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中国西南地区脊革菌属（担子菌门）两个新种

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摘　要：木腐真菌作为森林生态系统中的分解者发挥着关键作用。本研究基于形态学和分子系统学证据描述并绘制了来自中国西南地区云南省2个木腐真菌新种：小孢脊革菌 *Lopharia minispora* 和斑点脊革菌 *Lopharia punctata*。*Lopharia minispora* 的形态特征为革质担子果，具浅棕色有裂纹的子实层体，菌丝系统一体系具锁状联合，担孢子窄椭圆形，大小为(5.5–6.7)×(2.7–3.3) μm；*L. punctata* 的形态特征为膜质担子果，具白色至奶油色的子实层体，菌丝系统一体系且生殖菌丝具简单分隔，担孢子近球形至球形，大小为(9.5–12)×(7.5–10.1) μm。研究采用最大似然法、最大简约法和贝叶斯推断法对研究标本的 ITS+nLSU nrRNA 基因序列进行系统发育分析，分析表明 2 个新物种隶属于 *Lopharia*，其中 *L. minispora* 与 *L. erubescens* 聚为姐妹种，*L. punctata* 与 *L. ayresii* 和 *L. resupinata* 支系为近缘类群。

关键词：新种；木腐菌；分类；分子系统学；云南省

Two new species of *Lopharia* (Basidiomycota) from southwest China

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Abstract: Wood-decaying fungi play crucial roles as decomposers in forest ecosystems. In this study, two new *Lopharia* species from Yunnan Province in southwest China, *Lopharia minispora* and *Lopharia punctata,* are described and illustrated based on the morphological and molecular evidence. *Lopharia minispora* is characterized by its slightly brown and cracked

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basidiomata when dry, a monomitic hyphal system with clamp connections, and oblong-ellipsoid basidiospores measuring (5.5–6.7)×(2.7–3.3) µm; *L. punctata* is characterized by its membranous, white to cream basidiomata, a monomitic hyphal system with simple-septa on generative hyphae and subglobose to globose basidiospores measuring (9.5–12)×(7.5–10.1) µm. Sequences of ITS and nLSU rRNA markers of the studied samples were employed, and phylogenetic analyses were performed with maximum likelihood, maximum parsimony and Bayesian inference methods, ensuring the reliability of our findings. The dataset analyses showed that the two new species clustered into the genus *Lopharia*, in which *L. minispora* was sister of *L. erubescens*; *L. punctata* grouped with the lineage of *L. ayresii* and *L. resupinata*.

Keywords: new species; wood-decaying fungi; taxonomy; molecular systematics; Yunnan Province

INTRODUCTION

Fungi play vital roles in forest ecosystem as endophytes, pathogens and saprobes (Wei & Dai 2004; Dai 2012; Bhunjun *et al.* 2022; Dong *et al.* 2023; Yuan *et al.* 2023; Hyde *et al.* 2024b). The number of species of kingdom *Fungi* is estimated to be in the range of 2.2 to 13.2 million, with the latest estimate of 2 to 3 million species, but only around 150 000 species have been named and classified to date (Dai & Zhuang 2010; Bhunjun *et al.* 2022; He *et al.* 2024; Hyde *et al.* 2024b; Zhao *et al.* 2024). Undescribed fungi could therefore represent a massive potential at a time when there is a need to find new sources of food, novel antibiotics, novel metabolites with biotechnological, industrial and pharmaceutical applications (Hyde *et al.* 2019). Hjortstam & Ryvarden (1990) compiled the first nomenclature of the genus *Lopharia* Kalchbr. & MacOwan, which is an important group of the wood-decaying fungi.

The genus *Lopharia* s.s. (Polyporales), typified by *L. mirabilis* (Berk. & Broome) Pat., is stereoid fungi, and the identifying features of this genus are resupinate and effused-reflexed basidiomata, a monomitic or dimitic hyphal system, generative hyphae with clamp connection, presence of the large basidia and basidiospores and large, encrusted, hyaline, thick-walled lamprocystidia (Kalchbrenner 1881; Liu *et al.* 2018). Based on the MycoBank database (http://www.mycobank.org, accessed on 28 February 2025) and the Index Fungorum (http://www.indexfungorum.org, accessed on 28 February 2025), the genus *Lopharia* has registered 39 specific and infraspecific names, and 15 species are widely recognized (Hyde *et al.* 2024a).

Nowadays, DNA sequence-based classification and identification has become the standard approach in fungal taxonomy. The genus *Lopharia* was placed in the family Polyporaceae Fr. ex Corda in their phylogenetic analysis of the nrLSU, nrITS, and rpb1 dataset (Justo *et al*. 2017; He *et al.* 2024). The phylogenetic analyses of *Lopharia* based on the nuc rDNA ITS1-5.8S-ITS2 (ITS), D1-D2 domains of uc 28S rDNA (28S) and RNA polymerase II second-largest subunit (rpb2) sequences revealed that *L. resupinata* S.H. He, S.L. Liu & Y.C. Dai was closely related to *L. ayresii* (Berk. ex Cooke) Hjortstam, and *L. sinensis* S.H. He, S.L. Liu & Y.C. Dai was related to *L. cinerascens* (Schwein.) G. Cunn. and *L. mirabilis* (Berk. & Broome) Pat., in which *Lopharia mirabilis* specimens from temperate to tropical areas with varied hymenophore configurations all cluster together in a fully supported clade (Liu *et al.* 2018). Phylogenetic reconstruction for *Dentocorticium* (Parmasto) M.J. Larsen & Gilb., *Lopharia*, *Phlebiopsis* Jülich, and *Porostereum* Pilát inferred from a combined dataset of ITS and nLSU indicated that quite similar tree topologies and small or no significant differences in the statistical support values, in which two specimens clustered in a well-supported clade within the equally well-supported *Lopharia* s.s. clade, and confirmed that those sequences belonged to a new species as *L. erubescens* Xavier de Lima (Xavier de Lima *et al*. 2020).

