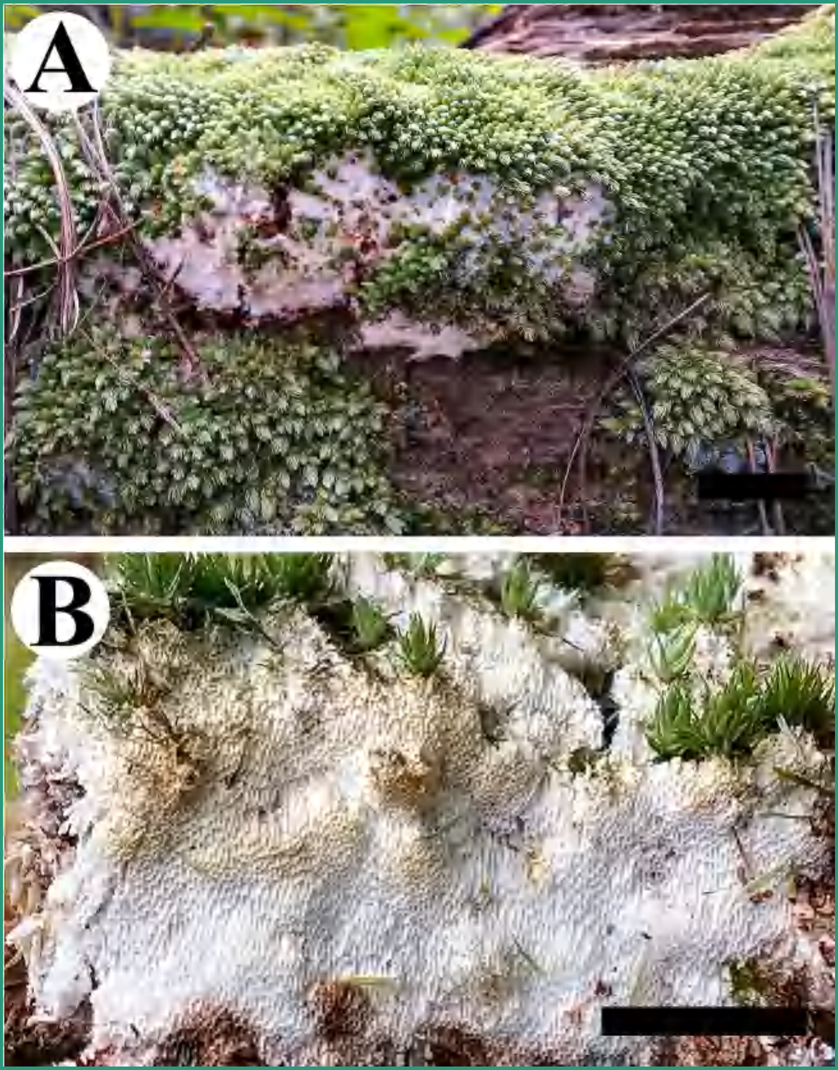
MYCOTAXON

THE INTERNATIONAL JOURNAL OF FUNGAL TAXONOMY & NOMENCLATURE

VOLUME 137 (2) APRIL–JUNE 2022



Cinereomyces wuliangshanensis sp. nov.
(Luo & Zhao— FIG. 2, p. 215)

ISSN (PRINT) 0093-4666 https://doi.org/10.5248/137-2 ISSN (ONLINE) 2154-8889
MYXNAE 137(2): 173–398 (2022)

ISSN 0093-4666 (print)

ISSN 2154-8889 (online)

MYCOTAXON

THE INTERNATIONAL JOURNAL OF FUNGAL TAXONOMY & NOMENCLATURE

April–June 2022

Volume 137 (2)

http://dx.doi.org/10.5248/137-2

www.mycotaxon.com &
www.ingentaconnect.com/content/mtax/mt
p.o. box 264, Ithaca, NY 14581-0264, USA

MYCOTAXON

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publication date for volume one hundred thirty-seven (1)

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was issued on April 28, 2022

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p. 21, line 19 for: Additional examinations … ***Phaeocollybia P.***
read: Additional examinations … ***P. spadicea***

Corrigenda for Mycotaxon 137(2)

Cited below is an omission present in files submitted for PDF conversion in the current issue but not detected by the authors until after the paper had gone to press.

p. 311, line 23 After the last sentence add: *Platismatia* is not closely related with the three other genera included in this study (Divakar et al. 2017).

