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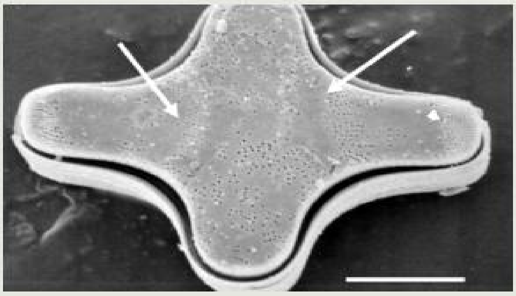

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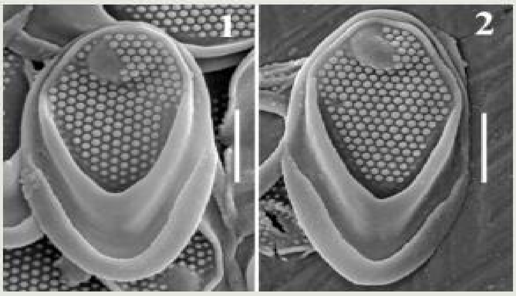

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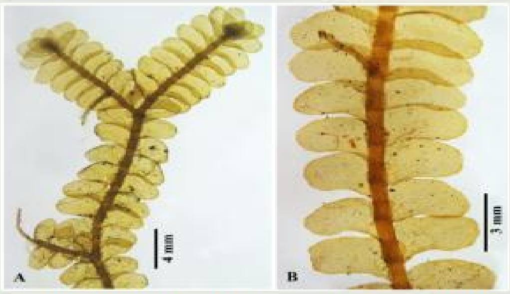

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Morphological characteristics and phylogenetic analyses revealed *Lopharia guangdongensis sp. nov*. (Polyporaceae, Basidiomycota) from Southern China

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Abstract

One new wood-inhabiting fungus, *Lopharia guangdongensis*, found in Guangdong Province, Southern China, is described here based on its morphology and phylogeny. *Lopharia guangdongensis* is characterized by its coriaceous basidiomata, smooth hymenial surface, a monomitic hyphal system with simple-septa generative hyphae, and oblong ellipsoid basidiospores measuring 8.8–11 × 5–6.5 µm. Phylogenetic analyses of the new species are carried out based on the nuclear ribosomal internal transcribed spacer (ITS) and the nuclear large subunit (nLSU) of ribosomal DNA. The phylogenetic tree revealed that the studied materials represent a distinct lineage, closely related to *L. ayresii* within the genus *Lopharia*, based on ITS+nLSU sequences. A full description, illustrations, and phylogenetic analyses results of the new species are provided.

Key words: Guangdong Province, One new species, Taxonomy, Wood-inhabiting fungi

Introduction

Fungi play vital roles in forest ecosystems as endophytes, pathogens, and saprobes (Wei & Dai 2004, Dai 2010, Yuan *et al*. 2023). Among them, the Polyporaceae Fr. ex Corda (1839: 49) is a diverse group in Polyporales (Corda 1839, Justo *et al*. 2017), and is widely found in nature and has long been an important part of the field of traditional Chinese medicine (Wu *et al*. 2019, Cui *et al*. 2021, Xu *et al*. 2024).

The genus *Lopharia* Kalchbr & MacOwan (1881: 58) is an important group of the Polyporaceae, and it was established by Kalchbrenner (1881) with *L. lirellosa* Kalchbr & MacOwan (1881: 58) as its type species (Kalchbr & MacOwan 1881). The genus is characterized by stereoid, resupinate, and effused-reflexed basidiomata, a monomitic or dimitic hyphal system, generative hyphae with clamp connection or simple septa, large encrusted, thick-walled lamprocystidia, clavate to subclavate basidia, and cylindrical to ellipsoid basidiospores (Kalchbrenner 1881, Welden 1975, Liu *et al*. 2018, Gu *et al*. 2025, Larsson *et al*. 2025).

