) different to *F. cugenangense* (CBS 130308);
KUMCC 21-0717	*CaM* (CL1/CL2A)	1.93% (13/675 bp) different to *F. inflexum* (CBS 716.74);
		1.93% (13/675 bp) different to *F. curvatum* (NRRL 22902);
		1.93% (13/675 bp) different to *F. nirenbergiae* (CBS 744.97)
	RPB2 (RPB2-5f/RPB2-7cR)	2.18% (26/1194 bp) different to *F. inflexum* (CBS 716.74);
		1.76% (21/1194 bp) different to *F. cugenangense* (CBS 130308);
		2.43% (29/1194 bp) different to *F. curvatum* (NRRL 22902);
		2.51% (30/1194 bp) different to *F. nirenbergiae* (CBS 744.97)
	RPB1 (RPB1-FA/RPB1-G2R)	1.00% (16/1605 bp) different to *F. inflexum* (CBS 716.74);
		0.12% (18/1605 bp) different to *F. cugenangense* (CBS 130308);
		0.46% (7/1534 bp) different to *F. curvatum* (NRRL 22902)
	TUB (T1/T2)	0.59% (3/506 bp) different to *F. inflexum* (CBS 716.74);
		0.93% (5/537 bp) different to *F. curvatum* (NRRL 22902);
		0.93% (5/537 bp) different to *F. nirenbergiae* (CBS 744.97)
	TEF1-α (EF1/EF2)	2.77% (18/649 bp) different to *F. inflexum* (CBS 716.74);
		2.76% (17/615 bp) different to *F. cugenangense* (CBS 130308);
		2.82% (18/639 bp) different to *F. curvatum* (NRRL 22902);
		2.82% (18/639 bp) different to *F. nirenbergiae* (CBS 744.97)
Fusarium rhinolophicola	ITS (ITS5/ITS4)	0.52% (3/572 bp) different to *F. hainanense* (LC11638)
KUMCC 21-0449	*CaM* (CL1/CL2A)	0.15% (1/647 bp) different to *F. hainanense* (LC11638)
	RPB2 (RPB2-5f/RPB2-7cR)	2.33% (28/1201 bp) different to *F. hainanense* (LC11638)
	RPB1 (RPB1-FA/RPB1-G2R)	2.49% (40/1607 bp) different to *F. hainanense* (LC11638)
	TEF1-α (EF1/EF2)	2.52% (16/636 bp) different to *F. hainanense* (LC11638)

Supplementary Table 4 Continued.

Taxa	Locus	The sequences comparison result
Fusarium xishuangbannaensee KUMCC 21-0432	*CaM* (CL1/CL2A)	4.61% (36/781 bp) different to *F. annulatum* (CBS 258.54);
		2.88% (21/728 bp) different to *F. globosum* (CBS 428.97);
		3.11% (22/707 bp) different to *F. siculi* (CBS 142222)
	RPB2 (RPB2-5f/RPB2-7cR)	0.24% (2/818 bp) different to *F. annulatum* (CBS 258.54);
		1.89% (15/794 bp) different to *F. fujikuroi* (CBS 221.76);
		0.37% (3/818 bp) different to *F. globosum* (CBS 428.97);
		3.11% (3/707 bp) different to *F. siculi* (CBS 142222)
	RPB1 (RPB1-FA/RPB1-G2R)	2.34% (20/856 bp) different to *F. annulatum* (CBS 258.54);
		13.02% (>100/768 bp) different to *F. fujikuroi* (CBS 221.76);
		13.07% (>100/765 bp) different to *F. globosum* (CBS 428.97)
	TUB (T1/T2)	1.96% (26/1327 bp) different to *F. annulatum* (CBS 258.54);
		1.94% (11/568 bp) different to *F. fujikuroi* (CBS 221.76);
		1.23% (7/568 bp) different to *F. globosum* (CBS 428.97);
		1.63% (8/492 bp) different to *F. siculi* (CBS 142222)
	TEF1-α (EF1/EF2)	17.12% (>100/584 bp) different to *F. annulatum* (CBS 258.54);
		4.91% (32/652 bp) different to *F. fujikuroi* (CBS 221.76);
		4.02% (26/646 bp) different to *F. globosum* (CBS 428.97);
		5.48% (31/566 bp) different to *F. siculi* (CBS 142222)
Phialemoniopsis hipposiderocola KUMCC 21-0778	ITS (ITS1/ITS4)	0.34% (11/471 bp) different to *Ph. pluriloculosa* (UTHSC 04-7);
		1.94% (11/568 bp) different to *Ph. xishuangbannaensis* (KUMCC 21-0774)
	LSU (LR0R/LR5)	0.19% (1/536 bp) different to *Ph. pluriloculosa* (UTHSC 04-7);
		2.09% (19/909 bp) different to *Ph. xishuangbannaensis* (KUMCC 21-0774)
	TUB (TUB-F/TUB-R)	2.13% (8/375 bp) different to *Ph. pluriloculosa* (UTHSC 04-7);
		4.26% (24/564 bp) different to *Ph. xishuangbannaensis* (KUMCC 21-0774)
Ph. xishuangbannaensis KUMCC 21-0774	ITS (ITS1/ITS4)	0.42% (2/471 bp) different to *Ph. pluriloculosa* (UTHSC 04-7);
		1.94% (11/568 bp) different to *Ph. hipposiderocola* (KUMCC 21-0778)
	LSU (LR0R/LR5)	0.19% (1/536 bp) different to *Ph. pluriloculosa* (UTHSC 04-7);
		2.09% (19/909 bp) different to *Ph. hipposiderocola* (KUMCC 21-0778)
	Act (Act1/Act5ra)	0.85% (6/705 bp) different to *Ph. pluriloculosa* (UTHSC 04-7)
	TUB (TUB-F/TUB-R)	0.33% (5/375 bp) different to *Ph. pluriloculosa* (UTHSC 04-7);
		4.26% (24/564 bp) different to *Ph. hipposiderocola* (KUMCC 21-0778)