Reviewers — volume one hundred thirty-seven (2)

The Editors express their appreciation to the following individuals who have, prior to acceptance for publication, reviewed one or more of the papers prepared for this issue.

Krishnendu Acharya
D. Jayarama Bhat
Uwe Braun
Rafael F. Castaneda-Ruíz
Maria Martha Dios
Arun Kumar Dutta
Daria Erastova
Edit Farkas
Patricia Oliveira Fiuza
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Andrus Voitk

From the Editor-in-Chief

Mycotaxon style nuts and bolts—As this issue goes to press, we are in the process of editing a new set of instructions and manuscript templates to assist authors. In so doing, the supposedly helpful styles formatting of the previous Mycotaxon template will be eliminated. This past year, although it became obvious that several authors had carefully prepared manuscripts using those styles, their texts arrived at the editorial desk looking nothing like what the authors had intended. There seems to be a growing incompatibility among different computer operating systems and word processing applications that is causing problems. (The fact that one manuscript left Nomenclature Editor Pennycook's computer in perfect Times New Roman but arrived on Editor-in-Chief Norvell's computer displaying several sections written entirely in the Greek alphabet alerted us that there was trouble brewing between Shaun's Times New Roman font family on his PC and Lorelei's Times font family on her Mac.)

Therefore, until we post the 2022 author guides on our Mycotaxon website, we urge everyone to refer to the sample manuscript or a recent Mycotaxon publication for formatting suggestions. Use the current blank templates (all of which are sized for the Mycotaxon-size page) for all the required body-, legend-, and table-text files, but do not apply any built-in 'styles' or introduce your own author-defined character or paragraph styles to your document. Use instead the paragraph formatting menu built into your word-processing application. We hope to have the new guidelines available shortly!

Font-family reminder—Remember that the only font families permitted in a Mycotaxon manuscript are the serif **Times** and san-serif **Arial** families. Authors should begin any manuscripts intended for Mycotaxon using only those fonts to prevent the sudden and highly dismaying resurrection of an 'alien' font at press time.

No intervening space in °C—an editorial labor-saving device! For several years, we have advised inserting a space between the degree symbol ('°') and the temperature abbreviation ('C' or 'F'). Given the number of times scientific papers refer to temperature, it does not seem to make much sense to devote so much room to the lowly space. We feel that the degree symbol is analogous to the percent sign and that neither should be separated from its corresponding abbreviation. During editorial processing, the separate parts frequently fall on separate lines, requiring valuable editorial time to reunite. Henceforth, we ask all of you to join our Two-Elements-Together-Movement: 20°C and 100%.

The information above might not be of high scientific interest to readers, but your Editor-in-Chief thanks you!

The 2022 April–June Mycotaxon offers 21 contributions by 89 authors (representing 17 countries) as revised by 38 expert reviewers and the editors.

With 13 titles, the new taxa section proposes two new genera (*Andomyces* from Thailand & *Vesiculophora* from Brazil) and 15 species new to science representing *Adustochaete, Cinereomyces, Corynespora, Ellisembia, Gangliostilbe, Xylodon,* and *Zasmidium* from China; *Anapleurothecium, Podosporium, Vesiculophora* from Brazil; *Andomyces* from Thailand; *Chaetocapnodium* from Mexico; *Erysiphe* from Iran; and *Nephromopsis* and *Passalora* from India. We also offer one new combination in *Anapleurothecium* from Brazil.

The New ranges/hosts section contains six titles. New species range extensions are reported for [ascomycetes] *Elaphomyces* for Turkey; [basidiomycetes] *Anthracoidea* for Russia and *Lactocollybia* for Pakistan & Asia; [myxomycetes] *Diderma, Lamproderma, Lepidoderma, Meriderma,* and *Physarum* for the French and Spanish Pyrenees and *Fuligo* & *Stemonitis* for Russia; and [zygomycetes] *Coemansia* for Brazil & South America.

Mycotaxon 137(2) also provides identification keys to species in all cetrarioid lichen genera (*Cetraria, Melanelia, Nephromopsis, Platismatia*) and species in India as well as to species in *Adustochaete, Anapleurothecium, Gangliostilbe*, and *Coemansia.* Papers providing conclusions supported by sequence analyses cover five new species representing *Adustochaete, Chaetocapnodium, Cinereomyces, Erysiphe* and *Xylodon* and one range extension in *Lactocollybia*.

We also pleased to announce the posting on our mycobiota website of two new annotated species lists, which cover 1871 Indian cercosporoid fungi in India and 1619 basidiomycetes collected from Grosseto Province in Italy. Our issue concludes with book reviews of The Hidden Kingdom of Fungi (Seifert 2022) and The Boletes of China: Tylopilus s.l. (Chun & Yang 2021).

