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Article	8
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Arode	15 Views
Mountains of Northeast China	D EnossRef citations
Du Miao, Qingsong Dong, Yuanju Jin, A. K. Hasith Priyashantha, Wanzhu Jiang, Chunlan Zhang & Jite Xu Published online: 14 Oct 2024	0 Attracete

 Anthoxanthum od mycorrhizal fungi 	oratum (Poaceae) as a bioindicator of arbuscular	79 Views
soils >	abundance prior to marrie reseguation on agricultural	0 CrassRef citations
Sky Horton, Mandy Lowi?	er & janice Lard	D
Published online: 67 Oct 20	24	Alteneeric
Bacterial non-rib	osomal pentides: a sustainable approach for combatting	16
phytopathogenic fungi in agriculture >		Views

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RESEARCH ARTICLE



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Botryobasidium bambusinum (Botryobasidiaceae, Cantharellales): a new species from Yunnan, Southwest China, based on morphology and phylogeny

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ABSTRACT

Botryobasidium bambusinum sp. nov. was collected in Yunnan Province, China, is described here as a new species based on its morphology and phylogeny. In this study, the taxon Botryobasidium bambusinum is characterised by its resupinate, coriaceous conidiomata with a smooth, hypochnoid, rubiginous to slightly reddish-brown hymenial surface, a slightly thick-walled basal hyphae with simple septa, subcylindrical, septate subglobose to globose, slightly thick-walled conidia measuring as $7.2-9.5 \times 7-9 \mu m$. Phylogenetic analyses of the new species were based on the internal transcribed spacer (ITS) and large subunit (nrLSU) of ribosomal DNA (rDNA) sequences. The phylogenetic tree indicated that the new species belonged to the genus Botryobasidium, and was closely related to B. gossypirubiginosum, B. rubiginosum and B. simile. Botryobasidium gossypirubiginosum differs from B. bambusinum by having a floccose to cotton conidiomata. Botryobasidium rubiginosum differentiates from *B. bambusinum* by having a cottony conidiomata, and ovoid to ellipsoid, larger conidia $(14.5-16 \times 10.5-12.5 \ \mu m \ vs \ 7.2-9.5 \times 7-9 \ \mu m)$. Botryobasidium simile can be distinguished from B. bambusinum by having an ochraceous to fulvous conidiomata, and larger conidia $(21.5-27 \times 16-18 \,\mu\text{m}$ vs $7.2-9.5 \times 7-9 \,\mu\text{m})$. A detailed description, illustrations and phylogenetic analysis of the new species are provided.

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Introduction

Fungi comprise enormous species diversity with respect to morphological, ecological and nutritional modes (Song et al. 2024). Wood-inhabiting fungi play a fundamental role in ecosystem processes, particularly in wood degradation and the recycling of organic matter (Dong et al. 2024c). Recognised as pivotal contributors to the intricate balance of forest ecosystems, these fungi are renowned as 'key players' due to their enzymatic prowess, effectively breaking down woody components like lignin, cellulose, and hemicellulose (Hyde et al. 2016, 2017, 2020, 2022; Lu et al. 2024; Zhang et al. 2024; Dong et al. 2024c). Revealing and documentation of new fungal species in China have been

extensively done recent decades (Liu et al. 2015; Senanayake et al. 2015, 2017, 2020a, 2020b, 2020c, 2020d, 2023; Li et al. 2016, 2023; Tibpromma et al. 2017; Wanasinghe et al. 2018; Phookamsak et al. 2019; Liang et al. 2023; Hongsanan et al. 2023; Kularath-nage et al. 2022, 2023a, 2023b; Ma et al. 2023; Dong et al. 2024c).

The corticioid genus Botryobasidium Donk, belonging to the family Botryobasidiaceae Jülich (Cantharellales Gäum.), was established by Donk (1931) with B. subcoronatum (Höhn. & Litsch.) Donk as the type species. The genus is characterised by resupinate, thin, basidiomata, floccose, reticulate, arachnoid, hypochnoid to porulose hymenophore, a monomitic hyphal system with simple septa or clamp connections on generative hyphae, present or absent cystidia, subcylindrical to cylindrical basidia with (4)6-8-sterigmata and a basal simple septum, in clusters on hymenial hyphal branches, and variable, usually ellipsoid, allantoid or navicular, smooth or ornamented basidiospores (Donk 1931; Bernicchia and Gorjón 2010). Many species in the genus Botryobasidium are known in anamorph (Bernicchia and Gorjón 2010). Many asexual morph generic names, such as Acladium Link, Allescheriella Henn., Alysidium Kunze, Haplotrichum Link, Neoacladium P.N. Singh & S.K. Singh, Physospora Fr., and Sporocephalium Chevall., were congeneric with Botryobasidium, and were re-combined in the genus Botryobasidium (Stalpers et al. 2021). Many species of *Botryobasidium* conidial state were found to belonging to the genus Oidium Link (Eriksson and Ryvarden 1973). The genus Oidium is characterised by white or greyish to slightly yellow, rusty red or rusty brown colonies, erect or ascending, septate or nodose-septate conidiophores, spherical to ellipsoidal, smooth or internally or externally roughened conidia (Linder 1942). Based on the MycoBank database (http:// www.mycobank.org, accessed on 28 October 2024) and the Index Fungorum (http:// www.indexfungorum.org, accessed on 28 October 2024), the genus Botryobasidium has registered 115 specific and infraspecific names.

