Phytotaxa 601 (3): 203–211
https://www.mapress.com/pt/

Article

ISSN 1179-3155 (print edition)
PHYTOTAXA
ISSN 1179-3163 (online edition)

https://doi.org/10.11646/phytotaxa.601.3.1

Bambusicola autumnalis sp. nov., a bambusicolous ascomycete from Sichuan province, China

RUI-RU LIANG[1,2], SHENG-NAN ZHANG[1,3] & JIAN-KUI LIU[1,4*]

[1] *School of Life Science and Technology, Center for Informational Biology, University of Electronic Science and Technology of China, Chengdu 611731, P.R. China.*

[2] *lrr202206@163.com; https://orcid.org/0000-0001-7727-0998*

[3] *zhangshengnan@uestc.edu.cn; https://orcid.org/0000-0001-8602-5193*

[4] *liujiankui@uestc.edu.cn; https://orcid.org/0000-0002-9232-228X*

* *Corresponding author: JIAN-KUI LIU; liujiankui@uestc.edu.cn*

Abstract

During the survey of microfungi diversity in Sichuan province, China, a new bamboo inhabiting ascomycete *Bambusicola autumnalis* was identified and introduced in this study. *Bambusicola autumnalis* is characterized by having immersed to erumpent ascostromata, and fusiform, hyaline, 1-septate ascospores surrounded by an inconspicuous mucilaginous sheath, which fits well with the sexual morph of *Bambusicola*. The phylogenetic analysis based on multi-gene (SSU, ITS, LSU, *RPB2*, *TEF1-α*) dataset of taxa within the family Bambusicolaceae showed that *B. autumnalis* formed a sister lineage to *B. guttulata* within *Bambusicola* and representing as a distinct species. Morpho-phylogenetic evidence revealed *B. autumnalis* is distinct from other *Bambusicola* species. Notes on the phylogenetic placement and identification of the new species are provided.

Keywords: 1 new species, Dothideomycetes, multi-gene, phylogeny, taxonomy

Introduction

Dai *et al.* (2012) introduced the genus *Bambusicola*, which resembles *Massarina sensu lato* (Hirayama *et al.* 2010) and yet, was phylogenetically close to Trematosphaeriaceae and formed a distinct clade in Massarineae (Pleosporales). Hyde *et al.* (2013) established the family Bambusicolaceae to accommodate *Bambusicola* on account of its coelomycetous asexual morph different from that of Trematosphaeriaceae (hyphomycetous asexual morph), as well as a multi-gene (SSU, LSU, *RPB2* and *TEF1-α*) phylogeny. *Palmiascoma* (Liu *et al.* 2015), *Leucaenicola* (Jayasiri *et al.* 2019), and *Corylicola* (Wijesinghe *et al.* 2020) were subsequently added to this family based on morph-phylogenetic evidence. Sexual morphs of Bambusicolaceae are characterized by having immersed to erumpent, globose to subglobose ascomata, sometimes stromatic, with anastomosing and branched pseudoparaphyses, cylindrical, bitunicate asci with a well-developed ocular chamber and short furcate pedicel, and fusiform, hyaline or yellowish to brown, didymosporous ascospores, with or without a gelatinous sheath (Hongsanan *et al.* 2020, Wijesinghe *et al.* 2020). Asexual morphs are characterized by having pycnothyrial conidiomata, and holoblastic, annelidic or phialidic conidiogenous cells, producing cylindrical, globose or oblong to ellipsoidal, pale to dark brown, aseptate or 1–3-septate conidia (Wijesinghe *et al.* 2020, Phukhamsakda *et al.* 2022). The exterior appearance of ascomata, the shape of ascospores and/or conidia are diagnostic features to distinguish genera in this family. *Bambusicola* has immersed to erumpent, conical ascomata (in vertical section), and fusiform, hyaline ascospores, as well as the coelomycetous asexual morph, i.e., cylindrical, hyaline to pale brown, macro- and micro-conidia, which produced in culture or on the host substrate (Phukhamsakda *et al.* 2022). *Corylicola* and *Palmiascoma* different from *Bambusicola* in having didymosporous, clavate to ellipsoidal, brown ascospores, and aseptate, hyaline to pale brown conidia produced in culture (Liu *et al.* 2015, Monkai *et al.* 2021). Furthermore, *Corylicola* and *Palmiascoma* are phylogenetically distinct and differ in ascospores (brown to dark brown vs. yellowish brown) and conidia (oblong to ellipsoidal vs. subglobose to globose). *Leucaenicola* is only represented by its asexual morph which is similar to *Palmiascoma* and *Corylicola*. They are, however, formed distinct monophyletic clades within Bambusicolaceae (Jayasiri *et al.* 2019).

Accepted by Sinang Hongsanan: 20 Jun. 2023; published: 11 Jul. 2023

Bambusicola species are widespread and commonly known from Asia, most of them are saprobic and few are parasitic on branches or leaves of bamboo in terrestrial and freshwater habitats (Dai *et al.* 2012, 2015, Thambugala 2017, Yang *et al*. 2019, Phukhamsakda *et al.* 2022, Yu *et al.* 2022). Four species were found with their holomorphs, *viz. B. didymospora*, *B. dimorpha*, *B. massarinia* and *B. triseptatispora* (Dai *et al.* 2012, 2017, Thambugala *et al.* 2017), while the other species were reported based on either asexual or sexual morphs (Dai *et al.* 2015, Yang *et al.* 2019, Brahmanage *et al.* 2020, Monkai *et al.* 2021, Phukhamsakda *et al.* 2022, Yu *et al.* 2022). As known to current, almost all *Bambusicola* members were found or reported from bamboos. The aim of this study is to describe and introduce a new bambusicolous ascomycete *Bambusicola autumnalis* and the establishment is justified by morphological and phylogenetic evidence.