Morphologically, species in the genus *Lopharia* are distinct from related taxa, and were transferred to other genera, such as *Hjortstamia*, *Porostereum,* and *Phlebiopsis* (Ryvarden 2010, Xavier de Lima *et al*. 2020, Zhao *et al*. 2021). Three species, *Lopharia mexicana* A.L. Welden (1971: 19), *L. perplexa* D.A. Reid (1963: 297), and *L. rimosissima* (Berk. & M.A. Curtis) A.L. Welden (1975: 544) were recorded in *Lopharia*, but they were treated as species of *Hjortstamia* Boidin & Gilles (2002: 99) due to the shorter basidiospores (Boidin & Gilles *et al*. 2002). Five species of *Lopharia*: *L. fulva* (Lév.) Boidin (1959: 213), *L. phellodendri* (Pilát) Boidin (1959: 207), *L. sharpiana* A.L. Welden (1971: 18), *L. spadicea* (Pers.) Boidin (1959: 211), *L. umbrinoalutacea* (Wakef.) A.L. Welden (1975: 546) were categorized into *Porostereum* Pilát (1937: 330) because of the lack of clamp connections and a brownish cystidia wall (Hjortstam & Ryvarden 1990, Pilát 1936). Another seven species: *L. amethystea* (Hjortstam & Ryvarden)

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A.L. Welde (2010: 70), *L. crassa* (Lév.) Boidin (1959: 497), *L. dregeana* (Berk.) P.H.B. Talbot (1951: 57), *L. novae-granatae* A.L. Welden (1975: 540), *L. papyracea* (Bres.) D.A. Reid (1957: 131), *L. papyrina* (Mont.) Boidin (1959: 210), and *L. vinosa* (Berk.) G. Cunn (1956: 625) of *Lopharia* were transferred into *Phlebiopsis* Jülich (1978: 137) as the morphological similarity with the latter (Miettinen *et al*. 2016, Xavier de Lima *et al*. 2020, Zhao *et al*. 2021).

Currently, molecular phylogenetic analysis has become the standard in fungal taxonomy (Wu *et al*. 2016, 2022a, Chen *et al*. 2020, Zhao *et al*. 2023, Gu *et al*. 2025, Liu *et al*. 2025). All species of *Lopharia* were analyzed by molecular techniques (Liu *et al*. 2018, Xavier de Lima *et al*. 2020, Gu *et al*. 2025). The genus *Lopharia* was placed in the family Polyporaceae based on phylogenetic analysis of the ITS, nLSU, and *rpb1* datasets (Justo *et al*. 2017, He *et al*. 2024, Gu *et al*. 2025). Phylogenetic reconstructions of *Lopharia*, inferred from ITS, nLSU, and *rpb1* sequences, demonstrated that *L. resupinata* S.H. He, S.L. Liu & Y.C. Dai (2018: 29) formed a sister lineage to *L. ayresii* (Berk. ex Cooke) Hjortstam (1995: 188); additionally, *L. sinensis* S.H. He, S.L. Liu & Y.C. Dai (2018: 33) was closely related to *L. cinerascens* (Schwein.) G. Cunn. (1956: 622) and *L. mirabilis* (Berk. & Broome) Pat. (1895: 14), in which specimens of *L. mirabilis* from temperate to tropical areas with variable hymenophore configurations all clustered into a strongly supported clade (Liu *et al*. 2018, Gu *et al*. 2025). *Lopharia erubescens* Xavier de Lima (2020: 34) was described from the tropics based on the phylogenetic analyses of *Lopharia* s.l. using the ITS+nLSU dataset (Xavier de Lima *et al.* 2020).