Warm regards,

Lorelei L. Norvell (*Editor-in-Chief*)
14 July 2022

2022 Mycotaxon submission procedure

Prospective Mycotaxon authors should download the Mycotaxon 2022 guide, review & submission forms, and Mycotaxon sample manuscript by clicking the 'file download page' link on our Instructions to Authors page before preparing their manuscript. This page briefly summarizes our '4-step' submission process.

1—Peer review: Authors first contact peer reviewers (two for journal papers; three for mycobiota/fungae) before sending them formatted text & illustration files and the appropriate 2022 Mycotaxon journal or mycota reviewer comment form. Experts return revisions & comments to both the *Editor-in-Chief* <editor@mycotaxon.com> and authors. All co-authors must correct and *proof-read* their files before submitting them to the *Nomenclature Editor*.

2—Nomenclatural review: Authors email all **error-free** text, tables, legends, and graphics **in separate files** to the *Nomenclature Editor* <PennycookS@LandcareResearch.co.nz>. Place **first author surname** + **genus** + 'Mycotaxon' on the subject line, and (required) attach a completed submission form. The Nomenclature Editor will (i) immediately assign the accession number and (ii) after a few weeks return his notes and suggested revisions to the author(s) and *Editor-in-Chief*.

3—Final submission: All coauthors thoroughly revise and proof-read files to prepare error-free text and images ready for immediate publication. Poorly formatted copy will be rejected or returned for revision. E-mail the final manuscript to the *Editor-in-Chief* <editor@mycotaxon.com>, adding the **accession number** to the message and **all** files, which include a **(i)** revised 2022 submission form, all **(ii)** text files and **(iii)** jpg images, and **(iv)** FN, IF, or MB identifier verifications for each new name or typification. The *Editor-in-Chief* acknowledges submissions within two weeks of final submission but requests authors to wait at least 14 days before sending a follow-up query (without attachments).

4—Final editorial review & publication: The *Editor-in-Chief* conducts a final grammatical and scientific review and returns her editorial revisions to all expert reviewers and coauthors for final author approval. Author-approved files are placed in the publication queue.

The PDF proof and bibliographic & nomenclatural index entries are sent to all coauthors for final inspection. After PDF processing, the *Editor-in-Chief* corrects only PDF editorial/conversion and index entry errors; corrections of all other errors are listed in the Corrigenda of a subsequent issue for no charge. Authors pay fees for mycobiota uploads, optional open access, and correction of major author errors to the *Business Manager* <subscriptions@mycotaxon.com> at this time.

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The Mycotaxon journal publishes four quarterly issues per year. Both open access and subscription articles are offered.

Podosporium simile sp. nov.
(Monteiro & al.— Fɪɢ. 3, p. 234)

MYCOTAXON

ISSN (print) 0093-4666 (online) 2154-8889 Mycotaxon, Ltd. ©2022

April–June 2022—Volume 137, pp. 209–219
https://doi.org/10.5248/137.209

Cinereomyces wuliangshanensis sp. nov. from China

Kai-Yue Luo[1,3] & Chang-Lin Zhao[1,2,3,4*]

[1] *Yunnan Key Laboratory of Plateau Wetland Conservation, Restoration and Ecological Services;*
[2] *Key Laboratory for Forest Resources Conservation and Utilization in the Southwest Mountains of China, Ministry of Education; &*
[3] *College of Biodiversity Conservation;*
[1–3:] *Southwest Forestry University, Kunming, 650224, Yunnan, P.R. China*
[4] *Yunnan Key Laboratory for Fungal Diversity and Green Development,*
Kunming Institute of Botany, Chinese Academy of Science,
Kunming 650201, Yunnan, P.R. China

[*] Correspondence to: *fungichanglinz@163.com*

Abstract—A new poroid wood-inhabiting fungal species, *Cinereomyces wuliangshanensis,* is proposed based on morphological and molecular characters. The species is characterized by resupinate brittle basidiomata with a white pore surface, a dimitic hyphal system with clamped generative hyphae, and subglobose to broadly ellipsoid hyaline thin-walled smooth basidiospores (4.2–5.1 × 2.9–3.8 µm). Sequences were generated from the internal transcribed spacer (ITS) region of nuclear ribosomal RNA gene and phylogenetically analyzed using maximum likelihood, maximum parsimony, and Bayesian inference methods. The phylogeny strongly (100% BS, 100% BT, 1.00 BPP) supports *C. wuliangshanensis* in a monophyletic lineage grouping with *C. lindbladii* and a clade comprising *Obba rivulosa* and *O. valdiviana.*

