

Molecular phylogeny and morphology reveal a new wood-inhabiting fungal species, *Candelabrochaete tenuis* (Irpicaceae, Polyporales) from Yunnan Province, China

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Abstract

In this study, *Candelabrochaete tenuis* is described and illustrated as a novel species based on morphological characteristics and phylogenetic analyses of internal transcribed spacer (ITS) regions and the large subunit (nLSU) of nuclear ribosomal RNA genes. The species is characterized by smooth, membranaceous basidiomata with a cream to slightly brown hymenial surface, and allantoid to subcylindrical basidiospores. The phylogenetic analyses based on ITS+nLSU sequences inferred that the new species is nested within the genus *Candelabrochaete* and is closely related to *C. guangdongensis*. A description, illustrations, phylogenetic analysis results and comparisons with closely related taxa of the new species are provided.

Key words: Biodiversity, corticioid fungi, molecular systematics, new taxon, taxonomy

Introduction

The number of fungal species is estimated to range from 2.2 to 13.2 million, with recent assessments converging on approximately 2–3 million species (Niskanen *et al.* 2023, Hyde *et al.* 2024). However, only around 160,000 species have been formally named and classified, indicating that most fungal diversity remains undocumented and represents a substantial untapped resource (Hyde *et al.* 2019, Yang *et al.* 2025). Polyporales is a highly diverse order within Agaricomycetes and one of the most intensively studied fungal clades (Zhao *et al.* 2015, 2025, Justo *et al.* 2017, Cui *et al.* 2019; Mao *et al.* 2023, Wang *et al.* 2024a, Wijesinghe *et al.* 2025). As major wood-inhabiting fungi, species of Polyporales play critical roles in lignocellulose decomposition and are key drivers of forest carbon cycling (Floudas *et al.* 2012, Tedersoo *et al.* 2014, James *et al.* 2020, Zhang *et al.* 2022). Most species of Polyporales are saprotrophic wood decomposers, whereas a smaller proportion are plant pathogens that cause wood decay and economic losses in timber and woody crops (Dai *et al.* 2012, Hawksworth *et al.* 2017, Liu *et al.* 2023, Zhao *et al.* 2023, Cui *et al.* 2026).

The family Irpicaceae, typified by *Irpex* Fr., was established by Spirin (2003). The family belongs to the phlebioid clade of Polyporales and includes 14 genera, viz. *Byssomerulius* Parmasto, *Ceriporia* Donk, *Crystallicutis* El-Gharabawy, *Cytidiella* Pouzar, *Eftibula* Sheng H. Wu, Leal-Dutra & G.W. Griff., *Gloeoporus* Mont. *Irpex*, *Leptoporus* Quél., *Meruliopsis* Bondartsev, *Phanericium* (Parmasto) K.H. Larss. & Spirin, *Phanerochaetella* C.C. Chen & Sheng H. Wu, *Raduliporus* Spirin & Zmitr., *Resiniporus* Zmitr., and *Trametopsis* Tomšovský. Members within Irpicaceae

develops variable hymenophores, including corticioid and irpicoid species, and resupinate to pileate polypores (Wang *et al.* 2023, Larsson *et al.* 2025, Li *et al.* 2025, Deng *et al.* 2026).

The genus *Candelabrochaete* Boidin was originally described by Boidin (1970), and its type species, *C. africana* Boidin (1970: 24) (Burdsall 1984), formed an independent lineage in the phlebioid clade (Irpicaceae, Meruliaceae, Phanerochaetaceae) of Polyporales. Morphologically, the genus is characterized by resupinate basidiomata with a smooth to odontoid hymenophore, a monomitic hyphal system, thin- to thick-walled generative hyphae with simple septa, cylindrical cystidia, and ellipsoid to allantoid basidiospores (Eriksson *et al.* 1981, Maekawa 2021, Wang *et al.* 2024b). In recent studies, five species of *Candelabrochaete* formed three distinct lineages within the *Ceriporia* / *Candelabrochaete* / *Leptoporus* clade, which indicate that *Candelabrochaete* was polyphyletic, and the generic placement of these taxa remains uncertain, partly because the type species *C. africana* was not nested within the phlebioid clade in some analyses, highlighting a need for additional sampling and data (Justo *et al.* 2017, Li *et al.* 2022). According to Index Fungorum (www.indexfungorum.org; accessed on 7 June 2026), *Candelabrochaete* includes 16 specific and registered records, of which 13 species are currently accepted worldwide (Li *et al.* 2022, Wang *et al.* 2024b).

During surveys of wood-inhabiting fungi in China, we found a species of *Candelabrochaete* that does not match any known species. This species is characterized by smooth, membranaceous basidiomata with a cream to slightly brown hymenial surface, and allantoid to subcylindrical basidiospores. Morphological characteristics and multi-locus molecular analyses based on ITS+nLSU sequences indicate that it represents a new species and is described here.

