Phytotaxa

701

Magnolia Press, Auckland, New Zealand

Article

Morphological characteristics and phylogenetic analyses revealed *Gyrophanopsis changlinii sp. nov.* (Polyporales, Basidiomycota) from Southwest China

WENYUAN XIAO, YUNCHAO LI, ZIRUI GU, HONGMIN ZHOU

Published: 2025-05-20
DOI: 10.11646/phytotaxa.701.3.1
Page range: 223-234

PDF(6.94MB)

Solving the taxonomic identity of South American *Pseudognaphalium viravira* s.l. (Gnaphalieae, Asteraceae)

SUSANA E. FREIRE, MARIANA A. GROSSI, CLAUDIA MONTI, NÉSTOR D. BAYÓN

Published: 2025-05-20
DOI: 10.11646/phytotaxa.701.3.2
Page range: 235-249

PDF(19.96MB)

A new species of *Lycianthes* series *Meizonodontae* (Capsiceae, Solanaceae) from the Baja California Peninsula, Mexico

MARCO ANTONIO ANGUIANO-CONSTANTE, AARÓN RODRÍGUEZ

Published: 2025-05-20
DOI: 10.11646/phytotaxa.701.3.3
Page range: 250-260

PDF(11.55MB)

A new species of *Myrciaria* and botanical novelties in the family Myrtaceae for Bolivia

DANIEL VILLARROEL, ORIANA A. LINO-VILLALBA, LILIANA ARROYO-HERBAS, BENTE B. KLITGAARD

Published: 2025-05-20
DOI: 10.11646/phytotaxa.701.3.4
Page range: 261-270

PDF(22.87MB)

Dalechampia nivea (Euphorbiaceae), a new species from Brazil

LUIZA OLIVEIRA BRIGATO, DANIELA SANTOS CARNEIRO-TORRES, INÊS CORDEIRO, OTÁVIO LUIS MARQUES DA SILVA

A new species of the palmatisect *Anthurium* sect. *Dactylophyllium* (Araceae) from the Atlantic Forest of northern littoral of Bahia, Brazil

Phytotaxa 701 (3): 223–234
https://www.mapress.com/pt/

Article

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

https://doi.org/10.11646/phytotaxa.701.3.1

Morphological characteristics and phylogenetic analyses revealed *Gyrophanopsis changlinii sp. nov.* (Polyporales, Basidiomycota) from Southwest China

WENYUAN XIAO[1,3], YUNCHAO LI[1,4], ZIRUI GU[1,5] & HONGMIN ZHOU[1,6*]

[1] *The Key Laboratory of Forest Resources Conservation and Utilization in the Southwest Mountains of China, Ministry of Education, Key Laboratory of National Forestry and Grassland Administration on Biodiversity Conservation in Southwest China, Yunnan Provincial Key Laboratory for Conservation and Utilization of In-forest Resource, Southwest Forestry University, Kunming 650224, P.R. China*
[2] *College of Forestry, Southwest Forestry University, Kunming 650224, P.R. China*
[3] *fungixiaowenyuan@163.com; https://orcid.org/0009-0004-7482-3314*
[4] *fungiliyunchao@163.com; https://orcid.org/0009-0007-3500-3761*
[5] *fungiziruig@163.com; https://orcid.org/0000-0003-1476-9040*
[6] *zhouhongmin@swfu.edu.cn; https://orcid.org/0000-0002-0724-5815*
* *Corresponding author: H.M. Zhou: zhouhongmin@swfu.edu.cn*

Abstract

A new species, *Gyrophanopsis changlinii* is described and illustrated based on morphological and molecular evidence. This species is characterized by its white resupinate araneose basidiomata and cylindrical basidiospores (4.5–5.3 × 4.1–4.9 µm). Sequences of the internal transcribed spacer region (ITS) and the large subunit nuclear ribosomal RNA gene (nLSU) from the studied samples were generated, and phylogenetic analyses were performed using Maximum Likelihood, Bayesian Inference, and Maximum Parsimony methods. The phylogenetic analyses indicated that the new species, *G. changlinii* nested within the genus *Gyrophanopsis*, sister to three related species: *G. japonica*, *G. polonensis*, and *G. zealandica*.

Key words: Corticioid fungi, Molecular systematics, New taxa, Taxonomy, Yunnan Province

Introduction

Wood-inhabiting fungi are found on living and dead standing trees, decorticated trunks and fallen branches as well as manufactured wood products, in which these fungi of the cell walls and the components within the living cells secrete various enzymes that effectively degrade cellulose, hemicellulose and lignin into simple inorganic substances, in which as an important group of decomposers, thus they play an important role in forest ecosystems (Wei and Dai 2004, Dai 2011, Deng *et al.* 2024, Yang *et al.* 2024, Zhang *et al.* 2024). Basidiomycota constitutes a major phylum of wood-inhabiting fungi and is second in number of described species to Ascomycota in the kingdom fungi (Yang *et al.* 2023, Andjièrèyir *et al.* 2024, He *et al.* 2024, Wang *et al.* 2024a, Zhou *et al.* 2024a). With the frequent inclusion of data from DNA sequences and by using both fresh material and cultures, the fungal classification of the kingdom fungi has been updated continuously (Hibbett *et al.* 2007, Wu *et al*. 2022, Zhang *et al*. 2023a, Zhao *et al*. 2023, Zhou *et al*. 2023), and mycologists recollected more historic taxa and type specimens to accomplish taxonomy and phylogeny in 19 phyla of Fungi (Wijayawardene *et al.* 2024). The corticioid fungi are a cosmopolitan group with a rich diversity related to the high diversity of plants found in boreal, temperate, subtropical, and tropical regions (Gilbertson & Ryvarden 1987, Bernicchia & Gorjón 2010, Dai *et al.* 2015, 2021, Zhao *et al.* 2023).

The genus *Gyrophanopsis* Jülich (1979: 329) was established by Jülich (1979) as a monotypic genus, with *G. zealandica* (G. Cunn.) Jülich (1979: 329) designated as the type species. The genus *Gyrophanopsis* is characterized by the septocystidia and smooth, slightly thick-walled basidiospores (Jülich 1979, Maekawa *et al.* 2023). According to Index Fungorum (www.indexfungorum.org; accessed January 14, 2025), three species of *Gyrophanopsis* have been accepted worldwide.