Key words—*Gelatoporiaceae*, *Polyporales,* taxonomy, wood-inhabiting fungi, Yunnan Province

Introduction

Cinereomyces Jülich (*Gelatoporiaceae*, *Polyporales*) is characterized by resupinate poroid basidiomata with a white to cream to greyish pore surface with encrustations in trama or tube mouths, a dimitic hyphal system with clamp connections on generative hyphae, skeletal hyphae that dissolve in KOH, cystidia absent, and basidiospores that are cylindrical to allantoid, hyaline, thin-walled, smooth, non-dextrinoid, and acyanophilous (Jülich 1982, Miettinen & Rajchenberg 2012, Ryvarden & Melo 2014). The genus, which is typified by n *C. lindbladii* (Berk.) Jülich, contains two accepted species (Jülich 1982, Miettinen 2012).

Phylogenetically, Binder & al. (2005) distributed resupinate forms across the major clades of mushroom-forming fungi and nested *Cinereomyces lindbladii* in the core polyporoid clade, grouped with *Dentocorticium sulphurellum* (Peck) M.J. Larsen & Gilb. Nuclear and mitochondrial ribosomal DNA sequences used by Tomšovský & al. (2010) grouped *C. lindbladii* with *Gelatoporia subvermispora* (Pilát) Niemelä and *Obba rivulosa* (Berk. & M.A. Curtis) Miettinen & Rajchenb. Analysis of the taxonomic relationships of four genera—*Cinereomyces*, *Gelatoporia* Niemelä, *Obba* Miettinen & Rajchenb., *Sebipora* Miettinen—nested *C. lindbladii* in the *Cinereomyces* clade, grouped with *G. subvermispora*, *O. rivulosa*, and *S. aquosa* Miettinen. Miettinen & Rajchenberg (2012) grouped *C. lindbladii* with *G. subvermispora* and *Skeletocutis amorpha* (Fr.) Kotl. & Pouzar based on their molecular analysis of *Hymenochaetales* with poroid and hydnoid hymenophores. Further molecular analyses of *Polyporales* by Binder & al. (2013) nested *C. lindbladii* within the *Gelatoporia* clade, grouping *Cinereomyces* with *Gelatoporia*, *Obba*, and *Sebipora*. A revised family-level classification of the *Polyporales* based on nrLSU, nrITS, and RPB1 genes confirmed that *Cinereomyces* belongs in *Gelatoporiaceae* Miettinen & al. (Justo & al. 2017).

During investigations on wood-inhabiting fungi in southern China, an additional taxon was found that could not be assigned to any described species. After examining the morphology and generating a phylogeny from internal transcribed spacer (ITS) region sequences, we propose a new *Cinereomyces* species.

Materials & methods

The specimens studied are deposited at the herbarium of Southwest Forestry University, Kunming, Yunnan Province, P.R. China (SWFC). Macromorphological descriptions were based on field notes. Colour terms follow Petersen (1996). Micromorphological data were obtained from the dried specimens and observed under a light microscope. Abbreviations used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB– = acyanophilous, IKI = Melzer's reagent, IKI– = both non-amyloid and non-dextrinoid, L = mean spore length (arithmetic average of all basidiospores), W = mean spore width (arithmetic average of all basidiospores), Q = variation in the L/W ratios, |n (a/b) = (a) number of basidiospores measured from (b) number of specimens.

Table 1. Species, specimens, and sequences used in this study (new sequences in **bold**).