Materials and Methods

Collection and isolation

Fungi on dead bamboo branches were collected in Chengdu, Sichuan province, China. The samples were placed in envelopes and taken to the laboratory. Fungal fruiting bodies were examined by using stereomicroscope Motic SMZ 168 series. Fungal structures were photographed by using a Nikon E80i microscope-camera system. Measurements for all structural components were processed with the Tarosoft® Image Framework program v. 0.9.7 (Liu *et al*. 2010). The morphological examination and single spore isolation were carried out following the approaches laid out in Senanayake *et al.* (2020).

Type materials were deposited in the herbarium of Cryptogams Kunming Institute of Botany Academia Sinica (KUN-HKAS), Kunming, China, and the herbarium of the University of Electronic Science and Technology (HUEST), Chengdu, China. The ex-type strain was deposited at the China General Microbiological Culture Collection Center (CGMCC), Beijing, China, and duplicated at the University of Electronic Science and Technology Culture Collection (UESTCC), Chengdu, China. The name of the new species was registered in MycoBank (http://www.mycobank.org/).

DNA extraction, PCR amplification and sequencing

Fungal DNA was extracted from mycelium using the Trelief TM Plant Genomic DNA Kit. The primer pairs NS1/NS4, ITS5/ITS4, LR0R/LR5, fRPB2-5F/fRPB2-7cR and 983F/2218R were used to amplify the small subunit of nuclear ribosomal RNA gene region (SSU), the internal transcribed spacer (ITS), the large subunit of nuclear ribosomal RNA gene region (LSU), RNA polymerase II second largest subunit (*RPB2*) and the translation elongation factor 1-alpha (*TEF1-α*), respectively (Vilgalys & Hester 1990, White *et al.* 1990, Liu *et al.* 1999, Rehner & Buckley 2005). Polymerase chain reaction (PCR) amplification was carried out following the method in Dai *et al.* (2017). PCR products were purified and sequenced at Beijing Tsingke Biotechnology Co., Ltd., Chengdu, China.

Phylogenetic analyses

Sequences generated in this study were assembled by SeqMan in DNASTAR Lasergene v7.1 (DNASTAR, Inc. Madison, WI, USA), and deposited at NCBI GenBank (Table 1). The nucleotide blast searches were performed to find similar sequences that match our new isolates. The representative stains of Bambusicolaceae (Table 1) were derived from previous literatures (Dai *et al*. 2012, 2015, 2017, Thambugala *et al*. 2017, Yang *et al*. 2019, Brahmanage *et al*. 2020, Dong *et al*. 2020, Monkai *et al*. 2021, Phukhamsakda *et al*. 2022, Yu *et al*. 2022). Multiple-sequence alignments of each gene region were performed by MAFFT version 7 (http://mafft.cbrc.jp/alignment/server/) (Katoh *et al*. 2019) and edited manually with BioEdit 7.2.5 (Hall 1999) and trimmed by TrimAI (Capella-Gutiérrez *et al.* 2009). A concatenated dataset of SSU, ITS, LSU, *RPB2* and *TEF1-α* was finally used for phylogenetic analyses.

Phylogenetic analyses of maximum likelihood (ML), maximum parsimony (MP), and Bayesian inference (BI) were carried out as detailed in Dissanayake *et al*. (2020) and performed with RAxML-HPC2 on XSEDE 8.2.12, MrBayes v.3.2.7 and PAUP v. 4.0b (Stamatakis *et al*. 2008) in CIPRES Science Gateway (Miller *et al*. 2010), respectively. Phylogenetic trees were visualized with FigTree v.1.4.4 and the layout were made with Adobe Illustrator CS6 version 15.0 (Adobe Systems, USA).

TABLE 1. Taxa used in this study. Newly generated sequences are indicated with * and the ex-type strains are in bold.