Materials and methods

Sample Collection and Herbarium Specimen Preparation

Two fresh fruiting bodies of fungi growing on angiosperm branches were collected from Dehong, Lianghe County, Mengyang Town in Yunnan Province, China. The samples were photographed in situ using a Canon 80D camera (Tokyo, Japan). Fresh macroscopic details and collection data were recorded (Rathnayaka *et al.* 2025), and the samples were then taken to the Southwest Forestry University mycology laboratory in plastic collection boxes. Specimens were dried in an electric food dehydrator at 45 °C, then sealed in envelopes and zip-lock plastic bags, and labeled. The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macro morphology was based on fresh and dried specimens. The color terms in the description followed Petersen (1996). The micromorphological characteristics were systematically analyzed from the dried specimens and observed under a light microscope, in accordance with established methodologies. Sections mounted in 5% KOH and 2% phloxine B dye (C₂₀H₂Br₄Cl₄Na₂O₃). Other reagents were also used, including Cotton Blue and Melzer's reagent. Micro morphology was observed following the method of Dong *et al.* (2025). The following abbreviations were used: CB = Cotton Blue, CB– = acyanophilous, KOH = 5% potassium hydroxide, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid, W = mean spore width (arithmetic average for all spores), L = mean spore length (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 given number (b) of specimens (Dong *et al.* 2024).

DNA Extraction, PCR amplification, and Sequencing

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The nuclear ribosomal 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 newly generated sequences were deposited in GenBank (Table 1).

TABLE 1. A list of species, specimens and GenBank accession numbers of sequences used in this study. The new species is in bold and – refers to the data unavailability.

Species name	Sample no.	GenBank accessions no.		Country	References
		ITS	nLSU		
<i>Candelabrochaete africana</i>	FP-102821	KP135293	–	USA	Floudas & Hibbett (2015)
<i>Candelabrochaete africana</i>	FP-102901	KP135292	–	USA	Floudas & Hibbett (2015)
<i>Candelabrochaete africana</i>	FP-102987	KP135294	–	USA	Floudas & Hibbett (2015)
<i>Candelabrochaete guangdongensis</i>	He 5902	MZ422527	MZ422499	China	Li <i>et al.</i> (2022)
<i>Candelabrochaete tenuis</i>	CLZhao 50454	PX921698	PX921701	China	Present study
<i>Candelabrochaete tenuis</i>	CLZhao 48969	PX921699	PX921702	China	Present study
<i>Candelabrochaete yunnanensis</i>	CLZhao 26027	OR658994	OR999391	China	Wang <i>et al.</i> (2024)
<i>Ceriporia reticulata</i>	CBS 462.50	MH856710	MH868228	France	Vu <i>et al.</i> (2019)
<i>Ceriporia reticulata</i>	RLG-11354-Sp	KP135041	KP135204	USA	Justo <i>et al.</i> (2017)
<i>Efibula americana</i>	FP-102165	KP135016	KP135256	USA	Floudas & Hibbett (2015)
<i>Efibula americana</i>	HHB-8468	KP135012	–	USA	Floudas & Hibbett (2015)
<i>Efibula daweshanensis</i>	CLZhao 18946	OR094488	–	China	Dong <i>et al.</i> (2024)
<i>Efibula daweshanensis</i>	CLZhao 19002	OR094489	OR449958	China	Dong <i>et al.</i> (2024)
<i>Efibula gracilis</i>	FD-455	KP135027	MZ637116	USA	Chen <i>et al.</i> (2021)
<i>Efibula gracilis</i>	FP-102052	KP135028	–	China	Floudas & Hibbett (2015)
<i>Efibula yunnanensis</i>	He 4653	MZ636975	MZ637137	China	Chen <i>et al.</i> (2021)
<i>Irpex flavus</i>	WHC 1381	LC427029	LC427052	China	Chen <i>et al.</i> (2021)
<i>Irpex lacteus</i>	FD-9	KP135026	KP135224	USA	Chen <i>et al.</i> (2021)
<i>Irpex laceratus</i>	WHC 1372	MZ636990	MZ637151	China	Chen <i>et al.</i> (2021)
<i>Irpex latemarginatus</i>	Piatek 1997	KX752592	KX752592	China	Chen <i>et al.</i> (2021)
<i>Irpex lenis</i>	Wu 1608-14	MZ636991	MZ637152	China	Chen <i>et al.</i> (2021)
<i>Irpex lenis</i>	Wu 1608-22	MZ636992	MZ637153	China	Chen <i>et al.</i> (2021)
<i>Gloeoporus dichrous</i>	CBS 446.50	MH856705	MH868222	Canada	Vu <i>et al.</i> (2019)
<i>Gloeoporus dichrous</i>	Dai 16370A	KU360399	KU360406	China	Yuan <i>et al.</i> (2016)
<i>Gloeoporus pannocinctus</i>	FCUG 2109	AF141612	AF141612	Sweden	Yuan <i>et al.</i> (2016)
<i>Gloeoporus pannocinctus</i>	CBS 291.71	MH860130	MH871903	France	Vu <i>et al.</i> (2019)
<i>Gloeoporus thelephoroides</i>	BZ-2896	MG572757	MG572741	Belize	Jung <i>et al.</i> (2018)
<i>Leptoporus mollis</i>	TJV-93-174-T	KY948795	EU402510	USA	Li <i>et al.</i> (2025)
<i>Leptoporus mollis</i>	RLG 7163	KY948794	MZ637155	USA	Chen <i>et al.</i> (2021)