Species name	Sample no.	GenBank no.	Reference
		ITS	
Cinereomyces lindbladii	Kotiranta 19911	FN907909	Miettinen & Rajchenberg 2012
	FBCC 117	HQ659223	Miettinen & Rajchenberg 2012
	KH Larsson 12078	FN907906	Miettinen & Rajchenberg 2012
C. wuliangshanensis	**CLZhao 3405 [T]**	MT664802	Present study
	CLZhao 3409	MT664803	Present study
Gelatoporia subvermispora	Dai 3120	HQ659226	Miettinen & Rajchenberg 2012
	Miettinen 9079	HQ659229	Miettinen & Rajchenberg 2012
	Niemela 5978	HQ659227	Miettinen & Rajchenberg 2012
	BRNU 592909	FJ496694	Miettinen & Rajchenberg 2012
	Spirin 2156	HQ659228	Miettinen & Rajchenberg 2012
	Kinnunen 1052	HQ659225	Miettinen & Rajchenberg 2012
Lopharia cinerascens	EL6397	AY463440	Miettinen & Rajchenberg 2012
Obba rivulosa	Miettinen 8054	HQ659231	Miettinen & Rajchenberg 2012
	FBCC 938	HQ659233	Miettinen & Rajchenberg 2012
	Kotiranta 16702	HQ659232	Miettinen & Rajchenberg 2012
	Penttila 14135	HQ659234	Miettinen & Rajchenberg 2012
	Penttila 14441	FJ496691	Miettinen & Rajchenberg 2012
	Penttila 15077	HQ659230	Miettinen & Rajchenberg 2012
O. valdiviana	Gates FF503	HQ659235	Miettinen & Rajchenberg 2012
	CIEFAP 336	HQ659236	Miettinen & Rajchenberg 2012
Sebipora aquosa	Miettinen 8680	HQ659240	Miettinen & Rajchenberg 2012
	Miettinen 12032	HQ659241	Miettinen & Rajchenberg 2012
	Miettinen 8868	HQ659242	Miettinen & Rajchenberg 2012
	Miettinen 9265	HQ659243	Miettinen & Rajchenberg 2012

Genomic DNA was obtained from dried specimens using a CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd) following the manufacturer's instructions slightly modified by grinding a small (~30 mg) dried fungal sample to powder with liquid nitrogen; the powder was transferred to a 1.5 mL centrifuge tube, suspended in 0.4 mL of lysis buffer, and incubated in a 65 °C water bath for 60 min; thereafter 0.4 mL phenol-chloroform (24:1) was added to each tube and the suspension was shaken vigorously; after centrifugation at 13,000 rpm for 5 min, 0.3 mL supernatant was transferred to a new tube and mixed with

0.45 mL binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 mL inhibitor removal fluid was added in AC for a centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 mL washing buffer, the AC was transferred to a clean centrifuge tube, and 100 mL elution buffer was added to the middle of adsorbed film to elute the genomic DNA. The ITS region was amplified with primer pair ITS5 and ITS4 (White & al. 1990). 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 products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited at GenBank (Table 1).

Sequencher 4.6 (GeneCodes) was used to edit the DNA sequence. Sequences were aligned in MAFFT 7 (http://mafft.cbrc.jp/alignment/server/) using the "G-INS-i" strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 26522). Sequence of *Lopharia cinerascens* (Schwein.) G. Cunn. obtained from GenBank was used as an outgroup to root tree following Miettinen & Larsson (2011) in the ITS analysis.

Maximum parsimony analysis was performed using ITS sequences dataset. Approaches to phylogenetic analysis followed Zhao & Wu (2017) and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree (MPT). Sequences were also analyzed using Maximum Likelihood (ML) with RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org; Miller & al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes3.1.2 with a general time reversible (GTR+I+G) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 1 million generations, and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. A majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received maximum likelihood bootstrap (BS) > 70%, maximum parsimony bootstrap (BT) >50%, or Bayesian posterior probabilities (BPP) >0.95.

Phylogenetic results

The ITS dataset (Table 1) included sequences from 24 fungal specimens representing seven taxa. The dataset had an aligned length of 570 characters, of which 417 characters were constant, 26 parsimony-uninformative, and 127 parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 213, CI = 0.869, HI = 0.151, RI = 0.959, RC = 0.832). The best-fit model for ITS alignment estimated and applied in the Bayesian was lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian resulted in a similar topology with an average standard deviation of split frequencies = 0.009931 (BI).

The ITS phylogeny (Fig. 1) supported *Cinereomyces wuliangshanensis* as a new taxon in *Cinereomyces,* grouped with *C. lindbladii* and a clade comprising *Obba rivulosa* and *O. valdiviana* (Rajchenb.) Miettinen & Rajchenb.