Taxa	Vouchers/Strains	GenBank accession numbers				
		SSU	ITS	LSU	*RPB2*	*TEF1-α*
Bambusicola aquatica	MFLUCC 18-1031	MT864293	MT627729	MN913710	MT878462	MT954392
Bambusicola autumnalis*	CGMCC 3.24280	OQ427823	OQ427824	OQ427825	OQ507621	OQ507622
*Bambusicola autumnalis**	UESTCC 23.0001	OQ550209	OQ609612	OQ550210	OQ556791	OQ556792
Bambusicola bambusae	MFLUCC 11-0614	JX442039	JX442031	JX442035	KP761718	KP761722
Bambusicola didymospora	MFLUCC 10-0557	KU872110	KU940116	KU863105	KU940163	KU940188
Bambusicola dimorpha	MFLUCC 13-0282	KY038354	KY026582	KY000661	KY056663	–
Bambusicola ficuum	MFLUCC 17-0872	MT215581	–	MT215580	–	MT199326
Bambusicola fusispora	MFLUCC 20-0149	MW076529	MW076532	MW076531	MW034589	–
Bambusicola guttulata	CGMCC 3.20935	ON332919	ON332909	ON332927	ON383985	ON381177
Bambusicola irregulispora	MFLUCC 11-0437	JX442040	JX442032	JX442036	KP761719	KP761723
Bambusicola loculata	MFLUCC 13-0856	KP761735	KP761732	KP761729	KP761715	KP761724
Bambusicola massarinia	MFLUCC 11-0389	JX442041	JX442033	JX442037	KP761716	KP761725
Bambusicola nanensis	MFLUCC 21-0063	–	OK491656	OK491652	–	–
Bambusicola pustulata	MFLUCC 15-0190	KU872112	KU940118	KU863107	KU940165	KU940190
Bambusicola sichuanensis	SICAUCC 16-0002	MK253528	MK253473	MK253532	MK262830	MK262828
Bambusicola splendida	MFLUCC 11-0439	JX442042	JX442034	JX442038	KP761717	KP761726
Bambusicola subthailandica	SICAUCC 16-0005	MK253529	MK253474	MK253533	MK262831	MK262829
Bambusicola thailandica	MFLUCC 11-0147	–	KU940119	KU863108	KU940166	KU940191
Bambusicola triseptatispora	MFLUCC 11-0166	–	KU940120	KU863109	KU940167	–
Corylicola italica	MFLUCC 19-0500	MT554923	MT554925	MT554926	MT590776	–
Corylicola italica	MFLUCC 20-0111	MT633084	MT633085	MT626713	MT635596	MT590777
Leucaenicola aseptata	MFLUCC 17-2423	MK347853	MK347746	MK347963	MK434891	MK360059
Leucaenicola camelliae	NTUCC 18-093-4	MT071229	MT112302	MT071278	MT743283	MT374091
Leucaenicola osmanthi	NTUCC 18-101-1	MN908609	MN908565	MN908612	MN915020	MN918596
Leucaenicola phraeana	MFLUCC 18-0472	MK347892	–	MK348003	MK434867	MK360060
Palmiascoma gregariascomum	MFLUCC 11-0175	KP753958	KP744452	KP744495	KP998466	–
Palmiascoma qujingense	KUMCC 19-0201	MT477186	MT477183	MT477185	MT495782	–
Sulcatispora acerina	KT2982	LC014605	LC014597	LC014610	–	LC014615
Sulcatispora berchemiae	KT1607	AB797244	AB809635	AB807534	–	AB808509

"–" sequences were not obtained.

Result

Phylogenetic analyses

All the members of Bambusicolaceae (except for *Leucaenicola taiwanensis*) with their type stains were included in the phylogenetic analysis, and the tree was rooted to *Sulcatispora berchemiae* (KT1607) and *S. acerina* (KT2982). Five gene loci SSU, ITS, LSU, *RPB2*, and *TEF1-α* were used for determining the phylogenetic placement of our new isolates. The matrix comprised 29 strains with 4,242 characters after alignment (SSU: 998 bp, ITS: 452 bp, LSU: 799 bp, *RPB2*: 1, 042 bp, *TEF1-α*: 951 bp), including gaps.

RAxML analysis generated a best-sorting tree with the GAMMA model, a final optimization likelihood value of -17106.060700, and the matrix had 1,007 distinct alignment patterns, with 15.02% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.242512, C = 0.257235, G = 0.269298, T = 0.230955; substitution rates AC = 1.271399, AG = 3.015426, AT = 0.978251, CG = 0.962851, CT = 7.298393, GT = 1.000000; gamma distribution shape parameter α = 0.130337. Maximum parsimony analyses indicated that 3,355 characters were constant, 198 variable characters parsimony-uninformative, and 689 characters are parsimony-informative which resulted in 1, 000 trees with TL = 2, 184, CI = 0.559, RI = 0.660, RC = 0.369, and HI = 0.441. The evolutionary models for Bayesian analysis were selected for each locus using MrModeltest v. 2.3 (Nylander 2004), in which HKY+I model was selected for SSU, GTR+I+G model was selected for ITS, LSU, *RPB2* and *TEF1-α*. Bayesian analysis of six simultaneous Markov chains were run for 100,000,0 generations and trees were sampled every 100th generation (resulting in 10, 000 total trees). The first 20% (2, 000) trees, representing the burn-in phase of the analyses, were discarded and the remaining 80% (8, 000) trees used for calculating posterior probabilities (PP) in the majority rule consensus tree.

ML, MP and BI analyses based on the combined dataset resulted in similar topologies, and the best scoring RAxML tree is shown in FIGURE 1. The two isolates (CGMCC 3.24280, UESTCC 23.0001) of *Bambusicola autumnalis* nested in *Bambusicola* and formed a distinct lineage sister to *B. guttulata* (CGMCC 3.20935).