During investigations on wood-decaying fungi in Yunnan Province, two undescribed species were discovered and introduced. The aims of this study are to confirm the taxonomic affinities of the new species within this genus and to elucidate the relationships among representative species of *Lopharia*.

1 MATERIALS AND METHODS

1.1 Morphology studies

Samples were collected from Yunnan Province, China and deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China. The macro-morphology was based on fresh and dried specimens. The color terms in description followed Anonymous and Petersen (Anonymous 1969; Petersen 1996). The micromorphological characteristics data were systematically analyzed from the dried specimens, and observed under a light microscope align with established methodologies (Guan & Zhao 2021; Wu *et al.* 2022; Dong *et al.* 2023). Sections mounted in 5% KOH and 2% phloxine B dye ($C_{20}H_2Br_4Cl_4Na_2O_5$). Other reagents were also used, including Cotton Blue and Melzer's reagent. Micromorphology observation follows Wu *et al.* (2022).

The following abbreviations were used:

(1) CB = Cotton Blue, CB– = acyanophilous;

(2) KOH = 5% potassium hydroxide;

(3) IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid;

(4) W = mean spore width (arithmetic average for all spores);

(5) L = mean spore length (arithmetic average for all spores);

(6) Q = variation in the L/W ratios between the specimens studied;

(7) n (a/b) = number of spores (a) measured from given number (b) of specimens (Guan & Zhao 2021; Wu *et al.* 2022; Wang *et al.* 2023).

1.2 DNA extraction, polymerase chain reaction, 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 primer pair of ITS5 and ITS4 (Zhao *et al.* 2012; White *et al.* 1990) was amplified with ITS region. The primer pair LR0R and LR7 was amplified with nuclear LSU region. The PCR was performed following Dong *et al*. (Guan & Zhao 2021; Dong *et al.* 2024). All newly generated sequences were successfully deposited into the National Center for Biotechnology Information (NCBI) GenBank database. All the nucleotide sequences were systematically listed in Table 1.

1.3 Phylogenetic Analyses

The nucleotide sequences were aligned initially by using MAFFT (https://mafft.cbrc.jp/alignment/server/) using the “G-INS-I” algorithm and then manually optimized in BioEdit (Hall 1999; Guan & Zhao 2021; Dong *et al.* 2023). The multi-locus sequence dataset align firstly and then combine ITS and nLSU sequences with mesquite. To determine the phylogeny, we compiled ITS and LSU sequences matrix, and *Dentocorticium ussuricum* (Parmasto) M.J. Larsen & Gilb. was used as outgroup for phylogenetic reconstruction of ITS+nLSU phylogenetic tree (Fig. 1).

Maximum parsimony, maximum likelihood (ML), and Bayesian inference (BI) analysis was applied to the combined ITS+nLSU datasets followed the previous study by Gu and Zhao (2021). The combined dataset was also analyzed using maximum likelihood (ML) in RAxML-HPC2 through the Cipres Science Gateway. Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates (Gu & Zhao 2021; Guan & Zhao 2021; Dong *et al.* 2023; Wang *et al.* 2024).

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for dataset (ITS+nLSU) for the purposes of Bayesian inference (BI). Bayesian inference was performed using MrBayes3.2.7a (Ronquist *et al.* 2012). Four Markov chains were run for 2 runs from random starting trees for 250 thousand generations for

ITS+nLSU (Fig. 1). The first one-fourth of all generations was discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches exhibiting phylogenetic significance were considered as significantly supported if they received maximum likelihood bootstrap value (BS) > 70%, maximum parsimony bootstrap value (BT) > 50%, or Bayesian posterior probabilities (BPP) > 0.95 (Gu & Zhao 2021; Guan & Zhao 2021; Dong *et al.* 2023).

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

Species Name	Specimen No.	GenBank Accession No.		Country	References
		ITS	LSU		
Dentocorticium ussuricum	He 3294	MF626359	MF626383	China	Xavier de Lima *et al.*, 2020
D. ussuricum	He 3322	MF626360	MF626384	China	Xavier de Lima *et al.*, 2020
Lopharia ayresii	He 2778	MF626353	MF626376	China	Xavier de Lima *et al.*, 2020
L. ayresii	He 20120724	MF626352	MF626375	China	Xavier de Lima *et al.*, 2020
L. cinerascens	He 2188	MF626350	MF626373	USA	Liu *et al.*, 2018
L. cinerascens	He 2228	MF626351	MF626374	USA	Liu *et al.*, 2018
L. cinerascens	CBS 485.62	MH858220	MH869821	USA	Xavier de Lima *et al.*, 2020
L. erubescens	URM 93246	MK993641	MK993636	Brazil	Xavier de Lima *et al.*, 2020
L. erubescens	URM 93247	MK993642	—	Brazil	Xavier de Lima *et al.*, 2020
L. minispora	**CLZhao 21694**	**PQ362229**	**PQ363273**	**China**	**Present study**
L. minispora	**CLZhao 21779**	**PQ362230**	**PQ363274**	**China**	**Present study**
L. minispora	**CLZhao 21787***	**PQ362231**	**PQ363275**	**China**	**Present study**
L. mirabilis	Dai 5147	MF626342	MF626365	China	Liu *et al.*, 2018
L. mirabilis	Yuan 2532	MF626343	MF626366	China	Liu *et al.*, 2018
L. punctata	**CLZhao 32072**	**PQ362232**	**PQ363276**	**China**	**Present study**
L. punctata	**CLZhao 32105**	**PQ362233**	**PQ363277**	**China**	**Present study**
L. punctata	**CLZhao 32356**	**PQ362234**	**PQ363278**	**China**	**Present study**
L. punctata	**CLZhao 32688***	**PQ362235**	**PQ363279**	**China**	**Present study**
L. resupinata	He 4401	—	MF626377	China	Liu *et al.*, 2018
L. sinensis	He 2424	MF626349	MF626372	China	Liu *et al.*, 2018
L. sinensis	He 2428	MF626347	MF626370	China	Liu *et al.*, 2018
L. sinensis	He 2510	MF626348	MF626371	China	Liu *et al.*, 2018

Note: * is shown type material, holotype.

