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Molecular phylogeny and morphology reveal two new wood-inhabiting fungal species (Basidiomycota) from China

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Abstract

Wood-inhabiting fungi are found in living trees, decorticated wood of dead tree branches and trunks as well as manufactured wood products, and play an important role in forest ecosystems as an important group of decomposers. In this present study, two new wood-inhabiting fungal taxa, *Candelabrochaete yunnanensis* and *Hyphodermella sinensis* are proposed based on a combination of the morphological features and molecular evidence. *Candelabrochaete yunnanensis* is characterized by the farinaceous basidiomata with the flesh-pinkish to brownish vinaceous hymenial surface, a monomitic hyphal system with simple-septate generative hyphae, presence of the cylindrical septocystidia and ellipsoid basidiospores (4–5 × 2.5–3 µm). *Hyphodermella sinensis* is characterized by the membranaceous basidiomata having the white to slightly greyish hymenial surface, a monomitic hyphal system with clamp generative hyphae, presence of the clavate cystidia and ellipsoid basidiospores (4–6 × 3–4 µm). The phylogenetic tree inferred from ITS+nLSU sequences revealed that *Candelabrochaete yunnanensis* was nested into the family Irpicaceae within the order Polyporales, in which it was closely related to the species *C. africana*; *Hyphodermella sinensis* grouped into the genus *Hyphodermella* and clustered into the family Phanerochaetaceae, in which it grouped with *H. aurantiaca* and *H. zixishanensis*.

Key words: Biodiversity, Classification, Molecular systematics, Wood-inhabiting fungi

Introduction

The Polyporales is a diverse group of Agaricomycetes and one of the most intensively studied clades of Fungi (Kirk *et al.* 2008, Binder *et al.* 2013, Zhao *et al.* 2015, Justo *et al.* 2017, Virágh *et al.* 2021, Liu *et al.* 2022, 2023a, 2023b). As major wood-inhabiting fungi, Polyporales are key players in the carbon cycle (Floudas *et al.* 2012, Tedersoo *et al.* 2014, James *et al.* 2020, Zhang *et al.* 2022). A great majority of Polyporales are the saprotrophic wood-inhabiting fungi, while a few are plant pathogens causing timber damage (Dai *et al.* 2012a, Binder *et al.* 2013, Hawksworth *et al.* 2017, Liu *et al.* 2022, Zhao *et al* 2023, Hussain *et al.* 2024). The enzymatic capabilities of the Polyporales are not only important for the biogeochemical cycles but also make them prime candidates for industrial applications including biomass conversion, mycoremediation, paper pulping and the production of biofuels (Binder *et al.* 2013, Hibbett *et al.* 2016). As the major wood-decaying fungi, the morphological and developmental diversity of fruiting bodies of Polyporales are of interest to both fungal ecologists and applied scientists (Dai *et al.* 2012b, Wu *et al.* 2018, He 2019, Guan & Zhao 2021, Chen *et al.* 2021, Hyde *et al.* 2023, Li *et al.* 2023b, Liu *et al.* 2023b).

The genus *Candelabrochaete* Boidin (1970: 24) belonged to the order Polyporales (Basidiomycota), typified by *C. africana* Boidin (1970: 24) (Burdsall 1984). *Candelabrochaete* is characterized by the short-celled, simple-septate generative hyphae and the multiseptate cystidia (Bernicchia & Górjon 2010). According to Index Fungorum (www.indexfungorum.org; accessed on 2 February 2024), the genus *Candelabrochaete* has 16 specific and registered names with 14 species been accepted worldwide (Justo *et al.* 2017, Chen *et al.* 2020, Chen *et al.* 2021, Li *et al.* 2023b). The genus *Hyphodermella* J. Erikss. & Ryvarden (1976: 579) belongs to the family Phanerochaetaceae (Polyporales, Basidiomycota) and typified by *H. corrugata* (Fr.) J. Erikss. & Ryvarden (1976: 579) (Duhem *et al.* 2011). The genus is

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characterized by the resupinate, crustose basidiomata and a monomitic hyphal structure with simple septa on generative hyphae, presence of encrusted hyphal ends, clavate to suburniform basidia, and ellipsoid to globose, smooth, thin-walled basidiospores (Wang & Zhao 2020). According to Index Fungorum (www.indexfungorum.org; accessed on 2 February 2024), the genus *Hyphodermella* has thirteen specific and registered names and currently twelve species have been accepted worldwide (Telleria *et al.* 2010, Floudas & Hibbett 2015, Zhao *et al.* 2017, Wang *et al.* 2021, Wang & Zhao 2021, Li *et al.* 2023b, Shen *et al.* 2023).

In recent studies, three species of *Candelabrochaete* formed two distinct lineages in the *Ceriporia*/ *Candelabrochaete* s.l./ *Leptoporus*/ *Phanerochaete allantospora* clade, which indicate that *Candelabrochaete* was polyphyletic, and their generic position remained unresolved since the type species *C. africana* was not nested within the phlebioid clade, and the results indicated that the complicated relationships among these taxa may require additional data (Justo *et al.* 2017, Chen *et al.* 2020, Chen *et al.* 2021, Li *et al.* 2022). Recently, molecular studies involving the phylogeny of the genus *Hyphodermella* based on single- or multi-gene datasets have been carried out and the phylogenetic positions of some species within *Hyphodermella* in Phanerochaetaceae (Polyporales, Basidiomycota) were rearranged (Telleria *et al.* 2010, Floudas & Hibbett 2015, Zhao *et al.* 2017, Wang *et al.* 2021, Wang & Zhao 2021, Li *et al.* 2023b). The research focused on the taxonomy of a small wood-inhabiting fungal genus *Hyphodermella*, with the most comprehensive sampling to date, and the phylogenetic position of *Hyphodermella* within the family Phanerochaetaceae was rearranged by employing the same ITS and nLSU regions as in previous study and also the ITS, nLSU, rpb1, rpb2 and tef1 regions, in which the result showed that many taxa were transferred into other genera (Shen *et al.* 2023).

During the surveys of the wood-inhabiting fungi, we collected two species from the order Polyporales from Yunnan Province, China., which were not consistent with any known species of the wood-inhabiting fungi. We presented the morphological characteristics and multi-genes molecular analyses with ITS and nLSU DNA markers that supported the taxonomy and phylogenetics of *Candelabrochaete* and *Hyphodermella* species.

Materials and methods

Morphological studies

Fresh fruiting bodies of fungi growing on angiosperm branches were collected from Qujing of Yunnan Province, P.R. China. Specimens were dried in an electric food dehydrator at 40 °C, then sealed and stored in an envelope bag and deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China. The macromorphological descriptions were based on field notes and photos captured in the field and lab. Colour terms follow Petersen (1996). The micromorphological data were obtained from the dried specimens when observed under a light microscope following Dai *et al*. (2015). The following abbreviations were used: KOH = 5% potassium hydroxide water solution, CB = Cotton Blue, CB– = acyanophilous, CB+ = cyanophilous, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid, L = mean spores length (arithmetic average for all spores), W = mean spores width (arithmetic average for all spores), 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), Qm = the average of Q (arithmetic average for all spores).

Molecular procedures 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 specimens according to the manufacturer's instructions (Zhao *et al.* 2023). The nuclear ribosomal of the internal transcribed spacer (ITS) region was amplified with the primer pair ITS5/ITS4 (White *et al.* 1990), the nuclear large subunit (nLSU) region with the primer pair LR0R/LR7 (Vilgalys & Hester 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 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, P.R. China). All of the newly generated sequences were deposited in GenBank (Table 1).