Another generic name, *Hypochnicium* J. Erikss. (1958: 100) has treated *Gyrophanopsis* as a synonym based on phylogenetic analysis using the ITS region (Paulus *et al.* 2007). However, more recent research has shown that *Gyrophanopsis* formed an independent clade, and was sister to *Bulbillomyces* Jülich (1974: 69), rather than

Accepted by Samantha C. Karunarathna: 21 Apr. 2025; published: 20 May 2025

being positioned within *Hypochnicium* (Maekawa *et al.* 2023). Morphologically, the three genera *Bulbillomyces*, *Gyrophanopsis*, and *Hypochnicium*, share subclavate to suburniform (slightly constricted) basidia, clamped hyphae, and smooth, thick-walled and cyanophilous basidiospores. However, *Bulbillomyces* and *Gyrophanopsis* can be distinguished from *Hypochnicium* by forming sclerotia (Aegerita state) and septocystidia (Maekawa *et al.* 2023). *Bulbillomyces* distinguishes from *Hypochnicium* for its producing sclerotia (Aegerita state) associated with teleomorph (Jülich 1979, Stalpers & Buchanan 1991). *Gyrophanopsis* differs from *Hypochnicium* by the heavily encrusted septocystidia and only slightly thick-walled basidiospores (Jülich 1979, Stalpers & Buchanan 1991, Maekawa *et al.* 2023). Three species, *viz., G. japonica* N. Maek. & Kogi (2023: 28), *G. polonensis* (Bres.) Stalpers & P.K. Buchanan (1991: 333) and *G. zealandica* formed a monophyletic group in *Gyrophanopsis* (Stalpers & Buchanan 1991). The currently known species of *Gyrophanopsis* are rather rare; *Gyrophanopsis japonica* was described from Japan, *G. polonensis* (Bres.) Stalpers & P.K. Buchanan (1991) was described from Poland (Stalpers & Buchanan 1991), and *G. zealandica* occurs in New Zealand. Thus, the characteristics of its ecological environment still require further expansion.

In the present study, we collected material supposedly belonging to an undescribed species of corticioid fungi from Yunnan Province, China. Based on ITS and nLSU sequences, we present morphological and molecular phylogenetic evidence that supports the recognition of a new species within *Gyrophanopsis*.

Materials and Methods

Sample collections and herbarium specimens' preparation

The fresh basidiomata growing on fallen angiosperm branches were collected in Dehong, Yunnan Province, China. The collection information was recorded (Rathnayaka *et al.* 2024) and taken to the mycology laboratory at Southwest Forestry University (SWFC). The samples were photographed using a Jianeng 80D camera (Tokyo, Japan), and fresh macroscopic details were recorded. All the photographs were focus-stacked and merged using Helicon Focus Pro 7.7.5 software. Specimens were dried in an electric food dehydrator at 40 °C (Hu *et al.* 2022). Once dried, the specimens were sealed in an envelope and zip-lock plastic bags, labeled (Zhang *et al.* 2024), and then sealed and stored in an envelope bag before being deposited in the herbarium of SWFC, Kunming, Yunnan Province, China.

Morphology

The macromorphological descriptions were based on field notes and photos captured in the field and laboratory and followed the color terminology of Petersen (1996). Micromorphological data were obtained from the dried specimens following observation under a light microscope (Zhao & Wu 2017). Drawings were made using a fungus plotter (Zhao *et al.* 2023). The measurements and drawings were made from slide preparations stained with Cotton Blue (0.1 mg aniline blue dissolved in 60 g pure lactic acid), Melzer's reagent (3 g potassium iodide, 1 g crystalline iodine, 44 g chloral hydrate, and 40 mL distilled water), and 5% potassium hydroxide. Spore size data, excluding 5% of the measurements from each end of the range, are shown in parentheses. The following abbreviations were used: KOH = 5% potassium hydroxide water solution, CB+ = cyanophilous, CB = cotton blue, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid. Q = variation in the L/W ratios between the specimens studied and n = a/b (number of spores (a) measured from a given number (b) of specimens).

DNA extraction, PCR amplification, sequencing, and phylogenetic analyses

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing, China) was used to obtain genomic DNA from the dried fungal specimens according to the manufacturer's instructions (Zhao & Wu 2017). The nuclear ribosomal ITS region was amplified with the ITS5 and ITS4 primer pair (White *et al.* 1990). The nuclear nLSU region was amplified with the LR0R and LR7 primer pair (Vilgalys & Hester 1990, Rehner & 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 nLSU 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, China. All newly generated sequences were deposited in NCBI GenBank (https://www.ncbi.nlm.nih.gov/genbank) and are listed in Table 1.

TABLE 1. List of species, specimens, and GenBank accession numbers of sequences used in this study. The new species are bold.

Species Name	Sample No.	GenBank Accession No.		Locality	References
		ITS	nLSU		
Bulbillomyces farinosus	NH 9933 (GB)	DQ681201	DQ681201	Spain	Dong *et al.* 2024
*Gyrophanopsis japonica**	TUMH:61400 *	LC663668	LC663688	Japan	Maekawa *et al.* 2023
Gyrophanopsis polonensis	NH 11337 (GB)	DQ677511	DQ677511	Turkey	Larsson 2007
Gyrophanopsis polonensis	FCUG 2262	DQ309065	-	Turkey	Maekawa *et al.* 2023
Gyrophanopsis polonensis	FCUG 2675	DQ309067	-	Russia	Maekawa *et al.* 2023
Gyrophanopsis changlinii	**CLZhao 30151**	**PQ373196**	**-**	**China**	**Present study**
Gyrophanopsis changlinii	**CLZhao 30209**	**PQ373197**	**-**	**China**	**Present study**
Gyrophanopsis changlinii	**CLZhao 30310**	**PQ373201**	**-**	**China**	**Present study**
Gyrophanopsis changlinii*	**CLZhao 30338 ***	**PQ373198**	**PQ765773**	**China**	**Present study**
Gyrophanopsis changlinii	**CLZhao 30404**	**PQ373199**	**PQ765772**	**China**	**Present study**
Gyrophanopsis changlinii	**CLZhao 30533**	**PQ373200**	**-**	**China**	**Present study**
Gyrophanopsis zealandica	NH 15340	DQ309068	-	New Zealand	Dong *et al.* 2024
Hypochnicium bombycinum	Otto Miettinen 9441 (H)	KY415959	KY415959	Finland	Dong *et al.* 2024
Hypochnicium karstenii	NH 10924	DQ677510	DQ677510	Sweden	Dong *et al.* 2024
Hypochnicium lundellii	443	AY781277	-	Sweden	Maekawa *et al*. 2023
Hypochnicium lyndoniae	NL 041031	JX124704	JX124704	UK	Dong *et al.* 2024
Hypochnicium multiforme	TUMH 64581	LC663674	LC663693	Japan	Maekawa *et al.* 2023
Hypochnicium sp.	WY-DT1	KP980549	-	China	Maekawa *et al*. 2023

*Indicates type material (holotype); new sequences are in bold and - represents the data unavailability.

Sequencher 4.6 (GeneCodes, Ann Arbor, MI, USA) was used to assemble and edit the generated sequence reads. Sequences were aligned in MAFFT 7 (https://mafft.cbrc.jp/alignment/server/) using the "G-INS-I" strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was first aligned, and then the sequences of ITS+nLSU were combined using Mesquite version 3.51. The combined ITS+nLSU sequences were used to infer the position of the new species in the genus *Gyrophanopsis* and related species. Sequences of *Hypochnicium* sp. retrieved from GenBank were used as an outgroup in the combined ITS+nLSU analysis.

Maximum Parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined three datasets. Approaches to phylogenetic analyses followed (Zhao & Wu 2017). MP analysis 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 Tree Bisection and Reconnection (TBR) branch swapping and 1000 random sequence additions. The maximum number of trees was set to 5,000, branches of zero length were collapsed, and almost all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics, including tree length (TL), the consistency index (CI), the retention index (RI), the rescaled consistency index (RC), and the homoplasy index (HI), were calculated for each most parsimonious tree generated. ML was inferred using RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org) (Miller *et al.* 2012). Branch support (BS) for ML analysis was determined by 1,000 bootstrap replicates and evaluated under the gamma model.

