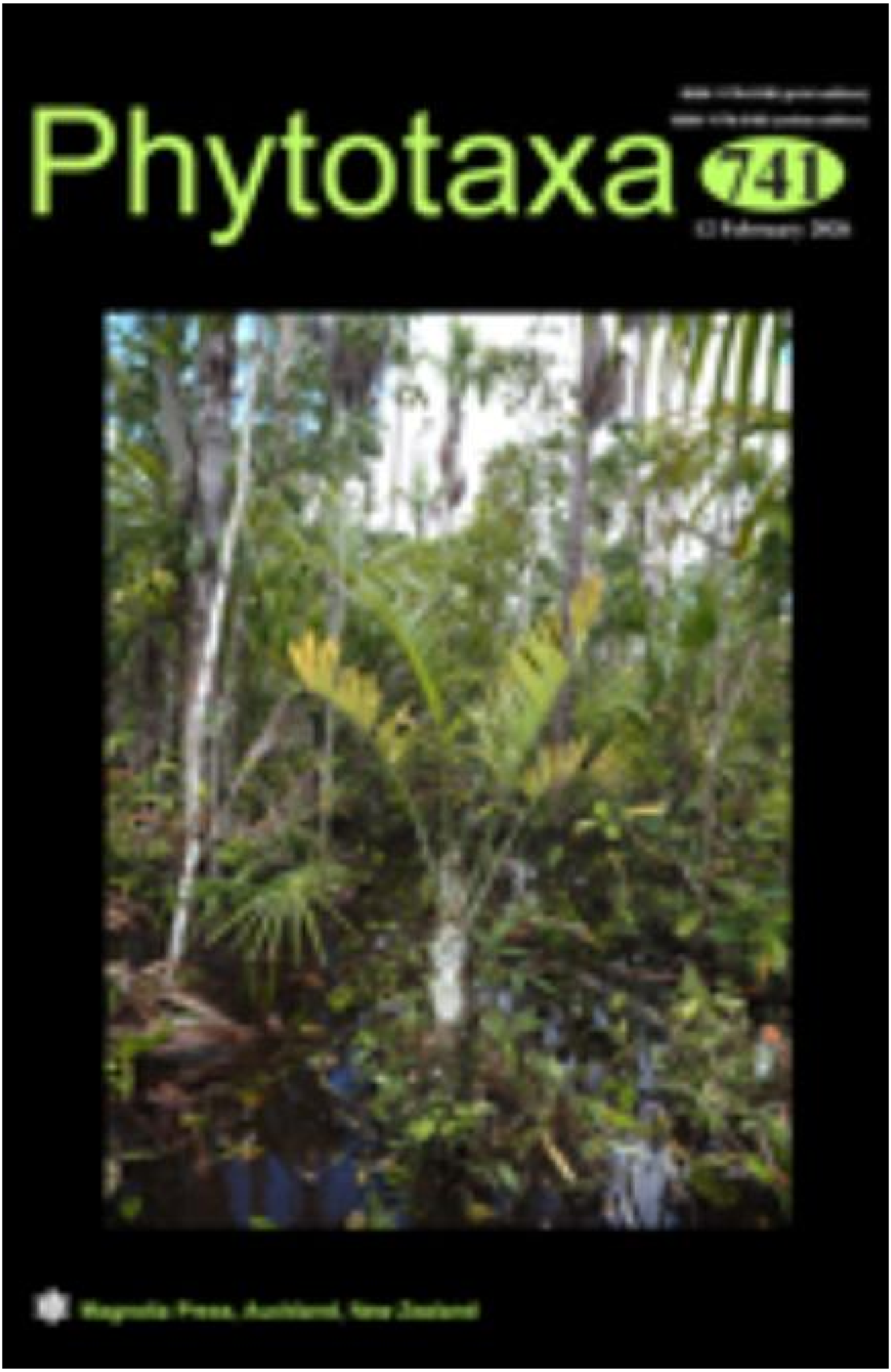

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Article

Updated data on *Psilocybe* (Hymenogastraceae, Agaricales) from the southern Brazil region and a newly proposed species

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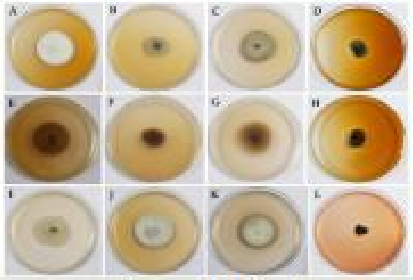

Discovery of a novel endophytic species of *Nigrograna* (Nigrogranaceae) associated with *Azadirachta indica* (Neem) from the Deccan Plateau

SHIWALI RANA, SANJAY K. SINGH

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Molecular phylogeny and morphology reveal a new *Cabalodontia* species (Polyporales, Basidiomycota) from Yunnan Province, China

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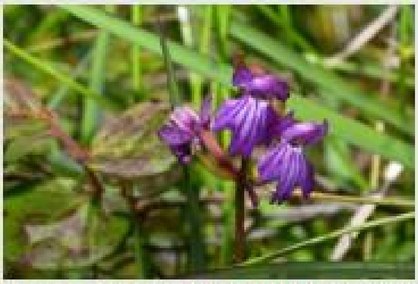

A new species of *Ponerorchis* (Orchidaceae, Orchideae) from Xizang, China

TIRTHA RAJ PANDEY, YAJUN WANG, CHAO YE, XILONG WANG, XIAO-HUA JIN

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Molecular phylogeny and morphology reveal a new *Cabalodontia* species (Polyporales, Basidiomycota) from Yunnan Province, China

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Abstract

The genus *Cabalodontia* belonging to the family Steccherinaceae, is an important member of wood-inhabiting fungi. In this study, one new species, *Cabalodontia aurantiaca sp. nov.* is collected from Yunnan, P.R. China, which is proposed based on a combination of morphological features and molecular evidence. This species *C. aurantiaca* is characterized by its orange basidiomata with odontoid hymenial surface, a monomitic hyphal system with clamped generative hyphae, thick-walled skeletocystidia and ellipsoid basidiospores (4–5 × 2.5–3.0 µm). Phylogenetic analysis of the new species is carried out based on the nuclear ribosomal internal transcribed spacer (ITS) and the nuclear large subunit (nLSU) of ribosomal DNA. The phylogenetic tree indicates that the new species belongs to the genus *Cabalodontia*, and it is retrieved as a sister to *C. delicata*. Full morphological description, illustrations, and phylogenetic analyses results for the new species are provided.