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

Species Name	**Sample No.**	**GenBank Accession No.**		**References**
		ITS	**nLSU**	
Bjerkandera adusta	HHB-12826	KP134983	KP135198	Floudas & Hibbett 2015
B. centroamericana	L-13104	KY948791	KY948855	Justo *et al.* 2017
Byssomerulius corium	FP-102382	KP135007	KP135230	Floudas & Hibbett 2015
B. corium	WEI 17-645	LC427006	LC427030	Chen *et al.* 2020
Candelabrochaete africana	FP-102987	KP135294	KP135199	Floudas & Hibbett 2015
C. guangdongensis	He 5902	MZ422527	MZ422499	Li *et al.* 2022
C. langloisi	FP-110343	KY948793	KY948886	Chen *et al.* 2021
C. septocystidia	FCUG 2027	MZ636933	MZ637097	Li *et al.* 2022
C. septocystidia	RLG-9759	MZ636934	GQ470631	Chen *et al.* 2021
C. yunnanensis	CLZhao 26027	OR658994	OR999391	**Present study**
Ceriporia arbuscula	GC 1708-338	LC427008	LC427040	Chen *et al.* 2020
C. mellita	GC 1508-71	LC427022	LC427044	Chen *et al.* 2020
C. viridans	GC 1708-211	LC427027	LC427049	Chen *et al.* 2020
Crepatura ellipsospora	CLZhao 1260	MK343693	MK343697	Ma & Zhao 2019
C. ellipsospora	CLZhao 1265	MK343692	MK343696	Ma & Zhao 2019
Crystallicutis rajchenbergii	MR-4310	KY948797	KY948888	Justo *et al.* 2017
C. serpens	HHB-15692	KP135031	KP135200	Floudas & Hibbett 2015
Cytidiella albida	GB 1833	KY948748	KY948889	Justo *et al.* 2017
C. albomarginata	He 5575	MZ422526	MZ422497	Li *et al.* 2022
Efibula americana	FP-102165	KP135016	KP135256	Floudas & Hibbett 2015
E. tropica	TNM:F33355	MZ636967	MZ637129	Chen *et al.* 2021
Gloeoporus orientalis	TNM:F31113	MZ636980	MZ637141	Chen *et al.* 2021
G. pannocinctus	L-15726	KP135060	KP135214	Floudas & Hibbett 2015
Hapalopilus eupatorii	Dammrich 10744	KX752620		Miettinen *et al.* 2016
H. rutilans	FP-102473	MZ636981	MZ637142	Chen *et al.* 2021
Hyphodermella aurantiaca	CLZhao 10487	MW209023	MW209012	Wang & Zhao 2021
H. aurantiaca	CLZhao 10500	MW209025	MW209014	Wang & Zhao 2021
H. corrugata	MA-Fungi 24238	FN600378	JN939586	Telleria *et al.* 2010
H. corrugata	MA-Fungi 5527	FN600372	JN939597	Telleria *et al.* 2010
H. laevigata	He 5427	ON964013	ON963996	Li *et al.* 2023b
H. laevigata	He 5430	ON964014	ON963997	Li *et al.* 2023b
H. poroides	Dai 10848	KX008368	KX011853	Zhao *et al.* 2017
H. poroides	Dai 12045	KX008367	KX011852	Zhao *et al.* 2017
H. rosae	FP-150552	KP134978	KP135223	Floudas & Hibbett 2015
H. rosae	TNM:F31698	MZ636986	MZ637147	Chen *et al.* 2021
H. sinensis	CLZhao 25866	OR658992	OR999388	**Present study**
H. sinensis	CLZhao 25922	OR658993	OR999389	**Present study**
H. tropica	He 3808	ON964010	ON963993	Li *et al.* 2023b
H. tropica	He 4004	ON964012	ON963995	Li *et al.* 2023b
H. zixishanensis	CLZhao 7159	MZ305278	MZ305287	Wang *et al.* 2021
H. zixishanensis	CLZhao 7204	MZ305279	MZ305288	Wang *et al.* 2021
Irpex alboflavescens	He 4719	MZ422501	MZ422472	Li *et al.* 2022
I. laceratus	TNM:F23945	MZ636990		Tian *et al.* 2022
I. rosea	CLZhao 18489	MW377574	MW377577	Wang & Zhao 2022
Leptoporus mollis	RLG-7163	KY948794	MZ637155	Justo *et al.* 2017
L. mollis	TJV-93-174T	KY948795		Justo *et al.* 2017
Meruliopsis leptocystidiata	Wu 1708-43	LC427013	LC427033	Chen *et al.* 2020

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TABLE 1 (Continued)

Species Name	**Sample No.**	**GenBank Accession No.**		**References**
		ITS	**nLSU**	
M. taxicola	GC 1704-60	LC427028	LC427050	Chen *et al.* 2020
Phaeophlebiopsis caribbeana	HHB-6990	KP135415		Floudas & Hibbett 2015
P. peniophoroides	FP-150577	KP135417		Floudas & Hibbett 2015
Phanerochaete albida	GC 1407-14	MZ422788	MZ637179	Floudas & Hibbett 2015
P. allantospora	KKN-111	KP135038	KP135238	Floudas & Hibbett 2015
P. arizonica	RLG-10248	KP135170	KP135239	Floudas & Hibbett 2015
Phanerochaete leptocystidiata	Dai 10468	MT235684	MT248167	Xu *et al.* 2020
Phlebiopsis friesii	He 5722	MT452528	MT447413	Zhao *et al.* 2021
P. gigantea	FP-70857	KP135390	KP135272	Floudas & Hibbett 2015
P. yunnanensis	CLZhao 3958	MH744140	MH744142	Zhao *et al.* 2019
Pirex concentricus	OSC-41587	KP134984	KP135275	Floudas & Hibbett 2015
Porostereum fulvum	LY:18491	MG649452	MG649454	Chen *et al.* 2021
P. spadiceum	TNM:F4022	MZ637062	MZ637263	Chen *et al.* 2021
Raduliporus aneirina	HHB-15629	KP135023	KP135207	Floudas & Hibbett 2015
R. aneirinus	Wu 0409-199	MZ637068		Chen *et al.* 2021
Resiniporus pseudogilvescens	Wu 1209-46	KY688203		Chen *et al.* 2021
R. resinascens	BRNM 710169	FJ496675		Tomšovský *et al.* 2010
Rhizochaete brunnea	MR11455	AY219389		Li *et al.* 2023b
R. fissurata	CLZhao 10407	MZ713642	MZ713846	Gu & Zhao 2021
R. grandinosa	CLZhao 3117	MZ713644	MZ713848	Gu & Zhao 2021
Russula begonia	HBAU15564	MZ573252	OQ077072	Li *et al.* 2023a
Terana caerulea	FP-104073	KP134980	KP135276	Floudas & Hibbett 2015
T. caerulea	TNM:F29079	MZ637090	MZ637287	Chen *et al.* 2021
Trametopsis aborigena	Robledo 1236	KY655336		Lopes *et al.* 2017
T. cervina	TJV-93-216T	JN165020	JN164796	Justo & Hibbett 2011

The sequences were aligned in MAFFT version 7 using the G-INS-i strategy (Katoh *et al.* 2019). The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The sequence alignments were deposited in TreeBase (ID 31308). The combined ITS and nLSU sequences and ITS datasets were used to infer the position of the two new species in the genus *Candelabrochaete* and *Hyphodermella* and related species. *Russula begonia* G.J. Li, T.Z. Liu & T.Z. Wei was assigned as an outgroup to root trees in the ITS+nLSU analysis (Figure 1) (Li *et al.* 2023a).

Maximum parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined datasets following a previous study (Zhao & Wu 2017), and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All of the characters were equally weighted, and gaps were treated as missing data. Using the heuristic search option with TBR branch swapping and 1000 random sequence additions, trees were inferred. Max trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics, 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 maximum parsimonious tree generated. The multiple sequence alignment was also analyzed using maximum likelihood (ML) in RAxML-HPC2 (Miller *et al.* 2012). 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 datasets for Bayesian inference (BI), which was performed using MrBayes 3.2.7a with a GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run twice from a random starting tree, for 2 million generations of the datasets (Figure 1) and the tree was sampled every 1000 generations. The first one fourth of all generations were discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received a maximum likelihood bootstrap value (BS) >70%, maximum parsimony bootstrap value (BT) >70% or Bayesian posterior probabilities (BPP) >0.95.