2 RESULTS

2.1 Molecular phylogeny

In *Lopharia* analyses, the ITS+nLSU dataset (Fig. 1) included sequences from 22 fungal specimens representing 9 taxa. The phylogram inferred from ITS+nLSU sequences within the genus *Lopharia* revealed that the presence of two previously undescribed species embedded within the genus, in which *L. minispora* was sister of *L. erubescens* with a medium supported lineage (71% BT and 1.00 BPP); *L. punctata* was grouped with the lineage of *L. ayresii* and *L. resupinata* (100% BT and 1.00 BPP).

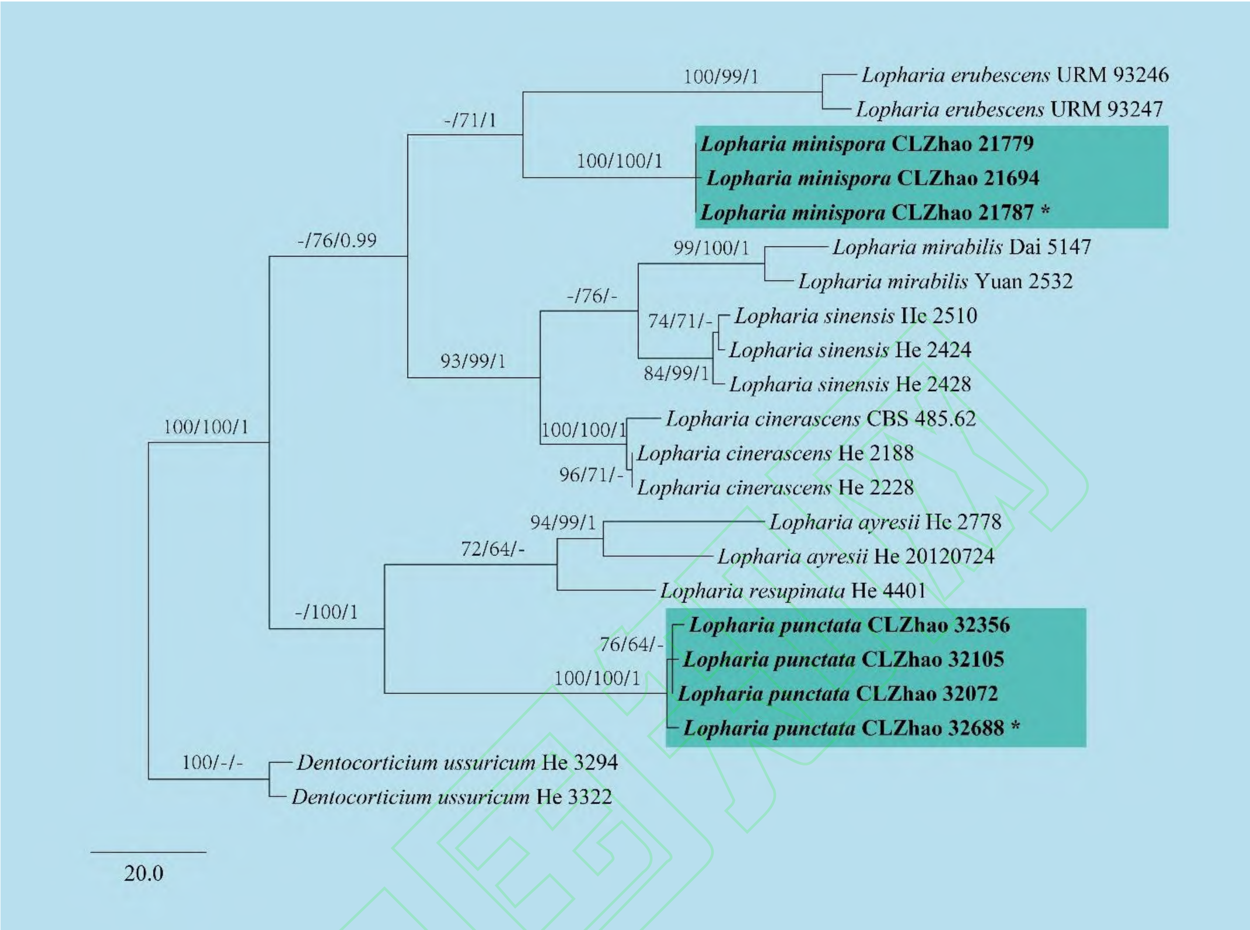

Fig. 1 Phylogeny of *Lopharia* (in bold) and related species by ML analysis based on combined ITS and LSU rDNA sequences. Branches are labeled with maximum likelihood bootstrap values > 70%, parsimony bootstrap values > 50%, and Bayesian posterior probabilities > 0.95, respectively.

2.2 Taxonomy

Lopharia minispora **Z.R. Gu & C.L. Zhao, sp. nov.** (Fig.2, Fig.3, Fig.4)

MycoBank no.: 856035

Holotype. China. Yunnan Province, Lijiang, Heilongtan Forest Park, GPS coordinates 26°52'N, 100°14'E, elev. 2 000 m asl., on the fallen angiosperm branch, 21 July 2021, leg. C.L. Zhao, CLZhao 21787 (SWFC).