Key words: One new species, Phylogenetic analysis, Steccherinaceae, Taxonomy, Wood-inhabiting fungi

Introduction

Fungi are the third category of eukaryotes besides plants and animals, and one of the key factors bridging the biotic and abiotic environments (He *et al.* 2024, Hibbett *et al.* 2025). Fungi occur in nearly every habitat on earth, including the air, marine environments, exposed rock surfaces, soils and every tissue of land plants, the fungal kingdom has diversified to more than two million species, with over 95% still undescribed (Case *et al.* 2025). According to estimates, only around 155,000 species have been named and classified to date (Dai & Zhuang 2010, Bhunjun *et al.* 2022, Tarafder *et al.* 2022, 2023, He *et al.* 2024, Hyde *et al.* 2024, Zhao *et al.* 2024, Gu *et al.* 2025, Hibbett *et al.* 2025). Wood-inhabiting fungi are a cosmopolitan group in the kingdom Fungi, in which many natural product discoveries from fungi for drug development and description of novel chemistry has been a tremendous success, which recently led to the discovery of an unparalleled biodiversity in the fungal kingdom (Lambert *et al.* 2025, Schrey *et al.* 2025). These fungi secrete various enzymes that effectively degrade cellulose, hemicellulose, and lignin into simple inorganic substances. As an important group of decomposers, they play a crucial role in forest ecosystems (Wei & Dai 2004, Dai 2011, Deng *et al.* 2024, Yang *et al.* 2024, Su *et al.* 2024, Zhang *et al.* 2024, Xiao *et al.* 2025).

Traditionally, wood-inhabiting fungi with a poroid hymenophore are known as polypores (Gibertoni *et al.* 2016, Chung *et al.* 2017). They grow on various substrates, such as living trees, dead standing trees, fallen trunks, rotten wood, stumps, fallen branches and twigs; some are associated with trees as ectomycorrhizal fungi (Alem *et al.* 2021, Wu *et al.* 2022, Liu *et al.* 2023, Zhao *et al.* 2024). The earliest polypore studies mostly focused on Europe and North America. The systematic studies of polypores carried on by many mycologists (Ryvarden & Gilbertson 1993, 1994, Ryvarden &

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Melo 2014, 2017, Lowe 1957, 1966, 1975, Zhao *et al.* 2024), and they have provided a strong foundation for numerous subsequent researchers to publish extensive academic paper on polypores (Zhao *et al.* 2024). The classification of the order Polyporales within the kingdom Fungi undergoes continual revision, driven by the integration of DNA sequence data in modern phylogenetic studies (Cui *et al*. 2019, Wijayawardene *et al*. 2022, Hyde *et al*. 2024, Dong *et al*. 2024, Yang *et al.* 2025).

The family Steccherinaceae Parmasto, belonging to the order Polyporales (Basidiomycota), was typified by the genus *Steccherinum* Gray (1821: 651). Twenty-four genera were placed in this family Steccherinaceae as *Antella* Miettinen (2016: 158), *Antrodiella* Ryvarden & I. Johans. (1980: 256), *Atraporiella* Ryvarden (2007: 38), *Austeria* Miettinen (2016: 159), *Butyrea* Miettinen (2016: 161), *Cabalodontia* Piątek (2004: 2), *Caudicicola* Miettinen, M. Kulju & Kotir. (2017: 163), *Citripora* Miettinen (2016: 163), *Elaphroporia* Z.Q. Wu & C.L. Zhao (2018: 88), *Etheirodon* Banker (1902: 441), *Flabellophora* G. Cunn. (1965: 88), *Flaviporus* Murrill (1905: 360), *Frantisekia* Spirin & Zmitr. (2007: 142), *Junghuhnia* Corda (1842: 195), *Lamelloporus* Ryvarden (1987: 529), *Loweomyces* (Kotl. & Pouzar) Jülich (1982: 424), *Metuloidea* G. Cunn. (1965: 263), *Mycorrhaphium* Maas Geest. (1962: 394), *Niemelaea* Zmitr., Ezhov & Khimich (2015: 27), *Nigroporus* Murrill (1905: 361), *Rhomboidia* C.L. Zhao (2020: 656), *Steccherinum* Gray, *Trullell*a Zmitr. (2018: 104), and *Xanthoporus* Audet (2010: 451) according to recent studies (He *et al.* 2024).

The genus *Cabalodontia* M. Piątek. is typified by the species *C. queletii* (Bourdot & Galzin) M. Piątek (2004: 3). It is characterized by basidiomata resupinate, ceraceous to subgelatinous, with odontoid, tuberculate or smooth hymenial surface, hyphal system monomitic, generative hyphae with clamps, cystidia lacking or present; basidia narrowly clavate, basidiospores non-amyloid, allantoid or ellipsoidal (Piatek 2004). Miettinen *et al.* (2012) confirmed by phylogenetic evidence that only the type species, *C. queletii*, belonged to *Cabalodontia*. Westphalen *et al*. (2021) expanded *Cabalodontia* by including two other species as *C. albofibrillosa* (Hjortstam & Ryvarden) Westph (2021: 795), from Asia, and *C. delicata* Westph. & Motato-Vásq (2021: 795), from the Neotropics. Currently, 7 species have been accepted worldwide in *Cabalodontia* (Piątek 2004, Westphalen *et al*. 2021). *Cabalodontia* has registered 7 specific and infraspecific names on Index Fungorum (http://www.indexfungorum.org) and MycoBank (https://www.mycobank.org).