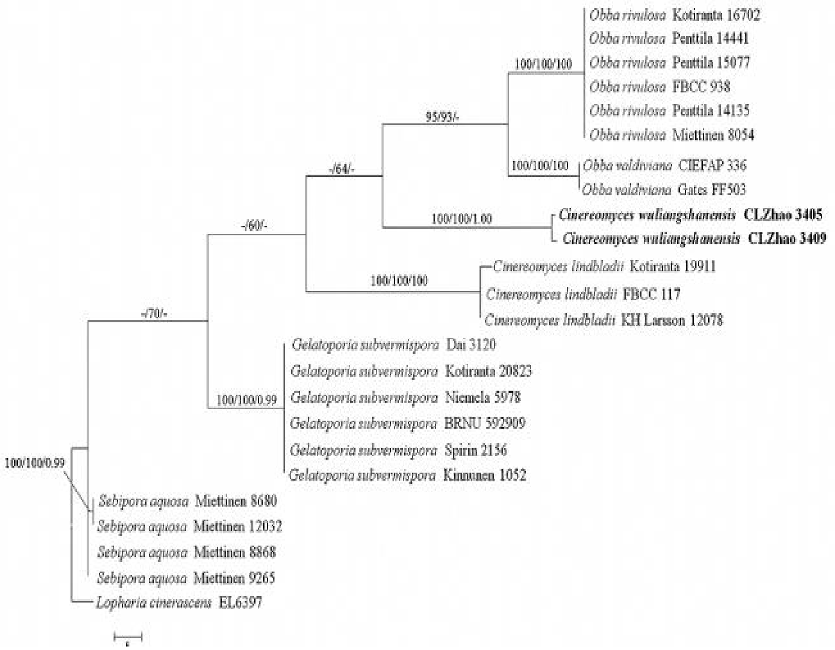

Fig. 1. Maximum Parsimony strict consensus tree illustrating the phylogeny of *Cinereomyces wuliangshanensis* and related species based on ITS sequence analyses. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50%, and Bayesian posterior probabilities >0.95.

Taxonomy

Cinereomyces wuliangshanensis C.L. Zhao & K.Y. Luo, **sp. nov.** FIGS 2, 3

MB 836265

Differs from *C. lindbladii* by its white to cream to olivaceous buff pore surface and smaller basidiospores.

TYPE: Yunnan Province, Puer, Zhenyuan County, Wuliangshan National Nature Reserve, Xieqipo Park, on angiosperm trunk, 1 October 2017, CLZhao 3405 (**Holotype**, SWFC 003405; GenBank MT664802).

ETYMOLOGY: The specific epithet *wuliangshanensis* (Lat.) refers to the collection locality (Wuliangshan) of the type specimen.

BASIDIOMATA annual, resupinate, soft, without odor or taste when fresh, becoming brittle upon drying, ≤9 cm long, 4.5 cm wide, and 1.5 mm thick at centre. Pore surface white when fresh, white to cream to olivaceous buff upon drying; pores round to elongated, 5–6 per mm; dissepiments thin, entire. Sterile margin narrow, white, ≤5 mm wide. Subiculum white, thin, ≤0.5 mm thick. Tubes white, corky, ≤1 mm long.

HYPHAL STRUCTURE dimitic; generative hyphae with clamp connections, skeletal hyphae IKI–, CB–; tissues swelling in KOH.

SUBICULUM generative hyphae hyaline, thin-walled, unbranched, 1.5–2.2 µm in diam.; skeletal hyphae rare, hyaline, thick-walled with a wide lumen, frequently branched, interwoven, 4–5 µm in diam.

TUBES generative hyphae hyaline, thin-walled, unbranched, 1–1.7 µm in diam.; skeletal hyphae dominant, hyaline, thick-walled with a wide lumen, frequently branched, interwoven, 3.5–4 µm in diam. Cystidia and cystidioles absent; basidia 15.2–16.1 × 5.1–5.3 µm, barrel-shaped, with four sterigmata and a basal clamp connection; basidioles dominant, mostly barrel-shaped, but slightly smaller than basidia.

BASIDIOSPORES (n = 60/2), (3.7–)4.2–5.1(–6.2) × (2.6–)2.9–3.8(–4.4) µm, L = 4.81 µm, W = 3.39 µm, Q = 1.40–1.43, subglobose to broadly ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–.

TYPE OF ROT: white.

ADDITIONAL SPECIMEN EXAMINED: **CHINA. YUNNAN PROVINCE. Puer:** Zhenyuan County, Wuliangshan National Nature Reserve, Xieqipo Park, on angiosperm trunk, 1 October 2017, CLZhao 3409 (SWFC 003409; GenBank MT664803).

Discussion

The current study proposes and describes a new species, *Cinereomyces wuliangshanensis,* based on phylogenetic and morphological analyses.