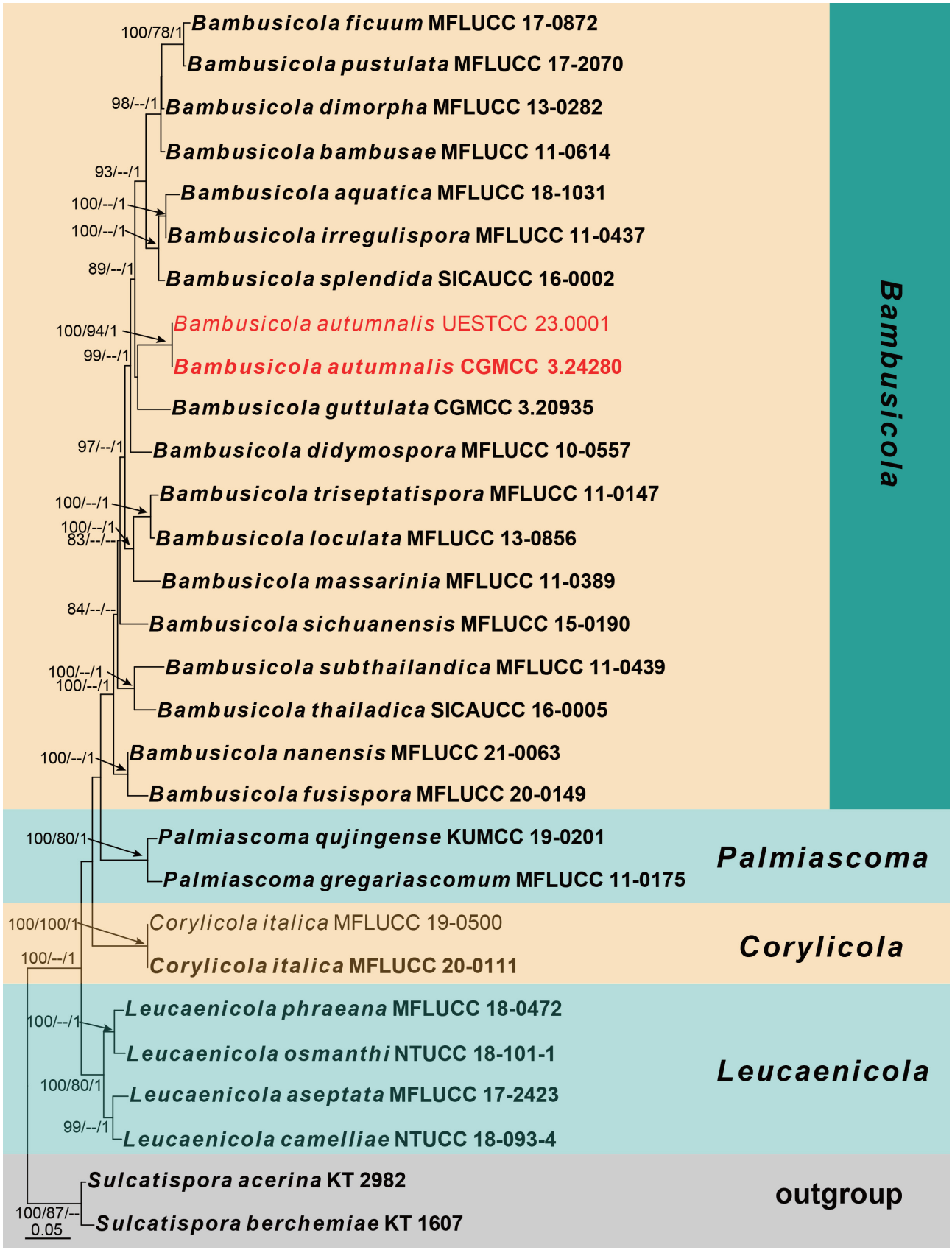

FIGURE 1. Maximum likelihood (RAxML) tree based on a combined sequence dataset (SSU, ITS, LSU, *RPB2* and *TEF1-α*) of taxa from Bambusicolaceae. Bootstrap values for ML and MP equal or greater than 75%, and BI posterior probabilities equal or greater than 0.95 are indicated. New isolated strains are indicated in red and ex-type strains are indicated in bold.