Etymology. *minispora* (Lat.): refer to the species having small basidiospores.

Diagnosis. It differs from other *Lopharia* species by its slightly brown and cracked basidiomata, a monomitic hyphal system with clamp connections, oblong-ellipsoid basidiospores measuring (5.5–6.7)×(2.7–3.3) μm.

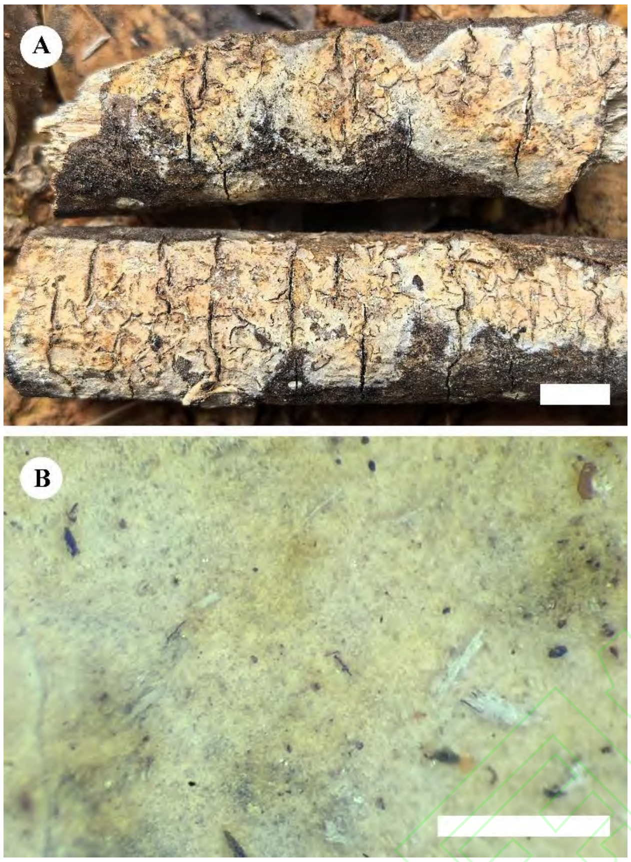

Fig. 2 Basidiomata of *Lopharia minispora*, (holotype, CLZhao 21787). Bars: A=1 cm; B=1 mm.

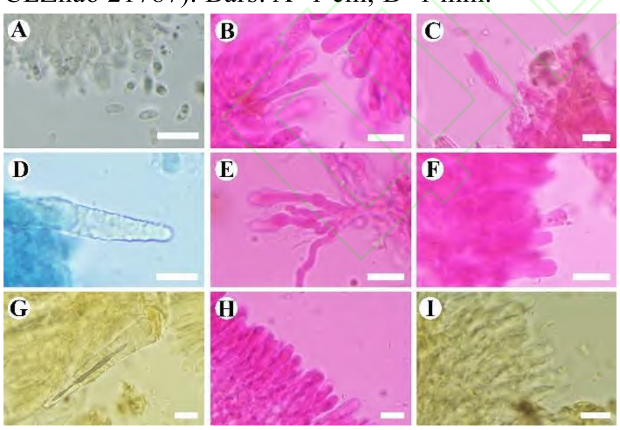

Fig. 3 Sections of hymenium of *Lopharia minispora* (holotype, CLZhao 21787). A: Basidiospores; B, E: Cystidia; C, F, H, I: Basidia and basidioles; D, G: Lamprocystidia. Bars: A–I = 10 μm. 10×100 Oil.

Basidiomata. Annual, resupinate, coriaceous, without odor or taste when fresh, up to 11 cm long, 2.1 cm wide, less than 1 mm thick. Hymenial surface cream to ochraceous when fresh, ochraceous to slightly brown when dry, cracking. Sterile margin narrow, cream, up to 1 mm wide.

Hyphal structure. Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin- to slight thick-walled, unbranched, interwoven, 2–3 μm in diameter, IKI–, CB–; tissues unchanged in KOH.

Hymenium. Subiculum thin, with numerous small crystals; generative hyphae colorless, thin- to slightly thick-walled, unbranched, interwoven, 2–3 μm in diam. Subhymenium slightly thick-walled, up to 120 μm thick; generative hyphae colorless, slightly thick-walled, vertically arranged, 2–4 μm in diam. Lamprocystidia abundant, arising from subhymenium, subulate, heavily encrusted with crystals, distinctly thick-walled, embedded in subhymenium or exerted, (41–54)×(7–10) μm. Basidia clavate, with a basal clamp connection and four sterigmata, (22–28)×(5–7) μm; basidioles dominating in hymenium, similar to basidia but smaller.

Basidiospores. Oblong ellipsoid, colorless, thin-walled, smooth, containing guttules, IKI–, CB–, (5.3–)5.5–6.7(–7)×(2.5–)2.7–3.3(–3.6) μm, L = 6.12 μm, W=2.99 μm, Q=2.04–2.07 (n=90/3).