During investigations on the wood-inhabiting fungi from Biluo Snow Mountain in Yunnan province of China, three specimens of Steccherinaceae were collected that could not be assigned to any described species. To clarify the placement and relationships of these specimens, we carried out a phylogenetic and taxonomic study on Steccherinaceae, based on the combined ITS+nLSU sequences analysis. These specimens are identified as an undescribed species of *Cabalodontia*, and the detailed description and illustrations of the new species are provided here.

Materials and methods

Sample collection and herbarium specimen preparation

Fresh basidiomata of fungi growing on angiosperm branches were collected from Weixi of Yunnan Province, P.R. China. The samples were photographed in situ and fresh macroscopic details were recorded. Photographs were recorded using a Jianeng 80D camera (Tokyo, Japan). All of the photos were 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), then sealed and stored in an envelope bag and deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

Macromorphological descriptions are based on field notes and photos captured in the field and lab. Color terminology follows Petersen (Petersen 1996). The micromorphological data were obtained from the dried specimens after observation under a light microscope with a magnification of 10 × 100 oil (Zhao *et al.* 2023, Dong *et al*. 2024). The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB = Cotton Blue, CB– = acyanophilous, IKI = Melzer's Reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied and n = a/b (number of spores (a) measured from given number (b) of specimens). The new species was registered in the MycoBank database (http://www.mycobank.org).

DNA extraction and sequencing

The CTAB rapid plant genome extraction kit DN14 (Aidlab Biotechnologies Co. Ltd., Beijing) was used to obtain genomic DNA from dried specimens following the manufacturer's instructions. The extracted DNA was maintained at –20 °C for long-term storage. Two molecular markers were investigated, i.e., internal transcribed spacer (ITS), the ITS region was amplified with the primer pair ITS5 and ITS4 (White *et al.* 1990), nuclear large subunit ribosomal RNA (nLSU), the nLSU region with primer pair LR0R and LR7 (Vilgalys & Hester 1990). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min; followed by 35 cycles of 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 (Dong *et al.* 2024). 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 directly sequenced at the Kunming Tsingke Biological Technology Ltd. Co. (Yunnan, P.R. China). All newly generated sequences were deposited in GenBank (https://www.ncbi.nlm.nih.gov/genbank/) (Table 1).

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

Species Name	Sample No.	GenBank Accession No.		References
		ITS	nLSU	
Antella americana	KHL 11949	JN710509	JN710509	Miettinen *et al.* 2012
Antella tibetica	BJFC 037905	NR_182983	NG_149046	Du *et al.* 2022
Antrodiella faginea	KHL 11977	JN710514	JN710514	Miettinen *et al.* 2012
Antrodiella semisupina	X242	JN710521	JN710521	Miettinen *et al.* 2012
Atraporiella neotropica	Ryvarden 44447	HQ659221	HQ659221	Miettinen *et al.* 2012
Atraporiella yunnanensis	CLZhao 604	MF962482	MF962485	Wu *et al.* 2017
Butyrea japonica	10202	JN710556	JN710556	Cao *et al.* 2021
Butyrea luteoalba	5403	JN710558	JN710558	Cao *et al.* 2021
Cabalodontia albofibrillosa	Sanyal 6903	KP401770	KP401770	Westphalen *et al.* 2021
Cabalodontia albofibrillosa	CLZhao 8722	MZ713669	MZ713811	Dong *et al.* 2024
Cabalodontia aurantiaca	**CLZhao 34896**	**PX115615**	**PX115618**	**Present study**
Cabalodontia aurantiaca	**CLZhao 34508**	**PX115613**	**PX115616**	**Present study**
Cabalodontia aurantiaca	**CLZhao 34601**	**PX115614**	**PX115617**	**Present study**
Cabalodontia delicata	MCW 670/19	MT849296	MT849296	Westphalen *et al.* 2021
Cabalodontia delicata	MCW 693/19	MT849297	MT849297	Westphalen *et al.* 2021
Cabalodontia queletii	CBS:233. 56	MH857599	MH869147	Westphalen *et al.* 2021
Cabalodontia queletii	CBS 234. 56	MH857600	MH869148	Vu *et al.* 2019
Climacocystis borealis	KHL 13318	JN710527	JN710527	Cao *et al.* 2021
Elaphroporia ailaoshanensis	CLZhao 595	MG231568	MG748854	Wu *et al.* 2018
Elaphroporia ailaoshanensis	CLZhao 596	MG231572	MG748855	Wu *et al.* 2018
Etheirodon fimbriatum	KHL 11905	JN710530	JN710530	Miettinen *et al.* 2012
Etheirodon fimbriatum	CLZhao 10114	MZ713671	MZ713841	Dong *et al.* 2024
Etheirodon roseoalbum	CLZhao 24770	OR096187	OR461452	Dong *et al.* 2024
Etheirodon roseoalbum	CLZhao 24903	OR096188	OR461453	Dong *et al.* 2024
Flaviporus brownii	Gates 22.V. 2007	JN710538	JN710538	Miettinen *et al.* 2012
Flaviporus liebmannii	Ryvarden 44553	JN710540	JN710540	Miettinen *et al.* 2012
Frantisekia fissiliformis	CBS 436.72	MH860521	MH872232	Vu *et al.* 2019
Frantisekia mentschulensis	BRNM 710170	FJ496670	FJ496728	Tomšovský *et al.* 2010
Junghuhnia crustacea	X262	JN710553	JN710553	Miettinen *et al.* 2012
Junghuhnia crustacea	X1127	JN710554	JN710554	Yuan *et al.* 2019