Holubová-Jechová (1980) recognised the genus Haplotrichum Link for the asexual morphs of the genus Botryobasidium, and it was accepted in a monographic account of the genus Botryobasidium (Langer 1994). The Haplotrichum species with or without asexual morphs, clamp connections, smooth or ornamented basidiospores, and chlamydospores or cystidia were included the genus Botryobasidium (Langer 1994). The genus Botryobasidium formed a well-supported monophyletic group as previously demonstrated based on the micromorphological and ultrastructural characters (Langer 1994; Langer and Langer 1998). Molecular data have been confirmed these relations, placing the genus Botryobasidium in the cantharelloid clade, with the genera Cantharellus Adans. ex Fr., Clavulina J. Schröt., Craterellus Pers., and Hydnum L. (Moncalvo et al. 2006). Based on nuclear ribosomal DNA large subunit (nrLSU) analysis, Moncalvo et al. (2006) demonstrated that the genus Botryobasidium included taxa with asexual morphs and smooth basidiospores (e.g. B. candicans J. Erikss., B. conspersum J. Erikss. and B. simile Pouzar & Hol.-Jech.), and species without asexual morphs and smooth basidiospores (e.g. B. obtusisporum J. Erikss. and B. vagum (Berk. & M.A. Curtis) D.P. Rogers), and species without an asexual morph and ornamented basidiospores (e.g. B. subcoronatum and B. isabellinum (Fr.) D.P. Rogers). Based on the Stalpers et al. (2021) research, the genus Botryobasidium included a greater number of names, thus, the genus Botryobasidium was recommend for protection and 17 new combination species. Recently, nine species of Botryobasidium have been found in China, viz. B. acanthosporum L.J. Zhou & H.S. Yuan, B. coniferarum S.L. Liu & L.W. Zhou,

B. gossypirubiginosum Qian Zhou & C.L. Zhao, B. incanum Qian Zhou & C.L. Zhao, B. leptocystidiatum L.J. Zhou & H.S. Yuan, B. subincanum S.L. Liu & L.W. Zhou, B. subovalibasidium L.J. Zhou & H.S. Yuan, B. xizangense S.L. Liu & L.W. Zhou, B. yunnanense Qian Zhou & C.L. Zhao (Liu et al. 2024; Wang et al. 2024; Zhou et al. 2024b, 2024c).

During investigations on the corticioid fungi in Yunnan Province, China, some *Botryobasidium* specimens were collected. To clarify the placement and relationships of these specimens, we carried out a phylogenetic and taxonomic study based on the ITS and ITS + nrLSU sequences. This specimen is identified as a previously undescribed species of *Botryobasidium* and named *Botryobasidium bambusinum*. A description, illustrations, and phylogenetic analysis of the new species are provided.

Materials and methods

Sample collection and herbarium specimens preparation

The fresh fruiting bodies were collected on the dead stems of *Dendrocalamus sinicus* Chia et J.L. Su which from Dehong of Yunnan Province, China. The samples were photographed in situ, and fresh macroscopic details were recorded. Photographs were recorded by a Nikon D7100 camera. All the photos were focus-stacked using Helicon Focus software. Macroscopic details were recorded and transported to a field station where the fruit body was dried on an electronic food dryer at 45°C (Hu et al. 2022; Dong et al. 2024c). Once dried, the specimens were sealed in an envelope and zip-lock plastic bags and labelled (Senanayake et al. 2020d; Rathnayaka et al. 2024; Dong et al. 2024c). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macromorphological descriptions were based on field notes and photos captured in the field and lab. Petersen (1996) was followed for the colour terminology. The micromorphological data were obtained from the dried specimens after observation under a light microscope with a magnification of 10×100 oil (Zhao et al. 2023; Dong et al. 2024c). Sections mounted in 5% KOH and 2% phloxine B ($C_{20}H_2Br_4C_{14}Na_2O_5$), and we also used other reagents, including Cotton Blue and Melzer's reagent to observe micromorphology following as per Wu et al. (2022b). To show the variation in spore sizes, 5% of measurements were excluded from each end of the range and shown in parentheses. At least thirty basidiospores from each specimen were measured. Stalks were excluded from basidia measurements, and the hilar appendage was excluded from basidiospores measurements. The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB- = acyanophilous, IKI- = both inamyloid and non-dextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, Q_m represented the average Q of basidiospores measured \pm standard deviation, and n = a/b (number of spores (a) measured from given number (b) of specimens). The MycoBank number will be registered in the MycoBank database (http://www.mycobank.org).

Molecular phylogeny

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The nuclear ribosomal of the internal transcribed spacer (ITS) region was amplified with ITS5 and ITS4 primers (White et al. 1990). The nuclear large subunit (nrLSU) region was amplified with the LROR and LR7 primer pair (Vilgalys and Hester 1990; Rehner and Samuels 1994). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 ° C for 40 s, 58 °C for 45 s and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for nrLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P.R. China). The newly generated sequences were deposited in NCBI GenBank (Table 1).

The sequences were aligned in MAFFT version 7 (Katoh et al. 2019) using the G-INS-i strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was aligned first, and then the sequences of ITS + nrLSU were combined with Mesquite version 3.51. The combined ITS + nrLSU sequences and ITS datasets were used to infer the position of the new species in the genus *Botryobasidium* and related species. Sequences of *Trichosporon insectorum* Fuent., S.O. Suh, Landell, Faganello, A. Schrank, Vainstein, M. Blackw. & P. Valente was retrieved from GenBank and used as outgroup taxa in the ITS + nrLSU analysis (Figure 1); *Hydnum repandum* L. was selected as outgroup taxa in the ITS analysis (Figure 2) as in Liu et al. (2024).

Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined two datasets following a previous study (Zhou et al. 2024a). Maximum Likelihood (ML) analysis was performed with RAxML-HPC BlackBox in CIPRES Science Gateway (https://www.phylo.org/portal2/login!input.action, Miller et al. 2012) using a GTRCAT model of evolution with 1,000 bootstrap replicates. jModelTest v2 (Darriba et al. 2012) was used to determine the best-fit evolution model for each dataset for the purposes of Bayesian inference (BI), Bayesian inference was performed using MrBayes 3.2.7a (Ronquist et al. 2012). Four Markov chains were run from random starting trees. Trees were sampled every 1000 generation. The first 25% of sampled trees were discarded as burn-in, whereas other trees were used to construct a 50% majority consensus tree and for calculating Bayesian posterior probabilities (BPPs). Branches were considered significantly supported if they received a maximum likelihood bootstrap value (BS) of \geq 70%, Bayesian posterior probabilities (BPP) of \geq 0.95.

Results

Molecular phylogeny

The aligned ITS + nrLSU dataset comprised 45 specimens representing 33 species. Four Markov chains were run for two runs from random starting trees, each for one million generations for the combined ITS + nrLSU (Figure 1) data set with trees and parameters sampled every 1000 generations. The best model for the ITS + nrLSU dataset, estimated and applied in the Bayesian analysis, was SYM + I + G.