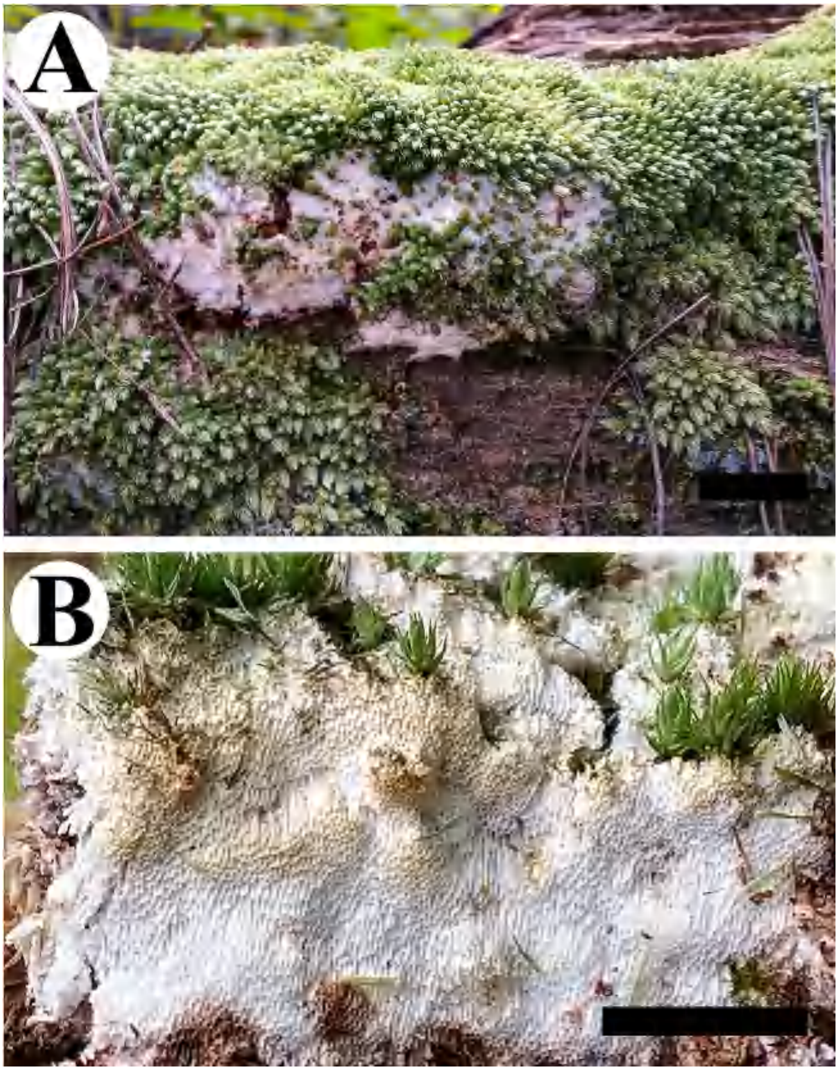

Fig. 2. *Cinereomyces wuliangshanensis* (holotype, SWFC 003405).
Basidiomata. Scale bars: A = 2 cm; B = 0.5 mm.

The phylogenetic analysis of the nrDNA ITS region by Miettinen & Rajchenberg (2012) grouped *Cinereomyces* closely with three related genera—*Obba, Sebipora*, and *Gelatoporia*. Our current phylogeny strongly (100% BS,