......continued on the next page

TABLE 1. (Continued)

Species Name	Sample No.	GenBank Accession No.		References
		ITS	nLSU	
Junghuhnia pseudocrustacea	Yuan6160	MF139551	-	Yuan *et al.* 2019
Junghuhnia pseudocrustacea	Zhou283	MF139552	-	Yuan *et al.* 2019
Loweomyces fractipes	Setliff 19.8.2007	JN710569	JN710569	Miettinen *et al.* 2012
Loweomyces tomentosus	MCW 366/12	KX378870	KX378870	Westphalen *et al.* 2016
Metuloidea murashkinsky	X449	JN710588	JN710588	Westphalen *et al.* 2019
Metuloidea reniformis	MCW 542/17	MT849303	MT849303	Westphalen *et al.* 2021
Metuloidea rhinocephala	X460	JN710562	JN710562	Westphalen *et al.* 2019
Mycorrhaphium adustum	KHL 12255	JN710573	JN710573	Miettinen *et al.* 2012
Mycorrhaphium hispidum	MCW 429/13	MH475307	MH475307	Westphalen *et al.* 2019
Nigroporus vinosus	Yuan12916	MT681923	MT675108	Cao *et al.* 2021
Nigroporus vinosus	Seitzman 2008-100	JN710575	JN710575	Miettinen *et al.* 2012
Steccherinum austrosinense	Dai 17540	MN871755	MN877768	Du *et al.* 2022
Steccherinum austrosinense	Dai 17679	MN871756	MN877769	Du *et al.* 2020
Steccherinum larssonii	MCW 593/17	MT849306	MT849306	Westphalen *et al.* 2021
Steccherinum larssonii	MCW 594/17	MT849307	MT849307	Westphalen *et al.* 2021
Steccherinum meridionale	CBS 125887	MH864086	MH875544	Vu *et al.* 2019
Steccherinum meridionale	Cui 16691	ON417195	ON417247	Liu *et al.* 2023
Steccherinum ochraceum	2060	JN710589	JN710589	Miettinen *et al.* 2012
Steccherinum ochraceum	KHL 11902	JN710590	JN710590	Miettinen *et al.* 2012
Steccherinum puerense	CLZhao 3122	MW682341	-	Wu *et al.* 2021
Steccherinum puerense	CLZhao 3644	MW682342	MW682338	Wu *et al.* 2021
Steccherinum rubigimaculatum	CLZhao 4069	MW682343	MW682339	Wu *et al.* 2021
Steccherinum rubigimaculatum	CLZhao 10638	MW682344	MW682340	Wu *et al.* 2021
Steccherinum tenue	KHL 12316	JN710598	JN710598	Miettinen *et al.* 2012
Steccherinum tenue	FP102082sp	KY948817	-	Justo *et al.* 2017
Steccherinum tenuispinum	X311	JN710599	JN710599	Miettinen *et al.* 2012
Steccherinum tenuispinum	X453	JN710600	JN710600	Miettinen *et al.* 2012
Steccherinum undigerum	MCW 426/13	KY174986	KY174986	Westphalen *et al.* 2018
Steccherinum undigerum	MCW 496/14	KY174988	KY174988	Westphalen *et al.* 2018
Steccherinum wumengshanense	CLZhao 23586	OR658995	OR999392	Wang *et al.* 2024
Steccherinum yunnanense	CLZhao 1445	MW290042	MW290056	Dong *et al.* 2022
Steccherinum yunnanense	CLZhao 2822	MW290043	MW290057	Dong *et al.* 2022
Trullella dentipora	Ryvarden 40822	JN710512	JN710512	Miettinen *et al.* 2012
Trullella duracina	MCW 41012	MH475309	MH475309	Westphalen *et al.* 2019
Trullella duracina	RP 96	MH475310	MH475310	Westphalen *et al.* 2019
Xanthoporus syringae	X339	JN710606	JN710606	Miettinen *et al.* 2012
Xanthoporus syringae	Jeppson 2264	JN710607	JN710607	Miettinen *et al.* 2012

Phylogenetic analyses

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). Each dataset was aligned separately at first and then the ITS and nLSU regions were combined with Mesquite version 3.51. Sequence of *Climacocystis borealis* (Fr.) Kotl. & Pouzar obtained from GenBank was used as an outgroup to root trees in the ITS+nLSU analysis for the family Steccherinaceae (Fig. 1) by a previous study (Cao *et al.* 2021).