Supplementary Table 5 List of fungal and fungus-like organisms isolated from bats and bat carcasses.

Fungal species	Host	Bat species	Country	References
Ascomycota				
Acaulium caviariforme	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Acremonium sp. 1	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Acremonium berkeleyanum	Bat	*Myotis septentrionalis*	Canada, USA	Vanderwolf et al. (2013b, 2016)
Acremonium cereale	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Acremonium murorum	Bat	Unknown species	Mexico	Vanderwolf et al. (2013b)
Acrodontium cf. *crateriforme*	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Alternaria sp.	Bat and bat carcasses	*Miniopterus orianae oceanensis, Myotis capaccini*	Australia, Italy	Voyron et al. (2011), Vanderwolf et al. (2013b), Holz et al. (2018), Nováková et al. (2018)
Alternaria betae-kenyensis	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Alternaria kulundii	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Alternaria tenuissima	Bat	Unknown species	Slovakia	Vanderwolf et al. (2013b)
Amphichorda yunnanensis	Bat	*Rhinolophus affinis, Rhinolophus siamensi*	China	This study
Aphanocladium album	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Apiospora arundinis	Bat	*Miniopterus schreibersii, Myotis pilosus*	China	This study
Apiospora marii	Bat	*Rhinolophus sinicus*	China	This study
Apiospora vietnamensis	Bat	*Hipposideros pomona*	China	This study
Apiospora xishuangbannaensis	Bat	*Rhinolophus pusillus*	China	This study
Apodospora sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Arachniotus sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Arachniotus ruber	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)
Arachnopeziza aurata	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Arbusculina fragmentans	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Arthrinium sphaerospermum	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Arthroderma quadrifidum	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)
Arthroderma sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Arthroderma silverae	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Arthrographis kalrae	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Arthrographis sp.	Bat	Unknown species	Canada, France	Vanderwolf et al. (2013b)
Ascomycete sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Ascomycota sp.	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Aspergillus aureolatus	Bat	Unknown species	Romania	Nováková et al. (2018)
Aspergillus baeticus	Bat and bat carcasses	Unknown species	Slovakia	Vanderwolf et al. (2013b), Nováková et al. (2018)

Supplementary Table 5 Continued.