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TABLE 1. (Continued)

Species name	Sample no.	GenBank accessions no.		Country	References
		ITS	nLSU		
<i>Meruliopsis leptocystidiata</i>	Wu 1708-15	LC427012	LC427032	China	Li <i>et al.</i> (2025)
<i>Meruliopsis leptocystidiata</i>	Wu 1708-43	LC427013	LC427033	China	Li <i>et al.</i> (2025)
<i>Phanerochaetella angustocystidiata</i>	Wu 9606-39	MZ637020	GQ470638	China	Chen <i>et al.</i> (2021)
<i>Phanerochaetella leptoderma</i>	Chen 1362	MZ637025	GQ470646	China	Chen <i>et al.</i> (2021)
<i>Trametopsis aborigena</i>	Robledo 1236	KY655336	KY655338	Argentina	Gomez-Montoya <i>et al.</i> (2017)
<i>Trametopsis aborigena</i>	Robledo 1238	KY655337	KY655339	Argentina	Gomez-Montoya <i>et al.</i> (2017)
<i>Trametopsis brasiliensis</i>	Meijer 3637	JN710510	JN710510	Brazil	Gomez-Montoya <i>et al.</i> (2017)
<i>Trametopsis cervina</i>	PRM900574	AY684175	AY855907	Czech Republic	Tomšovský <i>et al.</i> (2006)
<i>Phanerochaete rhodella</i>	FD-18	KP135187	KP135258	USA	Justo <i>et al.</i> (2017)

Molecular Phylogeny

The newly generated sequences were compared using the Basic Local Alignment Search Tool (BLAST) from GenBank. Additionally, sequences from previous studies on species in the genus containing ex-type or representative sequences were downloaded from GenBank (Spirin *et al.* 2018, Wu *et al.* 2020, Deng *et al.* 2025, Gu *et al.* 2025, Xu *et al.* 2025, Yang *et al.* 2025). Two datasets were created: one containing ITS sequences and the other containing nLSU sequences. Each dataset was aligned in MAFFT version 7 using the G-INS-i strategy (Katoh *et al.* 2019). The alignments were adjusted manually using AliView version 1.27 (Larsson 2014). Both datasets were combined using Mesquite version 3.51.

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 characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1,000 random sequence additions. Max trees were set to 5,000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics, tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each maximum parsimonious tree generated. The combined dataset was analyzed using maximum likelihood (ML) in RAxML-HPC2 (Miller *et al.* 2012). Branch support (BS) for ML analysis was determined by 1,000 bootstrap replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each dataset for Maximum Likelihood (ML) and Bayesian inference (BI), which was performed with MrBayes 3.2.7a using a general time-reversible model of DNA substitution and a gamma distribution of rate variation across sites (Ronquist *et al.* 2012). Four Markov chains were run twice from a random starting tree for 0.8 million generations of the datasets (Figure 1) and for 0.8 million generations of the datasets (Figure 2); the tree was sampled every 1,000 generations. The first one-fourth of all generations were discarded as burnin. The majority rule consensus tree of all remaining trees was calculated. Branches were considered significantly supported if they received a maximum likelihood bootstrap value (BS) $\geq 70\%$, a maximum parsimony bootstrap value (BT) $\geq 50\%$, or Bayesian posterior probabilities (BPP) ≥ 0.95 .