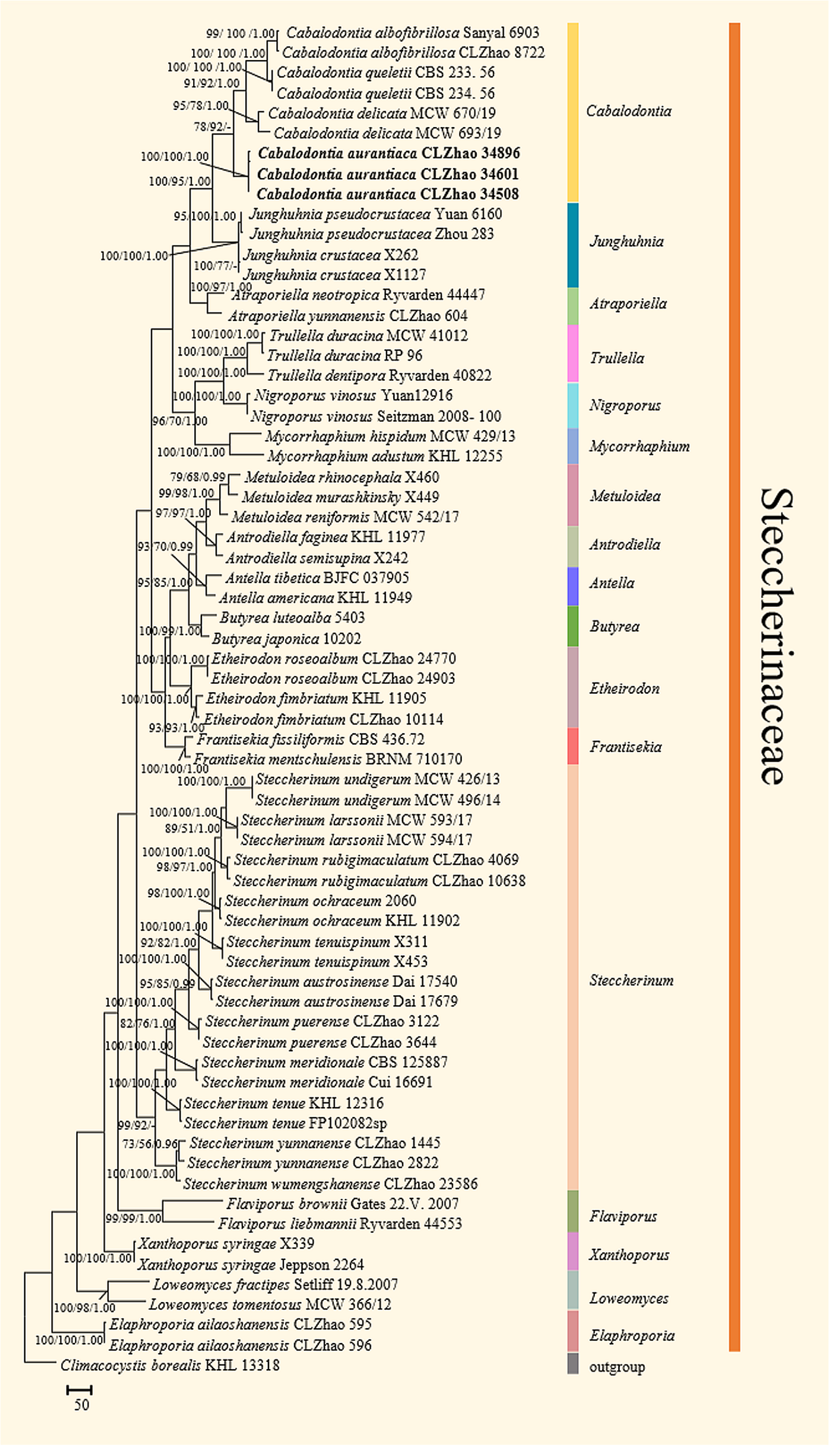

FIGURE 1. Maximum Parsimony strict consensus tree illustrating *Cabalodontia* and related genera in the family Steccherinaceae based on the combined ITS+nLSU sequences. Branches are labeled with Maximum Likelihood bootstrap values ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95. The newly generated sequences are in red-bold.

Maximum parsimony (MP), maximum likelihood (ML) and Bayesian Inference (BI) analyses were applied to the three combined datasets. Maximum parsimony analysis in PAUP* version 4.0b10 (http://phylosolutions. com/paup-test/) was applied to the combined ITS+nLSU dataset following a previous study (Fig. 1, Zhao & Wu 2017). All of the characteristics were equally weighted and gaps were treated as missing data. Max-trees were set to 5,000, branches of zero length were collapsed and all most-parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1,000 replicates (Felsenstein 1985).

MrModeltest 2.3 was used to determine the best-fit evolution model for each dataset for the purposes of Bayesian inference (BI) (Nylander 2004), 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 *et al.* 2012). A total of four Markov chains were run for two runs from random starting trees for 1.7 million generations for ITS+nLSU (Fig. 1); with trees and parameters sampled every 1,000 generations. The first one-fourth generations were discarded as burn-in. A majority rule consensus tree was computed from the remaining trees. Branches were considered as significantly supported if they received a maximum likelihood bootstrap support value (BS) of ≥ 70%, a maximum parsimony bootstrap support value (BT) of ≥ 50% or a Bayesian posterior probability (BPP) of ≥ 0.95.

Results

Molecular phylogeny

The aligned ITS+nLSU dataset (Fig. 1) comprised 67 specimens representing 44 species. The aligned length of the dataset was 2283 characters, of which 1522 characters were constant, 178 were variable and parsimony-uninformative and 583 were parsimony-informative. Maximum parsimony analysis yielded three equally parsimonious trees (TL = 3303, CI = 0.3803, HI = 0.6197, RI = 0.6436, RC = 0.2447). At the end of the BI runs, the average standard deviation of split frequencies was 0.008520 (BI) and the effective sample size (ESS) across the two runs is double the average ESS (avg. ESS) = 156.

In phylogenetic reconstruction of Steccherinaceae (Polyporales), based on combined ITS + nLSU sequences (Fig. 1), 17 genera were included in the present study. Among them, the new species *Cabalodontia aurantiaca* was assigned to the genus *Cabalodontia*, and it is closely related to *C. delicata*.