Fungal species	Host	Bat species	Country	References
Aspergillus candidus	Bat	*Hipposideros armiger*	China	This study
Aspergillus carbonarius	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Aspergillus creber	Bat	*Rhinolophus affinis*	China	This study
Aspergillus cf. *wentii*	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Aspergillus flavofurcatus	Bat	Unknown species	Mexico	Vanderwolf et al. (2013b)
Aspergillus flavus	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Aspergillus fumigatus	Bat	*Myotis myotis*	France, Italy, Poland	Vanderwolf et al. (2013b), Ogórek et al. (2020)
Aspergillus fumigatus var. *fumigatus*	Bat	*Tadarida teniotis, Pipistrellus nathusii*	Italy	Voyron et al. (2011)
Aspergillus jensenii	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)
Aspergillus parasiticus	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Aspergillus penicillioides	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Aspergillus piperis	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Aspergillus restrictus	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Aspergillus sp. 1	Bat	Unknown species	Mexico	Vanderwolf et al. (2013b)
Aspergillus sp. 2	Bat carcasses	*Miniopterus schreibersii*	Italy	Voyron et al. (2011)
Aspergillus sp. 4 section *Nidulantes*	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Aspergillus sp. 4 section *Nigri*	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Aspergillus sp. 4 section *Nigri*	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Aspergillus sp. 4 section *Aspergillus*	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Aspergillus sulphureus	Bat	Unknown species	Mexico	Vanderwolf et al. (2013b)
Aspergillus sydowii	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil, Italy, Mexico	Vanderwolf et al. (2013b), Cunha et al. (2020)
Aspergillus terreus	Bat	Unknown species	Mexico, USA	Vanderwolf et al. (2013b)
Aspergillus versicolor	Bat	Unknown species	Canada, Mexico	Vanderwolf et al. *(*2013b)
Aspergillus westerdijkiae	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Aureobasidium pullulans	Bat	*Miniopterus orianae oceanensis, Myotis lucifugus, Myotis septentrionalis*	Australia, Canada	Vanderwolf et al. (2016), Holz et al. (2018)
Auxarthron cf. *californiense*	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Bartalinia robillardoides	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)

Supplementary Table 5 Continued.

Fungal species	Host	Bat species	Country	References
Bagadiella koalae	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Beauveria bassiana	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada	Vanderwolf et al. (2013b, 2016)
Beauveria bassiana cf. *brongniartii*	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Beauveria sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Blastobotrys chiropterorum	Bat	Unknown species	Columbia	Vanderwolf et al. (2013b)
Cadophora sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Cadophora malorum	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Camarosporium sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Candida athensensis	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Candida deformans	Bat	Unknown species	Mexico	Vanderwolf et al. (2013b)
Candida glabrata	Bat	Unknown species	USA	Vanderwolf et al. (2013b)
Candida orthopsilosis	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Candida palmioleophila	Bat carcasses	*Myotis capaccini*	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Candida parapsilosis	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Candida sp.	Bat	*Pipistrellus nathusii*	Canada, Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Capnobotryella sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Capnodiales sp.	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Cenococcum sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Cephalotrichum stemonitis	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada, Slovakia	Vanderwolf et al. (2013b, 2016), Nováková et al. (2018)
Ceratocystis sp.	Bat	Unknown species	France	Vanderwolf et al. (2013b)
Ceratocystis autographa	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Chaetomium fimeti	Bat	Unknown species	Mexico	Vanderwolf et al. (2013b)
Chaetomium globosum	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)
Chalara microspora	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Chrysosporium chiropterorum	Bat	Unknown species	France	Vanderwolf et al. (2013b)
Chrysosporium merdarium	Bat and bat carcasses	*Myotis capaccini, Myotis lucifugus, Myotis* sp., *Myotis septentrionalis, Miniopterus schreibersii, Pipistrellus* sp.	Canada, France, Hungary, Italy	Zeller (1966), Voyron et al. (2011), Vanderwolf et al. (2013b, 2016)
Chrysosporium pseudomerdarium	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Cladosporiaceae sp.	Bat	Unknown species	South Korea	Kim et al. (2023)
Cladorrhinum sp. 1	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Cladorrhinum sp. 2	Bat carcasses	Unknown species	Italy	Vanderwolf et al. (2013b)

Supplementary Table 5 Continued.