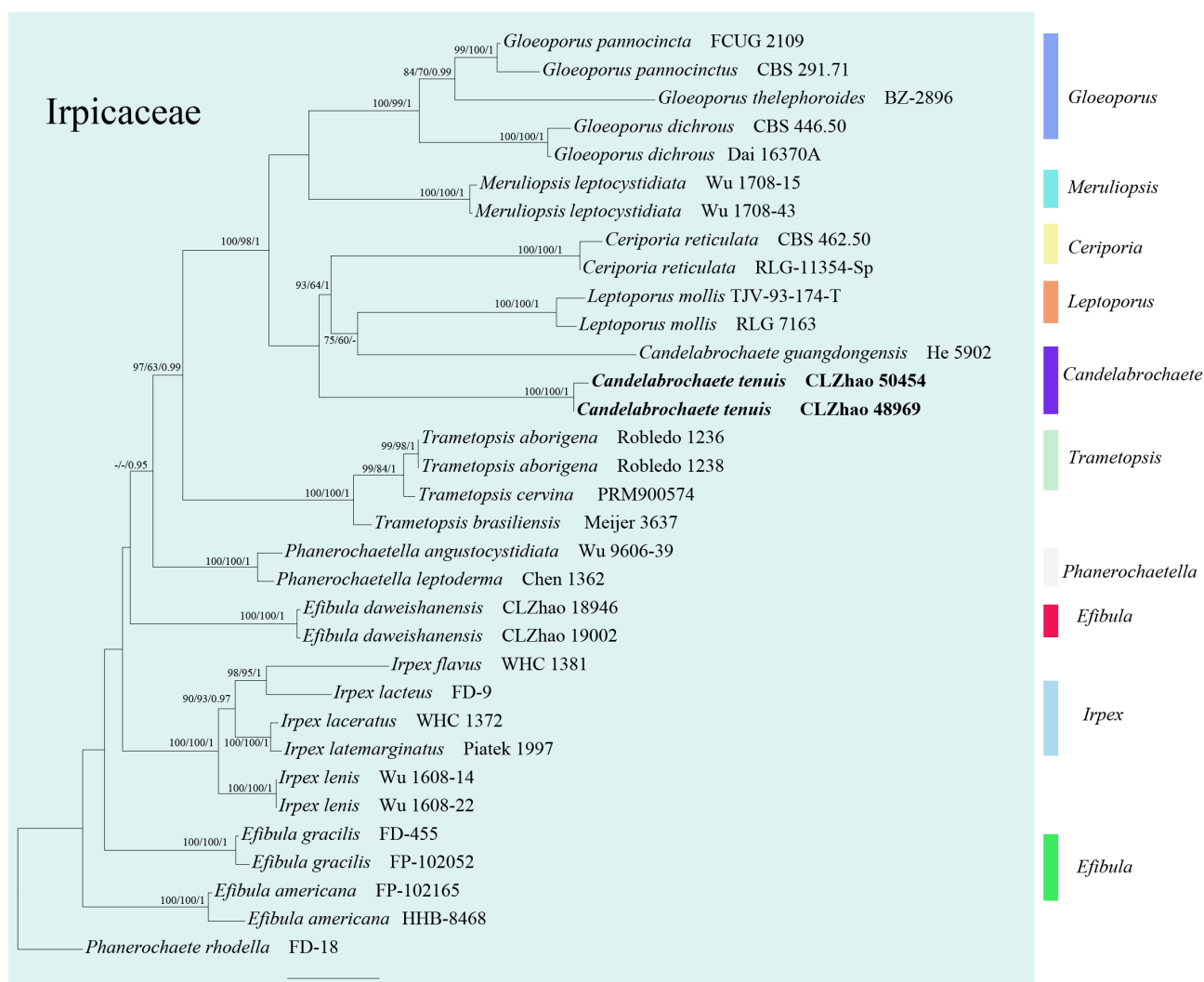


FIGURE 1. Maximum Likelihood tree illustrating the *Candelabrochaete tenuis* and related species in the family Irpicaceae based on the combined ITS+nSU sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, Parsimony bootstrap values $\geq 50\%$, and Bayesian Posterior Probabilities ≥ 0.95 . The new species is in bold.