Taxonomy

Cabalodontia aurantiaca J.Q. Su & C.L. Zhao, *sp. nov.* Figs. 2–4
MycoBank no.: 860763

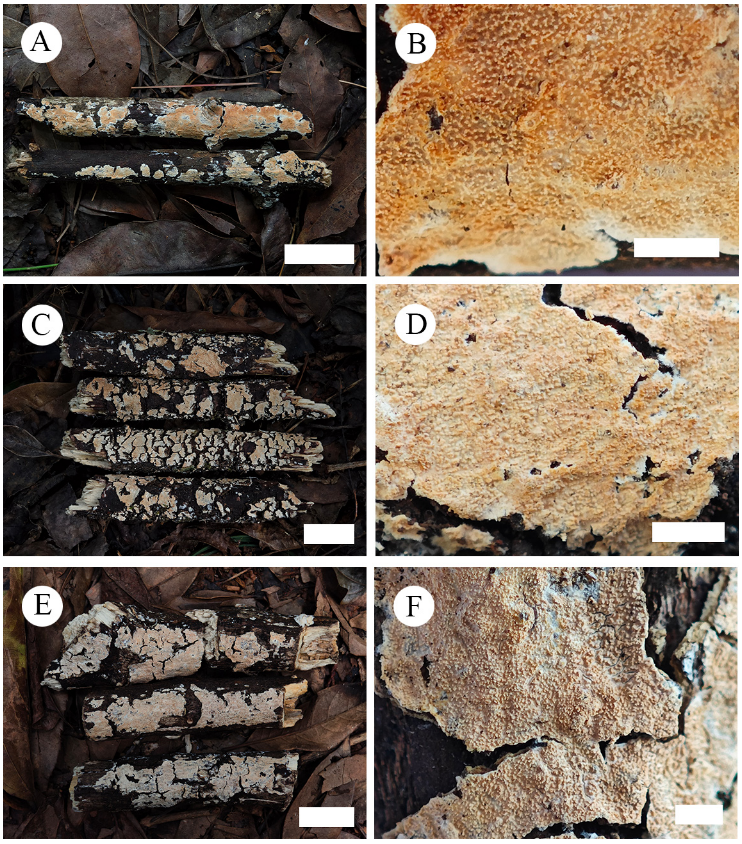

FIGURE 2. Basidiomata of *Cabalodontia aurantiaca* (A, B) CLZhao 34601 (holotype); (C, D) CLZhao 34896; (E, F) CLZhao 34508. Scale bars: A, C, E = 2 cm; B, D, F = 2 mm.

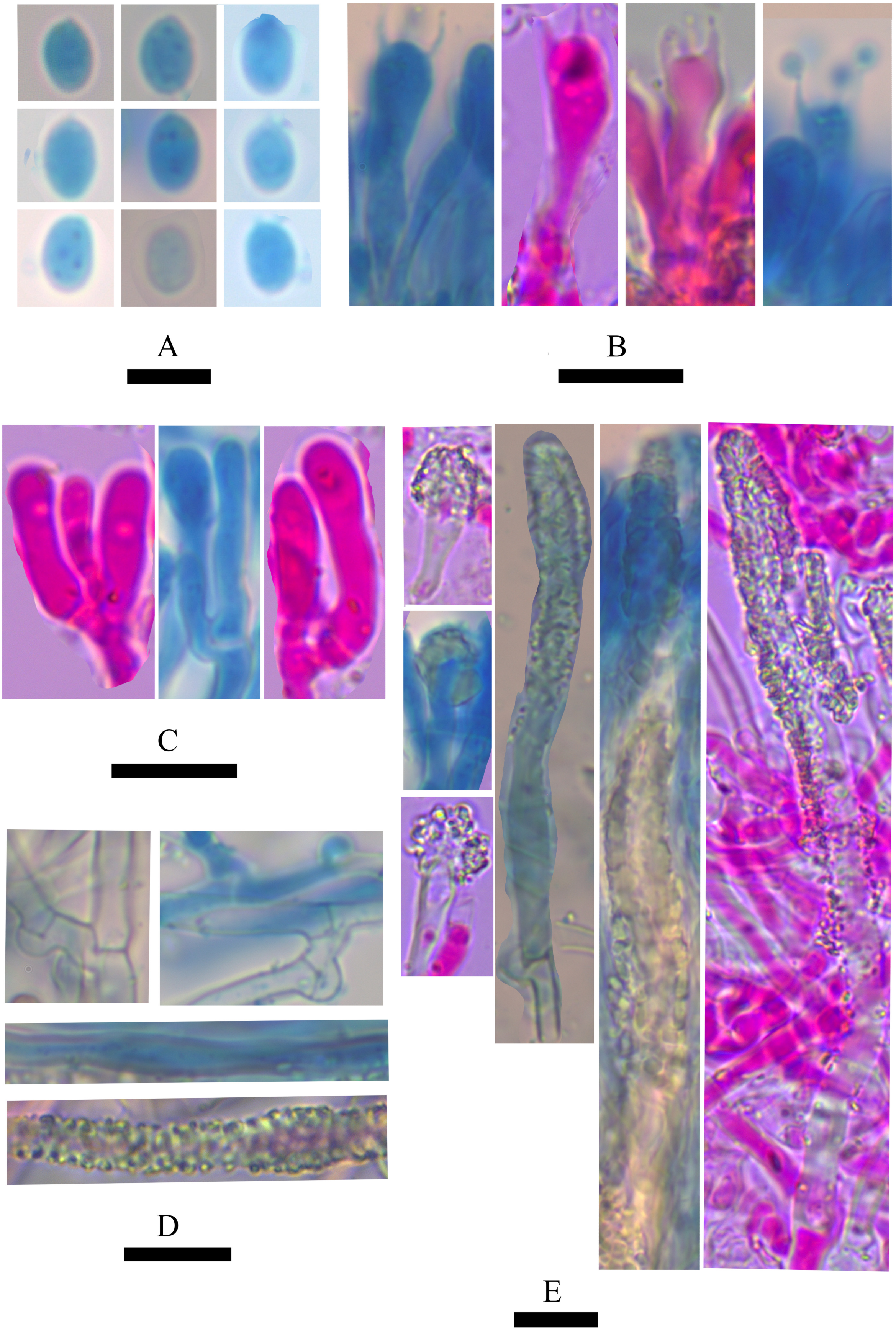

FIGURE 3. Sections of hymenium of *Cabalodontia aurantiaca* (holotype, CLZhao 34601). (A) Basidiospores; (B) Basidia; (C) Basidioles; (D) Generative hyphae; (E) Cystidia. Scale bars: A = 5 µm, B–E = 10 µm.