Fungal species	**Host**	**Bat species**	**Country**	**References**
Cladorrhinum sp. 3	Bat	Unknown species	Canada, France, USA	Vanderwolf et al. (2013b)
Cladosporium cladosporioides	Bat and bat carcasses	*Hypsugo savii*, *Myotis capaccini*	Canada, Italy, Slovakia	Voyron et al. (2011), Vanderwolf et al. (2013b), Nováková et al. (2018)
Cladosporium delicatulum	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Cladosporium herbarum	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Cladosporium macrocarpum	Bat	Unknown species	Slovakia	Vanderwolf et al. (2013b)
Cladosporium rosea	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Cladosporium sphaerospermum	Bat	*Myotis myotis*	Poland, Slovakia	Nováková et al. (2018), Ogórek et al. (2020)
Cladosporium sp.	Bat	*Myotis lucifugus*, *Myotis septentrionalis*	Canada, France, USA	Vanderwolf et al. (2016)
Chrysosporium sp. 1	Bat carcasses	*Myotis capaccini*	Italy	Voyron et al. (2011)
Chrysosporium sp. 2	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Chrysosporium sp. 3	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Cladosporium sp. 1 *C. sphaerospermum* complex	Bat	*Carollia perspicillata*, *Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Cladosporium sp. 1 *C. sphaerospermum* complex	Bat	*Carollia perspicillata*, *Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Clonostachys rhinolophicola	Bat	*Hipposideros larvatus*, *Rhinolophus stheno*	China	This study
Cochliobolus sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Coelomycete unidentified	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Curvularia sp.	Bat	*Carollia perspicillata*, *Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Cylindrocarpon destructans	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Cylindrocarpon o btusiusculum	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Cylindrocarpon sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Cylindrodendrum album	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Davidiella tassiana	Bat	*Miniopterus orianae bassanii*, *Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Debaryomyces subglobosus	Bat	Unknown species	Mexico	Vanderwolf et al. (2013b)
Debaryomyces udenii	Bat	*Miniopterus orianae bassanii*, *Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Deniquelata quercina	Bat	*Carollia perspicillata*, *Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Dictyosporium toruloides	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Didymella exigua	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Dothideomycetes sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Dothioraceae sp.	Bat	Unknown species	South Korea	Kim et al. (2023)

Supplementary Table 5 Continued.

Fungal species	Host	Bat species	Country	References
Eremomyces sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Eurotiomycetes sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Exophiala sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Fusarium dimerum	Bat carcasses	Undetermined bat	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Fusarium equiseti	Bat carcasses	*Myotis* sp., *Miniopterus schreibersii*	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Fusarium incarnatum	Bat carcasses	Unknown species	China	Karunarathna et al. (2020)
Fusarium luffa	Bat	*Rhinolophus malayanus*	China	This study
Fusarium merismoides	Bat	Unknown species	Brazil, Slovakia	Nováková et al. (2018)
Fusarium sp. 1	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Fusarium sp. 2	Bat	Unknown species	Canada, USA	Vanderwolf et al. (2013b)
Fusarium sp. *F. fujikuroi* complex	Bat	*Carollia perspicillata*, *Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Fusarium septata	Bat	*Rhinolophus malayanus*, *Rhinolophus stheno*	China	This study
Fusarium hipposiderocola	Bat	*Hipposideros pomona*	China	This study
Fusarium menglaense	Bat	*Rhinolophus malayanus*	China	This study
Fusarium menglunense	Bat	*Hipposideros pomona, Rhinolophus malayanus*	China	This study
Fusarium xishuangbannaensee	Bat	*Rhinolophus malayanus*	China	This study
Fusarium rhinolophicola	Bat	*Rhinolophus malayanus*	China	This study
Fusarium yunnanensis	Bat	*Rhinolophus malayanus*	China	This study
Geomyces destructans	Bat	*Eptesicus fuscus, Myotis austroriparius, Myotis leibii, Myotis lucifugus, Myotis septentrionalis, Myotis sodalis, Myotis velifer, Perimyotis subflavus*	USA	Swezey & Garrity (2011)
Geomyces pannorum	Bat	Unknown species	Canada, USA	Vanderwolf et al. (2013a, b)
Geomyces sp.	Bat	Unknown species	Canada, USA	Vanderwolf et al. (2013b)
Geomyces pannorum	Bat	Unknown species	USA	Vanderwolf et al. (2014b)
Geosmithia carolliae	Bat	*Carollia perspicillata*	Brazil	Cunha et al. (2020)
Gimnoascacea unidentified	Bat carcasses	*Myotis capaccini*	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Gliomastix chartarum	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Gymnascella aurantiaca	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)
Gymnoascus dankaliensis	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Gymnoascus intermedius	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Gymnoascus reessii	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)

Supplementary Table 5 Continued.