The best evolutionary model for each alignment was estimated using jModelTest (Guindon & Gascuel 2003; Posada 2008) under the Akaike information criterion. MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for the Bayesian Inference (BI) dataset. Bayesian Inference was performed using MrBayes 3.1.2, with a general time-reversible (GTR+I+G) model of DNA substitution and a gamma distribution of rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for two independent runs from random starting trees, each comprising 10 million generations of combined ITS+nLSU sequences (Fig. 1), with trees and parameters sampled every 100 generations. The first quarter of all the generations was discarded as burn-in. A majority rule consensus tree of all remaining trees and posterior probabilities was calculated. Branches were considered significantly supported if they received a Maximum Likelihood bootstrap value (BS) of ≥70%, a Maximum Parsimony bootstrap value (BT) of ≥70%, or Bayesian posterior probabilities (BPP) of ≥0.95.

FIGURE 1. Phylogeny of species in *Gyrophanopsis* and related taxa generated using Maximum Likelihood based on ITS and nLSU sequence data. Branches are labeled with Maximum Likelihood bootstrap ≥ 70% and Bayesian posterior probabilities ≥ 0.95, respectively. New species are in bold.

Results

Phylogenetic analyses

The ITS+nLSU dataset included sequences from 18 fungal specimens representing 11 species (Figure 1). The dataset includes 1,436 characters, all of which are aligned for length. Of these, 1,175 characters are constant, 192 are parsimony-informative, and 69 are variable and parsimony-uninformative. Maximum parsimony analysis yielded one equally parsimonious tree (TL = 439, CI =0.7244, HI = 0.2756, RI = 0.8246, RC = 0.5973). Bayesian analysis and ML analysis yielded a topology similar to that of MP analysis, with the effective sample size (ESS) across the two runs being double the average ESS (avg ESS) of 3432.5. The phylogram based on ITS+nLSU sequences (Figure 1) shows that the new taxon clusters within the genus *Gyrophanopsis* and forms a well-supported lineage within the order Polyporales.

All samples of *Gyrophanopsis* form a monophyletic clade that exhibits a close relationship with *Bulbillomyces* and *Hypochnicium*. All specimens of *Gyrophanopsis* form two clades. The six Chinese specimens formed a well-supported clade, named *Gyrophanopsis changlinii*, sister to *G. japonica.* Three Polish specimens occupy another clade, sister to the Japanese specimens, named *G. japonica*.

Table 2 gives the BLAST result for the new species, including the closest top 10 taxa and their corresponding parameters.

TABLE 2. The BLAST result of the new species for the closest top 10 taxa and their corresponding parameters.

Scientific Name	Specimens	Sequence Number	Max score	Total score	Query cover	E value	Per. Ident.	Acc. len.	Accession
Gyrophanopsis changlinii			1219	1219	100%	0	100%	660	PQ373196
			1199	1199	100%	0	99.55%	661	PQ373199
			1192	1192	99%	0	99.54%	659	PQ373201
			1175	1175	99%	0	99.24%	662	PQ373197
	CLZhao 30151	PQ373196	1101	1101	92%	0	99.18%	615	PQ373200
			1096	1096	93%	0	98.70%	617	PQ373198
			571	571	97%	4e-158	83.51%	618	KJ140731
			569	569	86%	1e-157	85.34%	617	PP982817
			566	566	95%	2e-156	83.86%	639	KP980549
			558	558	98%	3e-154	82.95%	662	NR_185386
			1223	1223	100%	0	100.00%	662	PQ373197
			1194	1194	99%	0	99.69%	661	PQ373199
			1184	1184	99%	0	99.39%	659	PQ373201
			1175	1175	98%	0	99.24%	660	PQ373196
	CLZhao 30209	PQ373197	1122	1122	93%	0	99.67%	615	PQ373200
			1094	1094	93%	0	98.54%	617	PQ373198
			582	582	96%	2e-161	83.80%	618	KJ140731
			575	575	94%	3e-159	84.13%	639	KP980549
			568	568	97%	5e-157	83.28%	662	NR_185386
			568	568	85%	5e-157	85.51%	617	PP982817
			1214	1214	100%	0	100.00%	659	PQ373201
			1197	1197	99%	0	99.69%	661	PQ373199
			1192	1192	99%	0	99.54%	660	PQ373196
			1184	1184	99%	0	99.39%	662	PQ373197
	CLZhao 30310	PQ373201	1110	1110	93%	0	99.35%	615	PQ373200
			1103	1103	93%	0	98.86%	617	PQ373198
			582	582	96%	2e-161	83.78%	618	KJ140731
			577	577	94%	8e-160	84.13%	639	KP980549
			569	569	86%	1e-157	85.34%	617	PP982817
			564	564	98%	7e-156	83.00%	662	NR_185386
			1122	1122	100%	0	100.00%	617	PQ373198
			1103	1103	99%	0	98.86%	661	PQ373199
			1103	1103	99%	0	98.86%	659	PQ373201
			1096	1096	99%	0	99.70%	660	PQ373196
			1094	1094	99%	0	98.54%	662	PQ373197
	CLZhao 30338	PQ373198	1088	1088	99%	0	98.53%	615	PQ373200
			556	556	92%	1e-153	84.67%	617	PP982817
			545	545	88%	2e-150	85.32%	639	KP980549
			544	544	91%	8e-150	84.45%	618	KJ140731
			540	540	91%	1e-148	84.45%	593	KJ140683

.....continued on the next page

TABLE 2. (Continued)

Scientific Name	Specimens	Sequence Number	Max score	Total score	Query cover	E value	Per. Ident.	Acc. len.	Accession
	CLZhao 30404	PQ373199	1221	1221	100%	0	100.00%	661	PQ373199
			1199	1199	100%	0	99.55%	660	PQ373196
			1197	1197	99%	0	99.69%	659	PQ373201
			1194	1194	98%	0	99.69%	662	PQ373197
			1112	1112	92%	0	99.51%	615	PQ373200
			1103	1103	93%	0	98.86%	617	PQ373198
			582	582	96%	2e-161	83.80%	618	KJ140731
			575	575	94%	3e-159	84.13%	639	KP980549
			569	569	98%	1e-157	83.23%	662	NR_185386
			569	569	86%	1e-157	85.37%	617	PP982817
	CLZhao 30553	PQ373200	1133	1133	100%	0	100.00%	615	PQ373200
			1122	1122	100%	0	99.67%	662	PQ373197
			1112	1112	99%	0	99.51%	661	PQ373199
			1110	1110	100%	0	99.35%	659	PQ373201
			1101	1101	99%	0	99.18%	660	PQ373196
			1088	1088	99%	0	98.53%	617	PQ373198
			564	564	91%	6e-156	85.34%	617	PP982817
			560	560	88%	8e-155	86.06%	639	KP980549
			558	558	90%	3e-154	85.48%	612	HM008934
			556	556	91%	1e-153	85.13%	618	KJ140731

Taxonomy

Gyrophanopsis changlinii W.Y. Xiao & H.M. Zhou, *sp. nov.* Figures. 2–3.
MycoBank no.: 856152

Etymology:—*Changlinii* (Lat.) in honor of the Chinese mycologist, Prof. Changlin Zhao.