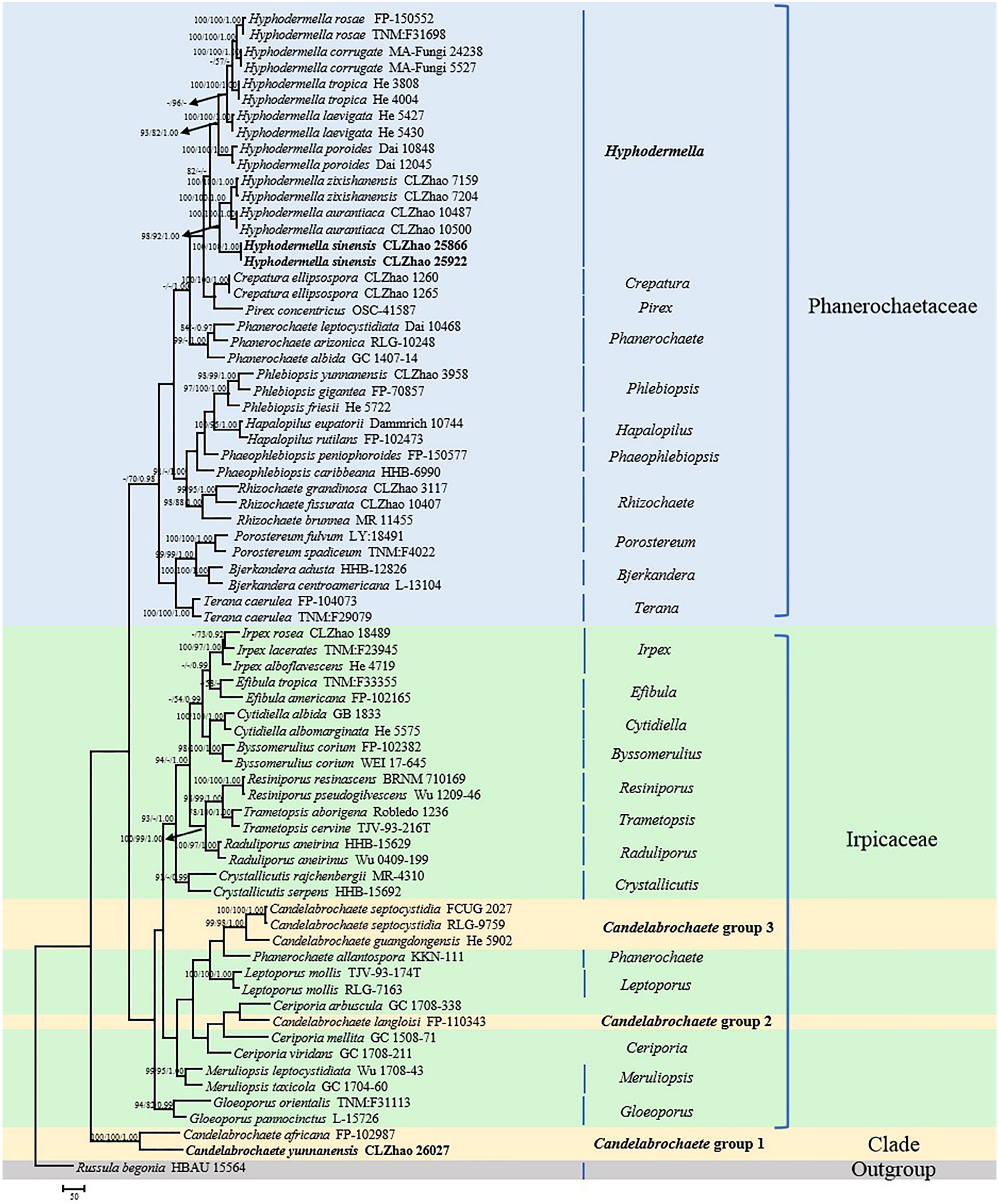

FIGURE 1. Maximum parsimony strict consensus tree illustrating the phylogeny of two new species and related species in Phanerochaetaceae and Irpicaceae within Polyporales based on ITS+nLSU se-quences. The branch is labeled with a maximum likelihood lead value greater than 70%, a reduced lead value greater than 50% and a Bayesian posterior probability greater than 0.95. The new species are in bold.

Results

Phylogenetic analyses

The dataset based on ITS+nLSU (Figure 1) comprises sequences from 71 fungal specimens representing 59 species. The dataset had an aligned length of 2362 characters, of which 1424 characters are constant, 332 are variable and parsimony-uninformative, and 606 are parsimony-informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 4563, CI = 0.3364, HI = 0.6636, RI = 0.5502, RC = 0.1851). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.008061 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 299. The phylogenetic tree (Figure 1) inferred from ITS and nLSU sequences revealed that *Candelabrochaete yunnanensis* was nested into the family Irpicaceae, and the genus *Candelabrochaete* is polyphyletic. *Hyphodermella sinensis* grouped into genus *Hyphodermella* and clustered into the family Phanerochaetaceae, in which *H. sinensis* was sister to *H. aurantiaca* C.L. Zhao and *H. zixishanensis* C.L. Zhao (Figure 1).

Taxonomy

Candelabrochaete yunnanensis L. Wang & C.L. Zhao, *sp. nov.* Figs. 2 and 3.
MycoBank no.: 851547

***Etymology*:**—*yunnanensis* (Lat.): refers to the locality (Yunnan Province) of the type specimen.

***Holotype*:**—CHINA. Yunnan Province, Qujing, Qilin District, Cuishan Forest Park, GPS coordinates: 25°55′ N, 103°69′ E, altitude: 2245 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 24 November 2022, CLZhao 26027 (SWFC).

***Basidiomata*:**—Annual, resupinate, closely adnate, farinaceous, up to 12 cm long, 5 cm wide and 0.3 mm thick. Hymenial surface smooth, flesh-pinkish to brownish vinaceous when fresh, become pinkish buff to buff when dry. Sterile margin thinning, adnate, pinkish buff to buff, up to 1 mm.

***Hyphal system*:**—Monomitic; generative hyphae simple-septate, colorless, distinctly thick-walled, usually branched at a right angle, interwoven, 3.5–6 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

***Hymenium*:**—Septocystidia abundant, cylindrical, slightly sinuous, frequently septate, colorless, thick-walled, arising from the subiculum, mostly embedded, 80–105 × 7–9 µm. Basidia barreled, colorless, thin-walled, encrusted with crystals, with a basal simple septum and four sterigmata, 16–18 × 4.5–5.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller.

***Spores*:**—Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, 4–5 × 2.5–3(–4) µm, L = 4.84 µm, W = 3.18 µm, Q = 1.53 (n = 30/1).

Hyphodermella sinensis L. Wang & C.L. Zhao, *sp. nov.* Figs. 4 and 5.
MycoBank no.: 851548.

***Etymology*:**—*sinensis* (Lat.): refers to the locality (China) of the type specimen.

***Holotype*:**—CHINA. Yunnan Province, Qujing, Qilin District, Cuishan Forest Park, GPS coordinates: 25°55′ N, 103°69′ E, altitude: 2245 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 27 October 2022, CLZhao 25866 (SWFC).

***Basidiomata*:**—Annual, resupinate, adnate, membranaceous, and up to 10 cm long, 4 cm wide and 0.1 mm thick. Hymenial surface smooth, white to slightly greyish when fresh, become greyish to honey yellow when dry. Sterile margin indistinct, white to slightly greyish, up to 1 mm.

***Hyphal system*:**—Monomitic; generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 3–4.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

***Hymenium*:**—Cystidia clavate, colorless, thin-walled, 18–30 × 2–3 µm. Basidia clavate, colorless, thin-walled, with a basal clamp connection and four sterigmata, 14.5–16 × 3–4 µm; basidioles dominant, in shape similar to basidia, but slightly smaller.

***Spores*:**—Basidiospores broadly ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, 4–6(–6.5) × (2.5–)3–4 µm, L = 5.24 µm, W = 3.63 µm, Q = 1.32–1.44 (n = 90/3).

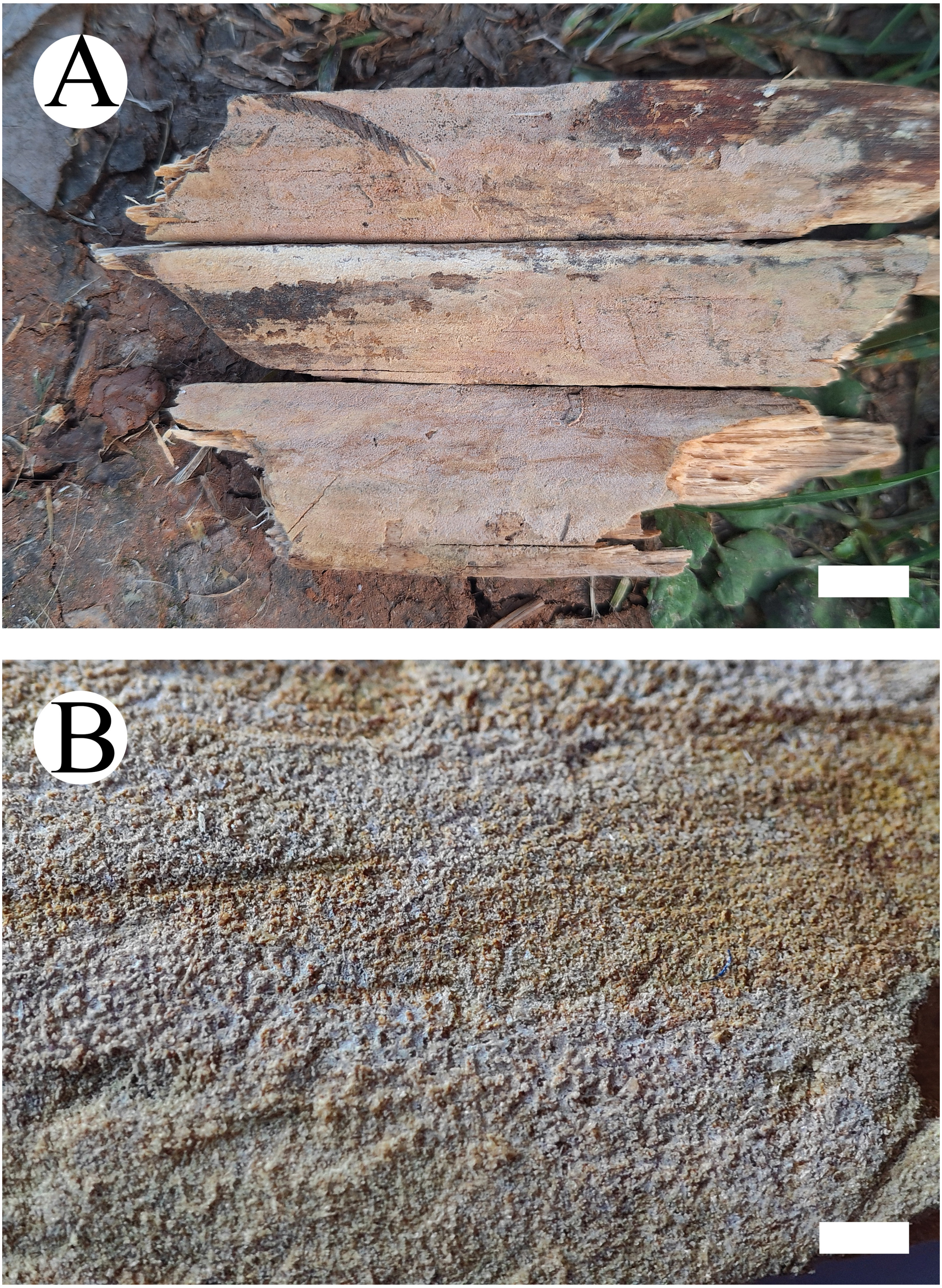

FIGURE 2. *Candelabrochaete yunnanensis* (holotype, CLZhao 26027): basidiomata on the substrate (A), macroscopic characteristics of hymenophore (B). Bars: (A) = 1 cm and (B) = 1 mm.