Fungal species	**Host**	**Bat species**	**Country**	**References**
Gymnoascus sp.	Bat and bat carcasses	*Miniopterus orianae bassanii*	Australia, Brazil, Italy	Vanderwolf et al. (2013b), Holz et al. (2018)
Gymnostellatospora sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Humicola sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Humicola sp. 1	Bat	*Myotis lucifugus*, *Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Hypocreales sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Hypoxylon sp. 1	Bat	Unknown species	Australia	Holz et al. (2018)
Hypoxylon sp. 2	Bat	*Carollia perspicillata*, *Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Isaria farinosa	Bat	*Myotis lucifugus*, *Myotis septentrionalis*	Canada, Slovakia	Vanderwolf et al. (2013b, 2016)
Kickxella alabastrina	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Lasiosphaeriaceae sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Lecanicillium lecanii	Bat carcasses	Unknown species	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Lecythophora sp.	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Leotiomycetes sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Leptodontidium elatius	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Leptosphaeriaceae sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Letendraea sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Leuconeurospora polypaeciloides	Bat	*Myotis lucifugus*, *Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Leuconeurospora capsici	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Leuconeurospora sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Malbranchea aurantiaca	Bat	Unknown species	Mexico	Vanderwolf et al. (2013b)
Malbranchea sp.	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Mammaria echinobotryoides	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Mammaria sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Meyerozyma cf. *caribbica*	Bat	*Carollia perspicillata*, *Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Microascus caviariformis	Bat	*Myotis lucifugus*, *Myotis septentrionalis*	Canada	Vanderwolf et al. (2013b, 2016)
Microascus longirostris	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Microascus sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Microsporum canis	Bat	Unknown species	Columbia	Vanderwolf et al. (2013b)
Monodictys sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Myceliophthora sp.	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Mycosphaerella tassiana	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Mycosphaerellaceae sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)

Supplementary Table 5 Continued.

Fungal species	Host	Bat species	Country	References
Myriangiales sp.	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Myriodontium sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Myrothecium sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Myxotrichum sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Nectriaceae sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Neocatenulostroma microsporum	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Neocosmospora pallidimors	Bat carcasses	*Rhinolophus affinis*	China	Karunarathna et al. (2020)
Neodevriesia capensis	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Neopestalotiopsis xishuangbannaensis	Bat	*Kerivoula hardwickii*	China	This study
Neopestalotiopsis paeoniae-suffruticosae	Bat	*Rhinolophus stheno*	China	This study
Neophaeosphaeria sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Neophysalospora eucalypti	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Nothophoma sp.	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Pestalotiopsis trachicarpicola	Bat	*Rhinolophus pusillus*	China	This study
Phialemoniopsis hipposiderocola	Bat	*Hipposideros larvatus*	China	This study
Phialemoniopsis xishuangbannaensis	Bat	*Hipposideros larvatus*	China	This study
Ochroconis cf. *musae*	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Oidiodendron cereale	Bat	*Miniopterus orianae bassanii*	Australia	Kokurewicz et al. (2016)
Oidiodendron griseum	Bat	Unknown species	Canada, Slovakia	Vanderwolf et al. (2013b), Nováková et al. (2018)
Oidiodendron myxotrichoides	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada	Vanderwolf et al. (2013b, 2016)
Oidiodendron sp. 1	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Oidiodendron sp. 2	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Oidiodendron sp. 3	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Oidiodendron truncatum	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada	Vanderwolf et al. (2013b, 2016)
Ophiostomataceae Unidentified	Bat carcasses	*Miniopterus schreibersii*, undetermined bat	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Paecilomyces carneus	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Paecilomyces cf. *formosus*	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Paecilomyces inflatus	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)

Supplementary Table 5 Continued.

Fungal species	Host	Bat species	Country	References
Paecilomyces sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Paraconiothyrium archidendri	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Paraconiothyrium variabile	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Paraphaeosphaeria sp.	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Pararamichloridium caricicola	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)
Penicillium aurantiogriseum	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Penicillium bialowiezense	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Penicillium brevicompactum	Bat	*Rhinolophus affinis, Rhinolophus rex, Rhinolophus siamensis, Rhinolophus sinicus*	China	This study
Penicillium brevistipitatum	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)
Penicillium chrysogenum	Bat	*Myotis myotis*	Canada, Poland, Slovakia	Vanderwolf et al. (2013b), Nováková et al. (2018), Ogórek et al. (2020)
Penicillium citreonigrum	Bat	*Myotis myotis*	Canada, Poland	Vanderwolf et al. (2013b), Ogórek et al. (2020)
Penicillium citrinum	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Penicillium commune	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Penicillium concentricum	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Penicillium coprophilum	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)
Penicillium corylophilum	Bat	Unknown species	Canada, Slovakia	Vanderwolf et al. (2013b), Nováková et al. (2018)
Penicillium crustosum	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Penicillium decumbens	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Penicillium dierckxii	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Penicillium griseofulvum	Bat carcasses	*Pipistrellus* sp.	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Penicillium guaibinense	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Penicillium miczynskii	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Penicillium olsonii	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Penicillium polonicum	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Penicillium solitum	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Penicillium spinulosum	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Penicillium sp. 1	Bat and bat carcasses	*Myotis lucifugus, Myotis septentrionalis* and undetermined bat	Canada, Italy, USA	Voyron et al. (2011), Vanderwolf et al. (2013b, 2016)
Penicillium sp. 2	Bat carcasses	Unknown species	UK	Wibbelt et al. (2010)
Penicillium rhinolophicola	Bat	*Rhinolophus sinicus*	China	This study

Supplementary Table 5 Continued.