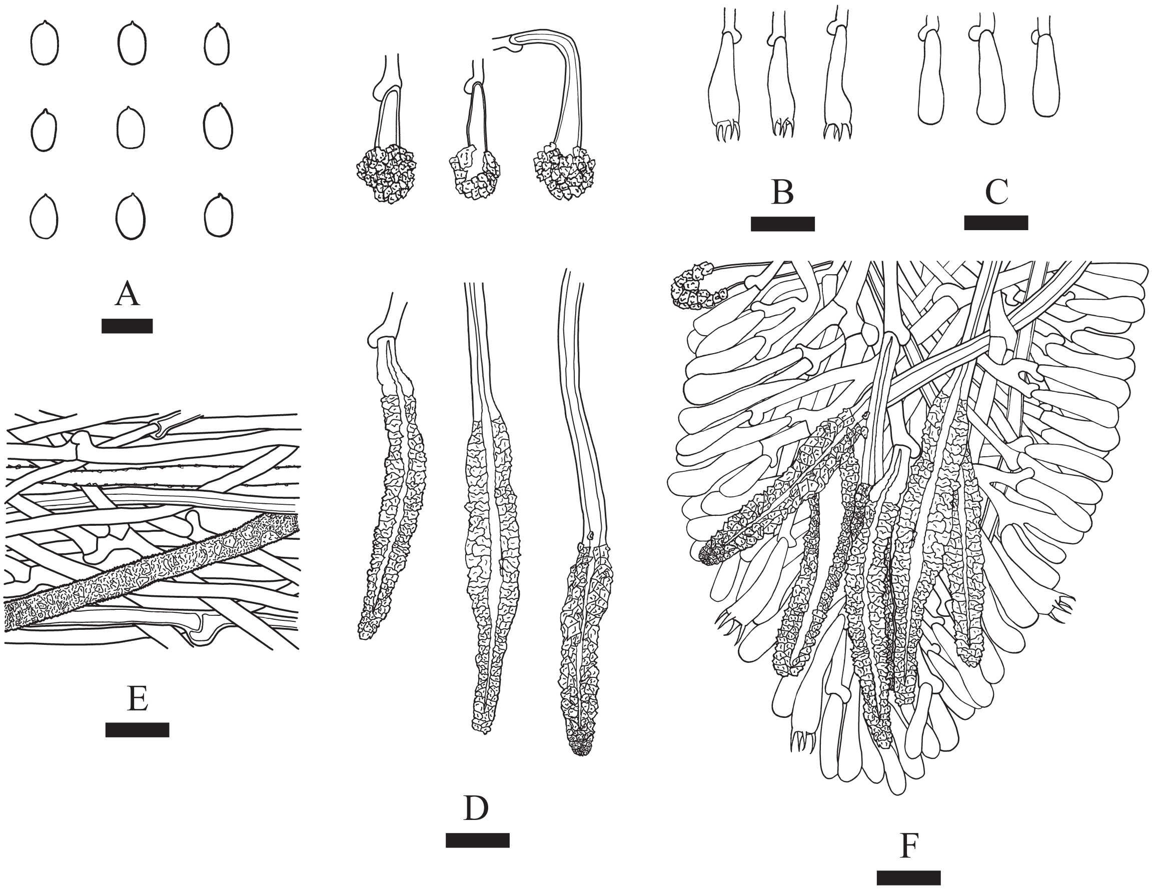

FIGURE 4. Microscopic structures of *Cabalodontia aurantiaca* (holotype, CLZhao 34601). (A) Basidiospores; (B) Basidia; (C) Basidioles; (D) Cystidia; (E) A section of subhymenial hyphae; (F) A section of the hymenium. Scale bars: A = 5 µm, B–F = 10 µm.

***Etymology*:**—*Aurantiaca* (Lat.): referring to the orange-colored hymenial surface of the type specimens.

***Diagnosis*:**—Differs from other species of *Cabalodontia* by its orange basidiomata with odontoid hymenial surface, a monomitic hyphal system with clamped generative hyphae, thick-walled skeletocystidia measuring 34.5–88 × 5–9 µm and ellipsoid basidiospores measuring 4–5 × 2.5–3.0 µm.

***Holotype*:**—CHINA. Yunnan Province, Diqing Prefecture, Weixi County, Weideng Township, Songpo Village, GPS coordinates 27°5′N, 99°13′E, altitude 2693 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 13 October 2023, CLZhao 34601 (SWFC 00034601).

***Basidiomata*:**—Annual, resupinate, adnate, soft coriaceous, white to orange when fresh, becoming slightly darker upon drying, up to 18 cm long, 2 cm wide, and 50–100 µm thick. Hymenial surface odontoid, pale orange to orange when fresh, orange upon drying. Sterile margin white, thinning out, up to 1 mm wide.

***Hyphal structure*:**—Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin to thick- walled, often branching near the clamp connections, interwoven, 2.5–5 µm in diameter; IKI–, CB–, tissues unchanged in KOH; subhymenial hyphae covered by crystals.

***Hymenium*:**—Skeletocystidia numerous, thick-walled, dominating in the trama, encrusted portion 34.5–88 × 5–9 µm. Basidia clavate, slightly sinuous or constricted from the middle, colorless, thin-walled, with 4 sterigmata and a basal clamp connection, 13–19 × 3–5 µm; basidioles dominant, similar to basidia in shape, but slightly smaller.

***Basidiospores*:**—Ellipsoid, thin-walled, smooth, colorless, IKI–, CB–, (3.5–)4–5 × (2–)2.5–3.0 (–3.5) µm, L = 4.32 µm, W = 2.93 µm, Q = 1.47 (n = 60/2).