Based on the MycoBank database (http://www.mycobank.org, accessed on 31 December 2025) and the Index Fungorum (http://www.indexfungorum.org, accessed on 31 December 2025), the genus *Lopharia* has registered 43 specific and infraspecific names, and 18 species are widely recognized (Hyde *et al*. 2024, Zhao *et al*. 2024). Among them, three species of *Lopharia avellanea* (Bres.) K.H. Larss. & E. Larss. (2025: 14), *L. ochracea* G. Cunn. (1963:145), and *L. pseudocinerascens* Boidin & Gilles (2002: 96) were found to have come from Europe, Oceania, and Africa, respectively (Cunningham 1963, Boidin & Gilles 2002, Larsson *et al*. 2025). Seven species, *L. albida* Rick (1938: 13), *L. americana* Rick (1928: 435), *L. bambusae* Rick (1960: 199), *L. cinerascens*, *L. erubescens*, *L. pilosiuscula* (Hjortstam & Ryvarden) A.L. Welden (2010: 73), *L. rimosissima* Rick (1960: 199) were discovered in America (Rick 1928, Rick 1938, Cunningham 1956, Rick 1960, Welden 1975, Welden 2010, Xavier de Lima *et al*. 2020). Another eight species, *L. cystidiosa* (Rehill & B.K. Bakshi) Boidin (1969: 191), *L. javanica* Henn. & E. Nyman (1900: 144), *L. lilacina* (Berk. & Broome) A.L. Welden (2010: 71), *L. minispora* Z.R. Gu & C.L. Zhao (2025: 6), *L. mirabilis*, *L. punctata* Z.R. Gu & C.L. Zhao (2025: 8), *L. resupinata* and, *L. sinensis* were noticed in Asia, of which four new species, *L. minispora*, *L. punctata*, *L. resupinate*, and *L. sinensis*, and a known species *L. mirabilis* have been continuously discovered in China (Patouillard 1895, Hennings 1900, Boidin 1969, Liu *et al*. 2018, Gu *et al*. 2025).

During investigations of wood-inhabiting fungi in Guangdong Province, Southern China, two specimens, identified as *Lopharia* based on morphological characteristics, were collected. To clarify the position and relationships of two specimens, we conducted phylogenetic and taxonomic analyses of the genus *Lopharia* using a combined ITS+nLSU dataset. The two specimens are identified as an undescribed species of *Lopharia*. A description, illustrations, and phylogenetic analysis results of the new species are provided.

Materials and methods

Specimen collection and morphological studies

Fresh basidiomata were collected from the wood-inhabiting fungi growing on fallen angiosperm branches in Guangzhou, Guangdong Province, Southeast China, in October 2024. The samples were photographed in situ, and fresh macroscopic details, as well as other important collection information, were recorded (Rathnayaka *et al*. 2024). The samples were photographed with a Nikon D7100. All the photos were focus-stacked using Helicon Focus software. The macroscopic details were recorded, and basidiomata were transported to a field station and dried on an electronic food drier at 45 °C (Hu *et al*. 2022). Once dried, the specimens were sealed in envelopes and zip-lock plastic bags, and labelled (Senanayake *et al*. 2020, Rathnayaka *et al*. 2024, Zhang *et al*. 2024). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macro-morphological descriptions were based on field notes and photos collected in the field and in the lab.

Petersen (1996) was followed in the use of the color terminology, while the macro-morphological data were obtained from the dried specimens when observed under a light microscope following the previous study (Zhao & Wu 2017, Ma *et al*. 2019, Dong *et al*. 2024, Wang *et al*. 2024, Xiao *et al*. 2025). The measurements and drawings were made from slide preparations stained with Cotton Blue (0.1 mg aniline blue dissolved in 60 g pure lactic acid), Melzer's reagent (3 g potassium iodide, 1 g crystalline iodine, 44 g chloral hydrate, and 40 mL distilled water), and 5% potassium hydroxide. Spore size variation is presented as the 90% range (excluding 5% of measurements from each extreme), with values in parentheses. At least thirty basidiospores per specimen were measured, excluding hilar appendages. Basidia measurements excluded stalks. The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB– = acyanophilous, IKI– = both inamyloid and non-dextrinoid, 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, China) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The nuclear ribosomal of the internal transcribed spacer (ITS) region was amplified with ITS5 and ITS4 primers (White *et al*. 1990), while the nuclear large subunit (nLSU) region was amplified with the LR0R and LR7 primer pair (Vilgalys & Hester 1990, Rehner & Samuels 1994). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles of denaturation at 94 °C for 40 s, annealing at 58 °C for 45 s, extension at 72 °C for 1 min, and a final extension at 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 of denaturation at 94 °C for 30 s, annealing at 48 °C for 1 min, extension at 72 °C for 1.5 min, and a final extension at 72 °C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P.R. China). The newly generated sequences were deposited in NCBI GenBank (Table 1).