Fungal species	**Host**	**Bat species**	**Country**	**References**
Penicillium yuxiensis	Bat	*Rhinolophus sinicus*	China	This study
Penicillium thomii	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada	Vanderwolf et al. (2013b, 2016)
Penicillium vulpinum	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Pestalotiopsis maculiformans	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Pestalotiopsis sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Petriella cf. *boulangeri*	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Phaeothecoidea minutispora	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Phaeotrichum hystricinum	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Phialemonium atrogriseum	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)
Phaeoacremonium sp.	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Phialocephala sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Phialophora hyalina	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Phialophora sp.	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2013b, 2016)
Phoma calidophila	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Phoma radicina	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Pleospora herbarum	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Pleosporaceae sp1.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Pleosporaceae sp2.	Bat	Unknown species	South Korea	Kim et al. (2023)
Pleosporales sp.	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Pleosporales unidentified	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Podospora glutinans	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Polyschema sp.	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Polytolypa sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Preussia sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Pseudeurotiaceae sp.	Bat	Unknown species	South Korea	Kim et al. (2023)
Pseudogymnoascus destructans	Bat	*Myotis lucifugus, Myotis myotis, Myotis daubentonii, Myotis septentrionalis*	Canada, Poland	Kokurewicz et al. (2016), Vanderwolf et al. (2016), Ogórek et al. (2020)
Pseudogymnoascus pannorum	Bat	*Myotis lucifugus, Myotis septentrionalis*	Slovakia	Vanderwolf et al. (2016), Nováková et al. (2018)
Pseudogymnoascus roseus	Bat	*Myotis lucifugus, Miniopterus orianae oceanensis, Myotis septentrionalis*	Australia, Canada	Vanderwolf et al. (2013a, 2016), Holz et al. (2018)
Pseudoarachniotus ruber	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Purpureocillium cf. *lilacinum*	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Pyrenochaeta sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)

Supplementary Table 5 Continued.

Fungal species	**Host**	**Bat species**	**Country**	**References**
Readeriella angustia	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Rhinocladiella similis	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Rhinocladiella sp.	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Saccharomycetaceae sp.	Bat	Unknown species	South Korea	Kim et al. (2023)
Sagenomella sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Schizothecium carpinicola	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Schizothecium sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Scopulariopsis brevicaulis	Bat	*Myotis myotis, Rhinolophus siamensis*	China, France, Poland	Vanderwolf et al. (2013b), Ogórek et al. (2020), This study
Scopulariopsis sp.	Bat	Unknown species	Mexico	Vanderwolf et al. (2013b)
Septonema secedens	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Shanorella sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Simplicillium aogashimaense	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Simplicillium lamellicola	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Simplicillium sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Sordariomycetes sp.	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Sporendonema sp.	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Sporothrix sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Sporothrix schenckii	Bat	Unknown species	Columbia	Vanderwolf et al. (2013b)
Stachylidium sp.	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Strelitziana albiziae	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Talaromyces allahabadensis	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Talaromyces sp. 1 section *Talaromyces*	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Talaromyces sp. 2 section *Talaromyces*	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Teratosphaeria capensis	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Teratosphaeriaceae sp.	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Tetracladium furcatum	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Thelebolus sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Thelebolus crustaceus	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada	Vanderwolf et al. (2013b, 2016)
Thelebolus globosus	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Thielavia sp.	Bat carcasses	*Myotis* sp., *Miniopterus schreibersii, Pipistrellus* sp.	Italy	Voyron et al. (2011)
Thysanophora penicillioides	Bat	*Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)

Supplementary Table 5 Continued.