Holotype:—CHINA. Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates 23°48′N, 97°38′E, evel. 1500 m a.s.l., on fallen angiosperm branch, leg. C.L. Zhao, 19 July 2023, CLZhao 30338 (SWFC).

Basidiomes:—Annual, resupinate, effused, byssoid, without odor or taste when fresh, up to 8 cm long, 7 cm wide, and 100 μm thick. Hymenophore surface white when fresh, white to slightly buff, flocculent when dry. Sterile margin narrow, slightly buff, up to 1 mm.

Hyphal system:—Monomitic; generative hyphae with clamp connections, colorless, thin- to thick-walled, frequently branched, IKI–, CB+, 3–5 μm in diameter; tissues unchanged in KOH. Cystidia clavate to subcylindrical, smooth, thin- to thick-walled, with 2–3 clamp connections, 9–13 × 4–5 μm. Basidia barrel-shaped with a slight median constriction, colorless, thin-walled, with four sterigmata and a basal clamp connection, 8–15 × 3.5–5 μm; basidioles in shape similar to basidia, but slightly smaller.

Spores:—Basidiospores subglobose to globose, colorless, thick-walled, IKI–, CB+, 4.5–5.3(–5.5) × (4–)4.1–4.9(–5) μm, L = 5 μm, W = 4.5 μm, Q = 1.01–1.08 (n = 180/6).

Additional specimens examined (paratypes):—CHINA. Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates 23°48′ N, 97°38′ E, evel. 1500 m a.s.l., on fallen angiosperm branch, 19 July 2023, CLZhao 30151, CLZhao 30209, CLZhao 30310, CLZhao 30404, CLZhao 30533 (SWFC).

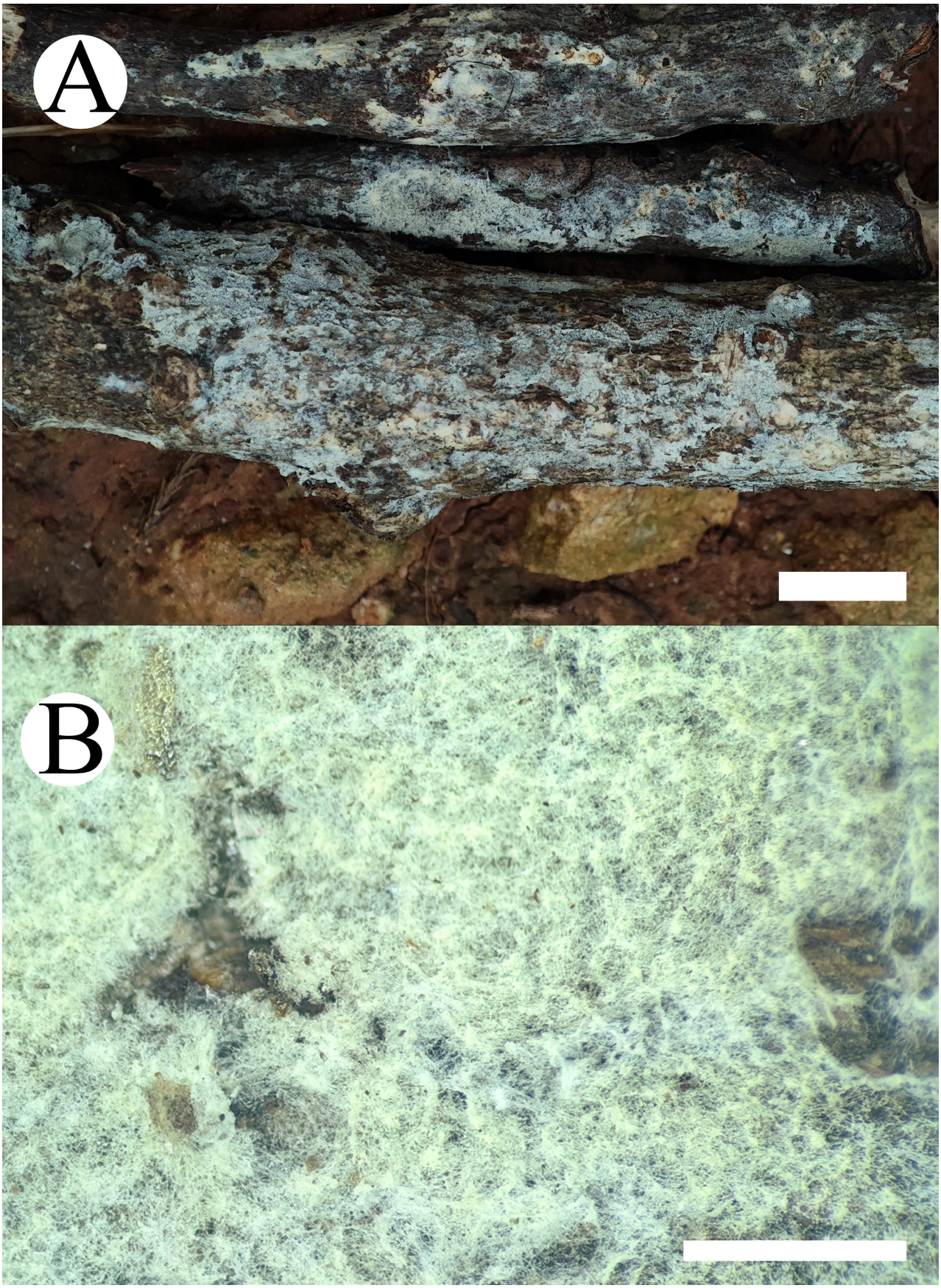

FIGURE 2. *Gyrophanopsis changlinii* (holotype, CLZhao 30338): (A) Basidiomata on the substrate; (B) Macroscopic characteristics of hymenophore. Bars: (A) = 1 cm, (B) = 2 mm.