Table 1. Names, sample number	s, references and corresponding	g GenBank accession	numbers of th	e taxa used in	the phylogen	etic analyses of this study.
			GenBank ac	cession no.		
Order/family	Species name	Sample no.	ITS	nrLSU	Country	References
Cantharellales /Botryobasidiaceae	Botryobasidium acanthosporum	Yuan16326	PP229497	I	China	Zhou et al. (2024b)
	B. acanthosporum	Yuan17989	PP229511	I	China	Zhou et al. (2024b)
	B. acanthosporum	Yuan18083*	PP229512	PP218361	China	Zhou et al. (2024b)
	B. acanthosporum	Yuan18128	PP229517	I	China	Zhou et al. (2024b)
	B. asperulum	RAS552	OR471090	OR470959	USA	Swenie et al. (2024)
	B. asperulum	FP102150	OR471075	OR47094	USA	Swenie et al. (2024)
	B. asperulum	RAS578	OR471100	OR470964	USA	Swenie et al. (2024)
	B. aureum	RAS571	OR471098	OR470963	USA	Swenie et al. (2024)
	B. bambusinum	CLZhao 29916	PQ539057	PQ539060	China	Present study
	B. bambusinum	CLZhao 29936*	PQ539058	PQ539061	China	Present study
	B. bambusinum	CLZhao 29938	PQ539059	PQ539062	China	Present study
	B. botryosum	AFTOL-ID 604	DQ267124	FJ176881	USA	Matheny et al. (2006)
	B. botryosum	KHL11081	AY463387	AY586638	Sweden	Larsson et al. (2004)
	B. candicans	UC2022891	KP814227	I	USA	Rosenthal et al. (2017)
	B. candicans	UC2022944	KP814546	I	USA	Rosenthal et al. (2017)
	B. candicans	UC2022893	KP814200	I	USA	Rosenthal et al. (2017)
	B. candicans	RC_OTU_512	MW472198	I	Canada	Bazzicalupo et al. (2022)
	B. coniferarum	LWZ20210928-3*	OR557259	OR527282	China	Liu et al. (2024)
	B. coniferarum	LWZ20210928-4	OR557260	OR527283	China	Liu et al. (2024)
	B. coniferarum	LWZ20210928-5	OR557261	OR527285	China	Liu et al. (2024)
	B. coniferarum	LWZ20171016-15	OR557262	OR527286	China	Liu et al. (2024)
	B. conspersum	AFTOL-ID 1766	DQ911612	DQ521414	USA	Matheny et al. (2006)
	B. conspersum	RAS259	OR471145	I	USA	Swenie et al. (2024)
	B. conspersum	MES-1018	OR471157	I	USA	Swenie et al. (2024)
	B. gossypirubiginosum	CLZhao 26052*	OR668924	OR708665	China	Zhou et al. (2024c)
	B. incanum	CLZhao 26697*	OR668923	OR708664	China	Zhou et al. (2024c)
	B. indicum	Yuan18434	PP209217	PP218365	China	Unpublished
	B. indicum	NFCCI 4480	NR_171230	NG_070816	India	Zhou et al. (2024c)
	B. indicum	AMH:10054	MK391496	MK391493	India	Zhou et al. (2024c)
	B. indicum	CLZhao 21791	ON406471	I	China	Zhou et al. (2024c)
	B. intertextum	UC2022959	KP814540	I	USA	Rosenthal et al. (2017)
	B. isabellinus	RAS5799 SV1	OR471108	OR470966	USA	Swenie et al. (2024)
	B. laeve	RAS762	OR471128	I	USA	Swenie et al. (2024)
	B. leptocystidiatum	Yuan17548	PP209211	PP218178	China	Zhou et al. (2024b)
	B. leptocystidiatum	Yuan17557	PP204173	PP218180	China	Zhou et al. (2024b)

(Continued)

			GenBank a	ccession no.		
Order/family	Species name	Sample no.	ITS	nrLSU	Country	References
	B. leptocystidiatum	Yuan17706	PP209200	PP218353	China	Zhou et al. (2024b)
	B. leptocystidiatum	Yuan17708*	PP209197	PP218354	China	Zhou et al. (2024b)
	B. leptocystidiatum	Yuan17709	PP209198	PP218355	China	Zhou et al. (2024b)
	B. robustius	CBS:945.69	MH859491	MH871272	Netherlands	Vu et al. (2019)
	B. robustius	iNaturalist 162067551	PP436446	I	USA	Unpublished
	B. rubiginosum	RAS776	OR471136	I	USA	Swenie et al. (2024)
	B. simile	RAS793	OR471146	I	USA	Swenie et al. (2024)
	B. simile	RAS794	OR471147	I	USA	Swenie et al. (2024)
	B. subcoronatum	RAS620 SV1	OR471110	OR470967	USA	Swenie et al. (2024)
	B. subcoronatum	RAS789	OR471144	OR470974	USA	Swenie et al. (2024)
	B. subcoronatum	FP101015	OR471077	OR470948	USA	Swenie et al. (2024)
	B. subcoronatum	FP151108	OR471078	OR470949	USA	Swenie et al. (2024)
	B. subovalibasidium	Yuan16439	PP209199	PP218152	China	Zhou et al. (2024b)
	B. subovalibasidium	Yuan18179*	PP209196	PP218362	China	Zhou et al. (2024b)
	B. tubulicystidium	DK14_139	OL436769	I	USA	Zhou et al. (2024c)
	B. vagum	GEL3330 SV1	OR471082	OR470953	USA	Swenie et al. (2024)
	B. yunnanense	CLZhao 24877*	OR668925	OR708666	China	Zhou et al. (2024c)
-/Ceratobasidiaceae	Ceratobasidium chavesanum	CML 3481	KX870116	I	Brazil	de Melo et al. (2018)
	C. globisporum	CBS:569.83	MH873365	MH873365	Netherlands	Vu et al. (2019)
	C. pseudocornigerum	CBS:568.83	MH861653	MH873364	Netherlands	Vu et al. (2019)
	C. ramicola	PP-1	PP493928	PP493932	China	Unpublish
-/Hydnaceae	Hydnum repandum	H 6003710	KX388650	I	Finland	Niskanen et al. (2018)
	Sistotrema confluens	AFTOL-ID 613	DQ267125	AY647214	USA	Liu et al. (2024)
	Sistotremella perpusilla	CBS:126048	MH864061	MH875516	Netherlands	Vu et al. (2019)
-/Oliveoniaceae	Oliveonia fibrillosa	VS 8257	MT235628	MT235607	Russia	Unpublished
	O. pauxilla	SREF104	MN660332	I	Poland	Schneider-Maunoury et al. (2019)
Trichosporonales /Trichosporonaceae	CBS:10422	KY105746	KY109953	CBS:10422	Netherlands	Vu et al. (2019)

New species is shown in bold; * is shown type material, holotype.