Fungal species	Host	Bat species	Country	References
Thysanophora sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Tolypocladium inflatum	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Toxicocladosporium strelitziae	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Torula sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Trichocladium opacum	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Trichocomaceae sp.	Bat	Unknown species	South Korea	Kim et al. (2023)
Trichoderma harzianum	Bat carcasses	Unknown species	China	Karunarathna et al. (2020)
Trichoderma obovatum	Bat	*Hipposideros pomona, Miniopterus schreibersii, Rhinolophus rex*	China	This study
Trichoderma sp. 1	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Trichoderma sp. 2	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Trichoderma hipposiderocola	Bat	*Hipposideros pomona, Miniopterus schreibersii, Rhinolophus affinis*	China	This study
Trichoderma rhinolophicola	Bat	*Rhinolophus malayanus*	China	This study
Trichoderma xishuangbannaense	Bat	*Rhinolophus sinicus*	China	This study
Trichocomaceae sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Trichophyton mentagrophytes	Bat	Unknown species	Columbia	Vanderwolf et al. (2013b)
Trichophyton terrestre	Bat	Unknown species	Canada, USA	Vanderwolf et al. (2013b)
Trichosporiella multisporum	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Trichosporiella sp. 1	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Trichosporiella sp. 2	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Tubercularia sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Ulocladium chartarum	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Verticillium lecanii	Bat carcasses	*Myotis capaccini*	Italy	Voyron et al. (2011)
Wardomyces sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Wardomyces humicola	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Wardomyces inflatus	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Wickerhamia fluorescens	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Xenophacidiella pseudocatenata	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Zopfiella pleuropora	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Basidiomycota				
Agaricales sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Agaricomycetes sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Agaricostilbum hyphaenes	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Asterotremella sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Atheliaceae sp.	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)

Supplementary Table 5 Continued.

Fungal species	**Host**	**Bat species**	**Country**	**References**
Auricularia mesenterica	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Baeospora sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Bandoniozyma noutii	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Basidiomycete sp.	Bat	*Myotis lucifugus*, *Myotis septentrionalis*	Canada	Vanderwolf et al. (2013b, 2016)
Basidiomycota sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Brevicellicium olivascens	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Bullera sp. 1	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Bullera sp. 2	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Cerrena unicolor	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Chaetocladium jonesiae	Bat	Unknown	Czech Republic	Nováková et al. (2018)
Chondrostereum sp.	Bat	*Carollia perspicillata*, *Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Cryptococcus aff *amylolyticus*	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Cryptococcus albidus	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Cryptococcus albidus var. *albidus*	Bat	Unknown species	Mexico	Vanderwolf et al. (2013b)
Cryptococcus friedmannii	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Cryptococcus laurentii	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Cryptococcus sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Cryptococcus victoriae	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Cystofilobasidium capitatum	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Cystofilobasidium sp.	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2013b, 2016)
Cylindrobasidium laeve	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)
Cystobasidium ongulense	Bat	*Myotis myotis*	Poland	Ogórek et al. (2020)
Duportella sp. 1	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Duportella sp. 2	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Gloeocystidiellum sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Hannaella luteola	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Hormomyces aurantiacus	Bat	Unknown species	Canada	Vanderwolf et al. (2013)
Kondoa aeria	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Kwoniella cf. *dendrophila*	Bat	*Carollia perspicillata*, *Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Leucosporidium fellii	Bat	Unknown species	Canada	Vanderwolf et al. (2013)
Limonomyces sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Lycoperdon utriforme	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Malassezia vespertilionis	Bat	*Myotis grisescens*, *Myotis lucifugus*, *Myotis septentrionalis*, *Myotis sodalis*	USA	Lorch et al. (2018)
Ossicaulis lachnopus	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)

Supplementary Table 5 Continued.

Fungal species	Host	Bat species	Country	References
Peniophoraceae sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Polyporales sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Polyporus tricholoma	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Pseudozyma sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013)
Pyrofomes demidoffii	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Rhodotorula mucilaginosa	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Rhodotorula cf. *mucilaginosa*	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Rhodotorula slooffiae	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Rhodotorula taiwanensis	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Sakaguchia sp.	Bat	*Carollia perspicillata, Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Sporidiobolales sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Sporobolomyces phyllomatis	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Sporobolomyces roseus	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Sporobolomyces ruberrimus	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Sporotrichum sp.	Bat	Unknown species	Canada	Vanderwolf et al. (2013)
Trametes pubescens	Bat	Unknown species	Canada	Vanderwolf et al. (2013)
Trametes versicolor	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Tremella indecorata	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Tremellomycetes sp.	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Trichosporon chiropterorum	Bat and bat carcasses	*Myotis capaccini*, *Myotis* sp., *Tadarida teniotis*	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Trichosporon coprophilum	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Trichosporon cutaneum	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Trichosporon dulcitum	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada	Vanderwolf et al. (2013b, 2016)
Trichosporon guehoae	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Trichosporon lignicola	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Trichosporon sp.	Bat	*Myotis lucifugus, Myotis septentrionalis*	Canada, Mexico	Vanderwolf et al. (2013b, 2016)
Tubulicrinis sp.	Bat	*Miniopterus orianae oceanensis, Myotis septentrionalis*	Australia	Vanderwolf et al. (2016), Holz et al. (2018)
Undetermined basidiomycetes	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Udeniomyces puniceus	Bat	*Miniopterus orianae bassanii, Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)

Supplementary Table 5 Continued.