TABLE 1. A list of species, specimens, and GenBank accession numbers of sequences used in this study. [New species are shown in bold; * is shown as type material, holotype; — indicates sequence unavailability].

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. avellanea	EL19-10	OR822098	OR822098	Spain	Larsson *et al*. 2025
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	VXL619	MK993641	MK993636	Brazil	Xavier de Lima *et al*. 2020
L. erubescens	VXL620 *	MK993642	—	Brazil	Xavier de Lima *et al*. 2020
L. guangdongensis	**HMZhou 1163 ***	**PV746220**	**PX050999**	China	**Present study**
L. guangdongensis	**HMZhou 1167**	**PV746221**	**PX051000**	China	**Present study**
L. minispora	CLZhao 21694	PQ362229	PQ363273	China	Gu *et al*. 2025
L. minispora	CLZhao 21779	PQ362230	PQ363274	China	Gu *et al*. 2025
L. minispora	CLZhao 21787 *	PQ362231	PQ363275	China	Gu *et al*. 2025
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	Gu *et al*. 2025
L. punctata	CLZhao 32105	PQ362233	PQ363277	China	Gu *et al*. 2025
L. punctata	CLZhao 32356	PQ362234	PQ363278	China	Gu *et al*. 2025
L. punctata	CLZhao 32688 *	PQ362235	PQ363279	China	Gu *et al*. 2025
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

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. Sequences of *Dentocorticium ussuricum* (Parmasto) M.J. Larsen & Gilb. (1974: 226) was selected as an outgroup in the ITS+nLSU analysis (Fig. 1) as inspired by a previous study (Gu *et al.* 2025).