Table 1. Continued.

NEW ZEALAND JOURNAL OF BOTANY 7



Figure 1. Maximum Likelihood strict consensus tree illustrating the Botryobasidium and related genera in the order Cantharellales based on the combined ITS + nrLSU sequences. Branches are labelled with Maximum Likelihood bootstrap values equal to or above 70%, and Bayesian posterior probabilities equal to or above 0.95.



Figure 2. Maximum Likelihood strict consensus tree illustrating the phylogeny of the new species Botryobasidium bambusinum and related species in the genus Botryobasidium based on ITS sequences. Branches are labelled with Maximum Likelihood bootstrap values equal to or above 70%, and Bayesian posterior probabilities equal to or above 0.95.

Maximum Likelihood (ML) and Bayesian Inference (BI) analysis resulted in a similar topology with an average standard deviation of split frequencies = 0.006240 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg. ESS) = 214.

The aligned ITS dataset comprised 53 specimens representing 24 species. Four Markov chains were run for two runs from random starting trees, each for 0.8 million generations for the ITS-only (Figure 2) data set with trees and parameters sampled every 1000 generations. The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was GTR + I + G. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis resulted in a similar topology with an average standard deviation of split frequencies = 0.016186 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg. ESS) = 225.

The phylogram based on the combined ITS + nrLSU sequences (Figure 1) indicated that the new species *Botryobasidium bambusinum* was assigned to the genus *Botryobasidium*. The topology based on ITS sequences (Figure 2), revealed that *B. bambusinum* was clustered with *B. gossypirubiginosum* Qian Zhou & C.L. Zhao, *B. rubiginosum* (Fr.) Rossman & W.C. Allen and *B. simile* Pouzar & Hol.-Jech.

Taxonomy

Botryobasidium bambusinum J.H. Dong & C.L. Zhao, sp. nov. (Figures 3-5)

MycoBank: MB 856464

Etymology: bambusinum (Lat.): is referring to grow on bamboo.

Holotype: China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 23°48′N, 97°38′E, altitude 1000 m asl., on the dead stems of *Dendrocalamus sinicus* Chia et J.L.Su, leg. C.L. Zhao, 18 July 2023, CLZhao 29916 (SWFC).

Conidiomata: Resupinate, originating as thin, then developing as minute conidiiferous cushions, forming colonial aggregations of many gregarious cushions; without odour and taste when fresh, becoming coriaceous upon drying, up to 10 cm long, 5 cm wide, $50-150 \mu m$ thick. Hymenial surface smooth, hypochnoid, terreous to rubiginous when fresh, turning to rubiginous to slightly reddish-brown upon drying. Sterile margin thinning out, terreous to rubiginous, up to 1 mm wide.

Hyphae: Basal hyphae scattered, simple septa, colourless, yellowish, or more deeply coloured near the substratum, slightly thick-walled, branched, more or less interwoven in subiculum, $7-8.5 \mu m$ in diameter, IKI–, CB–, tissues unchanged in KOH.

Conidiophores: Subcylindrical, septate, thin- to slightly thick-walled, hyaline to yellowish, relatively uniform in diameter or gradually tapering distally, up to 35 μ m long, 6–9 μ m in diameter, straight in the distal part, basally curved or flexuose, the distal cells bear sporogeneous teeth, most on the apical cell, in basal direction fewer.

Conidia: Subglobose to globose, hyaline to yellowish, slightly thick-walled, IKI–, CB+, $(7-)7.2-9.5(-9.7) \times (6.5-)7-9$ (-9.3) µm, L = 8.48 µm, W = 8.15 µm, Q = 1.01–1.08, Q_m = 1.04 ± 0.03 (n = 90/3).

Additional specimens (paratypes) examined. China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates 23°48'N, 97°38'E, altitude 1000 m asl., on the dead stems of *Dendrocalamus sinicus* Chia et J.L.Su, leg. C.L. Zhao, 18 July 2023, CLZhao 29936, CLZhao 29938 (SWFC).



Figure 3. Basidiomata of *Botryobasidium bambusinum* **A**, **B**, CLZhao 29916. **C**, **D**, CLZhao 29936 (holo-type). **E**, **F**, CLZhao 29938.

Discussion

The wood-rotting fungi have been extensively studied especially in recent years, which includes a number of poroid, smooth, grandinoid, odontioid and hydnoid basidiomata in China (Cui et al. 2019; Ji et al. 2022; Wu et al. 2022a, 2022b; Liu et al. 2023; Dong et al. 2023a, 2023b, 2024a, 2024b, 2024c; Liu et al. 2024; Zhao et al. 2024; Zhou et al. 2024a, 2024b, 2024c). To date, only nine species of the genus *Botryobasidium* have been found in China (Liu et al. 2024; Wang et al. 2024; Zhou et al. 2024b, 2024c). Thus, the species diversity of *Botryobasidium* is still not well known in China. This paper enriches our knowledge of fungal diversity in this area, and likely, more new taxa will be found with further fieldwork and molecular analyses.

In the present study, a new fungal species, *Botryobasidium bambusinum* is described based on the phylogenetic analyses and morphological characteristics.



Figure 4. Sections of hymenium of *Botryobasidium bambusinum* (holotype, CLZhao 29936). **A**, Basal hyphae. **B**–**F**, Conidiophores. **G**–**P**, Conidia. Scale bars: **A** = 20 μ m; **B**–**P** = 10 μ m.

The genus *Sistotrema* Fr. resembles *Botryobasidium* in having resupinate basidiomata, simple septa or clamp connections generative hyphae. However, *Sistotrema* is distinct from *Botryobasidium* by palisade hymenium and umiform basidia, whereas the latter having clustered hymenium and cylindrical basidia (Bernicchia and J. DONG ET AL.



Figure 5. Microscopic structures of Botryobasidium bambusinum (holotype, CLZhao 29936). A, Basal hyphae. **B**, Conidiophores. **C**, Conidia. Scale bars: $\mathbf{A}-\mathbf{C} = 10 \ \mu m$.