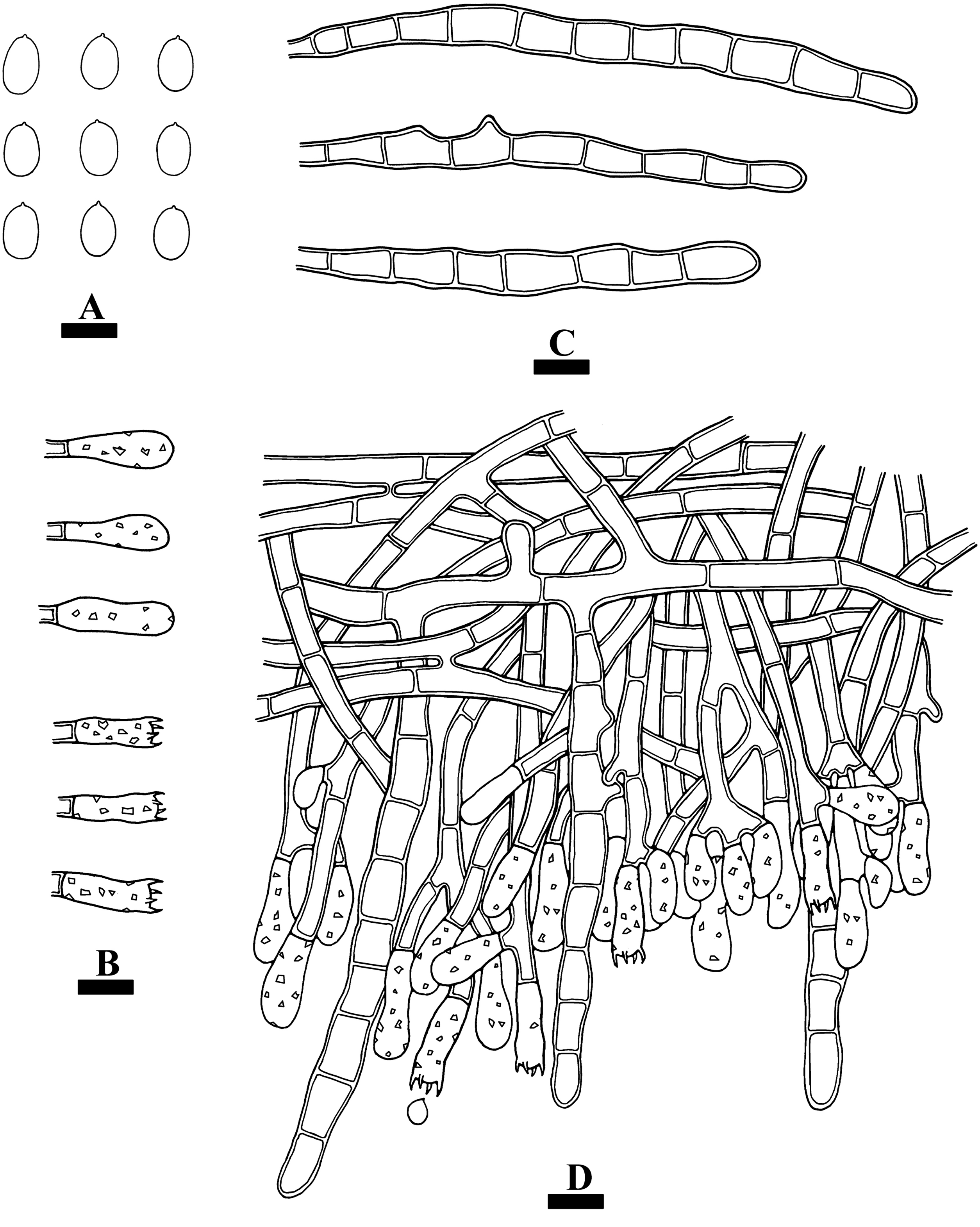

FIGURE 3. Microscopic structures of *Candelabrochaete yunnanensis* (holotype, CLZhao 26027): basidiospores (A), basidia and basidioles (B), cystidia (C), a section of the hymenium (D). Bars: A= 5 µm, (B–D) = 10 µm.

***Additional specimens examined*:**—CHINA. Yunnan Province, Wenshan, Xichou County, Dongma Town, Xinzhai Village, GPS coordinates: 23°45′ N, 104°90′ E, altitude: 1205 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 16 January 2019, CLZhao 11267; Qujing, Qilin District, Cuishan Forest Park, GPS coordinates: 25°55′ N, 103°69′ E, altitude: 2245 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 27 October 2022, CLZhao 25922 (SWFC).

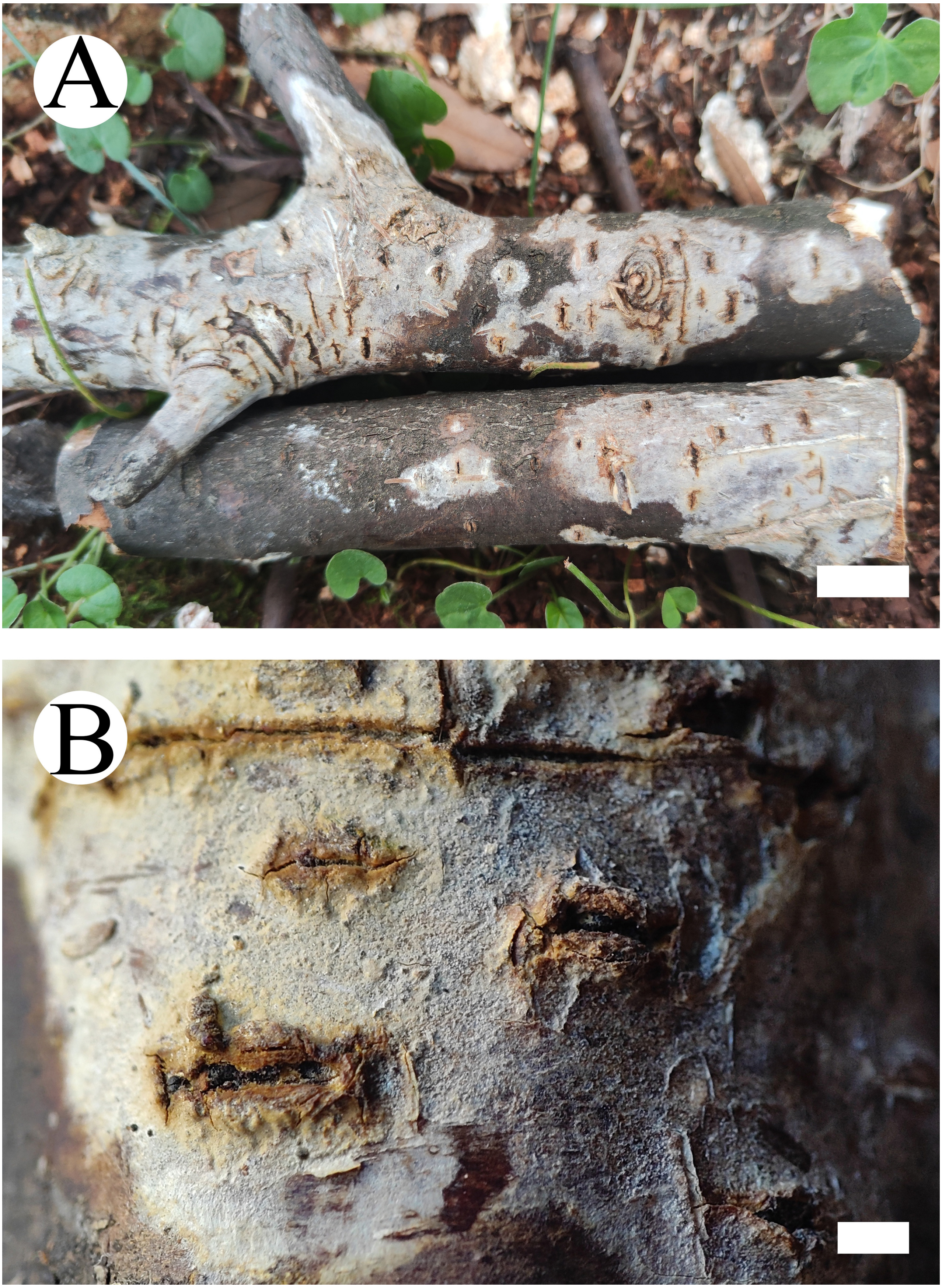

FIGURE 4. *Hyphodermella sinensis* (holotype, CLZhao 25866): basidiomata on the substrate (A), macroscopic characteristics of hymenophore (B). Bars: (A) = 1 cm and (B) = 1 mm.