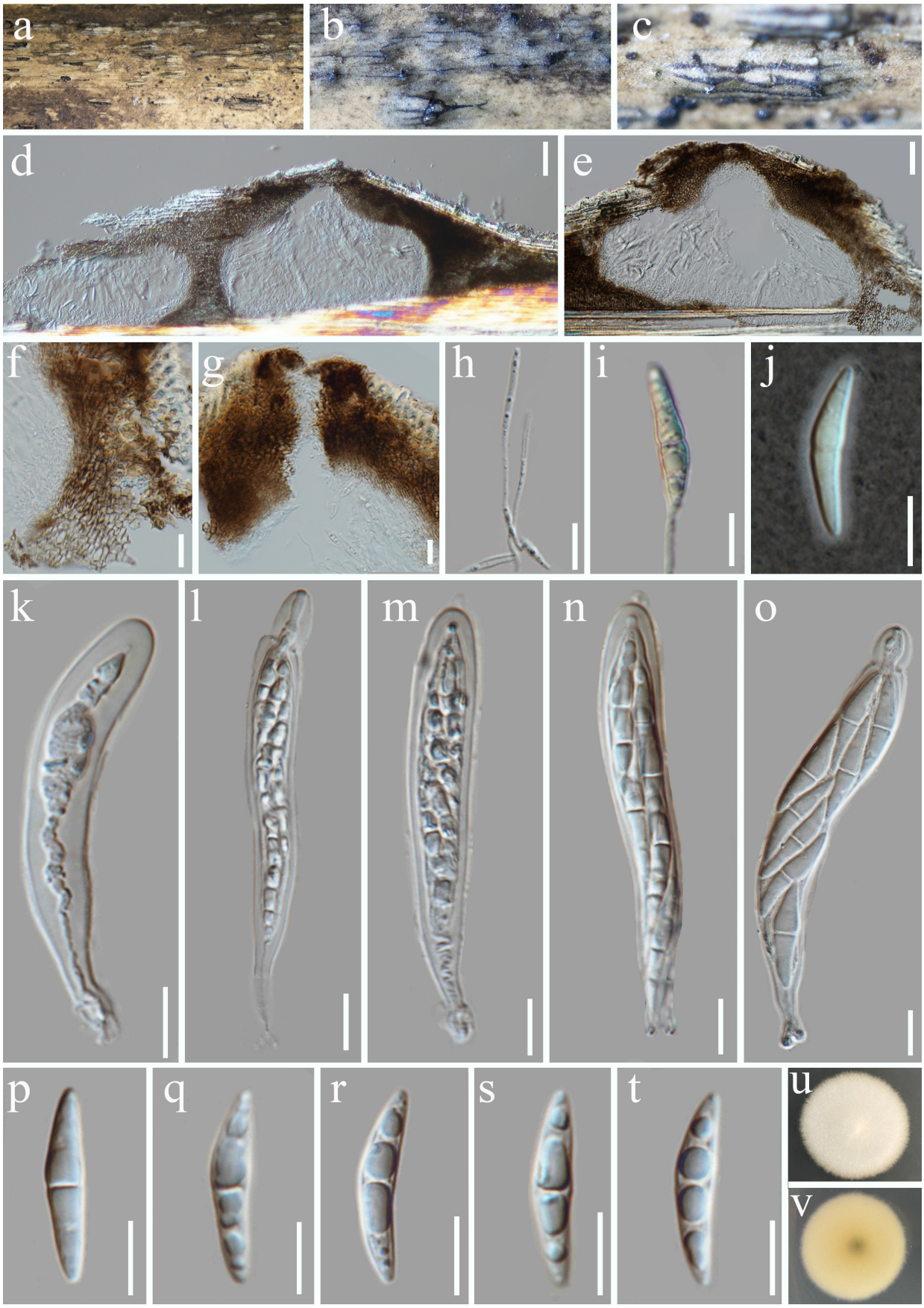

FIGURE 2. ***Bambusicola autumnalis*** (HKAS 126508, holotype) **a**–**c** Ascostromata on host substrate. **d**, **e** Vertical section of Ascostroma, which shows pseudostromatic structure. **f** Peridium. **g** Ostiole. **h** Trabeculate pseudoparaphyses. **i** Germinating ascospore. **j** Ascospore stained in India ink which shows a gelatinous sheath. **k**–**o** Asci. **p**–**t** Ascospores. **u**, **v** Colony on PDA, above (u) and below (v). Scale bars: d =100 µm, e = 50 µm, f, g, i = 20 µm, h, j, k–t = 10 µm.

Taxonomy

Bambusicola autumnalis R.R. Liang, S.N. Zhang and Jian K. Liu, *sp. nov.*
MycoBank: 847551; FIGURE 2.

Etymology:—The epithet "*autumnalis*" refers to the season "autumn" when the fungus was collected.

Holotype:—HKAS 126508

Saprobic on dead bamboo branches. **Sexual morph:** *Ascostromata* solitary to gregarious, rarely scattered, immersed to erumpent, pseudostromatic, visible as bumped areas with cracks and a central black minute papilla, in vertical section conical to subglobose, ostiolate, periphysate, individual locules 190–325 µm high, 215–295 µm diam ($\overline{x}$ = 280 × 250 µm, n = 10). *Peridium* 19–43 µm, composed of several layers of thick-walled, brown cells of *textura angularis*. *Hamathecium* 1–1.9 µm wide, trabecular pseudoparaphyses, anastomosing, hyaline, remotely septate. *Asci* 52–102 × 8–17 µm ($\overline{x}$ = 71 × 12 µm, n = 20), 8-spored, bitunicate, fissitunicate, long cylindric-clavate, shortly pedicellate, apically rounded with a minute ocular chamber. *Ascospores* 22–30 × 4.5–7 µm ($\overline{x}$ = 27 × 5 µm, n = 30), overlapping bi-seriate or multi-seriate, fusiform, 1-septate, constricted at the septum, guttulate, smooth-walled, surrounded by a thin, inconspicuous mucilaginous sheath. **Asexual morph:** Undetermined.

Culture characteristics:—Colonies on PDA reaching 28–32 mm after 4 weeks incubated at 25 °C in dark, circular, dry, mycelium velvety, milky white to pale yellow, reverse yellow to light brown.

Material examined:—CHINA, Sichuan province, Chengdu city, Chengdu Botanical Garden, 30°76.48' N, 104°13.03' E, 516 m elevation, on dead branches of bamboo in a terrestrial environment, 21 Nov. 2022, R.R. Liang, (HKAS 126508, holotype), ex-holotype living culture CGMCC 3.24280; *ibid*., HUEST 23.0001, isotype, ex-isotype living culture UESTCC 23.0001.

Notes:—Multi-gene phylogenetic analysis showed that our isolates belong to *Bambusicola* and are closely related to *B. guttulata* (FIGURE 1). However, it is not able to compare their morphology as the latter species only represented by a coelomycetous asexual morph. Nevertheless, *Bambusicola autumnalis* differs from *B. guttulata* in their nucleotide sequences, *viz.* SSU (6/950), ITS (44/450), LSU (17/800), *RPB2* (73/993) and *TEF1-α* (49/959), respectively. Morphologically, *Bambusicola autumnalis* resembles *B. loculata* in having stromatic ascomata, 8-spored, cylindric asci, and narrowly fusiform, 1-septate ascospores surrounded by an inconspicuous sheath (Dai *et al.* 2015). However, they have different dimensions of asci (52–102 × 8–17 µm vs. 80–105 × 8–13 µm) and ascospores (22–30 × 4.5–7 µm vs. 22–26.5 × 5–6), and the bumped ascostromata with cracks of *B. autumnalis* also differs from *B. loculata*. Moreover, the two species are phylogenetically distinct (FIGURE 1).