Gorjón 2010). In addition, many species in the genus Botryobasidium have known anamorphs that were useful in distinguishing related taxa (Bernicchia and Gorjón 2010).

Species name	Anamorph	Conidiophores	Conidia	References
Botryobasidium aureum	Haplotrichum aureum	Septate	Smooth, thin-walled, lemon-shaped; $20-30 \times 10-15 \ \mu m$	Bernicchia and Gorjón (2010)
B. bambusinum	B. bambusinum	Septate	Smooth, slightly thick-walled, subglobose to globose; 7.2–9.5 × 7– 9 μm	Present study
B. candicans	H. capitatum	Septate	Smooth, thin- to thick-walled, subglobose to citriform; 15–20×8– 10 μm	Bernicchia and Gorjón (2010)
B. conspersum	H. conspersum	Septate	Smooth, thin-walled, ellipsoid to subglobose; $15-20 \times 9-12 \ \mu m$	Bernicchia and Gorjón (2010)
B. curtisii	H. curtisii	Septate	Roughened or rarely smooth, thin- walled, globose to subglobose; 10– 13.5 × 10–12 µm	Linder (1942)
B. ellipsosporum	H. ellipsosporum	Septate	Smooth, thick-walled, ellipsoid; 20– 24 × 11–12.5 μ m	Holubová- Jechová (1969)
B. medium	H. medium	Septate	Smooth, thin-walled, fusiform; 15–25 \times 5–7 μm	Eriksson and Ryvarden (1973)
B. robustius	B. robustius	Septate	Smooth, thick-walled, globose; 13– 17 × 13–15 μm	Bernicchia and Gorjón (2010)

Table 2. A morphological comparison between the new species Botryobasidium bambusinum and eight similar species with the anamorph in the genus *Botryobasidium*.

12

Phylogenetically, *Botryobasidium bambusinum* forming a monophyletic lineage (100% BS, 1.00 BPP) closely associated with *B. gossypirubiginosum*, *B. rubiginosum* and *B. simile* (Figure 1). However, *Botryobasidium gossypirubiginosum* differs from *B. bambusinum* by having a floccose to cotton conidiomata (Zhou et al. 2024c). *Botryobasidium rubiginosum* differentiates from *B. bambusinum* by having a cottony conidiomata, and ovoid to ellipsoid, larger conidia (14.5–16 × 10.5–12.5 µm vs 7.2–9.5 × 7–9 µm; Linder 1942). *Botryobasidium simile* can be distinguished from *B. bambusinum* by having an ochraceous to fulvous conidiomata, and larger conidia (21.5–27 × 16–18 µm vs 7.2–9.5 × 7–9 µm; Linder 1942).

Botryobasidium bambusinum morphologically resembles with B. aureum, B. candicans, B. conspersum, B. curtisii, B. ellipsosporum, B. medium and B. robustius in having septate conidiophores. A morphological comparison between the new Botryobasidium species and eight similar species of the anamorph are presented in Table 2.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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References

- Bazzicalupo AL, Erlandson S, Branine M, Ratz M, Ruffing L, Nguyen NH, Branco S. 2022. Fungal community shift along steep environmental gradients from geothermal soils in Yellowstone National Park. Microbial Ecology. 84(1):33–43. doi:10.1007/s00248-021-01848-y.
- Bernicchia A, Gorjón SP. 2010. Fungi Europaei 12: Corticiaceae s.l. Edizioni Candusso, Lomazzo. 1–1008.
- Cui BK, Li HJ, Zhou JX, Song JL, Si J, Yang J, Dai ZL, C Y. 2019. Species diversity, taxonomy and phylogeny of Polyporaceae (Basidiomycota) in China. Fungal Diversity. 97:137–392. doi:10. 1007/s13225-019-00427-4.
- Darriba D, Taboada GL, Doallo R, Posada D. 2012. jModelTest 2: more models, new heuristics and parallel computing. Nature Methods. 9:772. doi:10.1038/nmeth.2109.
- de Melo MP, Matos KS, Moreira SI, Silva FF, Conceição GH, Nechet KL, Halfeld-Vieira BA, Beserra Júnior JEA, Ventura JA, Costa H, et al. 2018. Two new *Ceratobasidium* species

14 🕢 J. DONG ET AL.

causing white thread blight on tropical plants in Brazil. Tropical Plant Pathology. 43:559–571. doi:10.1007/s40858-018-0237-x.