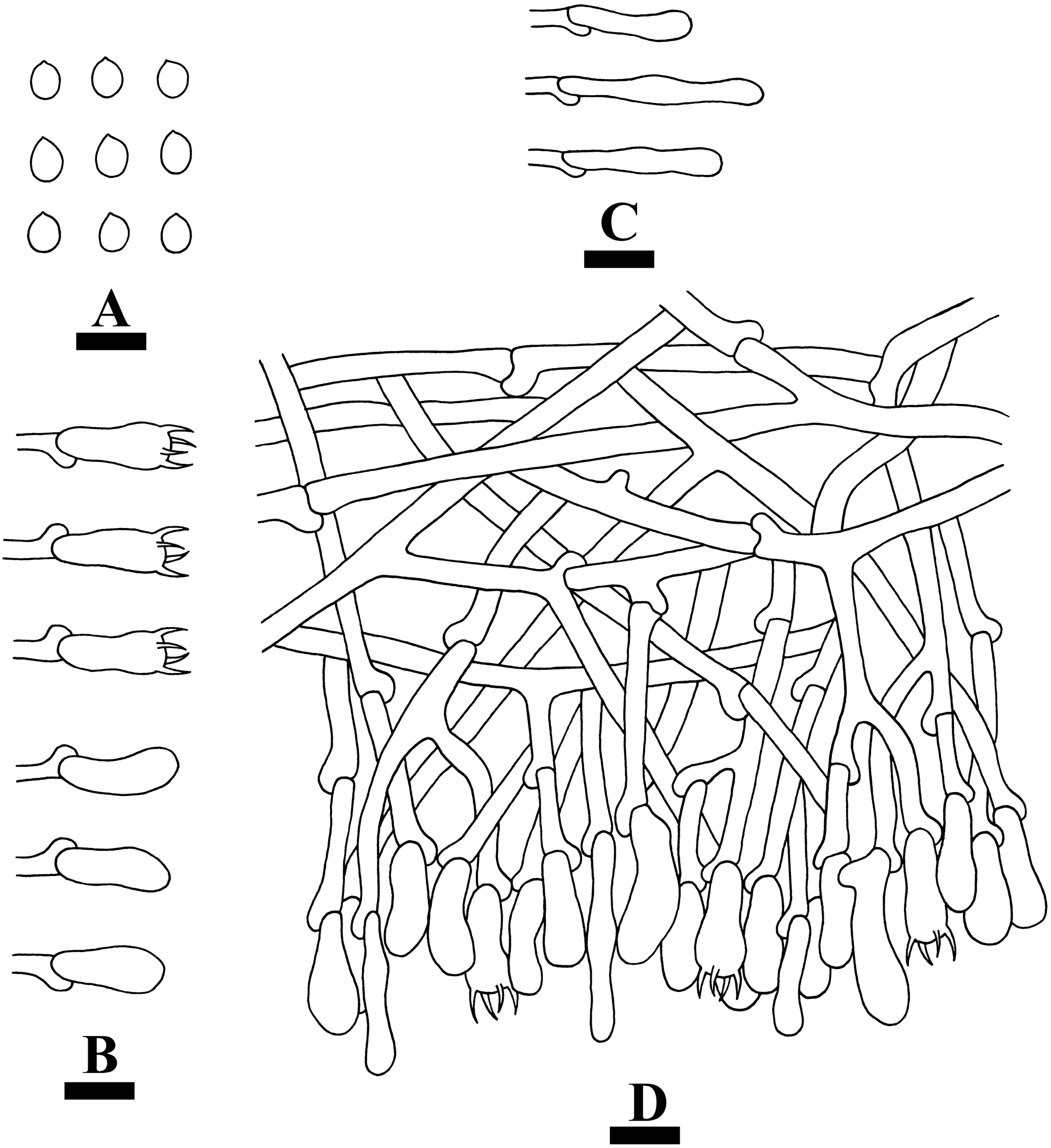

FIGURE 5. Microscopic structures of *Hyphodermella sinensis* (holotype, CLZhao 25866): basidiospores (A), basidia and basidioles (B), cystidia (C), a section of the hymenium (D). Bars: (A–D) = 10 µm.

Discussion

In the phylogenetic tree (Figure 1), *Candelabrochaete yunnanensis* is closely related to *C. africana.* However, *C. africana* is distinguished from *C. yunnanensis* by having the thin-walled generative hyphae and narrower basidia (12–18 × 3–4.5 µm) and its longer septocystidia (70–140 × 8–12 µm) (Boidin 1970). *Hyphodermella sinensis* is grouped with *H. aurantiaca* and *H. zixishanensis.* However, *H. aurantiaca* differs from *H. sinensis* by having the ceraceous hymenophore with orange to rose hymenial surface, smaller basidiospores (3–4 × 2–2.8 µm), and its simple-septate generative hyphae (Wang & Zhao 2021); *H. zixishanensis* is separated from *H. sinensis* by the tuberculate hymenophore with the reddish to brown hymenial surface, longer basidia (17.5–27 × 3–5.5 µm), its simple-septate generative hyphae and smaller basidiospores (3.7–5.8 × 2.6–4.0 µm) (Wang & Zhao 2021).

Morphologically, *Candelabrochaete guangdongensis* Yue Li & S.H. He, *C. neocaledonica* Duhem & Buyck and *C. septocystidia* (Burt) Burds. are similar to *C. yunnanensis* by having the large septocystidia. However, *C. guangdongensis* differs from *C. yunnanensis* by having the ceraceous hymenophore with orange to reddish orange hymenial surface and longer cystidia (145–190 × 6–10 µm) (Li *et al.* 2022); *C. neocaledonica* is distinct from *C. yunnanensis* by having the distinctly hydnoid hymenophore and allantoid basidiospores (Duhem & Buyck 2011); *C. septocystidia* is separated from *C. yunnanensis* by having the distinctly encrusted septocystidia and allantoid, narrower basidiospores (4.5–6.5 × 1.5–2 µm) (Burdsall 1984). *Hyphodermella laevigata* Yue Li & S.H. He, *H. poroides* Y.C. Dai & C.L. Zhao, *H. rosae* (Bres.) Nakasone and *H. tropica* Yue Li & S.H. He are similar to *H. sinensis* by having the ellipsoid, thin-walled, smooth basidiospores (Zhao *et al.* 2017, Li *et al.* 2022). However, *H. laevigata* differs in *H. sinensis* by having the pale yellow to grayish yellow hymenial surface and simple-septate generative hyphae (Li *et al.* 2022); *H. poroides* differs from *H. sinensis* by having the ceraceous to crustaceous hymenophore with cream to orange hymenial surface and thick-walled, simple-septate generative hyphae (Zhao *et al.* 2017); *H. rosae* is separated from *H. sinensis* by having the subceraceous to crustaceous hymenophore with odontoid hymenial surface and larger basidia (24–35 × 6–8 µm); *H. tropica* is distinct from *H. sinensis* by having the grandinioid hymenophore with grayish orange to brownish orange hymenial surface and wider crystal cystidia (20–50 × 6–10 µm) (Li *et al.* 2022).

The estimation of fungal species ranges from 1 to 11 million, depending on the criteria employed by various researchers (Hyde *et al.* 2020). The researches of fungal species numbers are still ongoing, and the value of fungi is, however, indisputable with both beneficial and negative impacts (Hyde *et al.* 2023). Our focusing on two species *Candelabrochaete yunnanensis* and *Hyphodermella sinensis* are new to science, which enrich the fungal diversity, and both taxa were found in Yunnan Province, southwest China, which is a hotspot for biodiversity, and more new taxa have been discovered in here by mycologists in the recent years (Dong *et al.* 2022, 2023, Yang *et al.* 2023a, 2023b, Yuan *et al.* 2023, Zhang *et al.* 2024).

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References

Bernicchia, A. & Gorjón, S.P. (2010) Corticiaceae s.l. *In: Fungi Europaei* 12. Ed. Candusso. Italia.

Binder, M., Justo, A., Riley, R., Salamov, A., Lopez-Giraldez, F., Sjökvist, E., Copeland, A., Foster, B., Sun, H., Larsson, E., Larsson, K.H., Townsend, J.P., Grigoriev, I.V. & Hibbett, D. (2013) Phylogenetic and phylogenomic overview of the Polyporales. *Mycologia* 105: 1350–1373.
https://doi.org/10.3852/13-003

Boidin, J. (1970) Basidiomycètes Corticiaceae de la République Centrafricaine. II. — Les genres Botryobasidium Donk et *Candelabrochaete* nov. gen. *Cahiers de la Maboké* 8: 17–25.

Burdsall, H.H. (1984) The genus *Candelabrochaete* (Corticiaceae) in North America and a note on *Peniophora mexicana*. *Mycotaxon* 19: 389–395.

Chen, C.C., Chen, C.Y., Lim, Y.W. & Wu, S.H. (2020) Phylogeny and taxonomy of *Ceriporia* and other related taxa and description of three new species. *Mycologia* 112: 64–82.
https://doi.org/10.1080/00275514.2019.1664097

Chen, C.C., Chen, C.Y. & Wu, S.H. (2021) Species diversity, taxonomy and multi-gene phylogeny of phlebioid clade (Phanerochaetaceae, Irpicaceae, Meruliaceae) of Polyporales. *Fungal Diversity* 111: 337–442.
https://doi.org/10.1007/s13225-021-00490-w

Dai, Y.C. (2012a) Pathogenic wood-decaying fungi on woody plants in China. *Mycosystema* 31: 493–509.