***Additional specimens examined (paratypes)*:**—CHINA. Yunnan Province, Diqing Prefecture, Weixi County, Weideng Township, Songpo Village, GPS coordinates 27°5′N, 99°13′E, altitude 2475 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 13 October 2023, CLZhao 34508 (SWFC 00034508); Weixi County, Zhonglu Township, Lagaluo Village, GPS coordinates 27°10′N, 99°8′E, altitude 1742 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 14 October 2023, CLZhao 34896 (SWFC 00034896).

TABLE 2. A morphological comparison between *Cabalodontia aurantiaca* and three similar species in the genus *Cabalodontia*.

Species name	Generative hyphae	Cystidia	Basidia	Basidiospores	References
Cabalodontia albofibrillosa	Hyphae with clamps, thin-walled or with slightly thickened walls, 3 µm wide.	Cystidia, usually more than 100 µm long, strongly encrusted, thick-walled and often with several adventitious septa and with a basal clamp.	Basidia subclavate, thin-walled, with 4 sterigmata and a basal clamp, 20–25 × 5 µm.	Basidiospores subglobose, thin-walled, 4–4.5 × 3.5–4 µm.	(Hjortstam & Ryvarden 1984)
C. aurantiaca	**Hyphae with clamps, thin to thick- walled, 2.5–5 µm wide.**	**Skeletocystidia thick-walled, dominating in the trama, encrusted portion 34.5–88 × 5–9 µm.**	**Basidia clavate, slightly sinuous or constricted from the middle, thin-walled, with 4 sterigmata and a basal clamp connection, 13–19 × 3–5 µm.**	**Basidiospores ellipsoid, thin-walled, 4–5 × 2.5–3.0 µm.**	**Present study**
C. delicata	Hyphae with clamps, thin- to thick-walled, 2–5 µm wide.	Cystidia of two types: (i) thin-walled leptocystidia in the hymenium, clavate, 3.5–6 µm wide; (ii) thick-walled cystidia projecting toward the trama and the hymenium, wide at the middle portion and narrow at the apex, heavily encrusted, encrusted portion 4.5–11.5 µm wide.	Basidia clavate, with 4 sterigmata, and a basal clamp, 12–16 × 4–5.5 µm.	Basidiospores subglobose to oblong-ellipsoid, thin-walled, 3.5–4.0 × 2.5–3.0 µm.	(Westphalen *et al.* 2021)
C. queletii	Hyphae with clamps, thin-walled, 2–4 µm wide.	Cystidia conical, 60–100 × 6–8 µm, heavily encrusted, with thin to usually thick-walled.	Basidia clavate,with 4 sterigmata, and a basal clamp, 15–25 × 4–5 µm.	Basidiospores narrowly ellipsoid to cylindrical, thin-walled, 5–6 × 3–3.5 µm.	(Bernicchia & Gorjón 2010)

Discussion

Based on the morphological and phylogenetic methods, a number of wood-inhabiting fungi were recorded in China (Luo & Zhao 2021, Zhao *et al*. 2023, Dong *et al*. 2024, Su *et al*. 2024, Dai *et al.* 2025, Deng *et al.* 2025, Yang *et al.* 2025). Biluo Snow Mountain nationanl natural reserve is located in Weixi, Yunnan Province, China, in which it is situated in the western part of the mountainous region in southwestern China, and it is one of the 34 world's biodiversity hotspots. The region has a complex terrain and diverse ecosystems, with abundant fungal resources. The present study, the new species *C. aurantiaca* was reported based on a combination of morphological features and molecular evidence.

Phylogenetically, DNA sequence-based classification and identification has become the standard approach in fungal taxonomy (Hibbett *et al*. 2007, Xu 2020, Lücking *et al*. 2021). In this study, the phylogram inferred from the ITS+nLSU gene regions (Fig. 1), revealed that the new species grouped into the genus *Cabalodontia*, in which *C. aurantiaca* closely related to *C. delicata*, *C. queletii* and *C. albofibrillosa*. However, morphologically *C. delicata* is distinct from *C. aurantiaca* by having white to cream basidiomata and thin-walled clavate leptocystidia (3.5–6 µm wide, Westphalen *et al.* 2021); *C. queletii* differs from *C. aurantiaca* by ceraceous basidiomata and narrowly ellipsoid to cylindrical basidiospores (5–6 × 3–3.5 um, Bernicchia & Gorjón 2010); *C. albofibrillosa* is separated from *C. aurantiaca* by having larger cystidia and subglobose basidiospores (4–4.5 × 3.5–4 um, Hjortstam & Ryvarden 1984).

Morphologically, *C. aurantiaca* is similar to *C. delicata*, *C. queletii* and *C. albofibrillosa* by having the odontioid hymenial surface, monomitic hyphal system, encrusted thick-walled cystidia and smooth basidiospores. The morphological distinctions among *Cabalodontia* species, including the newly described taxon *C. aurantiaca*, are delineated through the comparative analysis presented in Table 2.

Biluo Snow Mountain belongs to the northwestern Yunnan of the Hengduan Mountains in The Qinghai-Xizang Plateau, serving as a transitional zone between The Qinghai-Xizang Plateau and Yunnan. Its climate and vegetation exhibit significant vertical distribution. It is rich in woody plant species, providing excellent substrates for wood-inhabiting fungi. Hence, studying the diversity of wood-inhabiting fungi in the northwestern Yunnan of China is of great significance. In this study, one new species is identified from the northwestern Yunnan, which will further enrich our knowledge of fungal diversity in this area, and more new taxa if this genus *Cabalodontia* will be found with further fieldwork and molecular analyses, the result will enrich the species diversity of fungi worldwide and promote the progress of fungi-related research.

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