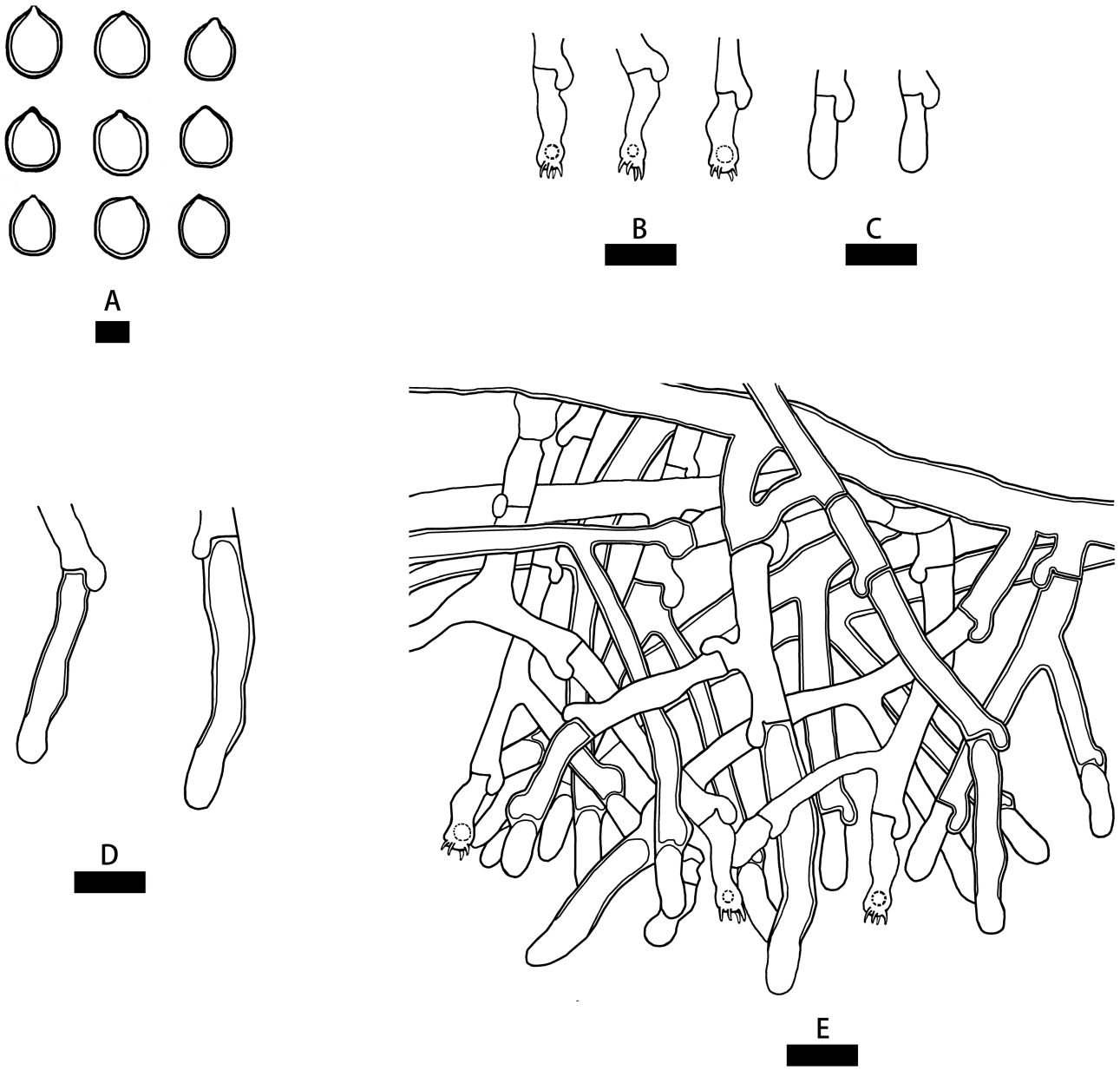

FIGURE 3. Microscopic structures of *Gyrophanopsis changlinii* (holotype, CLZhao 30338): (A) Basidiospores; (B) Basidia; (C) Basidioles; (D) Cystidia; (E) A section of the hymenium. Bars: (A)= 5 µm, (B–E) = 10 µm.

Discussion

The present study describes *Gyrophanopsis changlinii* as a new species based on phylogenetic analyses and morphological characteristics.

Previously, three species of *Gyrophanopsis* were accepted primarily based on morphological examination, and their confirmation was subsequently supported by phylogenetic analyses (Maekawa *et al.* 2023). In the present study, a distinct taxon of *Gyrophanopsis* is identified in China as *G. changlinii*, based on morphological and molecular evidence. The phylogenetic relationship among the three *Gyrophanopsis* taxa is then analyzed (Figure 1). However, *Gyrophanopsis japonica* is distinct from *G. changlinii* in having cylindrical septocystidia that are heavily covered with subhyaline crystals and larger basidia (14–20 × 5–5.5 µm vs. 8–15 × 3.5–5 µm, Maekawa *et al.* 2023). *Gyrophanopsis zealandica* differs from *G. changlinii* in its septocystidia, which are covered with a sheath of yellowish-brown crystalline material, and in its longer basidiospores (5.5–7 µm vs. 4.5–5.3 µm; Jülich 1979; Stalpers & Buchanan 1991). *Gyrophanopsis polonensis* is distinguished from *G. changlinii* by its longer basidiospores (6.5–8.5 × 4–5 µm

vs. 4.5–5.3 × 4.1–4.9 µm, Maekawa *et al*. 2023). Moreover, a key to the species of *Gyrophanopsis* known from China is provided.

Recent advances have been made in studying fungal species diversity (He *et al.* 2019; Dai *et al.* 2021). Approximately 165,000 species of fungi have been described, accounting for around 7% of an estimated 2.5 million species (Hawksworth & Lücking 2017, Hyde 2022, Index Fungorum 2025). Additionally, based on fossil evidence, determining the divergence within Basidiomycota has yielded a robust set of age estimates for higher taxa (He *et al*. 2019). The discovery of new fungal species has rapidly increased with the development of molecular techniques, drawing attention to the enormous fungal diversity that exists on earth, and the definition of many genera and families were revised (Cui *et al.* 2019, Dai *et al.* 2021, Wu *et al.* 2022, Duan *et al.* 2023, Liu *et al.* 2023, Mao *et al*. 2023, Wang *et al.* 2023, Yuan *et al.* 2023a, Yuan *et al.* 2023b, Zhang *et al.* 2023b, Zhao *et al.* 2023, Tian *et al.* 2024, Wang *et al.* 2024b, Zhao *et al.* 2024, Zhou *et al.* 2024b), but the generic concept of *Gyrophanopsis* has not been resolved yet (Maekawa *et al.* 2023). Our new contribution to *Gyrophanopsis* provides new data on the genus.

Key to species of the genus *Gyrophanopsis* worldwide

1a. Basidiospores ellipsoid 2
1b. Basidiospores subglobose 3
2a. Basidiospores > 6.5 µm ..... *G. polonensis*
2b. Basidiospores mearing < 6.5 µm ..... *G. zealandica*
3a. Septocystidia encrusted with crystalloid material ..... *G. japonica*
3b. Septocystidia without subhyaline crystalline material ..... *G. changlinii*

Acknowledgements

The research was supported by the National Natural Science Foundation of China (Project No. 3246006), the Scientific Research Fund of Yunnan Provincial Department of Education (2024J0668), and the Forestry Innovation Programs of Southwest Forestry University (Grant No: LXXK-2023M07).

References

Andjièrèyir, K.S., Samson, N., Sylvie, N.R., Benovana, B., Edouard, S.K.J., Kounbo, D. & Elise, S. (2024) Taxonomic study of five parasitic polypores of the Hymenochaetaceae family of TIN vegetation in Western Burkina Faso. *American Journal of Plant Sciences* 15: 441–454. https://doi.org/10.4236/ajps.2024.156031

Bernicchia, A. & Gorjón, S.P. (2010) *Fungi europaei 12: Corticiaceae s.l.* Edizioni Candusso, Lomazzo, 1007 pp.