Fungal species	Host	Bat species	Country	References
Mortierellomycota				
Mortierella gamsii	Bat carcasses	*Rhinolophus hipposideros*	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Mortierella horticola	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Mortierella humilis	Bat	*Myotis myotis*	Czech Republic, Slovakia	Nováková et al. (2018)
Mortierella indohii	Bat	*Miniopterus orianae bassanii*	Australia	Holz et al. (2018)
Mortierella multispora	Bat carcasses	*Rhinolophus affinis*	China	Karunarathna et al. (2020)
Mortierella parvispora	Bat	*Miniopterus orianae bassanii*, *Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Mortierella polycephala	Bat carcasses	*Pipistrellus* sp., undetermined bat	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Mortierella rhinolophicola	Bat carcasses	*Rhinolophus affiffiffinis*	China	Karunarathna et al. (2020)
Mortierella sp. 1	Bat	*Miniopterus orianae oceanensis*	Australia	Holz et al. (2018)
Mortierella sp. 2	Bat	Unknown species	Romania, Spain	Nováková et al. (2018)
Mortierella sp. 3	Bat	*Myotis lucifugus*, *Myotis septentrionalis*	Canada, USA	Vanderwolf et al. (2016)
Mortierella verticillata	Bat	*Myotis lucifugus*	Canada, USA	Vanderwolf et al. (2013b, 2016)
Mortierella yunnanensis	Bat carcasses	*Rhinolophus affiffiffinis*	China	Karunarathna et al. (2020)
Mucoromycota				
Helicostylum elegans	Bat	Unknown species	Canada, USA	Vanderwolf et al. (2013b)
Mucor hiemalis	Bat and bat carcasses	Unknown species	China, Slovakia	Nováková et al. (2018), Karunarathna et al. (2020)
Mucor hiemalis f. *hiemalis*	Bat carcasses	*Myotis capaccini*, *Myotis* sp., *Miniopterus schreibersii*, *Pipistrellus* sp. and undetermined bat	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Mucor hiemalis f. *luteus*	Bat	Unknown species	Czech Republic	Nováková et al. (2018)
Mucor hiemalis f. *silvaticus*	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Mucor mucedo	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Mucor piriformis	Bat carcasses	Unknown species	UK	Vanderwolf et al. (2013b)
Mucor plumbeus	Bat and bat carcasses	*Pipistrellus* sp. and *Rhinolophus rex*	Italy	Voyron et al. (2011), Vanderwolf et al. (2013b)
Mucor racemosus	Bat and bat carcasses	*Myotis capaccini*, *Myotis* sp., and undetermined bat	Czech Republic, Italy, Slovakia	Voyron et al. (2011), Vanderwolf et al. (2013b), Nováková et al. (2018)
Mucor sp.	Bat	*Myotis lucifugus*, *Myotis septentrionalis*	Canada, USA	Vanderwolf et al. (2013b, 2016)
Mucor wosnessenskii	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Rhizomucor pusillus	Bat	Unknown species	Slovakia	Nováková et al. (2018)

Supplementary Table 5 Continued.

Fungal species	Host	Bat species	Country	References
Rhizopus arrhizus	Bat	*Carollia perspicillata*, *Diphylla ecaudata*	Brazil	Cunha et al. (2020)
Thamnidium elegans	Bat	*Myotis lucifugus*	Canada, Czech Republic	Vanderwolf et al. (2016), Nováková et al. (2018)
Mycetozoa (Slime moulds)				
Arcyria sp.	Bat	Unknown species	Puerto Rico	Vanderwolf et al. (2013b)
Oomycota (Slime moulds)				
Pythium sp.	Bat	*Myotis lucifugus*, *Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
unidentified yeast	Bat	*Myotis lucifugus*	Canada	Vanderwolf et al. (2016)
Sterile	Bat	*Myotis lucifugus*, *Myotis septentrionalis*	Canada	Vanderwolf et al. (2016)
Percolozoa (Protozoa)				
Mycelia sterilia	Bat	Unknown species	Canada	Vanderwolf et al. (2013b)
Undetermined				
Fungi sp.	Bat	*Miniopterus orianae bassanii*, *Miniopterus orianae oceanensis*, *Pleosporales* sp.	Australia	Holz et al. (2018)
Sterile dark pigmented mycelium	Bat	Unknown species	Slovakia	Nováková et al. (2018)
Undetermined yeast	Bat	Unknown species	Slovakia	Nováková et al. (2018)