Dai, Y.C. (2012b) Polypore diversity in China with an annotated checklist of Chinese polypores. *Mycoscience* 53: 49–80.
https://doi.org/10.1007/s10267-011-0134-3

Dai, Y.C., Cui, B.K., Si, J., He, S.H., Hyde, K.D., Yuan, H.S. & Liu, X.Y. (2015) Dynamics of the worldwide number of fungi with emphasis on fungal diversity in China. *Mycological Progress* 14: 1–9. https://doi.org/10.1007/s11557-015-1084-5

Duhem, B. & Buyck, B. (2011) *Hyphodermella brunneocontexta* sp. nov. de l'île de Mayotte (France) (Basidiomycota, Polyporales). *Cryptogamie Mycologie* 32: 413–420. https://doi.org/10.7872/crym.v32.iss4.2011.413

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

Floudas, D., Binder, M., Riley, R., Barry, K., Blanchette, R.A., Henrissat, B., Martínez, A.T., Otillar, R., Spatafora, J.W., Yadav, J.S., Aerts, A., Benoit, I., Boyd, A., Carlson, A., Copeland, A., Coutinho, P.M., De Vries, R.P., Ferreira, P., Findley, K., Foster, B., Gaskell, J., Glotzer, D., Górecki, P., Heitman, J., Hesse, C., Hori, C., Igarashi, K., Jurgens, J.A., Kallen, N., Kersten, P., Kohler, A., Kües, U., Kumar, T.K.A., Kuo, A., Labutti, K., Larrondo, L.F., Lindquist, E., Ling, A., Lombard, V., Lucas, S., Lundell, T., Martin, R., McLaughlin, D.J., Morgenstern, I., Morin, E., Murat, C., Nagy, L.G., Nolan, M., Ohm, R.A., Patyshakuliyeva, A., Rokas, A., Ruiz-Dueñas, F.J., Sabat, G., Salamov, A., Samejima, M., Schmutz, J., Slot, J.C., St. John, F., Stenlid, J., Sun, H., Sun, S., Syed, K., Tsang, A., Wiebenga, A., Young, D., Pisabarro, A., Eastwood, D.C., Martin, F., Cullen, D., Grigoriev, I.V. & Hibbett, D.S. (2012) The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. *Science* 336: 1715–1719. https://doi.org/10.1126/science.1221748

Floudas, D. & Hibbett, D.S. (2015) Revisiting the taxonomy of *Phanerochaete* (Polyporales, Basidiomycota) using a four gene dataset and extensive ITS sampling. *Fungal Biology* 119: 679–719. https://doi.org/10.1016/j.funbio.2015.04.003

Gu, Z.R. & Zhao, C.L. (2021) The hidden wood-decaying fungal diversity: *Rhizochaete* from East Asia. *Diversity* 13: 503. https://doi.org/10.3390/d13100503

Guan, Q.X. & Zhao, C.L. (2021) Taxonomy and phylogeny of the wood-inhabiting fungal genus *Hyphoderma* with descriptions of three new species from East Asia. *Journal of Fungi* 7: 308. https://doi.org/10.3390/jof7040308

Hawksworth, D.L. & Lücking, R. (2017) Fungal diversity revisited: 2.2 to 3.8 million species. *Microbiology Spectrum* 5. https://doi.org/10.1128/9781555819583.ch4

Hibbett, D., Abarenkov, K., Kõljalg, U., Öpik, M., Chai, B., Cole, J., Wang, Q., Crous, P., Robert, V., Helgason, T., Herr, J.R., Kirk, P., Lueschow, S., O'Donnell, K., Nilsson, R.H., Oono, R., Schoch, C., Smyth, C., Walker, D.M., Porras-Alfaro, A., Taylor, J.W. & Geiser, D.M. (2016) Sequence-based classification and identification of Fungi. *Mycologia* 108: 1049–1068. https://doi.org/10.3852/16-130

Hussain, S., Nisar, M. & Sher, H. (2024) Taxonomic study and diversity of *Postia* s.lat. in Swat, Pakistan: addition of five brown rot Polypores to the country. Arch Microbiology 206: 66. https://doi.org/10.1007/s00203-023-03795-3

Hyde, K.D., Abdel-Wahab, M.A., Abdollahzadeh, J., Abeywickrama, P.D., Absalan, S., Afshari, N., Ainsworth, A.M., Akulov, O.Y., Aleoshin, V.V., Al-Sadi, A.M., Alvarado, P., Alves, A., Alves-Silva, G., Amalfi, M., Amira, Y., Amuhenage, T.B., Anderson, J., Antonín, V., Aouali, S., Aptroot, A., Apurillo, C.C.S., Araújo, J.P.M., Ariyawansa, H.A., Armand, A., Arumugam, E., Asghari, R., Assis, D.M.A., Atienza, V., Avasthi, S., Azevedo, E., Bahkali, A.H., Bakhshi, M., Banihashemi, Z., Bao, D.F., Baral, H.O., Barata, M., Barbosa, F., Barbosa, R.N., Barreto, R.W., Baschien, C., Belamesiatseva, D.B., Bennett, R.M., Bera, I., Bezerra, J.D.P., Bezerra, J.L., Bhat, D.J., Bhunjun, C.S., Bianchinotti, M.V., Błaszkowski, J., Blondelle, A., Boekhout, T., Bonito, G., Boonmee, S., Boonyuen, N., Bregant, C., Buchanan, P., Bundhun, D., Burgaud, G., Burgess, T., Buyck, B., Cabarroi-Hernández, M., Cáceres, M.E.S., Caeiro, M.F., Cai, L., Cai, M.F., Calabon, M.S., Calaça, F.J.S., Callalli, M., Camara, M.P.S., Cano-Lira, J.F., Cantillo, T., Cao, B., Carlavilla, J.R., Carvalho, A., Castañeda-Ruiz, R.F., Castlebury, L., Castro-Jauregui, O., Catania, M.D.V., Cavalcanti, L.H., Cazabonne, J., Cedeño-Sanchez, M.L., Chaharmiri-Dokhaharani, S., Chaiwan, N., Chakraborty, N., Chaverri, P., Cheewangkoon, R., Chen, C., Chen, C.Y., Chen, K.H., Chen, J., Chen, Q., Chen, W.H., Chen, Y.P., Chethana, K.W.T., Coleine, C., Condé, T.O., Corazon-Guivin, M.A., Cortés-Pérez, A., Costa-Rezende, D.H., Courtecuisse, R., Crouch, J.A., Crous, P.W., Cui, B.K., Cui, Y.Y., da Silva, D.K.A., da Silva, G.A., da Silva, I.R., da Silva, R.M.F., da Silva Santos, A.C., Dai, D.Q., Dai, Y.C., Damm, U., Darmostuk, V., Daroodi, Z., Das, K., Das, K., Davoodian, N., Davydov, E.A., Dayarathne, M.C., Decock, C., de Groot, M.D., De Kesel, A., dela Cruz, T.E.E., De Lange, R., Delgado, G., Denchev, C.M., Denchev, T.T., de Oliveira, N.T., de Silva, N.I., de Souza, F.A., Dentinger, B., Devadatha, B., Dianese, J.C., Dima, B., Diniz, A.G., Dissanayake, A.J., Dissanayake, L.S., Doğan, H.H., Doilom, M., Dolatabadi, S., Dong, W., Dong, Z.Y., Dos Santos, L.A., Drechsler-Santos, E.R., Du, T.Y., Dubey, M.K., Dutta, A.K., Egidi, E., Elliott, T.F., Elshahed, M.S., Erdoğdu, M., Ertz, D., Etayo, J., Evans, H.C., Fan, X.L., Fan, Y.G., Fedosova, A.G., Fell, J., Fernandes, I., Firmino, A.L., Fiuza, P.O., Flakus, A., Fragoso de Souza, C.A., Frisvad, J.C., Fryar, S.C., Gabaldón, T., Gajanayake, A.J., Galindo, L.J., Gannibal, P.B., García, D., García-Sandoval, S.R., Garrido-Benavent, I., Garzoli, L., Gautam, A.K., Ge, Z.W., Gené, D.J., Gentekaki, E., Ghobad-Nejhad, M., Giachini, A.J., Gibertoni, T.B., Góes-Neto, A., Gomdola, D., Gomes de Farias, A.R., Gorjón, S.P., Goto, B.T., Granados-Montero, M., Griffith,