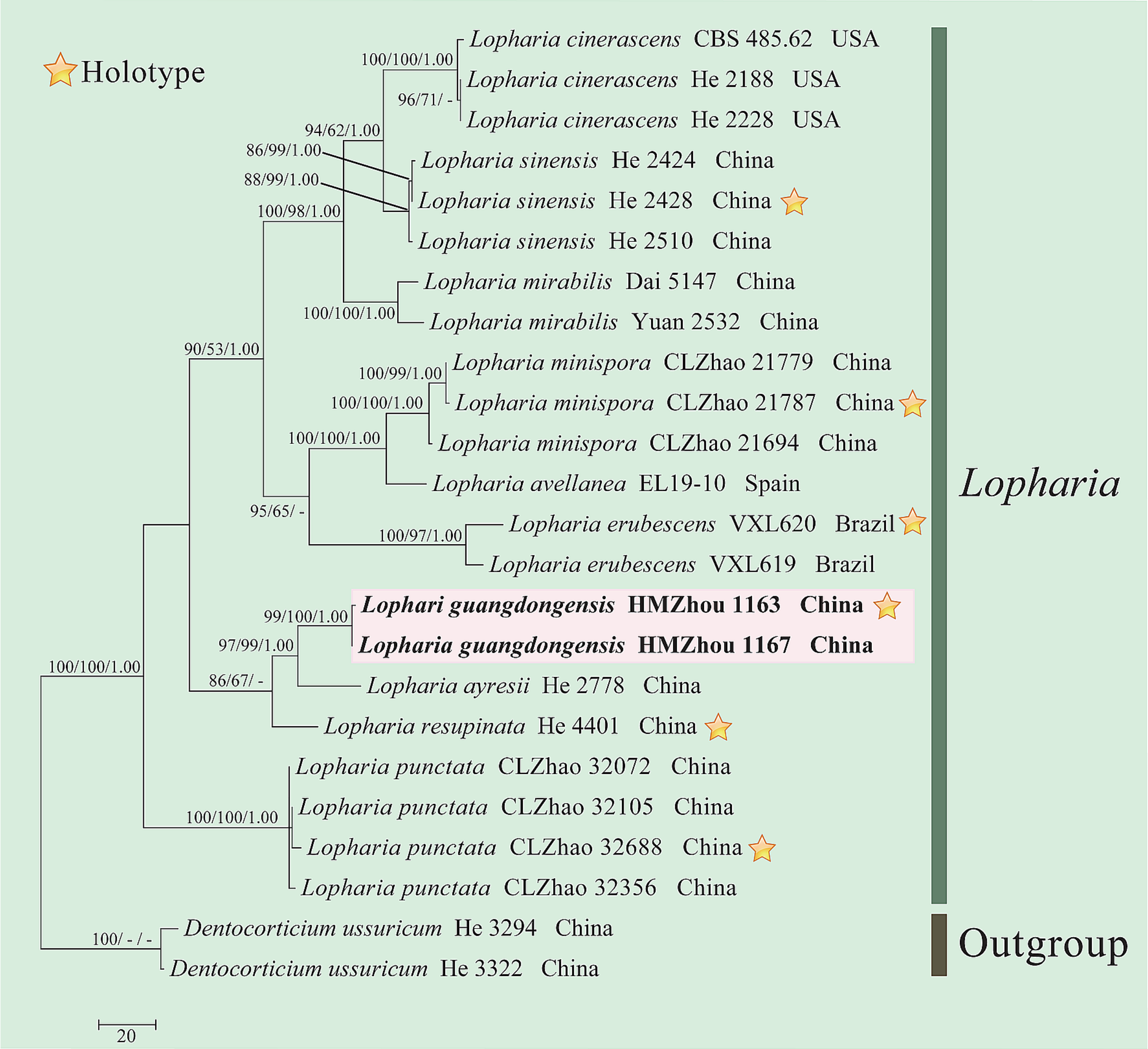

FIGURE 1. Maximum Parsimony strict consensus tree illustrating the *Lopharia guangdongensis* and related species in the genus *Lopharia* based on the combined ITS+nLSU sequences. Branches are labeled with Maximum Likelihood bootstrap values ≥ 70%, parsimony bootstrap values ≥ 50%, and Bayesian posterior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

Maximum parsimony analysis in PAUP* version 4.0b10 (http://phylosolutions. com/paup-test/) was applied to the ITS+nLSU dataset following a previous study (Zhao & Wu 2017). All characters were equally weighted, and gaps were treated as missing data. The tree was 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 pseudo-replicates (Felsenstein 1985). Descriptive tree statistics—tree length (TL), composite consistency index (CI), composite retention index (RI), composite rescaled consistency index (RC), and composite homoplasy index (HI)—were calculated for each maximum parsimonious tree generated. The combined dataset was also analyzed using Maximum Likelihood (ML) in RAxML-HPC2 through the CIPRES Science Gateway (Miller *et al.* 2012). Branch support (BS) for the ML analysis was determined using 1,000 bootstrap replicates.

MrModeltest 2.3 (Posada & Crandall 1998, Nylander 2004) was used to determine the best-fit evolutionary model for each data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes 3.1.2 using a general time-reversible (GTR+G+I) model of DNA substitution and a gamma distribution of rate variation across sites (Ronquist *et al*. 2012). Four Markov chains were run for 2 runs from random starting trees for 0.5 million generations (Fig. 1), and trees were sampled every 100 generations. The first one-fourth generation was discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches were considered significantly supported if they received a maximum likelihood bootstrap (ML) ≥ 70%, a maximum parsimony bootstrap (MP) ≥ 50%, or a Bayesian posterior probability (PP) ≥ 0.95.