- Dong J, Gu Z, Wang Y, Shi Y, Zhao C. 2024a. A new corticioid fungus, *Alloexidiopsis sinensis* (Auriculariales, Basidiomycota), in China, evidenced by morphological characteristics and phylogenetic analyses. Phytotaxa. 658(3):227–239. doi:10.11646/phytotaxa.658.3.1.
- Dong J, Wang L, Chen D, Zheng W, Wang Y, Zhao C. 2024b. Morphological and molecular identification of *Asterostroma roseoalbum* sp. nov. (Peniophoraceae, Russulales), from southwestern China. New Zealand Journal of Botany. 62:1–14. doi:10.1080/0028825X. 2024.2415054.
- Dong JH, Gu JY, Zhao CL. 2023a. Diversity of wood-decaying fungi in Wenshan Area, Yunnan Province, China. Mycosystema. 42:638–662. doi:10.13346/j.mycosystema.220205.
- Dong JH, Li Q, Yuan Q, Luo YX, Zhang XC, Dai YF, Zhou Q, Liu XF, Deng YL, Zhou HM, et al. 2024c. Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. Mycosphere. 15(1):1110–1293. doi:10.5943/mycosphere/15/1/10.
- Dong JH, Zhang XC, Chen JJ, Zhu ZL, Zhao CL. 2023b. A phylogenetic and taxonomic study on *Steccherinum* (Polyporales, Basidiomycota): focusing on three new *Steccherinum* species from Southern China. Frontiers in Cellular and Infection Microbiology. 12:1103579. doi:10.3389/ fcimb.2022.1103579.
- Donk MA. 1931. Revisie van de Nederlandse Heterobasidiomycetae en Homobasidiomycetae Aphyllophoraceae I. Mededelingen van de Nederlandse Mycologische Vereeniging. 18:67–200.
- Eriksson J, Ryvarden L. 1973. The Corticiaceae of North Europe Volume 2, Aleurodiscus-Confertobasidium. pp. 60-261.
- Holubová-Jechová V. 1969. New species of the genus *Oidium* Link ex Fr. emend. Linder. Ceská Mykologie. 23(4):209–221.
- Holubová-Jechová V. 1980. Revision and subdivision of *Haplotrichum*: anamorphs of *Botryobasidium*. Mycotaxon. 12:122–130.
- Hongsanan S, Norphanphoun C, Senanayake IC, Jayawardena RS, Manawasinghe IS, Abeywickrama PD, Khuna S, Suwannarach N, Senwanna C, Monkai J, et al. 2023. Annotated notes on *Diaporthe* species. Mycosphere. 14(1):918–1189. doi:10.5943/mycosphere/14/1/12.
- Hu Y, Karunarathna SC, Li H, Galappaththi MC, Zhao CL, Kakumyan P, Mortimer PE. 2022. The impact of drying temperature on basidiospore size. Diversity. 14(4):239. doi:10.3390/ d14040239.
- Hyde KD. 2022. The numbers of fungi. Fungal Diversity. 114(1):1. doi:10.1007/s13225-022-00507-y.
- Hyde KD, Dong Y, Phookamsak R, Jeewon R, Bhat DJ, Gareth Jones EB, Liu NG, Abeywickrama PD, Mapook A, Wei D, et al. 2020. Fungal diversity notes 1151–1276: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity. 100:5–277. doi:10. 1007/s13225-020-00439-5.
- Hyde KD, Hongsanan S, Rajesh J, Jayarama BD, McKenzie EHC, Jones EBG, Phookamsak R, Ariyawansa HA, Boonmee S, Zhao Q, et al. 2016. Fungal diversity notes 367–490: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity. 80:1–270. doi:10.1007/s13225-016-0373-x.
- Hyde KD, Norphanphoun C, Abreu VP, Bazzicalupo A, Chethana KT, Clericuzio M. 2017. Fungal diversity notes 603–708: taxonomic and phylogenetic notes on genera and species. Fungal Diversity. 87:1–235. doi:10.1007/s13225-017-0391-3.
- Ji X, Zhou JL, Song CG, Xu TM, Wu DM, Cui BK. 2022. Taxonomy, phylogeny and divergence times of *Polyporus* (Basidiomycota) and related genera. Mycosphere. 13:1–52. doi:10.5943/ mycosphere/13/1/1.
- Katoh K, Rozewicki J, Yamada KD. 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics. 20(4):1160–1166. doi:10.1093/bib/bbx108.
- Kularathnage ND, Senanayake IC, Wanasinghe DN, Doilom M, Stephenson SL, Song J, Dong W, Xu B. 2023a. Plant-Associated novel *Didymellaceous* taxa in the South China Botanical Garden (Guangzhou, China). Journal of Fungi. 9:182. doi:10.3390/jof9020182.

- Kularathnage ND, Tennakoon DS, Zhu X, Zhou J, Su B, Xie Y, Chen Q, Calabon MS, Kirk PM, Senanayake IC, et al. 2023b. Reinstating Dyfrolomyces and introducing *Melomastia pyriformis* sp. nov. (Pleurotremataceae, Dyfrolomycetales) from Guangdong Province, China. Current Research in Environmental & Applied Mycology (Journal of Fungal Biology). 13(1):426–438. doi:10.5943/cream/13/1/16.
- Kularathnage ND, Wanasinghe DN, Senanayake IC, Yang Y, Manawasinghe IS, Phillips AJL, Hyde KD, Dong W, Song J. 2022. Microfungi associated with ornamental palms: *Byssosphaeria phoenicis* sp. nov. (Melanommataceae) and *Pseudocoleophoma rhapidis* sp. nov. (Dictyosporiaceae) from south China. Phytotaxa. 568(2):149–169. doi:10.11646/phytotaxa.568.2.2.
- Langer G. 1994. Die Gattung *Botryobasidium* Donk (Corticiaceae, Basidiomycetes). Bibliotheca Mycologica. 158:1–459.
- Langer G, Langer E. 1998. *Haplotrichum parmastii* sp. nov. collected in Costa Rica. Folia cryptogamica Estonica. 33:63–69.
- Larsson A. 2014. AliView: a fast and lightweight alignment viewer and editor for large data sets. Bioinformatics (Oxford, England). 30(22):3276–3278. doi:10.1093/bioinformatics/btu531.
- Larsson KH, Larsson E, Kõljalg U. 2004. High phylogenetic diversity among corticioid homobasidiomycetes. Mycological Research. 108:983–1002. doi:10.1017/s0953756204000851.
- Li GJ, Hyde KD, Zhao RL, Hongsanan S, FA A-A, Wahab A-, Alvarado MA, Alves-Silva P, Ammirati G, Ariyawansa JF, A H, et al. 2016. Fungal diversity notes: 253–366: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity. 78:1–237. doi:10.1007/s13225-016-0366-9.
- Li H, Manawasinghe IS, Zhang Y, Senanayake IC. 2023. Taxonomic and phylogenic appraisal of *Pestalotiopsis linguae* sp. nov., and a new record of *P. nanjingensis* from *Pyrrosia lingua* (Polypodiaceae) in Southern China. Phytotaxa. 587(3):229–250. doi:10.11646/phytotaxa.587. 3.3.
- Liang JR, Senanayake IC, Dong ZY, Hongsanan S, Luo M. 2023. *Digitopodium citri* sp. nov.; an endophytic species associated with *Citrus medica* L. var. sarcodactylis from Guangdong Province, China. Phytotaxa. 616(1):69–78. doi:10.11646/phytotaxa.616.1.5.
- Linder DH. 1942. A contribution towards a monograph of the genus *Oidium* (fungi imperfecti). Lloydia. 5(3):165–207.
- Liu JK, Hyde KD, Jones EBG, Ariyawansa HA, Bhat DJ, Boonmee S, Maharachchikumbura SSN, McKenzie EHC, Phookamsak R, Phukhamsakda C, et al. 2015. Fungal diversity notes 1–110: taxonomic and phylogenetic contributions to fungal species. Fungal Diversity. 72:1–197. doi:10.1007/s13225-015-0324-y.
- Liu S, Shen LL, Xu TM, Song CG, Gao N, Wu DM, Sun YF, Cui BK. 2023. Global diversity, molecular phylogeny and divergence times of the brown-rot fungi within the Polyporales. Mycosphere. 14:1564–1664. doi:10.5943/mycosphere/14/1/18.
- Liu SL, Wang XW, Li GJ, Deng CY, Rossi W, Leonardi M, Liimatainen K, Kekki T, Niskanen T, Smith ME, et al. 2024. Fungal diversity notes 1717–1817: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity. 124:1–216. doi:10.1007/ s13225-023-00529-0.
- Lu W, Suwannarach N, Lumyong S, Elgorban AM, Dai DQ, Dutta AK, Han LH, Tibpromma S, Karunarathna SC. 2024. Molecular phylogeny and morphology reveal two new species of *Conocybe* (Bolbitiaceae, Agaricales) from southwest China. New Zealand Journal of Botany. 62(2/3):501–518. doi:10.1080/0028825X.2024.2327117.
- Ma S, Xu B, Senanayake IC, Song J. 2023. Addition to *Erysiphe quercicola*, a powdery mildew fungus on urena lobata in South China. Chiang Mai Journal of Science. 50(3):1–10. doi:10. 12982/CMJS.2023.030.
- Matheny PB, Curtis JM, Hofstetter V, MC A, Moncalvo JM, Ge ZW, Slot JC, Ammirati JF, Baroni TJ, Bougher NL, et al. 2006. Major clades of Agaricales: a multilocus phylogenetic overview. Mycologia. 98:982–995. doi:10.1007/s13225-019-00432-7.
- Miller MA, Pfeiffer W, Schwartz T. 2012. The CIPRES science gateway. In Proceedings of the 1st Conference of the Extreme Science and Engineering Discovery Environment: Bridging from the Extreme to the Campus and Beyond, Chicago, IL, USA. pp. 1–39. doi:10.1145/2335755.2335836.