Cui, B.K., Li, H.J., Ji, X., Zhou, J.L., Song, J., Si, J., Yang, Z.L. & Dai, Y.C. (2019) Species diversity, taxonomy and phylogeny of Polyporaceae (Basidiomycota) in China. *Fungal Diversity* 97: 137–392. https://doi.org/10.1007/s13225-019-00427-4

Dai, Y.C. (2011) A revised checklist of corticioid and hydnoid fungi in China for 2010. *Mycoscience* 52: 69–79. https://doi.org/10.1007/S10267-010-0068-1

Dai, Y.C., Yang, Z.L., Cui, B.K., Wu, G., Yuan, H.S., Zhou, L.W., He, S.H., Ge, Z.W., Wu, F., Wei, Y.L., Yuan, Y. & Si, J. (2021) Diversity and systematics of the important macrofungi in Chinese forests. *Mycosystema* 40 (4): 770–805. https://doi.org/10.13346/j.mycosystema.210036

Dai, Y.C., Cui, B.K., Si, J., He, S.H., Hyde, K.D., Yuan, H.S., Liu, X.Y. & Zhou, L.W. (2015) Dynamics of the worldwide number of fungi with emphasis on fungal diversity in China. *Mycological Progress* 14: 62. https://doi.org/10.1007/s11557-015-1084-5

Deng, Y.L., Jabeen, S. & Zhao, C.L. (2024) Species diversity and taxonomy of *Vararia* (Russulales, Basidiomycota) with descriptions of six species from Southwestern China. *MycoKeys* 103: 97–128. https://doi.org/10.3897/mycokeys.103.118980

Dong, J.H., Li, Q., Yuan, Q., Luo, Y.X., Zhang, X.C., Dai, Y.F., Zhou, Q., Liu, X.F., Deng, Y.L., Zhou, H.M., Muhammad, A. & Zhao, C.L. (2024) Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. *Mycosphere* 15 (1): 1110–1293. https://doi.org/10.5943/mycosphere/15/1/10

Duan, Z.Y., Guan, Q.X., Luo, K.Y. & Zhao, C.L. (2023) Morphological and molecular identification of three new resupinate species of

Hyphoderma (Hyphodermataceae, Agaricomycetes) from East Asia. *Phytotaxa* 599 (1): 001–019. https://doi.org/10.11646/phytotaxa.599.1.1

Felsenstein, J. (1985) Confidence intervals on phylogenetics: an approach using bootstrap. *Evolution* 39: 783–791. https://doi.org/10.1111/j.1558-5646.1985.tb00420.x

Gilbertson, R.L. & Ryvarden, L. (1987) *North American Polypores 1–2*. Fungiflora, Oslo, Norway, 433 pp.

Guindon, S. & Gascuel, O. (2003) A simple, fast and accurate algorithm to estimate large phylogenies by Maximum Likelihood. *Systematic Biology* 52 (5): 696–704. https://doi.org/10.1080/10635150390235520

Hawksworth, D.L. & Lücking, R. (2017) Fungal diversity revisited: 2.2 to 3.8 million species. *Microbiology Spectrum* 5 (4): 1–17. https://doi.org/10.1128/microbiolspec.FUNK-0052-2016

He, M.Q., Cao, B., Liu, F., Boekhout, T., Denchev, T.T., Schoutteten, N., Denchev, C.M., Kemler, M., Gorjón, S.P., Begerow, D., Valenzuela, R., Davoodian, N., Niskanen, T., Vizzini, A., Redhead, S.A., Ramírez-Cruz, V., Papp, V., Dudka, V.A., Dutta, A.K., García-Sandoval, R., Liu, X.Z., Kijpornyongpan, T., Savchenko, A., Tedersoo, L., Theelen, B., Trierveiler-Pereira, L., Wu, F., Zamora, J,C., Zeng, X.Y., Zhou, L.W., Liu, S.L., Ghobad-Nejhad, M., Giachin, A.J., Li, G.J., Kakishima, M., Olariaga, I., Haelewaters, D., Sulistyo, B., Sugiyama, J., Svantesson, S., Yurkov, A., Alvarado, P., Antonín, V., Silva, A.F.D., Druzhinina, I., Gibertoni, T.B., Guzmán-Dávalos, L., Justo, A., Karunarathna, S.C., Galappaththi, M.A.C., Toome-Heller, M., Hosoya, T., Liimatainen, K., Márquez, R., Mešić, A., Moncalvo, J.M., Nagy, L.G., Varga, T., Orihara, T., Raymundo, T., Salcedo, I., Silva-Filho, A.G.S., Tkalčec, Z., Wartchow, F., Zhao, C.L., Bau, T., Cabarroi-Hernández, M., Cortés-Pérez, A., Decock, C., Lange, R.D., Weiss, M., Menolli Jr, N., Nilsson, R.H., Fan, Y.G., Verbeken, A., Gafforov, Y., Meiras-Ottoni, A., Mendes-Alvarenga, R.L., Zeng, N.K., Wu, Q., Hyde, K.D., Kirk, P.M. & Zhao, R.L. (2024) Phylogenomics, divergence times and notes of orders in Basidiomycota. *Fungal Diversity* 126 (1): 127–406. https://doi.org/10.1007/s13225-024-00535-w

He, M.Q., Zhao, R.L., Hyde, K.D., Begerow, D., Kemler, M., Yurkov, A., McKenzie, E.H.C., Raspé, O., Kakishima, M., Sánchez-Ramírez, S., Vellinga, E.C., Halling, R., Papp, V., Zmitrovich, I.V.,Buyck, B., Ertz, D., Wijayawardene, N.N., Cui, B.K., Schoutteten, N., Liu, X.Z., Li, T.H., Yao, Y.J., Zhu, X.Y., Liu, A.Q., Li, G.J., Zhang, M.Z., Cao, B., Antonín, V., Boekhout, T., Silva, B.D.B.D., Crop, E.D., Decock, C., Dima,B., Dutta, A.K., Fell, J.W., Geml, J., Ghobad-Nejhad, M., Giachini, A.J., Gibertoni, T.B., Gorjón, S.P., Haelewaters, D., He, S.H., Hodkinson, B.P., Horak, E., Hoshino, T., Justo, A., Lim, Y.W., Menolli Jr, N., Mešić, A., Moncalvo, J.M., Mueller, G.M., Nagy, L.G., Nilsson, R.H., Noordeloos, M., Nuytinck, J., Orihara, T., Ratchadawan, C., Rajchenberg, M., Silva-Filho, A.G.S., Sulzbacher, M.A., Tkalčec, Z., Valenzuela, R., Verbeken, A., Vizzini, A., Wartchow, F., Wei, T.Z., Weiß, M., Zhao, C.L. & Kirk, P.M. (2019) Notes, outline and divergence times of Basidiomycota. *Fungal Diversity* 99: 105–367. https://doi.org/10.1007/s13225-019-00435-4