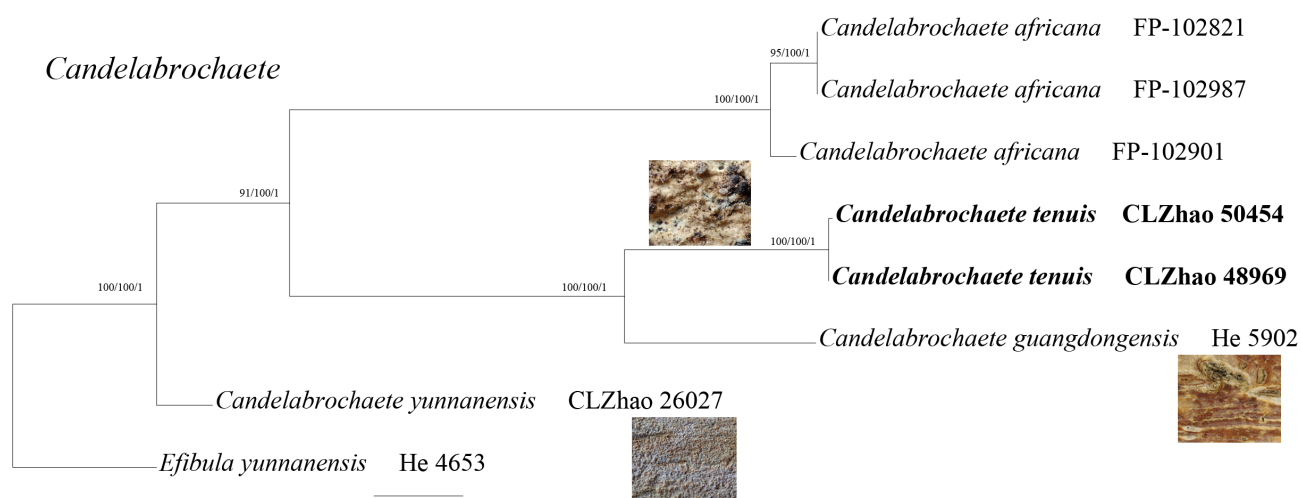


FIGURE 2. Maximum Likelihood tree illustrating the *Candelabrochaete tenuis* and related species in the genus *Candelabrochaete* based on the combined ITS sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, Parsimony bootstrap values $\geq 50\%$, and Bayesian Posterior Probabilities ≥ 0.95 . The new species is in bold.

Results

Phylogenetic analyses

The combined dataset ITS+nLSU (Figure 1) comprised sequences from 33 fungal specimens representing 22 species. The datasets had an aligned length of 2,043 characters, of which 1,476 were constant, 148 were variable and parsimony-uninformative, and 419 were parsimony-informative. Maximum Parsimony analysis yielded 1 equally parsimonious tree (TL = 1451, CI = 0.5376, HI = 0.4624, RI = 0.6939, RC = 0.3730). Bayesian and ML analyses yielded a similar topology to the MP analysis, with an average standard deviation of split frequencies of 0.004405 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 412.5. The phylogenetic tree (Figure 1) inferred from ITS and nLSU sequences showed that the new species was grouped within the genus *Candelabrochaete*, which was clustered within the family Irpicaceae. The aligned sequence dataset of the phylogenetic analyses was deposited in figshare (10.6084/m9.figshare.30540785).

The datasets based on ITS+nLSU (Figure 2) comprise sequences from 8 fungal specimens representing 5 species. The datasets had an aligned length of 2,124 characters, of which 1,690 were constant, 159 were variable and parsimony-uninformative, and 275 were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 591, CI = 0.9425, HI = 0.0575, RI = 0.9218, RC = 0.8688). Bayesian and ML analyses resulted in a similar topology to the MP analysis, with an average standard deviation of split frequencies of 0.008329 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 262. The phylogenetic tree (Figure 2) inferred from ITS and nLSU sequences showed that the new species grouped within the genus *Candelabrochaete*, where it was recovered as a sister to *C. guangdongensis* Yue Li & S.H. He 2022. The aligned sequence dataset of the phylogenetic analyses was deposited in figshare (10.6084/m9.figshare.30540785).

Taxonomy

Candelabrochaete tenuis Wen Li & C.L. Zhao, *sp. nov.* Figs. 3–5

MycoBank no.: MB 862147

Holotype: CHINA. Yunnan Province, Dehong, Lianghe County, Mengyang Town (Lianghe County State-owned Forest Farm), 24°06' N, 98°02' E, elevation 1,395 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 5 October 2025, CLZhao 50454 (SWFC 00050454).

Etymology: *Tenuis* (Lat.) refers to the thin basidiomata.

Basidiomata: Annual, resupinate, adnate, membranaceous, without odor or taste when fresh, up to 60 mm long, 25 mm wide, and 0.1 mm thick. Hymenial surface smooth, cream when fresh, turning to cream to slightly brown upon drying. Sterile margin narrow, cream, up to 1 mm.

Hyphal system: Monomitic; generative hyphae with simple septa, colorless, thin- to slightly thick-walled, interwoven, 4.5–5 µm in diameter, IKI–, CB–; tissue unchanged in KOH.

Hymenium: Septocystidia abundant, cylindrical, slightly sinuous, frequently septate, colorless, slightly thick-walled, smooth, 88–107 × 8–10.5 µm. Basidia barrel-shaped, thin-walled, smooth, with four sterigmata and a simple septum at the base, 11.5–12.5 × 3.5–4 µm. Irregular crystals present among hyphae and hymenium.

Basidiospores: Allantoid to subcylindrical, colorless, thin-walled, smooth, usually with oil drops, IKI–, CB–, (3.5–)4–4.5(–5) × 2–2.5(–3) µm, L = 4.34 µm, W = 2.24 µm, Q = 1.94–1.95 (n = 60/2).