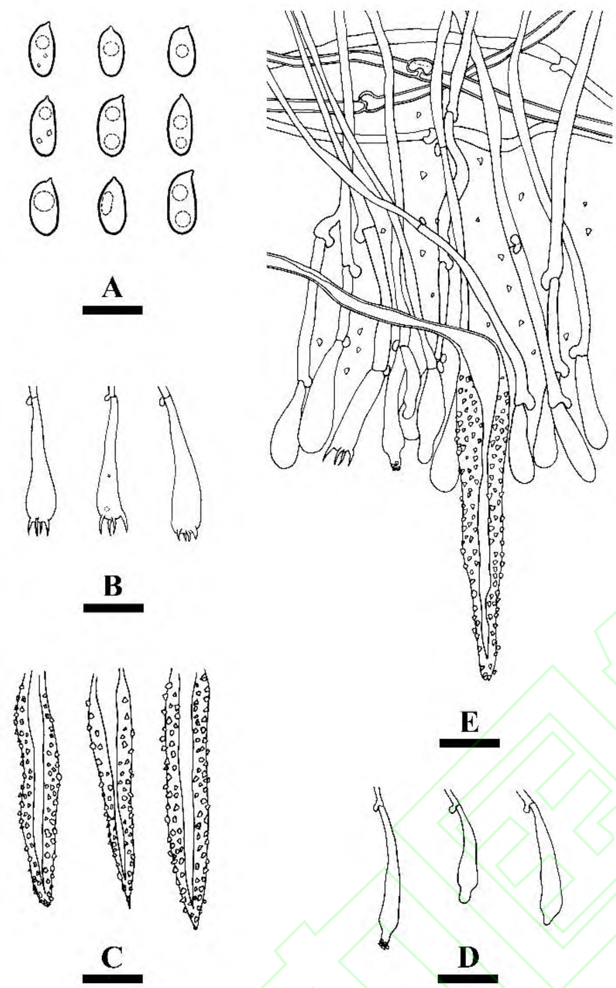

Fig. 4 Microscopic structures of *Lopharia minispora* (holotype, CLZhao 21787). A: Basidiospores; B: Basidia; C: Lamprocystidia; D: Cystidia; E: A cross section of hymenium. Bars: A=5 μm; B–E=10 μm.

Type of rot: white rot.

Additional specimens examined (paratypes). China. Yunnan Province, Lijiang, Heilongtan Forest Park, GPS coordinates 26°52'N, 100°14'E, elev. 2 000 m asl., on the fallen angiosperm branch, 21 July 2021, leg. C.L. Zhao, CLZhao 21694 (SWFC); CLZhao 21779 (SWFC).

***Lopharia punctata* Z.R. Gu & C.L. Zhao, sp. nov.** (Figs.5, Fig.6, Fig.7)

MycoBank no.: 856056.

Etymology. *punctata* (Lat.): refer to the species having dotted basidiomata.

Holotype. China. Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, GPS coordinates 27°77'N, 104°29'E, elev. 1 800 m asl., on the fallen angiosperm branch, 29 August 2023, leg. C.L. Zhao, CLZhao 32688 (SWFC).

Diagnosis. It differs from other *Lopharia* species by white to cream basidiomata, a monomitic hyphal system with simple-septa on generative hyphae and subglobose to globose basidiospores measuring (9.5–12)×(7.5–10.1) μm.

Fig. 5 Basidiomata of *Lopharia punctata* (holotype, CLZhao 32688). Bars: A=1 cm; B=1 mm.

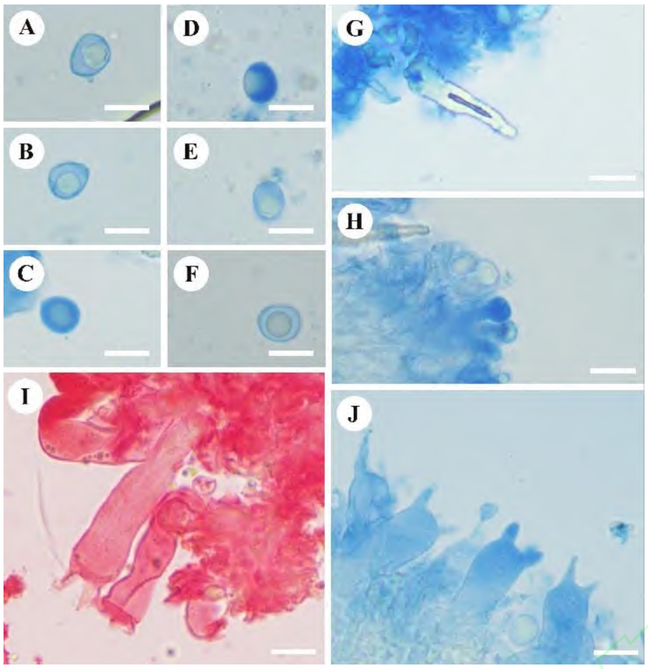

Fig. 6 Sections of hymenium of *Lopharia punctata* (holotype, CLZhao 32688). A–F: Basidiospores; G–H: Cystidia; I–J: Basidia. Bars: A–J=10 μm. 10 × 100 Oil.

Basidiomata. Annual, resupinate, membranous, without odor or taste when fresh, up to 3.2 cm long, 8 cm wide, less than 1 mm thick. Hymenial surface white to cream when fresh, cream when dry. Sterile margin narrow, white to cream, up to 1 mm.

Hyphal structure. Hyphal system monomitic, generative hyphae with simple septa, colorless, thin-walled, rarely branched, interwoven, 2–4 μm in diameter; IKI–, CB–; tissues unchanged in KOH.

Hymenium. Lamprocystidia in hymenium, colorless, thick-walled, slightly constricted, (19–21)×(5–7) μm; capitate cystidia, colorless, thin-walled, (17–19)×（3–4）μm. Basidia clavate with four sterigmata and a basal simple septum, (18–38)×(7–10.5) μm; basidioles similar to basidia in shape, but slightly smaller.

Basidiospores. Subglobose to globose, colorless, smooth, thin-walled, IKI–, CB–, (9.1–)9.5–12(–13.1)×(6.7–)7.5–10.1(–11.1) μm, L=10.66 μm, W=8.81 μm, Q=1.12–1.29 (n=120/4).