Hibbett, D.S., Binder, M., Bischoff, J.F., Blackwell, M., Cannon, P.F., Eriksson, O.E., Huhndorf, S., James, T., Kirk, P.M., Lücking, R., Lumbsch, H.T., Lutzoni, F., Matheny, P.B., McLaughlin, D.J., Powell, M.J., Redhead, S., Schoch, C.L., Spatafora, J.W., Stalpers, J.A., Vilgalys, R., Aime, M.C., Aptroot, A., Bauer, R., Begerow, D., Benny, G.L., Castleburry, L.A., Crous, P.W., Dai, Y.C., Gams, W., Geiser, D.M., Griffith, G.W., Gueidan, C., Hawksworth, D.L., Hestmark, G., Hosaka, K., Humber, R.A., Hyde,K.D., Ironside, J.E., Koljalg, U., Kurtzman, C.P., Larsson, K.H., Lichtwardt, R., Longcore, J., Miadlokowska, J., Miller, A., Moncalvo, J.M., Mozley-Standridge, S., Oberwinkler, F., Parmasto, E., Reeb, V., Rogers, J.D., Roux, C., Ryvarden, L., Sampaio, J.P., Schüssler, A., Sugiyama, J., Thorn, R.G., Tibell, L., Untereiner, W.A., Walker, C., Wang, Z., Weir, A., Weiss, M., White, M.M., Winka, K., Yao, Y.J. & Zhang, N. (2007) A higher-level phylogenetic classification of the Fungi. *Mycological Research* 111 (5): 509–547. https://doi.org/10.1016/j.mycres.2007.03.004

Hu, Y.W., Karunarathna, S.C., Li, H., Galappaththi, M.C., Zhao, C.L., Kakumyan, P. & Mortimer, P.E. (2022) The impact of drying temperature on basidiospore size. *Diversity* 14: 239. https://doi.org/10.3390/d14040239

Hyde, K.D. (2022) The numbers of fungi. *Fungal Diversity* 114: 1. https://doi.org/10.1007/s13225-022-00507-y

Jülich, W. (1979) Studies in resupinate Basidiomycetes–VI. On some new taxa. *Persoonia* 10 (3): 325–336.

Larsson, A. (2014) AliView: a fast and lightweight alignment viewer and editor for large data sets. *Bioinformatics* 30 (22): 3276–3278. https://doi.org/10.1093/bioinformatics/btu531

Larsson, K.H. (2007) Molecular phylogeny of *Hyphoderma* and the reinstatement of *Peniophorella*. *Mycological Research* 111: 186–195. https://doi.org/10.1016/j.mycres.2006.10.002

Liu, S., Chen, Y.Y., Sun, Y.F., He, X.L., Song, C.G., Si, J., Liu, D.M., Gates, G. & Cui, B.K. (2023) Systematic classification and phylogenetic relationships of the brown-rot fungi within the Polyporales. *Fungal Diversity* 118: 1–94. https://doi.org/10.1007/s13225-022-00511-2

Maekawa, N., Sugawara, R., Kogi, H., Norikura, S., Sotome, K., Endo, N., Nakagiri, A. & Ushijima, S. (2023) *Hypochnicium* sensu lato (Polyporales, Basidiomycota) from Japan, with descriptions of a new genus and three new species. *Mycoscience* 64: 19–34.

https://doi.org/10.47371/mycosci.2022.10.001

Mao, W.L., Wu, Y.D., Liu, H.G., Yuan, Y. & Dai, Y.C. (2023) A contribution to *Porogramme* (Polyporaceae, Agaricomycetes) and related genera. *IMA Fungus* 14: 5.
https://doi.org/10.1186/s43008-023-00110-z

Miller, M.A., Pfeiffer, W. & Schwartz, T. (2012) The CIPRES science gateway: enabling high–impact science for phylogenetics researchers with limited resources. *Association for Computing Machinery* 39: 1–8.
https://doi.org/10.1145/2335755.2335836

Nylander, J.A.A. (2004) *MrModeltest v2.* Evolutionary Biology Centre, Uppsala University, Uppsala, Sweden.

Paulus, B., Nilsson, H. & Hallenberg, N. (2007) Phylogenetic studies in *Hypochnicium* (Basidiomycota), with special emphasis on species from New Zealand. *New Zealand Journal of Botany* 45: 139–150.
https://doi.org/10.1080/00288250709509709

Posada, D. (2008) jModelTest: Phylogenetic model averaging. *Molecular Biology and Evolution* 25 (7): 1253–1256.
https://doi.org/10.1093/molbev/msn083

Rathnayaka, A.R., Tennakoon, D.S., Jones, G.E., Wanasinghe, D.N., Bhat, D.J., Priyashantha, A.H., Stephenson, S.L. & Tibpromma, S. & Karunarathna, S.C. (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* 63 (2–3): 462–489.
https://doi.org/10.1080/0028825X.2024.2381734

Rehner, S.A. & Samuels, G.J. (1994) Taxonomy and phylogeny of *Gliocladium* analysed from nuclear large subunit ribosomal DNA sequences. *Mycological Research* 98 (6): 625–634.
https://doi.org/10.1016/S0953-7562(09)80409-7

Ronquist, F. & Huelsenbeck, J.P. (2003) MRBAYES 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19 (12): 1572–1575.
https://doi.org/10.1093/bioinformatics/btg180

Stalpers, J.A. & Buchanan, P.K. (1991) Type studies of the species of *Pellicularia* and *Peniophora* described by G. H. Cunningham. *New Zealand Journal of Botany* 29 (3): 331–340.
https://doi.org/10.1080/0028825X.1991.10416611

Swofford, D.L. (2002) PAUP*: Phylogenetic analysis using parsimony (*and Other Methods), Version 4.0b10. Sinauer Associates: Sunderland, MA, USA.

Tian, X.G., Bao, D.F., Karunarathna, S.C., Jayawardena, R.S., Hyde, K.D., Bhat, D.J., Luo, Z.L., Elgorban, A.M., Hongsanan, S., Rajeshkumar, K.C., Maharachchikumbura, S.S.N., Suwannarach, N., Dawoud, T.M., Lu, Y.Z., Han, J.J., Xiao, Y.P., Du, T.Y., Lu, L., Xu, R.F., Dai, D.Q., Liu, X.F., Liu, C. & Tibpromma, S. (2024) Taxonomy and phylogeny of Ascomycetes associated with selected economically important monocotyledons in China and Thailand. *Mycosphere* 15 (1): 1–274.
https://doi.org/10.5943/mycosphere/15/1/1

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

Wang, C.G., Dai, Y.C., Kout, J., Gates, G.M., Liu, H.G., Yuan, Y. & Vlasák, J. (2024b) Multi-gene phylogeny and taxonomy of *Physisporinus* (Polyporales, Basidiomycota). *Mycosphere* 15 (1): 1455–1521.
https://doi.org/10.5943/mycosphere/15/1/12

Wang, C.G., Zhao, H., Liu, H.G., Zeng, G.Y., Yuan, Y. & Dai, Y.C. (2023) A multi-gene phylogeny clarifies species diversity, taxonomy, and divergence times of *Ceriporia* and other related genera in Irpicaceae (Polyporales, Basidiomycota). *Mycosphere* 14 (1): 1665–1729.
https://doi.org/10.5943/mycosphere/17/1/9

Wang, L., Kang, Z.L., Zhou, H.M. & Zhao, C.L. (2024a) Molecular phylogeny and morphology reveal two new wood-inhabiting fungal species (Basidiomycota) from China. *Phytotaxa* 647 (3): 207–222.
https://doi.org/10.11646/phytotaxa.647.3.1

Wei, Y.L. & Dai, Y.C. (2004) The ecological function of wood-inhabiting fungi in forest ecosystem. *Chinese Journal of Applied Ecology* 15: 1935–1938. [in Chinese]