Additional specimen examined (paratype): CHINA. Yunnan Province, Dehong, Lianghe County, Mengyang Town (Lianghe County State-owned Forest Farm), 24°06' N, 98°02' E, elevation 1,395 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 5 October 2025, CLZhao 48969 (SWFC 00048969).

Discussion

Fungal specimens collected in Yunnan Province led to the identification of a new species, *Candelabrochaete tenuis*, which was described based on phylogenetic analyses and morphological characteristics. The phylogenetic tree constructed from the ITS+nLSU dataset demonstrates that *C. tenuis* is nested within the genus *Candelabrochaete* (Figure 1). Furthermore, ITS+nLSU sequence data indicate that *C. tenuis* is closely related to *C. guangdongensis*

(Figure 2). *Candelabrochaete guangdongensis* can be distinguished from *C. tenuis* by its ceraceous basidiomata, orange to reddish orange hymenial surface, and narrower basidiospores ($4\text{--}5 \times 1.5\text{--}2 \mu\text{m}$ vs. $4\text{--}4.5 \times 2\text{--}2.5 \mu\text{m}$, Li *et al.* 2022).

Morphologically, *Candelabrochaete tenuis* resembles *C. adnata* Hjortstam 1995, *C. africana*, and *C. yunnanensis* Lu Wang & C.L. Zhao 2024 due to its smooth hymenial surface. However, *C. adnata* differs from *C. tenuis* by its grey to green hymenial surface and larger basidiospores ($6.5\text{--}7 \times 2.8\text{--}3.5 \mu\text{m}$ vs. $4\text{--}4.5 \times 2\text{--}2.5 \mu\text{m}$, Duenas *et al.* 2008). *Candelabrochaete africana* is distinguished from *C. tenuis* by its longer basidiospores ($4.5\text{--}6 \times 2\text{--}3 \mu\text{m}$ vs. $4\text{--}4.5 \times 2\text{--}2.5 \mu\text{m}$, Li *et al.* 2025). *Candelabrochaete yunnanensis* can be differentiated from *C. tenuis* by its flesh-pinkish to brownish vinaceous hymenial surface and ellipsoid basidiospores (Wang *et al.* 2024b). A morphological comparison between *C. tenuis* and 11 similar species is presented in Table 2.

This study describes a new wood-inhabiting fungus, *Candelabrochaete tenuis*, from Yunnan Province, China. The discovery enhances understanding of species diversity within this genus and highlights the significance of ongoing regional biodiversity surveys and fungal resource exploration.