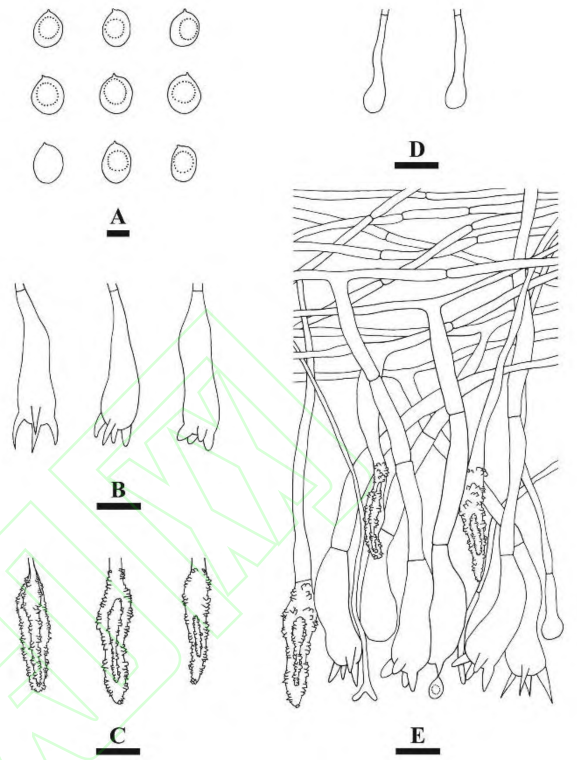

Fig. 7 Microscopic structures of *Lopharia punctata* (holotype, CLZhao 32688): A: Basidiospores; B: Basidia; C–D: Cystidia; E: A cross section of hymenium. Bars: A=5 μm; B–E=10 μm.

Type of rot: white rot.

Additional specimens examined (paratypes). China. Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, GPS coordinates 27° 77′ N, 104° 29′ E, elev. 1 800 m asl., on the fallen angiosperm branch, 27 August 2018, leg. C.L. Zhao, CLZhao 32105; CLZhao 32072 (SWFC); 28 August 2023, CLZhao 32356 (SWFC).

3 DISCUSSIONS

In the present study, two new species, *Lopharia minispora* and *L. punctata*, are described based on phylogenetic analyses and morphological characters. Previously *Lopharia* was defined by a dimitic hyphal system with clamped generative hyphae, large basidia and basidiospores and large, encrusted, colorless, thick-walled cystidia (Hjortstam &

Ryvarden 1990; Boidin & Gilles 2002). However, definition of *Lopharia* has been expanded to include additional features, such as a monomitic system, dextrinoid cystidia (Bernicchia & Gorjón 2010; Xavier de Lima *et al.* 2020). A comparison of the morphologies, type localities of *Lopharia* species are listed in Table 2.

Phylogenetically, two new taxa were grouped into the genus *Lopharia* based on the ITS+nLSU dataset, in which *L. minispora* was sister of *L. erubescens*. *L. punctata* was grouped with the lineage of *L. ayresii* and *L. resupinata* (Fig. 1), and the present topology observed is strongly supported and consistent with previous findings (Xavier de Lima *et al.* 2020). Morphologically, *Lopharia minispora* resembles *L. erubescens* in having white to pale yellow and smooth basidiomata, subulate cystidia, but *L. erubescens* has smaller basidiospores ((5–6)×(1.5–2.5) µm *vs*. (5.5–6.7)×(2.7–3.3) µm, Xavier de Lima *et al.* 2020). *Lopharia punctata* is closely related to *L. ayresii*, but the latter has shorter basidiospores (5.8–7 µm *vs.* 7.5–10.1 µm, Boidin & Gilles 1991). *L. resupinata* differs from *L. punctata* in having ceraceous basidiomata, pale orange, orange gray to grayish-orange hymenial surface, and smaller basidiospores ((7–9)×(4–5) µm, Liu *et al.* 2018).

Morphologically, *L. minispora* is similar to *L. ayresii*, having a monomitic hyphal system. However, *L. ayresii* differs in its larger basidiospores ((10–13)×(5.8–7) µm, Boidin & Gilles 1991; Hjortstam 1995; Liu *et al.* 2018). *L. minispora* is similar to *L. mirabilis* in having the coriaceous basidiomata, but *L. mirabilis* differs in its dimitic hyphae system and larger basidiospores ((10–16)×(6–8) µm, Hjortstam & Ryvarden 2004).

Lopharia punctata resembles *L. cystidiosa* (Rehill & B.K. Bakshi) Boidin, both sharing monomitic hyphal system, but differs in its smaller basidiospores ((9.5–12)×(7.5–10.1) µm *vs.* (6.6–9.1)×(4.5–5.8) µm, Boidin & Gilles 2002). *Lopharia punctata* is also similar to *L. sinensis* in having lamprocystidia, but *L. sinensis* differs in its coriaceous basidiomata, a dimitic hyphal system, and ellipsoid basidiospores (Liu *et al.* 2018).

The coriaceous fungi represent a frequently overlooked resupinate group of wood-decaying basidiomycetes. However, many species are widely distributed across diverse habitats due to their remarkable adaptability (Yang *et al.* 2023, 2024; Deng *et al.* 2024; Dong *et al.* 2024). These fungi possess a strong capacity to degrade fallen branches in broad-leaved forests (Dai 2009; Dai *et al.* 2021; Zhao *et al.* 2023; Dong *et al*. 2024; Gu *et al.* 2024; Wang *et al.* 2024; Zhou *et al.* 2023, 2024; Yang *et al.* 2025).

Further studies should be focused on the relationships between *Lopharia* species and their hosts as well as the evolutionary directions between hosts and *Lopharia* species.