Discussion

Bambusicola autumnalis, an additional saprobe to *Bambusicola*, was isolated, identified and well-described in this study, which contributed to the diversity of bamboo fungi, especially those in Sichuan province, China. It is noteworthy that members of *Bambusicola* appear to have host preferences, i.e., they were frequently reported from bamboo (16 of a total of 18 species were found on bamboo substratum, Index Fungorum June 2023). Moreover, *Bambusicola* species in saprobic and/or parasitic lifestyles have been successfully isolated and reported, which to some extent, indicates the genus *Bambusicola* could be a candidate for further research, such as the interaction or relationship between fungi and bamboo.

Acknowledgements

This study was supported by the Joint Fund of the National Natural Science Foundation of China and the Karst Science Research Center of Guizhou province (Grant No. U1812401).

References

Brahmanage, R.S., Dayarathne, M.C., Wanasinghe, D.N., Thambugala, K.M., Jeewon, R., Chethana, K.W.T., Samarakoon, M.C., Tennakoon, D.S., De Silva, N.I. & Camporesi, E., Raza, M., Yan, J.Y. & Hyde, K.D. (2020) Taxonomic novelties of saprobic Pleosporales from selected dicotyledons and grasses. *Mycosphere* 11 (1): 2481–2541.
http://doi.org/10.5943/mycosphere/11/1/15

Capella-Gutiérrez, S., Silla-Martínez, J.M. & Gabaldón, T. (2009) TrimAI: a tool for automated alignment trimming in large-scale phylogenetic analyses. *Bioinformatics* 25 (15): 1972–1973.
https://doi.org/10.1093/bioinformatics/btp348

Dai, D.Q, Bhat, D.J., Liu, J.K, Chukeatirote, E., Zhao, R.L. & Hyde, K.D. (2012) *Bambusicola*, a new genus from bamboo with asexual and sexual morphs. *Cryptogamie Mycologie* 33 (3): 363–379.
http://doi.org/10.7872/crym.v33.iss3.2012.363

Dai, D.Q., Bahkali, A.H., Li, W.J., Bhat, D.J., Zhao, R.L. & Hyde, K.D. (2015) *Bambusicola loculata* sp. nov. (Bambusicolaceae) from bamboo. *Phytotaxa* 213 (2): 122–130.
http://doi.org/10.11646/phytotaxa.213.2.5

Dai, D.Q., Phookamsak, R., Wijayawardene, N.N., Li, W.J., Bhat, D.J., Xu, J.C., Taylor, J.E., Hyde, K.D. & Chukeatirote, E. (2017) Bambusicolous fungi. *Fungal Diversity* 82 (1): 1–105.
http://doi.org/10.1007/s13225-016-0367-8

Dai, D.Q., Tang, L.Z. & Wang, H.B. (2018) A review of bambusicolous ascomycetes. *Bamboo: Current and future prospects* 165.
http://doi.org/10.5772/intechopen.76463

Dissanayake, A.J., Bhunjun, C.S., Maharachchikumbura, S.S.M. & Liu, J.K. (2020) Applied aspects of methods to infer phylogenetic relationships amongst fungi. *Mycosphere* 11: 2652–2676.
https://doi.org/10.5943/mycosphere/11/1/-18

Dong, W., Wang, B., Hyde, K.D., McKenzie, E.H.C, Raja, H.A., Tanaka, K., Abdel-Wahab, M.A., Abdel-Aziz, F.A., Doilom, M., Phookamsak, R., Hongsanan, S., Wanasinghe, D.N., Yu, X.D., Wang, G.N., Yang, H., Yang, J., Thambugala, K.M., Tian, Q., Luo, Z.L., Yang, J.B., Miller, A.N., Fournier, J., Boonmee, S., Hu, D.M., Nalumpang, S. & Zhang, H. (2020) Freshwater Dothideomycetes. *Fungal Diversity* 105: 319–575.
http://doi.org/10.1007/s13225-020-00463-5

Hall, T.A. (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for windows 95/98/NT. *Nuclc Acids Symposium Series* 41 (2): 95–98.
http://doi.org/10.14601/phytopathol_mediterr-14998u1.29

Hirayama, K., Tanaka, K., Raja, H.A., Miller, A.N. & Shearer, C.A. (2010) A molecular phylogenetic assessment of *Massarina ingoldiana sensu lato*. *Mycologia* 102 (3): 729–746.
https://doi.org/10.3852/09-230

Hyde, K.D., Jones, E.B.G., Liu, J.K., Ariyawansa, H., Boehm, E., Boonmee, S., Braun, U., Chomnunti, P., Crous, P.W. Dai, D.Q., Diederich, P., Dissanayake, A., Doilom, M., Doveri, F., Hongsanan, S., Jayawardena, R., Lawrey, J.D., Li, Y.M., Liu, Y.X., Lücking, R., Monkai, J., Muggia, L., Nelsen, M.P., Pang, K.L., Phookamsak, R., Senanayake, I.C., Shearer, C.I., Suetrong, S., Tanaka, K., Thambugala, K.M., Wijayawardene, N.N., Wikee, S., Wu, H.X., Zhang, Y., Aguirre-Hudson, B., Alias, S.A., Aptroot, A., Bahkali, A.H., Bezerra, J.L., Bhat, D.J., Camporesi, E., Chukeatirote, E., Gueidan, C., Hawksworth, D.L., Hirayama, K., Hoog, S.D., Kang, J.C., Knudsen, K., Li, W.J., Li,X.H., Liu, Z.Y., Mapook, A., McKenzie, E.H.C., Miller, A.N., Mortimer, P.E., Phillips, A.J.L., Raja, H.A., Scheuer, C., Schumm, F., Taylor, J.E., Tian, Q., Tibpromma, S., Wanasinghe, D.N., Wang, Y., Xu, J.C., Yacharoen, S., Yan, J.Y. & Zhang, M. (2013) Families of Dothideomycetes. *Fungal Diversity* 63 (1): 1–313.
http://doi.org/10.1007/s13225-013-0263-4