White, T.J., 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. (Eds.) *PCR protocols: A guide to methods and applications*. Academic Press, San Diego, pp. 315–322.
https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wijayawardene, N.N., Hyde, K.D., Mikhailov, K.V., Péter, G., Aptroot, A., Pires-Zottarelli, C., Goto, B.T., Tokarev, Y.S., Haelewaters, D., Karunarathna, S.C., Kirk, P.M., Santiago, A., Saxena, R.K., Schoutteten, N., Wimalasena, M.K., Aleoshin, V.V., Al-Hatmi, A.M.S., Ariyawansa, K.G.S.U., Assunção, A.R., Bamunuarachchige, T.C., Baral, H.O., Bhat, D.J., Błaszkowski, J., Boekhout, T., Boonyuen,

N., Brysch-Herzberg, M., Cao, B., Cazabonne, J., Chen, X.M., Coleine, C., Dai, D.Q., Daniel, H.M., Silva, S.B.G.D., Souza, F.A.D., Dolatabadi, S., Dubey, M.K., Dutta, A.K., Ediriweera, A., Egidi, E., Elshahed, M.S., Fan, X.L., Felix, J.R.B., Galappaththi, M.C.A., Groenewald, M., Han, L.S., Huang, B., Hurdeal, V.G., Ignatieva, A.N., Jerônimo, G.H., Jesus, A.L.D., Kondratyuk, S., Kumla, J., Kukwa, M., Li, Q.R., Lima, J.L.R., Liu, X.Y., Lu, W.H., Lumbsch, H.T., Madrid, H., Magurno, F., Marson, G., McKenzie, E.H.C., Menkis, A., Mešić, A., Nascimento, E.C.R., Nassonova, E.S., Nie, Y., Oliveira, N.V.L., Ossowska, E.A., Pawłowska, J., Peintner, U., Pozdnyakov, I.R., Premarathne, B.M., Priyashantha, A.K.H., Quandt, C.A., Queiroz, M.B., Rajeshkumar, K.C., Raza, M., Roy, N., Samarakoon, M.C., Santos, A.A., Santos, L.A., Schumm, F., Selbmann, L., Selçuk, F., Simmons, D.R., Simakova, A.V., Smith, M.T., Sruthi, O.P., Suwannarach, N., Tanaka, K., Tibpromma, S., Tomás, E.O., Ulukapı, M., Vooren, N.V., Wanasinghe, D.N., Weber, E., Wu, Q.Z., Yang, E.F., Yoshioka, R., Youssef, N.H., Zandijk, A., Zhang, G.Q., Zhang, J.Y., Zhao, H., Zhao, R.L., Zverkov, O.A., Thines, M. & Karpov, S.A. (2024) Classes and phyla of the kingdom Fungi. *Fungal Diversity* 128: 1–165. https://doi.org/10.1007/s13225-024-00540-z

Wu, F., Zhou, L.W., Vlasák, J. & Dai, Y.C. (2022) Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. *Fungal Diversity* 113: 1–192. https://doi.org/10.1007/s13225-021-00496-4

Yang, Y., Li, R., Liu, C.M. & Zhao, C.L. (2023) Morphological and molecular identification for two new species of wood-inhabiting macrofungi (Basidiomycota) from Yunnan-Guizhou Plateau, China. *Phytotaxa* 591 (1): 1–18. https://doi.org/10.11646/phytotaxa.591.1.1

Yang, Y., Li, R., Jiang, Q.Q., Zhou, H.M., Muhammad, A., Wang, H.J. & Zhao, C.L. (2024) Phylogenetic and taxonomic analyses reveal three new wood-inhabiting fungi (Polyporales, Basidiomycota) in China. *Journal of Fungi* 10 (1): 55: 1–17. https://doi.org/10.3390/jof10010055

Yuan, Q., Luo, K.Y., Zhang, Y. & Zhao, C.L. (2023a) Morphological characteristics and phylogenetic analyses revealed three new wood inhabiting fungi (Agaricomycetes, Basidiomycota) in Southern China. *Phytotaxa* 592 (3): 179–195. https://doi.org/10.11646/phytotaxa.592.3.1

Yuan, Y., Bian, L.S., Wu, Y.D., Chen, J.J., Wu, F., Liu, H.G., Zeng, G.Y. & Dai, Y.C. (2023b) Species diversity of pathogenic wood-rotting fungi (Agaricomycetes, Basidiomycota) in China. *Mycology* 14: 204–226. https://doi.org/10.1080/21501203.2023.2238779

Zhang, X.C., Li, Y.C., Wang, Y.Y., Xu, Z., Zhao, C.L. & Zhou, H.M. (2024) *Xylodon asiaticus* (Hymenochaetales, Basidiomycota), a new species of corticioid fungus from southern China. *Phytotaxa* 634 (1): 1–15. https://doi.org/10.11646/phytotaxa.634.1.1

Zhang, X.J., Yuan, Q., Su, J.Q. & Zhao, C.L. (2023b) Diversity of wood-decaying fungi in Zixishan area (Hengduan Mountains), Yunnan Province, China. *Phytotaxa* 612 (2): 113–138. https://doi.org/10.11646/phytotaxa.612.2.1

Zhang, Q.Y., Liu, H.G., Papp, V., Zhou, M., Dai, Y.C. & Yuan, Y. (2023a) New insights into the classification and evolution of *Favolaschia* (Agaricales, Basidiomycota) and its potential distribution, with descriptions of eight new species. *Mycosphere* 14: 777–814. https://doi.org/10.5943/mycosphere/14/1/10

Zhao, C.L. & Wu, Z.Q. (2017) *Ceriporiopsis kunmingensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. *Mycological Progress* 16 (1): 93–100. https://doi.org/10.1007/s11557-016-1259-8

Zhao, C.L., Qu, M.H., Huang, R.X. & Karunarathna, S.C. (2023) Multi-gene phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia* sensu lato (Polyporales, Basidiomycota). *Journal of Fungi* 9: 320. https://doi.org/10.3390/jof9030320

Zhao, H., Wu, Y.D., Yang, Z.R., Liu, H.G., Wu, F., Dai, Y.C. & 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: 2197–5620. https://doi.org/10.1016/j.fecs.2024.100200

Zhou, H.M., Gu, Z.R. & Zhao, C.L. (2024a) Molecular phylogeny and morphology reveal a new species of *Asterostroma* from Guizhou Province, China. *Phytotaxa* 635 (2): 173–181. https://doi.org/10.11646/phytotaxa.635.2.7

Zhou, M., Dai, Y.C., Vlasák, J., Liu, H.G. & Yuan, Y. (2023) Updated systematics of *Trichaptum* s.l. (Hymenochaetales, Basidiomycota). *Mycosphere* 14 (1): 815–917. https://doi.org/10.5943/mycosphere/14/1/11

Zhou, Q., Jiang, Q.Q., Yang, X., Zhao, C.L. & Zhao, J. (2024b) Phylogenetic and taxonomic analyses of five new wood-inhabiting fungi of *Botryobasidium*, *Coltricia* and *Coltriciella* (Basidiomycota) from China. *Journal of Fungi* 10 (3): 205: 1–22. https://doi.org/10.3390/jof10030205