16 👄 J. DONG ET AL.

- Moncalvo JM, Nilsson RH, Koster B, Dunham SM, Bernauer T, Matheny PB, Porter TM, Margaritescu S, Weiss M, Garnica S, et al. 2006. The cantharelloid clade: dealing with incongruent gene trees and phylogenetic reconstruction methods. Mycologia. 98:937–948. doi:10.1080/15572536.2006.11832623.
- Niskanen T, Liimatainen K, Nuytinck J, Kirk P, Ibarguren IO, Garibay-Orijel R, Norvell L, Huhtinen S, Kytövuori I, Ruotsalainen J, et al. 2018. Identifying and naming the currently known diversity of the genus *Hydnum*, with an emphasis on European and North American taxa. Mycologia. 110(5):890–918. doi:10.1080/00275514.2018.1477004.
- Petersen JH. 1996. Farvekort. In: The Danish Mycological Society's Colour-Chart, Foreningen til Svampekundskabens Fremme: Greve, Germany, pp. 1–16.
- Phookamsak R, Hyde KD, Jeewon R, Bhat DJ, Jones EBG, Maharachchikumbura SSN, Rasp O, Karunarathna SC, Wanasinghe DN, Hongsanan S, et al. 2019. Fungal diversity notes 929– 1035: taxonomic and phylogenetic contributions on genera and species of fungi. Fungal Diversity. 95:1–273. doi:10.1007/s13225-019-00421-w.
- Rathnayaka AR, Tennakoon DS, Jones GE, Wanasinghe DN, Bhat DJ, Priyashantha AH, Stephenson SL, Tibpromma S, Karunarathna SC. 2024. Significance of precise documentation of hosts and geospatial data of fungal collections, with an emphasis on plant-associated fungi. New Zealand Journal of Botany. 62:1–28. doi:10.1080/0028825X.2024.2381734.
- Rehner SA, Samuels GJ. 1994. Taxonomy and phylogeny of *Gliocladium* analysed from nuclear large subunit ribosomal DNA sequences. Mycological Research. 98(6):625–634. doi:10.1016/S0953-7562(09)80409-7.
- Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Hohna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. Mrbayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Molecular Systems Biology. 61:539–542. doi:10.1093/ sysbio/sys029.
- Rosenthal LM, Larsson KH, Branco S, Chung JA, Glassman SI, Liao HL, Peay KG, Smith DP, Talbot JM, Taylor JW, et al. 2017. Survey of corticioid fungi in North American pinaceous forests reveals hyper diversity, underpopulated sequence databases, and species that are potentially ectomycorrhizal. Mycologia. 109(1):115–127. doi:10.1080/00275514.2017.1281677.
- Schneider-Maunoury L, Deveau A, Moreno M, Todesco F, Belmondo S, Murat C, Courty PE, Jakalski M, Selosse MA. 2019. Two ectomycorrhizal truffles, *Tuber melanosporum* and *T. aestivum*, endophytically colonise roots of non-ectomycorrhizal plants in natural environments. New Phytologist. 225(6):2542–2556. doi:10.1111/nph.16321.
- Senanayake IC, Bhat JD, Cheewangkoon R, Xie N. 2020a. Bambusicolous Arthrinium species in Guangdong Province, China. Frontiers in Microbiology. 11:602773. doi:10.3389/fmicb.2020. 602773.
- Senanayake IC, Crous PW, Groenewald JZ, Maharachchikumbura SSN, Jeewon R, Phillips AJL, Bhat JD, Perera RH, Li QR, Li WJ, et al. 2017. Families of Diaporthales based on morphological and phylogenetic evidence. Studies in Mycology. 86:217–296. doi:10.1016/j.simyco.2017.07.003.
- Senanayake IC, Jeewon R, Hyde KD, Bhat JD, Cheewangkoon R. 2020b. Taxonomy and phylogeny of *Leptosillia cordylinea* sp. nov. from China. Phytotaxa. 435(3):213–226. doi:10.11646/ phytotaxa.435.3.1.
- Senanayake IC, Lian TT, Mai XM, Jeewon R, Maharachchikumbura SSN, Hyde KD, Zeng YJ, Tian SL, Xie N. 2020c. New geographical records of *Neopestalotiopsis* and *Pestalotiopsis* species in Guangdong Province, China. Asian Journal of Mycology. 3(1):512–533. doi:10.5943/ajom/3/1/19.
- Senanayake IC, Maharachchikumbura SSN, Hyde KD, Bhat JD, Jones EBG, Mckenzie EHC, Dai DQ, Daranagama DA, Dayarathne MC, Goonasekara ID, et al. 2015. Towards unraveling relationships in Xylariomycetidae (Sordariomycetes). Fungal Diversity. 73:73–144. doi:10. 1007/s13225-015-0340-y.
- Senanayake IC, Rathnayaka AR, Marasinghe DS, Calabon MS, Gentekaki E, Lee HB, Hurdeal V, Pem D, Dissanayake LS, Wijesinghe SN, et al. 2020d. Morphological approaches in studying fungi: collection, examination, isolation, sporulation and preservation. Mycosphere. 11 (1):2678–2754. doi:10.5943/mycosphere/11/1/20.