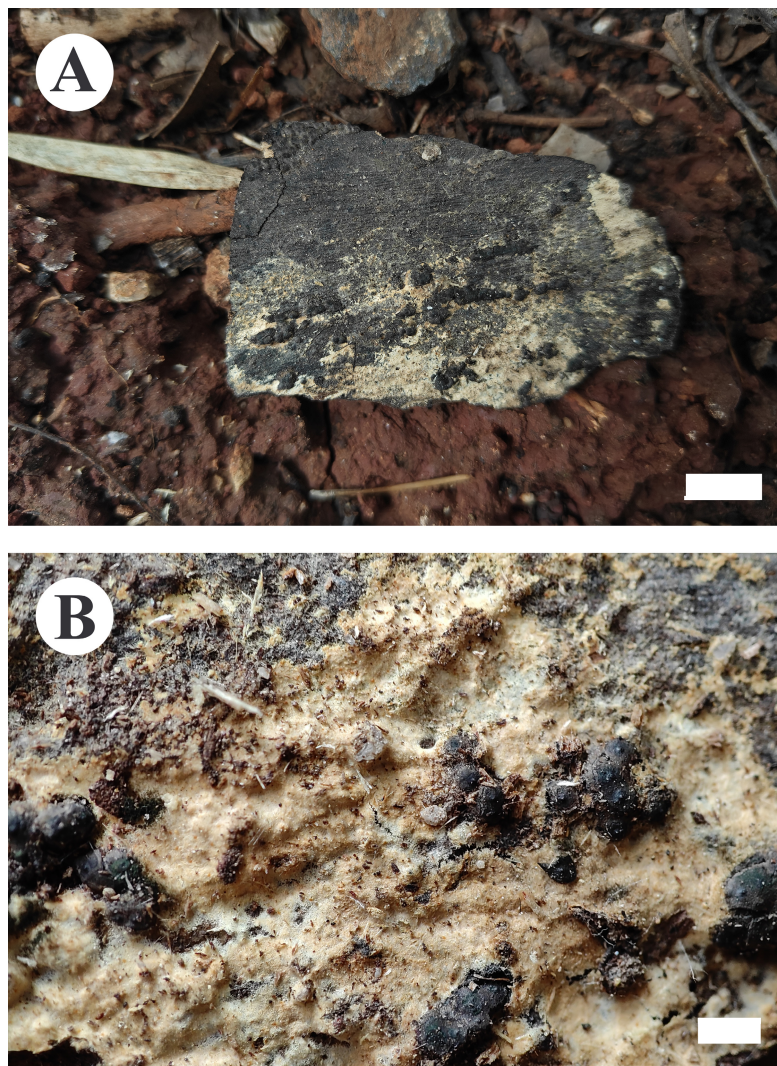


FIGURE 3. Basidiomata of *Candelabrochaete tenuis* sp. nov. (Holotype, CLZhao 50454): (A) Basidiomata on the substrate; (B) Macroscopic characteristics of hymenophore. Scale bars: (A) = 1 cm, (B) = 2 mm.

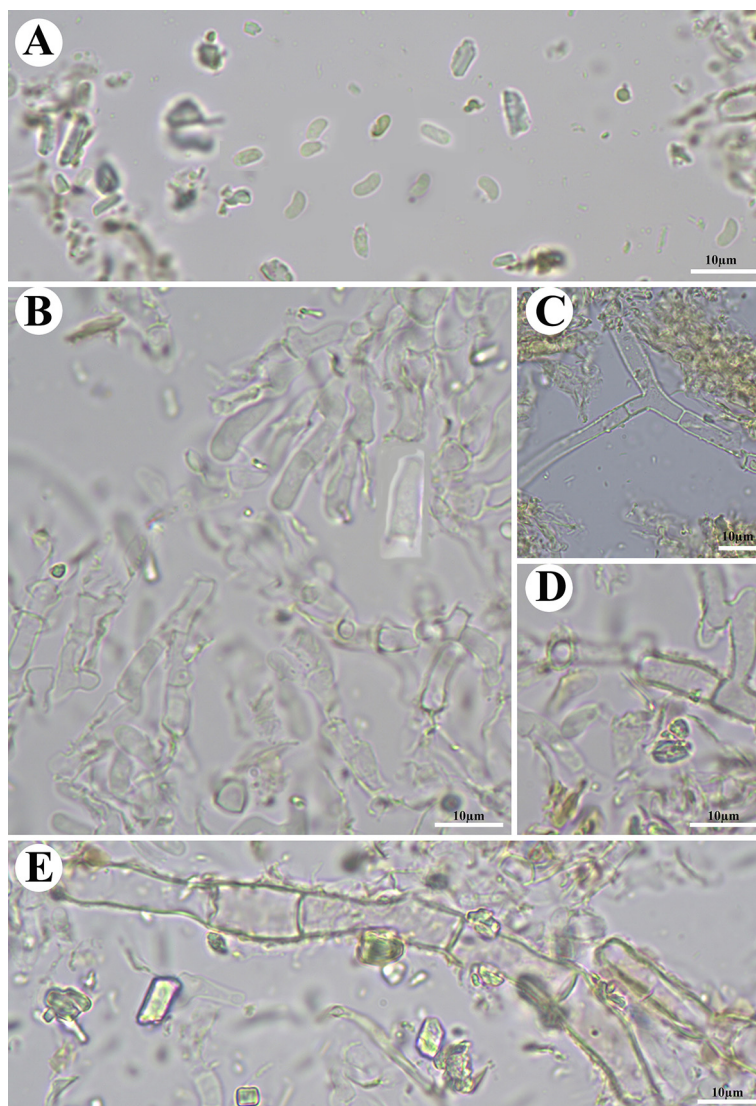


FIGURE 4. Sections of hymenium of *Candelabrochaete tenuis* sp. nov. (Holotype, CLZhao 50454). (A) Basidiospores; (B) Basidia and basidioles; (C–D) Generative hyphae; (E) Septocystidia.

TABLE 2. The morphological comparison of *Candelabrochaete* species. The new species is in bold.

Species name	Hymenial surface	Basidia size	Cystidia size	Basidiospores	References
<i>Candelabrochaete adnata</i>	Smooth	17–20 × 4–5 µm	40–60 × 6–8 µm	Ellipsoid; 6.5–7(–8) × 2.8–3.5 µm	Duenas <i>et al.</i> (2008)
<i>Candelabrochaete africana</i>	Smooth	13–17 × 5–6 µm	90 × 10 µm	Subcylindrical; 4.5–6 × 2–3 µm	Li <i>et al.</i> (2025)
<i>Candelabrochaete dispar</i>	Grandinoid to odontoid	(12–)15–17(–25) × 4–5(–6) µm	80–120(–200) × 6–9(–10) µm	Subglobose; 5–5.5 × 4–4.5 µm	Duenas <i>et al.</i> (2008)
<i>Candelabrochaete eruciformis</i>	Smooth to tuberculate	24–30 × 5–6 µm	40–90 × 6–10 µm	Ellipsoid; 7–9 × 3–5 µm	Duenas <i>et al.</i> (2008)
<i>Candelabrochaete guangdongensis</i>	Smooth	16–24 × 3.5–5 µm	Septocystidia abundant; 145–190 × 6–10 µm	short-cylindrical to allantoid; 4–5 × 1.5–2 µm	Li <i>et al.</i> (2025)
<i>Candelabrochaete macaronensis</i>	Smooth	(12–)16–18.5 × 5–5.5 µm	70–150 × 8–11 µm	Subcylindrical to narrowly ellipsoid; 5–6.5 × 2–3 µm	Duenas <i>et al.</i> (2008)