Hongsanan, S., Hyde, K.D., Phookamsak, R., Wanasinghe, D.N., McKenzie, E.H.C., Sarma, V.V., Lücking, R., Boonmee, S., Bhat, J.D., Liu, N.G., Tennakoon, D.S., Pem, D., Karunarathna, A., Jiang, S.H., Jones, G.E.B., Phillips, A.J.L., Manawasinghe, I.S., Tibpromma, S., Jayasiri, S.C., Sandamali, D., Jayawardena, R.S., Wijayawardene, N.N., Ekanayaka, A.H., Jeewon, R., Lu, Y.Z., Phukhamsakda, C., Dissanayake, A.J., Zeng, X.Y., Luo, Z.L., Tian, Q., Thambugala, K.M., Dai, D., Samarakoon, M.C., Chethana, K.W.T., Ertz, D., Doilom, M., Liu, J.K., Pérez-Ortega, S., Suija, A., Senwanna, C., Wijesinghe, S.N., Niranjan, M., Zhang, S.N., Ariyawansa, H.A., Jiang, H.B., Zhang, J.-F., Norphanphoun, C., de Silva, N.I., Thiyagaraja, V., Zhang, H., Bezerra, J.D.P., Miranda-González, R., Aptroot, A., Kashiwadani, H., Harishchandra, D., Sérusiaux, E., Abeywickrama, P.D., Bao, D.F., Devadatha, B., Wu, H.X., Moon, K.H., Gueidan, C., Schumm, F., Bundhun, D., Mapook, A., Monkai, J., Bhunjun, C.S., Chomnunti, P., Suetrong, S., Chaiwan, N., Dayarathne, M.C., Yang, J., Rathnayaka, A.R., Xu, J.C., Zheng, J., Liu, G., Feng, Y. & Xie, N. (2020) Refined families of Dothideomycetes: orders and families incertae sedis in Dothideomycetes. *Fungal Diversity* 105 (1): 17–318.
http://doi.org/10.1007/s13225-020-00462-6

Jayasiri, S.C., Hyde, K.D., Jones, E.B.G., McKenzie, E., Jeewon, R., Phillips, A.J.L., Bhat, D.J., Wanasinghe, D.N., Liu, J.K., Lu, Y.Z., Kang, J.C., Xu, J.C. & Karunarathna, S.C. (2019) Diversity, morphology and molecular phylogeny of Dothideomycetes on decaying wild seed pods and fruits. *Mycosphere* 10 (1): 1–186.
http://doi.org/10.5943/mycosphere/10/1/1

Katoh, K., Rozewicki, J. & Yamada, K.D. (2019) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Briefings in bioinformatics* 20 (4): 1160–1166.
http://doi.org/10.1093/bib/bbx108

Liu, Y.J., Whelen, S. & Hall, B.D. (1999) Phylogenetic relationships among ascomycetes: evidence from an RNA polymerse II subunit. *Molecular biology* 16 (12): 1799–1808.
http://doi.org/10.1093/oxfordjournals.molbev.a026092

Liu, J.K., Chomnunti, P., Cai, L., Phookamsak, R., Chukeatirote, E., Jones, E.B.G., Moslem, M. & Hyde, K.D. (2010) Phylogeny and morphology of Neodeightonia palmicola sp. nov. from palms. *Sydowia-Horn* 62: 261–276.

Liu, J.K., Hyde, K.D., Jones, E.B.G., Ariyawansa, H.A., Bhat, D.J., Boonmee, S., Maharachchikumbura, S.S.N., McKenzie, E.H.C., Phookamsak, R., Phukhamsakda, C., Shenoy, B.D., Abdel-Wahab, M.A., Buyck, B., Chen, J., Chethana, K.W.T., Singtripop, C., Dai, D.Q., Dai, Y.C., Daranagama, D.A., Dissanayake, A.J., Doilom, M., D'souza, M.J., Fan, X.L., Goonasekara, I.D., Hirayama, K., Hongsanan, S., Jayasiri, S.C., Jayawardena, R.S., Karunarathna, S.C., Li, W.J., Mapook, A., Norphanphoun, C., Pang, K.L., Perera, R.h., Peršoh, D., Pinruan, U., Senanayake, I.C., Somrithipol, S., Suetrong, S., Tanaka, K., Thambugala, K.M., Tian, Q., Tibpromma, S., Udayanga, D., Wijayawardene, N.N., Wanasinghe, D., Wisitrassameewong, K., Zeng, X.Y., Abdel-Aziz, F.A., Adamčík, S., Bahkali, A.H., Boonyuen, N., Bulgakov, T., Callac, P., Chomnunti, P., Greiner, K., Hashimoto, A., Hofstetter, V., Kang, J.C., Lewis, D., Li, X.H., Liu, X.Z., Liu, Z.Y., Matsumura, M., Mortimer, P.E., Rambold, G., Randrianjohany, E., Sato, G., Sri-Indrasutdhi, V., Tian, C.M., Verbeken, A., von Brackel, W., Wang, Y., Wen, T.C., Xu, J.C., Yan, J.Y., Zhao, R.L. & Camporesi, E. (2015) Fungal diversity notes 1–110: taxonomic and phylogenetic contributions to fungal species. *Fungal Diversity* 72 (1): 1–197.
http://doi.org/10.1007/s13225-015-0324-y.