G.W., Groenewald, J.Z., Groenewald, M., Grossart, H.P., Gueidan, C., Gunarathne, A., Gunaseelan, S., Gusmão, L.F.P., Gutierrez, A.C., Guzmán-Dávalos, L., Haelewaters, D., Halling, R., Han, Y.F., Hapuarachchi, K.K., Harder, C.B., Harrington, T.C., Hattori, T., He, M.Q., He, S., He, S.H., Healy, R., Herández-Restrepo, M., Heredia, G., Hodge, K.T., Holgado-Rojas, M.E., Hongsanan, S., Horak, E., Hosoya, T., Houbraken, J., Huang, S.K., Huanraluek, N., Hur, J.S., Hurdeal, V.G., Hustad, V.P., Iotti, M., Iturriaga, T., Jafar, E., Janik, P., Jayalal, R.G.U., Jayasiri, S.C., Jayawardena, R.S., Jeewon, R., Jerônimo, G.H., Jesus, A.L., Jin, J., Johnston, P.R., Jones, E.B.G., Joshi, Y., Justo, A., Kaishian, P., Kakishima, M., Kaliyaperumal, M., Kang, G.P., Kang, J.C., Karimi, O., Karpov, S.A., Karunarathna, S.C., Kaufmann, M., Kemler, M., Kezo, K., Khyaju, S., Kirchmair, M., Kirk, P.M., Kitaura, M.J., Klawonn, I., Kolarik, M., Kong, A., Kuhar, F., Kukwa, M., Kumar, S., Kušan, I., Lado, C., Larsson, K.H., Latha, K.P.D., Lee, H.B., Leonardi, M., Leontyev, D.L., Lestari, A.S., Li, C.J.Y., Li, D.W., Li, H., Li, H.Y., Li, L., Li, Q.R., Li, W.L., Li, Y., Li, Y.C., Liao, C.F., Liimatainen, K., Lim, Y.W., Lin, C.G., Linaldeddu, B.T., Linde, C.C., Linn, M.M., Liu, F., Liu, J.K., Liu, N.G., Liu, S., Liu, S.L., Liu, X.F., Liu, X.Z., Liu, Z.B., Lu, L., Lu, Y.Z., Luangharn, T., Luangsaard, J.J., Lumbsch, H.T., Lumyong, S., Luo, L., Luo, M., Luo, Z.L., Ma, J., Machado, A.R., Madagammana, A.D., Madrid, H., Magurno, F., Magyar, D., Mahadevan, N., Maharachchikumbura, S.S.N., Maimaiti, Y., Malosso, E., Manamgoda, D.S., Manawasinghe, I.S., Mapook, A., Marasinghe, D.S., Mardones, M., Marin-Felix, Y., Márquez, R., Masigol, H., Matočec, N., May, T., McKenzie, E.H.C., Meiras-Ottoni, A., Melo, R.F.R., Mendes, A.R.L., Mendieta, S., Meng, Q.F., Menkis, A., Menolli, N. Jr., Mešić, A., Meza Calvo, J.G., Mikhailov, K.V., Miller, S.L., Moncada, B., Moncalvo, J.M., Monteiro, J.S., Monteiro, M., Mora-Montes, H.M., Moreau, P.A., Mueller, G.M., Mukhopadhyay, S., Murugadoss, R., Nagy, L.G., Najafiniya, M., Nanayakkara, C.M., Nascimento, C.C., Nei, Y., Neves, M.A., Neuhauser, S., Niego, A.G.T., Nilsson, R.H., Niskanen, T., Niveiro, N., Noorabadi, M.T., Noordeloos, M.E., Norphanphoun, C., Núñez Otaño, N.B., O'Donnell, R.P., Oehl, F., Olariaga, I., Orlando, F.P., Pang, K.L., Papp, V., Pawłowska, J., Peintner, U., Pem, D., Pereira, O.L., Perera, R.H., Perez-Moreno, J., Perez-Ortega, S., Péter, G., Phillips, A.J.L., Phonemany, M., Phukhamsakda, C., Phutthacharoen, K., Piepenbring, M., Pires-Zottarelli, C.L.A., Poinar, G., Pošta, A., Prieto, M., Promputtha, I., Quandt, C.A., Radek, R., Rahnama, K., Raj, K.N.A., Rajeshkumar, K.C., Rämä, T., Rambold, G., Ramírez-Cruz, V., Rasconi, S., Rathnayaka, A.R., Raza, M., Ren, G.C., Robledo, G.L., Rodriguez-Flakus, P., Ronikier, A., Rossi, W., Ryberg, M., Ryvarden, L.R., Salvador-Montoya, C.A., Samant, B., Samarakoon, B.C., Samarakoon, M.C., Sánchez-Castro, I., Sánchez-García, M., Sandoval-Denis, M., Santiago, A.L.C.M.A., Santamaria, B., Santos, A.C.S., Sarma, V.V., Savchenko, A., Savchenko, K., Saxena, R.K., Scholler, M., Schoutteten, N., Seifollahi, E., Selbmann, L., Selcuk, F., Senanayake, I.C., Shabashova, T.G., Shen, H.W., Shen, Y.M., Silva-Filho, A.G.S., Simmons, D.R., Singh, R., Sir, E.B., Song, C.G., Souza-Motta, C.M. Sruthi, O.P., Stadler, M., Stchigel, A.M., Stemler, J., Stephenson, S.L., Strassert, J.F.H., Su, H.L., Su, L., Suetrong, S., Sulistyo, B., Sun, Y.F., Sun, Y.R., Svantesson, S., Sysouphanthong, P., Takamatsu, S., Tan, T.H., Tanaka, K., Tang, A.M.C., Tang, X., Tanney, J.B., Tavakol, N.M., Taylor, J.E., Taylor, P.W.J., Tedersoo, L., Tennakoon, D.S., Thamodini, G.K., Thines, M., Thiyagaraja, V., Thongklang, N., Tiago, P.V., Tian, Q., Tian, W.H., Tibell, L., Tibell, S., Tibpromma, S., Tkalčec, Z., Tomšovský, M., Toome-Heller, M., Torruella, G., Tsurykau, A., Udayanga, D., Ulukapi, M., Untereiner, W.A., Uzunov, B.A., Valle, L.G., Van Caenegem, W., Van den Wyngaert, S., Van Vooren, N., Velez, P., Verma, R.K., Vieira, L.C., Vieira, W.A.S., Vizzini, A., Walker, A., Walker, A.K., Wanasinghe, D.N., Wang, C.G., Wang, K., Wang, S.X., Wang, X.Y., Wang, Y., Wannasawang, F., Wartchow, F., Wei, D.P., Wei, X.L., White, J.F., Wijayawardene, N.N., Wijesinghe, S.N., Wijesundara, D.S.A., Wisitrassameewong, K., Worthy, F.R., Wu, F., Wu, G., Wu, H.X., Wu, N., Wu, W.P., Wurzbacher, C., Xiao, Y.P., Xiong, Y.R., Xu, L.J., Xu, R., Xu, R.F., Xu, R.J., Xu, T.M., Yakovchenko, L.S., Yan, J.Y., Yang, H., Yang, J., Yang, Z.L., Yang, Y.H., Yapa, N., Yasanthika, E., Youssef, N.H., Yu, F.M., Yu, Q., Yu, X.D., Yu, Y.X., Yu, Z.F., Yuan, H.S., Yuan, Y., Yurkov, A., Zafari, D., Zamora, J.C., Zare, R., Zeng, M., Zeng, N.K., Zeng, X.Y., Zhang, F., Zhang, H., Zhang, J.F., Zhang, J.Y., Zhang, Q.Y., Zhang, S.N., Zhang, W., Zhang, Y., Zhang, Y.X., Zhao, C.L., Zhao, H., Zhao, Q., Zhao, R.L., Zhou, L.W., Zhou, M., Zhurbenko, M.P., Zin, H.H. & Zucconi, L. (2023) Global consortium for the classification of fungi and fungus-like taxa. *Mycosphere* 14: 1960–2012.
https://doi.org/10.5943/mycosphere/14/1/23

Hyde, K.D., de Silva, N.I., Jeewon, R., Bhat, D.J., Phookamsak, R., Doilom, M., Boonmee, S., Jayawardena, R.S., Maharachchikumbura, S.S.N., Senanayake, I.C., Manawasinghe, I.S., Liu, N.G., Abeywickrama, P.D., Chaiwan, N., Karunarathna, A., Pem, D., Lin, C.G., Sysouphanthong, P., Luo, Z.L., Wei, D.P., Wanasinghe, D.N., Norphanphoun, C., Tennakoon, D.S., Samarakoon, M.C., Jayasiri, S.C., Jiang, H.B., Zeng, X.Y., Li, J.F., Wijesinghe, S.N., Devadatha, B., Goonasekara, I.D., Brahmanage, R.S., Yang, E.F., Aluthmuhandiram, J.V.S., Dayarathne, M.C., Marasinghe, D.S., Li, W.J., Dissanayake, L.S., Dong, W., Huanraluek, N., Lumyong, S., Liu, J.K., Karunarathna, S.C., Jones, E.B.G., Al-Sadi, A.M., Xu, J.C., Harishchandra, D., Sarma, V.V. & Bulgakov, T.S. (2020) AJOM new records and collections of fungi: 1–100. *Asian Journal of Mycology* 3: 22–294.
https://doi.org/10.5943/ajom/3/1/3

James, T.Y., Stajich, J.E., Hittinger, C.T. & Rokas, A. (2020) Toward a fully resolved fungal tree of life. *Annual Review of Microbiology* 74: 291–313.
https://doi.org/10.1146/annurev-micro-022020-051835

Justo, A. & Hibbett, D.S. (2011) Phylogenetic classifification of *Trametes* (Basidiomycota, Polyporales) based on a fifive-marker dataset. *Taxon* 60: 1567–1583.

https://doi.org/10.1002/tax.606003

Justo, A., Miettinen, O., Floudas, D., Ortiz-Santana, B., Sjökvist, E., Lindner, D., Nakasone, K., Niemelä, T., Larsson, K.H., Ryvarden, L. & Hibbett, D. (2017) A revised family-level classification of the Polyporales (Basidiomycota). *Fungal Biology* 121: 798–824. https://doi.org/10.1016/j.funbio.2017.05.010

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

Kirk, P.M., Cannon, P.F., Minter, D.W. & Stalpers, J.A. (2008) *Dictionary of the Fungi* CABI. Wallingford, UK.