Table 2 Main morphologies and type localities of *Lopharia* species

Species	Basidiomata	Size of Basidiospores	Hyphal System	Location	References
Lopharia ayresii	membranous	(10–13) × (5.8–7) µm	monomitic	Mauritius	Boidin & Gilles 1991
L. cinerascens	coriaceous	(8–16)× (5–8) µm	dimitic	USA	Cunningham 1956
L. cystidiosa	—	(6.6–9.1) ×(4.5–5.8) µm	monomitic	India	Boidin 1969
L. erubescens	ceraceous	(5–6) × (1.5–2.5) µm	monomitic	Brazil	Xavier de Lima *et al.*, 2020
L. minispora	**coriaceous**	**(5.5–6.7) ×(2.7–3.3) µm**	**monomitic**	**China**	**Present study**
L. mirabilis	coriaceous	(10–16) × (6–8) µm	dimitic	Sri Lanka	Liu *et al.*, 2018
L. pseudocinerascens	ceraceous	(8–14) × (4.5–6.5) µm	dimitic	Central African Republic	Boidin & Gilles 2002
L. punctata	**membranous**	**(9.5–12) ×(7.5–10.1) µm**	**monomitic**	**China**	**Present study**
L. resupinata	ceraceous	(7–9) × (4–5) µm	dimitic	China	Liu *et al.*, 2018
L. sinensis	coriaceous	(11–14) × (6.5–8) µm	dimitic	China	Liu *et al.*, 2018

Note: the new species are in bold.

Author contributions

Zirui Gu conducting field surveys and sampling, species identification, thesis conception and initial manuscript drafting; Yu Liu species identification and data analysis; Mei Li data analysis and literature search; Chunqin Zhou field survey and sampling; Hongmin Zhou providing guidance on species identification and manuscript writing; Changlin Zhao species identification, thesis conception, review and editorial oversight.

Declaration of competing interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

[REFERENCES]

Anonymous, 1969. Flora of British fungi: colour identification chart. Her Majesty's Stationery Office, London

Bernicchia A, Gorjón SP, 2010. Fungi Europaei 12: Corticiaceae s.l. Alassio: Edizioni, Candusso, Italy. 1-1008

Bhunjun CS, Niskanen T, Suwannarach N, *et al.* (more than 20 authors), 2022. The numbers of fungi: are the most speciose genera truly diverse? Fungal Diversity, 114: 387-462

Boidin J, 1969. A propos du genre *Lopharia* Kalchbr. et Mc Ow. em. Boidin 1959. Revue de Mycologie, 34(2-3): 187-191

Boidin J, Gilles G, 1991. Basidiomycètes Aphyllophorales de L'Île de La Réunion. XVI. Les genres *Hyphoderma*, *Hyphodermopsis*, *Chrysoderma* nov. gen. et *Crustoderma*. Cryptogamie Mycologie, 12: 97-132

Boidin J, Gilles G, 2002. À propos du genre *Lopharia* sensu lato (Basidiomycètes, Aphyllophorales). Bulletin de la Société Mycologique de France, 118(2): 91-115

Cunningham GH, 1956. Thelephoraceae of New Zealand. Part Ⅶ. The genus *Lopharia*. Part Ⅷ. The genera *Epithele* and *Mycobonia*. Transactions and Proceedings of the Royal Society of New Zealand, 83(4): 621-636

Dai YC, 2009. The checklist of Chinese polypores. Mycosystema, 28: 315-327 (in Chinese)

Dai YC, 2012. Pathogenic wood-decaying fungi on woody plants in China. Mycosystema, 31: 493-509 (in Chinese)

Dai YC, Yang ZL, Cui BK, Wu G, Yuan HS, Zhou LW, He SH, Ge ZW, Wu F, Wei YL, Yuan Y, Si J, 2021. Diversity and systematics of the important macrofungi in Chinese forests. Mycosystema, 40: 770-805 (in Chinese)

Dai YC, Zhuang JY, 2010. Numbers of fungal species hitherto known in China. Mycosystema, 29: 625-628 (in Chinese)

Deng YL, Li JF, Zhao CL, Zhao J, 2024. Four new fungal species in forest ecological system from southwestern China. Journal of Fungi, 10: 194

Dong JH, Gu JY, Zhao CL, 2023. Diversity of wood-decaying fungi in Wenshan Area, Yunnan Province, China. Mycosystema, 42(3): 638-662

Dong JH, Li Q, Yuan Qi, Luo YX, Zhang XC, Dai YF, Zhou Q, Liu XF, Deng YL, Zhou HM, Akmal M, Zhao CL, 2024. Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. Mycosphere, 15: 1110-1293

Gu ZR, Zhao CL, 2021. The hidden wood-decaying fungal diversity: *Rhizochaete* from East Asia. Diversity, 13: 503

Gu ZR, Zhou HM, Zhao CL, 2024. Morphological characteristics and phylogenetic analyses reveal *Scopuloides yunnanensis* (Polyporales, Basidiomycota), a new wood-decaying fungus from China. Phytotaxa, 665(2): 85-95

Guan QX, Zhao CL, 2021. Two new corticioid species, *Hyphoderma sinense* and *H. floccosum* (Hyphodermataceae, Polyporales), from southern China. Mycosystema, 40: 447-461

Hall TA, 1999. Bioedit: a user-friendly biological sequence alignment editor and analysis program for windows 95/98/NT. Nucleic Acids Symposium Series, 41: 95-98

He MQ, Cao B, Liu F, *et al.* (more than 20 authors), 2024. Phylogenomics, divergence times and notes of orders in Basidiomycota. Fungal Diversity, 126: 127-406

Hjortstam K, 1995. Two new genera and some new combinations of corticioid fungi (Basidiomycotina, Aphyllophorales) from tropical and subtropical areas. Mycotaxon, 54: 183-193

Hjortstam K, Ryvarden L, 1990. *Lopharia* and *Porostereum* (Corticiaceae). Synopsis Fungorum 4, Fungiflora, Oslo, Norway. 1-68