Results

Molecular phylogeny

The dataset based on ITS+nLSU (Fig. 1) comprises sequences from 24 fungal specimens representing 11 species. The alignment length of this dataset is 2013 characters, of which 1,700 are constant, 65 are variable and parsimony-uninformative, and 248 are parsimony-informative. Maximum parsimony analysis yielded three equally parsimonious trees (TL = 559, CI = 0.7138, HI = 0.2862, RI = 0.8493, RC = 0.6062). Bayesian and ML analyses resulted in a similar topology to the MP analysis, with an average standard deviation of split frequencies of 0.006032 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 278.5.

The phylogenetic tree (Fig. 1) inferred from ITS+nLSU sequences shows that the new species, *Lopharia guangdongensis*, forms a sister lineage to *L. ayresii* and is also closely related to *L. resupinata*.

Taxonomy

Lopharia guangdongensis W. Guo & H.M. Zhou, *sp. nov*. Figs. 2–4
MycoBank no.: MB860558

Etymology:—*Guangdongensis* (Lat.): refers to the locality (Guangdong Province) of the type specimens.

Diagnosis:—Differs from *Lopharia ayresii* by its dull cream to buff hymenial surface, generative hyphae with clamp connections, and oblong ellipsoid basidiospores (9.5–12.5 × 6–8 µm).

Holotype:—CHINA. Guangdong Province, Guangzhou, Haizhu National Wetland Park, 23°07′N, 113°33′E, elev. 2 m, on fallen angiosperm branch, leg. H.M. Zhou, 14 October 2024, HMZhou 1163 (SWFC 00101163).

Basidiomata:—Annual, resupinate, tightly adnate, coriaceous, without odor or taste when fresh, sometimes slightly cracked when dry, up to 20 cm long, 4 cm wide, and less than 1 mm thick. Hymenial surface smooth, cream when dry. Sterile margin indistinct.

Hyphal structure:—Hyphal system monomitic, generative hyphae with simple septa, hyaline, rarely branched, interwoven, IKI–, CB–; tissues unchanged in KOH.

Hymenium:—Lamprocystidia abundant, arising from subhymenium, subulate, hyaline, thick-walled, heavily encrusted with crystals in the middle to tips, embedded in subhymenium or outside of hymenium, 68.5–94.5 × 17–22 µm. Cystidioles numerous, arising from the subiculum and subhymenium, narrowly clavate, hyaline, thin-walled, immersed or projecting above the hymenium 16–23.5 × 2.5–4.5 µm. Basidia subclavate, apically widened, with a big guttule, with four sterigmata and a basal simple septum, 36.5–50.5 × 8–10 µm; basidioles dominating in hymenium, similar to basidia but smaller.

Basidiospores:—Oblong ellipsoid, hyaline, thin-walled, smooth, with one or two guttules, IKI–, CB–, (8–)8.8–11(–11.5) × 5–6.5(–7) µm, L = 10.13 µm, W = 5.66 µm, Q = 1.73–1.87 (n = 60/2).

***Additional specimens examined* (*paratype*)**:—CHINA. Guangdong Province, Guangzhou, Haizhu National Wetland Park, 23°07′N, 113°33′E, elev. 2 m, on fallen angiosperm branch, leg. H.M. Zhou, 14 October 2024, HMZhou 1167 (SWFC 00101167).