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

Li, G.J., Liu, T.Z., Li, S.M., Zhao, S.Y., Niu, C.Y., Liu, Z.Z., Xie, X.J., Zhang, X., Shi, L.Y., Guo, Y.B., Wang, K., Cao, B., Zhao, R.L., Li, M., Deng, C.Y. & Wei, T.Z. (2023a) Four new species of *Russula* subsection *Sardoninae* from China. *Journal of Fungi* 9: 199. https://doi.org/10.3390/jof9020199

Li, Y., Chen, C.C. & He, S.H. (2023b) New corticioid taxa in Phanerochaetaceae (Polyporales, Basidiomycota) from East Asia. *Frontiers in Microbiology* 14: 1093096. https://doi.org/10.3389/fmicb.2023.1093096

Li, Y., He, S.H., Chen, C.C., Nakasone, K.K. & Ma, H.X. (2022) Global taxonomy and phylogeny of Irpicaceae (Polyporales, Basidiomycota) with descriptions of seven new species and proposals of two new combinations. *Frontiers in Microbiology* 13: 911978. https://doi.org/10.3389/fmicb.2022.911978

Liu, S, Chen, Y.Y., Sun, Y.F., He, X.L., Song, C.G., Si, J., Liu, D.M., Gates, G. & Cui, B.K. (2022) 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

Liu, S., Shen, L.L., Xu, T.M., Song, C.G., Gao, N., Wu, D.M., Sun, Y.F. & Cui, B.K. (2023a) Global diversity, molecular phylogeny and divergence times of the brown-rot fungi within the Polyporales. *Mycosphere* 14: 1564–1664. https://doi.org/10.5943/mycosphere/14/1/18

Liu, S., Zhou, J.L., Song, J., Sun, Y.F., Dai, Y.C. & Cui, B.K. (2023b) Climacocystaceae fam. nov. and Gloeoporellaceae fam. nov., two new families of Polyporales (Basidiomycota). *Frontiers in Microbiology* 14: 1115761. https://doi.org/10.3389/fmicb.2023.1115761

Lopes, M.T., Urcelay, C. & Robledo, G.L. (2017) New insights on *Trametopsis* Tomšovský (Polyporales Gäum) based on phylogenetic evidences and morphological analyses of neotropical species. *Phytotaxa* 311: 155–167. https://doi.org/10.11646/phytotaxa.311.2.3

Ma, X. & Zhao, C.L. (2019) *Crepatura ellipsospora* gen. et sp. nov. in Phanerochaetaceae (Polyporales, Basidiomycota) bearing a tuberculate hymenial surface. *Mycological Progress* 18: 785–793. https://doi.org/10.1007/s11557-019-01488-0

Miettinen, O., Spirin, V., Vlasák, J., Rivoire, B., Stenroos, S. & Hibbett, D. (2016) Polypores and genus concepts in Phanerochaetaceae (Polyporales, Basidiomycota). *MycoKeys* 17: 1–46. https://doi.org/10.3897/mycokeys.17.10153

Miller, M.A., 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. 39 pp. https://doi.org/10.1145/2335755.2335836

Nylander, J.A.A. (2004) *MrModeltest v2. Program Distributed by the Author*, Evolutionary Biology Centre, Uppsala University: Uppsala, Sweden.

Petersen, J.H. (1996) *Farvekort. The Danish Mycological Society's Colour-Chart*, Foreningen til Svampekundskabens Fremme: Greve, Germany 6 pp.

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

Shen, S., Liu, S.L. & Zhou, L.W. (2023) Taxonomy of *Hyphodermella*: a case study to show that simple phylogenies cannot always accurately place species in appropriate genera. *IMA Fungus* 14: 11. https://doi.org/10.1186/s43008-023-00116-7

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

Tedersoo, L., Bahram, M., Põlme, S., Kõljalg, U., Yorou, N.S., Wijesundera, R., Villarreal, R.L., Vasco-Palacios, A.M., Thu, P.Q., Suija,

A., Smith, M.E., Sharp, C., Saluveer, E., Saitta, A., Rosas, M., riit, T. & Abarenkov, K. (2014) Global diversity and geography of soil fungi. *Science* 346: 1256688.
https://doi.org/10.1126/science.1256688

Telleria, M.T., Dueñas, M., Melo, I. & Martín, M.P. (2010) Morphological and molecular studies of *Hyphodermella* in the Western Mediterranean area. *Mycological Progress* 9, 585–596.
https://doi.org/10.1007/s11557-010-0666-5

Tian, X.M., Man, X.W. & Liu, Z.B. (2022) *Irpex jinshaensis* sp. nov. and *I. subulatus* comb. nov. (Irpicaceae, Polyporales), evidenced by morphological characters and phylogenetic analysis. *Phytotaxa* 533: 73–82.
https://doi.org/10.11646/phytotaxa.533.1.4

Tomšovský, M., Menkis, A. & Vasaitis, R. (2010) Phylogenetic relationships in European *Ceriporiopsis* species inferred from nuclear and mitochondrial ribosomal DNA sequences. *Fungal Biology* 114: 350–358.
https://doi.org/10.1016/j.funbio.2010.02.004

Vilgalys, R. & Hester, M. (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172: 4238–4246.
http://doi.org/10.1128/jb.172.8.4238-4246.1990

Virágh, M., Merényi, Z., Csernetics, Á., Földi, C., Sahu, N., Liu, X.B., Hibbett, D.S. & Nagy, L.G. (2021) Evolutionary morphogenesis of sexual fruiting bodies in Basidiomycota: toward a new evo-devo synthesis. *Microbiology and Molecular Biology Reviews* 86 : e0001921.
https://doi.org/10.1128/MMBR.00019-21

Wang, H., Gu, Z.R. & Zhao, C.L. (2021) *Hyphodermella zixishanensis* (Polyporales, Basidiomycota), a new species with reddish hymenial surface. *Nordic Journal of Botany* 39.
https://doi.org/10.1111/njb.03329

Wang, H. & Zhao, C.L. (2021) *Hyphodermella aurantiaca* sp. nova (Polyporales, Basidiomycota) as evidenced by morphological characters and phylogenetic analyses. *Annales Botanici Fennici* 58: 61–68.
https://doi.org/10.5735/085.058.0110

Wang, H. & Zhao, C.L. (2022) *Flavodontia rosea* gen. and sp. nov. from southwestern China. *Mycotaxon* 136: 755–767.
https://doi.org/10.5248/136.755

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

Wu, Z.Q., Xu, T.M., Shen, S., Liu, X., Luo, K.Y. & Zhao, C.L. (2018) *Elaphroporia ailaoshanensis* gen. et sp. nov. in Polyporales (Basidiomycota). *MycoKeys* 29: 81–95.
https://doi.org/10.3897/mycokeys.29.22086

Xu, Y.L., Cao, Y.F., Nakasone, K.K., Chen, C.C. & He, S.H. (2020) Taxonomy and phylogeny of *Phanerochaete* sensu stricto (Polyporales, Basidiomycota) with emphasis on Chinese collections and descriptions of nine new species. (2020) *Mycosphere* 11: 1527–1552.
https://doi.org/10.5943/mycosphere/11/1/12

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

Yang, Y., Jiang, Q.Q., Li, Q., Yang, J.W., Cha, L., Cheng, L.J., Yang, S.Q., Zhao, C.L. & Zhou, H.M. (2023b) Molecular systematics and taxonomic analyses of three new wood-inhabiting fungi of *Hyphoderma* (Hyphodermataceae, Basidiomycota). *Journal of Fungi* 9: 1044.
https://doi.org/10.3390/jof9111044

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

Zhang, J.W., Markillie, L.M., Mitchell, H.D., Gaffrey, M.J., Orr, G. & Schilling, J.S. (2022) Distinctive carbon repression effects in the carbohydrate-selective wood decay fungus *Rhodonia placenta*. *Fungal Genetics and Biology* 159: 103673.
https://doi.org/10.1016/j.fgb.2022.103673

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

Zhao, C.L., Cui, B.K., Song, J. & Dai, Y.C. (2015) Fragiliporiaceae, a new family of Polyporales (Basidiomycota). *Fungal Diversity* 70:

115–126.
https://doi.org/10.1007/s13225-014-0299-0

Zhao, C.L., Liu, X.F. & Ma, X. (2019) *Phlebiopsis yunnanensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. *Nova Hedwigia* 108: 265–279.
https://doi.org/10.1127/nova_hedwigia/2018/0508

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, C.L., Ren, G.J. & Wu, F. (2017) A new species of *Hyphodermella* (Polyporales, Basidiomycota) with a poroid hymenophore. *Mycoscience* 58: 452–456.
https://doi.org/10.1016/j.myc.2017.06.007

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

Zhao, Y.N., He, S.H., Nakasone, K.K., Wasantha Kumara, K.L., Chen, C.C., Liu, S.L., Ma, H.X. & Huang, M.R. (2021) Global phylogeny and taxonomy of the wood-decaying fungal genus *Phlebiopsis* (Polyporales, Basidiomycota). *Frontiers in Microbiology* 12: 622460.
https://doi.org/10.3389/fmicb.2021.622460