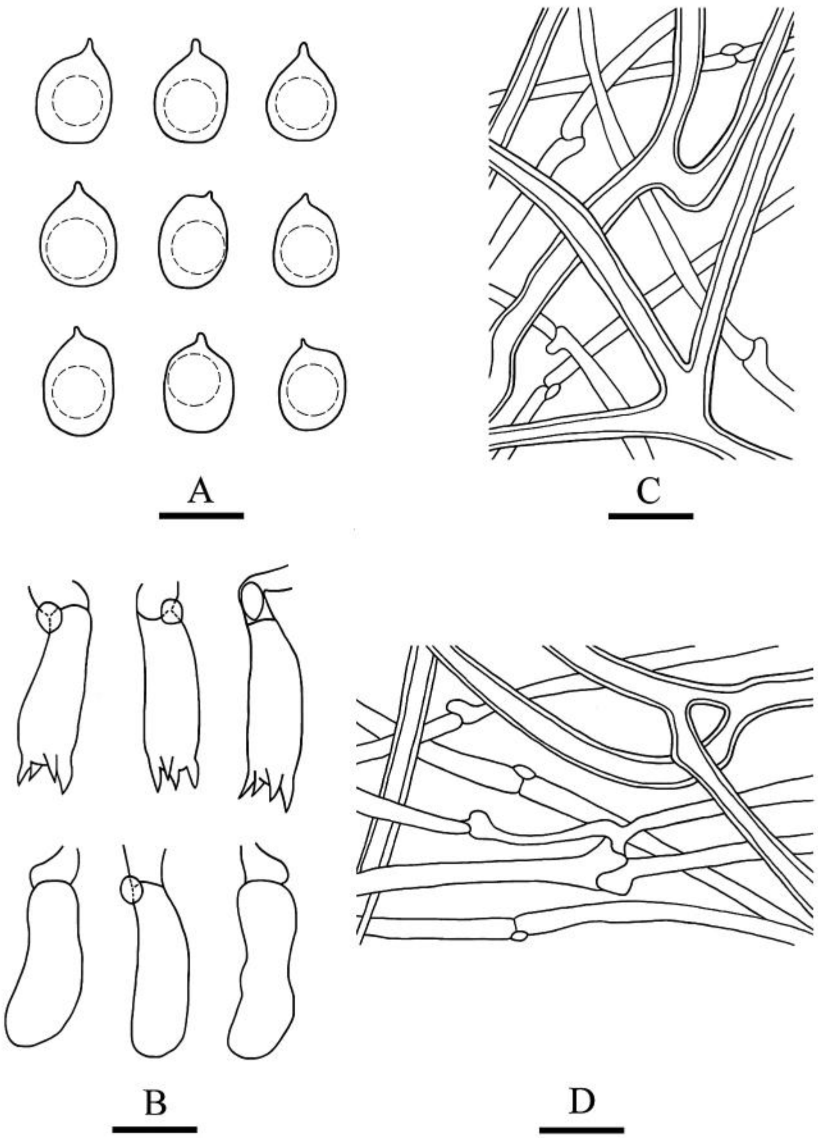

Fig. 3. *Cinereomyces wuliangshanensis* (holotype, SWFC 003405).
A. Basidiospores; B. Basidia and basidioles; C. Hyphae from trama;
D. Hyphae from subiculum. Scale bars: A = 5 ***µm;*** B–D = 10 µm.

100% BT, 1 BPP) supports the new taxon in a monophyletic lineage that groups with *C. lindbladii* and a clade comprising two species, *Obba rivulosa* and *O. valdiviana*.

Morphologically, *C. lindbladii* can be distinguished from *C. wuliangshanensis* by its greyish pore surface and larger basidiospores (5–7 × 1.5–2 µm; Ryvarden & Melo 2014); *O. rivulosa* differs from *C. wuliangshanensis* by a monomitic hyphal system and thin to slightly thick-walled and wider basidiospores (4.6–5.2 × 3.7–4.3; Miettinen & Rajchenberg 2012); *O. valdiviana,* also distinguished by its monomitic hyphal system, is further distinguished by its cyanophilous and wider basidiospores (4.6–5.3 × 4.2–5.0; Miettinen & Rajchenberg 2012).

Cinereomyces dilutabilis (Log.-Leite & J.E. Wright) Miettinen shares a dimitic hyphal system with *C. wuliangshanensis*. However, *C. dilutabilis* is distinguished by its light brownish basidiomata with smaller (6–8 per mm) pores and narrower basidiospores (4.8–5.5 × 2.4–2.8; Miettinen 2012).

With respect to distribution, *Cinereomyces* species are a rarely studied group of *Basidiomycota* (Loguercio-Leite & Wright 1998, Núñez & Ryvarden 2001, Dai 2012, Ryvarden & Melo 2014). Previously, only one species of *Cinereomyces*, *C. lindbladii,* was recorded in China (Dai 2012). However, the diversity of *Cinereomyces* species in China is still not well known, especially in southern China. In addition to our new species, *C. wuliangshanensis,* other related *Cinereomyces* taxa have been described from this region (Zhao & Cui 2012, Liu & al. 2017, Zhao & al. 2017, Zhao & Ma 2019). There is still a lot of room to explore the diversity of *Cinereomyces* species in southern China.

Acknowledgements

Special thanks are due to Drs. Mei-Ling Han (Langfang Normal University, Hebei, P.R. China) and Sana Jabeen (University of Education, Lahore, Pakistan) for expert presubmission review. The research was supported by the National Natural Science Foundation of China (Project No. 32170004), Yunnan Fundamental Research Project (Grant No. 202001AS070043), the High-level Talents Program of Yunnan Province (YNQRQNRC-2018-111), Yunnan Key Laboratory of Plateau Wetland Conservation, Restoration and Ecological Services (202105AG070002), and Science and Technology Innovation Project of Southwest Forestry University (KY21017).

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