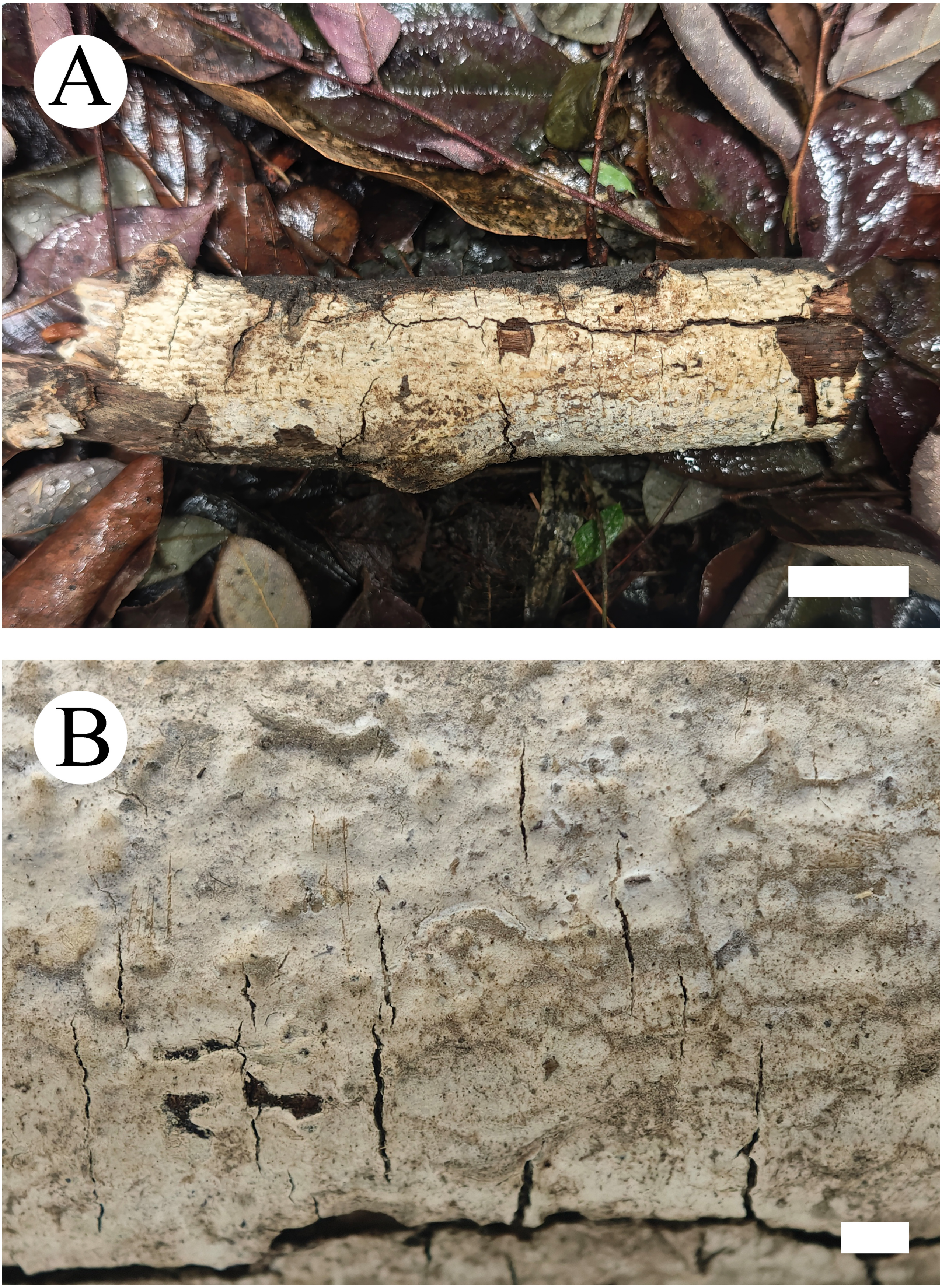

FIGURE 2. Basidiomata of *Lopharia guangdongensis* (A, B) HMZhou 1163. Scale bars: A = 2 cm; B = 2 mm.