- Senanayake IC, Rossi W, Leonardi M, Weir A, McHugh M, Rajeshkumar KC, Verma RK, Karunarathna SC, Tibpromma S, Ashtekar N, et al. 2023. Fungal diversity notes 1611–1716: taxonomic and phylogenetic contributions on fungal genera and species emphasis in south China. Fungal Diversity. 122:161–403. doi:10.1007/s13225-023-00523-6.
- Song J, Karunarathna SC, Senanayake IC, Yu FQ. 2024. Thyridium livistonae sp. nov. from Yunnan Province, China, with two new combinations. New Zealand Journal of Botany. 62. 1–15. doi:10.1080/0028825X.2024.2384470.
- Stalpers JA, Redhead SA, May TW, Rossman AY, Crouch JA, Cubeta MA, Dai YC, Kirschner R, Langer GJ, Larsson KH, et al. 2021. Competing sexual-asexual generic names in Agaricomycotina (Basidiomycota) with recommendations for use. IMA Fungus. 12(1):22. doi:10.1186/s43008-021-00061-3.
- Swenie RA, Looney BP, Ke YH, Rojas A, Cubeta J, Langer MA, Vilgalys GJ, Matheny R, B P. 2024. PacBio high-throughput multi-locus sequencing reveals high genetic diversity in mushroomforming fungi. Molecular Ecology Resources. 24(1):e13885. doi:10.1111/1755-0998.13885.
- Tibpromma S, Hyde KD, Jeewon R, Maharachchikumbura SSN, Liu JK, Bhat DJ, Gareth Jones EB, McKenzie EHC, Camporesi E, Bulgakov TS, et al. 2017. Fungal diversity notes 491–602: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity. 83(1):1–261. doi:10. 1007/s13225-017-0378-0.
- 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. doi:10.1128/jb.172.8.4238-4246.1990.
- Vu D, Groenewald M, de Vries M, Gehrmann T, Stielow B, Eberhardt U, Al-Hatmi A, Groenewald JZ, Cardinali G, Houbraken J, et al. 2019. Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. Studies in Mycology. 92:135–154. doi:10.1016/j. simyco.2018.05.001.
- Wanasinghe DN, Phukhamsakda C, Hyde KD, Jeewon R, Lee HB, Jones G, Tibpromma EB, Tennakoon S, Dissanayake DS, Jayasiri J, C S, et al. 2018. Fungal diversity notes 709–839: taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on Rosaceae. Fungal Diversity. 89:1–236. doi:10.1007/s13225-018-0395-7.
- Wang K, Liu S, Liu XZ, Hong P, Wei HW, Wang Y, Phurbud D, Zhou LW, Wei TZ. 2024. Catalogue of fungi in China 3. New taxa of macrofungi from southern Xizang, China. Mycology. 15:1–33. doi:10.1080/21501203.2024.2392014.
- White TJ, Bruns T, Lee S, Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis M.A., Gelfand D.H., Sninsky J.J., White T.J., editor. PCR protocols: a guide to methods and applications. San Diego: Academic Press; p. 315–322. doi:10. 1016/B978-0-12-372180-8.50042-1.
- Wu F, Man XW, Tohtirjap A, Dai YC. 2022a. A comparison of polypore funga and species composition in forest ecosystems of China, North America, and Europe. Forest Ecosystems. 9:100051. doi:10.1016/j.fecs.2022.100051.
- Wu F, Zhou LW, Vlasák J, Dai YC. 2022b. Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. Fungal Diversity. 113:1–192. doi:10.1007/s13225-021-00496-4.
- Zhang SF, Gui Y, Zhu GS, Shang NJ, Li B, Yang TJ, Gong GL, Huang WB, Liu ZB. 2024. *Laccaria guizhouensis* sp. nov. (Agaricales, Basidiomycota) from Southwest China. New Zealand Journal of Botany. 62:138–150. doi:10.1080/0028825X.2024.2304754.
- Zhao CL, Qu MH, Huang RX, Karunarathna SC. 2023. Multi-gene phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia sensu lato* (Polyporales, Basidiomycota). Journal of Fungi. 9:320. doi:10.3390/jof9030320.
- Zhao H, Wu YD, Yang ZR, Liu HG, Wu F, Dai YC, Yuan Y. 2024. Polypore funga and species diversity in tropical forest ecosystems of Africa, America and Asia, and a comparison with temperate and boreal regions of the Northern Hemisphere. Forest Ecosystems. 11:100200. doi:10. 1016/j.fecs.2024.100200.
- Zhou HM, Zhang XC, Li JT, Wu F, Zhao CL. 2024a. Morphological characteristics and phylogenetic analyses revealed four new wood inhabiting fungi (Agaricomycetes, Basidiomycota) in

18 👄 J. DONG ET AL.

Xizang Autonomous Region, China. MycoKeys. 106:201–224. doi:10.3897/mycokeys.106. 125831.

- Zhou LJ, Li XL, Yuan HS. 2024b. Three new wood inhabiting fungi of *Botryobasidium* (Cantharellales, Basidiomycota) from subtropical forests of Southwestern China. MycoKeys. 109:337–354. doi:10.3897/mycokeys.109.133325.
- Zhou Q, Jiang Q, Yang X, Yang J, Zhao C, Zhao J. 2024c. Phylogenetic and taxonomic analyses of five new wood-inhabiting fungi of *Botryobasidium*, *Coltricia* and *Coltriciella* (Basidiomycota) from China. Journal of Fungi. 10:205. doi:10.3390/jof10030205.