Hjortstam K, Ryvarden L, 2004. Some new and noteworthy corticioid fungi (Basidiomycotina, Aphyllophorales) from Japan. Synopsis Fungorum, 18: 8-13

Hyde KD, Noorabadi MT, Thiyagaraja V, *et al.* (more than 20 authors), 2024a. The 2024 Outline of Fungi and fungus-like taxa. Mycosphere, 15(1): 5146-6239

Hyde KD, Saleh A, Aumentado HDR, Boekhout T, Bera I, Khyaju S, Bhunjun CS, Chethana KWT, Phukhamsakda C, Doilom M, Thiyagaraja V, Mortimer PE, Maharachchikumbura SSN, Hongsanan S, Jayawardena RS, Dong W, Jeewon R, Al-Otibi F, Wijesinghe SN, Wanasinghe DN, 2024b. Fungal numbers: global needs for a realistic assessment. Fungal Diversity, 128(1): 191-225

Hyde KD, Xu JC, Rapior S, *et al.* (more than 20 authors), 2019. The amazing potential of fungi: 50 ways we can exploit fungi industrially. Fungal Diversity, 97: 1-136

Justo A, Miettinen O, Floudas D, Ortiz-Santana B, Sjokvist E, Lindner D, Nakasone KK, Niemela T, Larsson KH, Ryvarden L, Hibbett DS, 2017. A revised family-level classification of the Polyporales (Basidiomycota). Fungal Biology, 121: 798-824

Kalchbrenner C, 1881. Fungi MacOwaniani. Grevillea, 10(54): 52-59

Liu SL, Nakasone KK, Wu SH, He SH, Dai YC, 2018. Taxonomy and phylogeny of *Lopharia* s.s., *Dendrodontia*, *Dentocorticium* and *Fuscocerrena* (Basidiomycota, Polyporales). MycoKeys, 32: 25-48

Nylander JAA, 2004. MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University, Uppsala, Sweden. 1-146

Petersen JH, 1996. Farvekort. The Danish Mycological Society´s colour-chart. Foreningen til Svampekundskabens Fremme, Greve. 1-6

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology, 61: 539-542

Wang CG, Dai YC, Kout J, Gates GM, Liu HG, Yuan Y, Vlasák J, 2024. Multi-gene phylogeny and taxonomy of *Physisporinus* (Polyporales, Basidiomycota). Mycosphere, 15: 1455-1521

Wang CG, Zhao H, Liu HG, Zeng GY, Yuan Y, Dai YC, 2023. A multi-gene phylogeny clarifies species diversity, taxonomy, and divergence times of *Ceriporia* and other related genera in Irpicaceae (Polyporales, Basidiomycota). Mycosphere, 14(1): 1665-1729

Wei YL, Dai YC, 2004. The ecological function of wood-inhabiting fungi in forest ecosystem. Chinese Journal of Applied Ecology, 15: 1935-1938 (in Chinese)

White TJ, Bruns T, Lee S, Taylor J, 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR protocols: a guide to methods and applications, Academic Press, New York. 315-322

Wu F, Zhou LW, Vlasák J, Dai YC, 2022. Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. Fungal Diversity, 113: 1-192

Xavier de Lima V, de Sousa Lira C, dos Santos Chikowski R, Santos C, Lima N, Gibertoni TB, 2020. Additions to neotropical stereoid fungi (Polyporales, Basidiomycota): one new species of *Lopharia* and one new combination in *Phlebiopsis*. Mycological Progress, 19: 31-40

Yang X, Zhu YG, Duan SJ, Wu XX, Zhao CL, 2025. Morphology and multigene phylogeny revealed four new species of *Geastrum* (Geastrales, Basidiomycota) from China. MycoKeys, 113: 73-100

Yang Y, Jiang QQ, Li Q, Yang JW, Cha L, Cheng LJ, Yang SQ, Zhao CL, Zhou HM, 2023. Molecular systematics and taxonomic analyses of three new wood-inhabiting fungi of *Hyphoderma* (Hyphodermataceae, Basidiomycota). Journal of Fungi, 9(11): 1044

Yang Y, Li R, Jiang QQ, Zhou HM, Muhammad A, Wang HJ, Zhao CL, 2024. Phylogenetic and taxonomic analyses reveal three new wood-inhabiting fungi (Polyporales, Basidiomycota) in China. Journal of Fungi, 10: 55

Yuan Y, Bian LS, Wu YD, Chen JJ, Wu F, Liu HG, Zeng GY, Dai YC, 2023. Species diversity of pathogenic wood-rotting fungi (Agaricomycetes, Basidiomycota) in China. Mycology, 14: 204-226

Zhao CL, Cui BK, Dai YC, 2012. New species and phylogeny of *Perenniporia* based on morphological and molecular characters. Fungal Diversity, 58: 47-60

Zhao CL, Qu MH, Huang RX, Karunarathna SC, 2023. Multi-gene phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia* sensu lato (Polyporales,Basidiomycota). Journal of Fungi, 9: 320

Zhao H, Wu YD, Yang ZR, Liu HG, Wu F, Dai YC, Yuan Y, 2024. Polypore funga and species diversity in tropical forest ecosystems of Africa, America and Asia, and a comparison with temperate and boreal regions of the Northern Hemisphere. Forest Ecosystem, 11: 100200

Zhou HM, Gu ZR, Zhao CL, 2024. Molecular phylogeny and morphology reveal a new species of *Asterostroma* from Guizhou Province, China. Phytotaxa, 635(2): 173-181

Zhou M, Dai YC, Vlasák J, Liu HG, Yuan Y, 2023. Updated systematics of *Trichaptum* s.l. (Hymenochaetales, Basidiomycota). Mycosphere, 14(1):815-917