Miller, M., Pfeiffer, W. & Schwartz, T. (2010) Creating the CIPRES science gateway for inference of large phylogenetic trees. *In: Proceedings of the Gateway Computing Environments Workshop (GCE).* Institute of Electrical and Electronics Engineers, New Orleans. pp. 1–8.
http://doi.org/10.1109/GCE.2010.5676129

Monkai, J., Wanasinghe, D.N., Jeewon, R., Promputtha, I. & Phookamsak, R. (2021) Morphological and phylogenetic characterization of fungi within Bambusicolaceae: introducing two new species from the Greater Mekong Subregion. *Mycological Progress* 20 (5): 721–732.
http://doi.org/10.1007/s11557-021-01694-9

Nylander, J. (2004) MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University 2.

Phukhamsakda, C., Nilsson, R.H., Bhunjun, C.S., de Farias, A.R.G., Sun, Y.R., Wijesinghe, S.N., Raza, M., Bao, D.F., Lu, L. Tibpromma, S., Dong, W., Tennakoon, D.S., Tian, X.G., Xiong, Y.R., Karunarathna, S.C., Cai, L., Luo, Z.L., Wang, Y., Manawasinghe, I.S., Camporesi, E., Kirk, P.M., Promputtha, I., Kuo, C.H., Su, H.Y., Doilom, M., Li, Y., Fu, Y.P. & Hyde, K.D. (2022) The numbers of fungi: contributions from traditional taxonomic studies and challenges of metabarcoding. *Fungal Diversity* 114 (1): 327–386.
http://doi.org/10.1007/s13225-022-00502-3

Rehner, S.A. & Buckley, E. (2005) A Beauveria phylogeny inferred from nuclear ITS and *EF1-α* sequences: evidence for cryptic diversification and links to Cordyceps teleomorphs. *Mycologia* 97 (1): 84–98.
https://doi.org/10.1080/15572536.2006.11832842

Senanayake, I.C., Rathnayaka, A.R., Marasinghe, D.S., Calabon, M.S., Gentekaki, E., Lee, H.B., Hurdeal, V.G., Pem, D., Dissanayake, L.S., Wijesinghe, S.N., Bundhun, D., Nguyen, T.T., Goonasekara, I.D., Abeywickrama, P.D., Bhunjun, C.S., Jayawardena, R.S., Wanasinghe, D.N., Jeewon, R., Bhat, D.J. & Xiang, M.M. (2020) Morphological approaches in studying fungi: collection, examination, isolation, sporulation and preservation. *Mycosphere* 11 (1): 2678–2754.
http://doi.org/10.5943/mycosphere/11/1/20

Stamatakis, A., Hoover, P. & Rougemont, J. (2008) A rapid bootstrap algorithm for the RAxML web servers. *System Biology* 57 (5): 758–771.
http://doi.org/10.1080/10635150802429642

Thambugala, K., Wanasinghe, D.N., Phillips, A.J., Bulgakov, T., Phukhamsakda, C., Ariyawansa, H.A., Goonasekara, I.D., Phookamsak, R., Dissanayake, A.J., Tennakoon, D.S., Tibpromma, S., Chen, Y.Y., Liu, Z.Y. & Hyde, K.D. (2017) Mycosphere notes 1–50: Grass (Poaceae) inhabiting Dothideomycetes. *Mycosphere* 8 (84): 697–796.
http://doi.org/10.5943/mycosphere/8/4/13

Vilgalys, R. & Hester, M. (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several Cryptococcus species. *Journal of Bacteriology* 172 (8): 4238–4246.

https://doi.org/10.1128/jb.172.8.4238-4246.1990

White, T.J., Bruns, T., Lee, S. & Taylor, J.W. (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR protocols: a guide to methods and applicatons* 18 (1): 315–322.
https://doi.org/10.1016/b978-0-12-372180-8.50042-1.

Wijesinghe, S.N., Wang, Y., Camporesi, E., Wanasinghe, D.N., Boonmee, S. & Hyde, K.D. (2020) A new genus of Bambusicolaceae (Pleosporales) on Corylus avellana (Fagales) from Italy. *Biodiversity Data Journal* 8: e55957.
http://doi.org/10.3897/BDJ.8.e55957

Yang, C.L., Xu, X.L. & Liu, Y.G. (2019) Two new species of *Bambusicola* (Bambusicolaceae, Pleosporales) on *Phyllostachys heteroclada* from Sichuan, China. *Nova Hedwigia* 108 (3): 527–545.
http://doi.org/10.1127/nova_hedwigia/2019/0526

Yu, X.D., Zhang, S.N. & Liu, J.K. (2022) Morpho-phylogenetic evidence reveals novel Pleosporalean taxa from Sichuan Province, China. *Journal of Fungi* 8 (7): 720.
http://doi.org/10.3390/jof8070720