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TABLE 2. (Continued)

Species name	Hymenial surface	Basidia size	Cystidia size	Basidiospores	References
<i>Candelabrochaete magnahypha</i>	Smooth.	12–15 × 5.5–6 µm	100–150 × 9–12 µm	Subcylindrical; 6–7(–8) × 3–4 µm	Duenas <i>et al.</i> (2008)
<i>Candelabrochaete mexicana</i>	Continuous to pubescent	9–11.5 × 6.5–7µm	90–150 × 9–20 µm	Cylindrical; 7–10(–12) × (4–)5–6 µm	Duenas <i>et al.</i> (2008)
<i>Candelabrochaete simulans</i>	Smooth	20–25 × 4–5.5µm	100–250 × 9–12 µm	Ellipsoid; 4.5–5.5 × 3–3.2 µm	Duenas <i>et al.</i> (2008)
<i>Candelabrochaete tenuis</i>	Smooth	11.5–12.5 × 3.5–4 µm	Septocystidia abundant; 88–107 × 8–10.5 µm	Allantoid to subcylindrical; (3.5–)4–4.5(–5) × 2–2.5(–3) µm	Present study
<i>Candelabrochaete verruculosa</i>	Grandinioid to odontoid.	15–20 × 4.5–5 µm	70–140 × 8–12 µm	Ellipsoid; 5.5–6 × 3–3.25 µm	Duenas <i>et al.</i> (2008)
<i>Candelabrochaete yunnanensis</i>	Smooth	16–18 × 4.5–5.5 µm	Septocystidia abundant; 80–105 × 7–9 µm	Ellipsoid; 4–5 × 2.5–3(–4) µm	Wang <i>et al.</i> (2024)

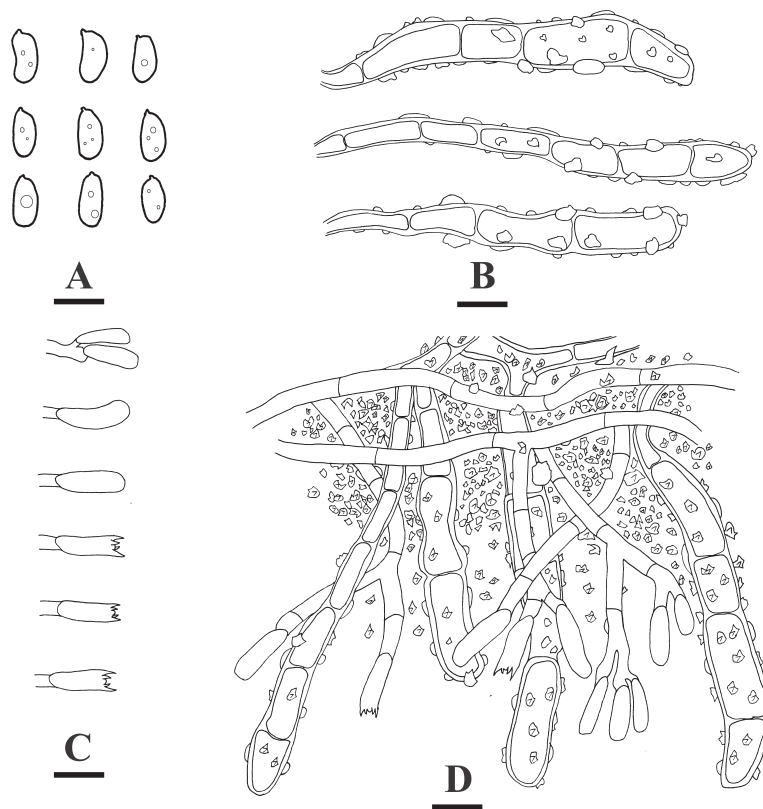


FIGURE 5. Microscopic structures of *Candelabrochaete tenuis* (Holotype, CLZhao 50454). (A) Basidiospores; (B) Septocystidia; (C) Basidia and basidioles; (D) Part of the vertical section of basidiomata. Scale bars: (A) = 5 µm, (B–D) = 10 µm.

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