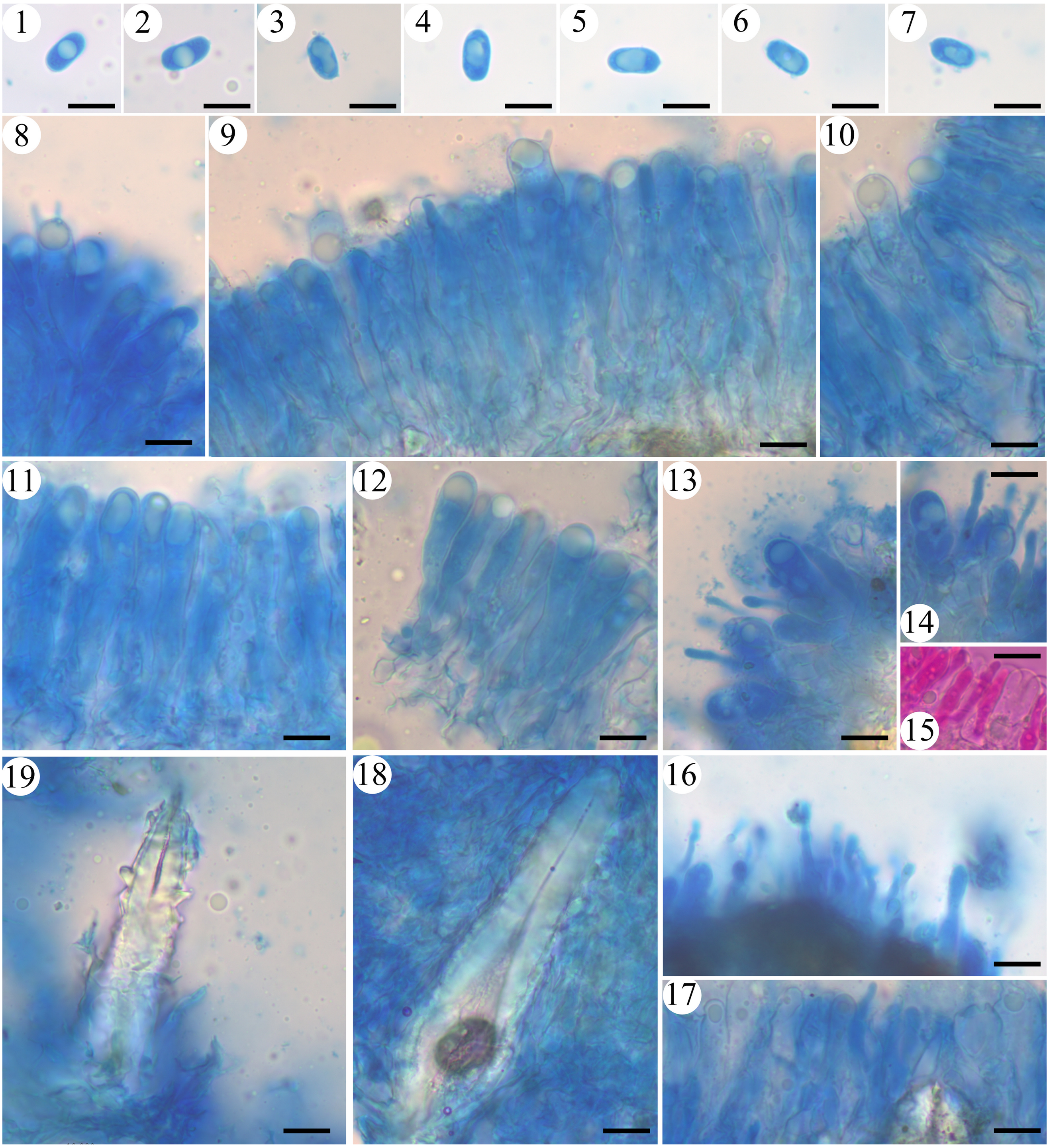

FIGURE 3. Sections of the hymenium of *Lopharia guangdongensis* (holotype, HMZhou 1163). (1–7) Basidiospores; (8–12) Basidia and basidioles in the hymenium; (13–17) Cystidia; (18–19) Lamprocystidia. Scale bars: 1–19 = 10 μm.

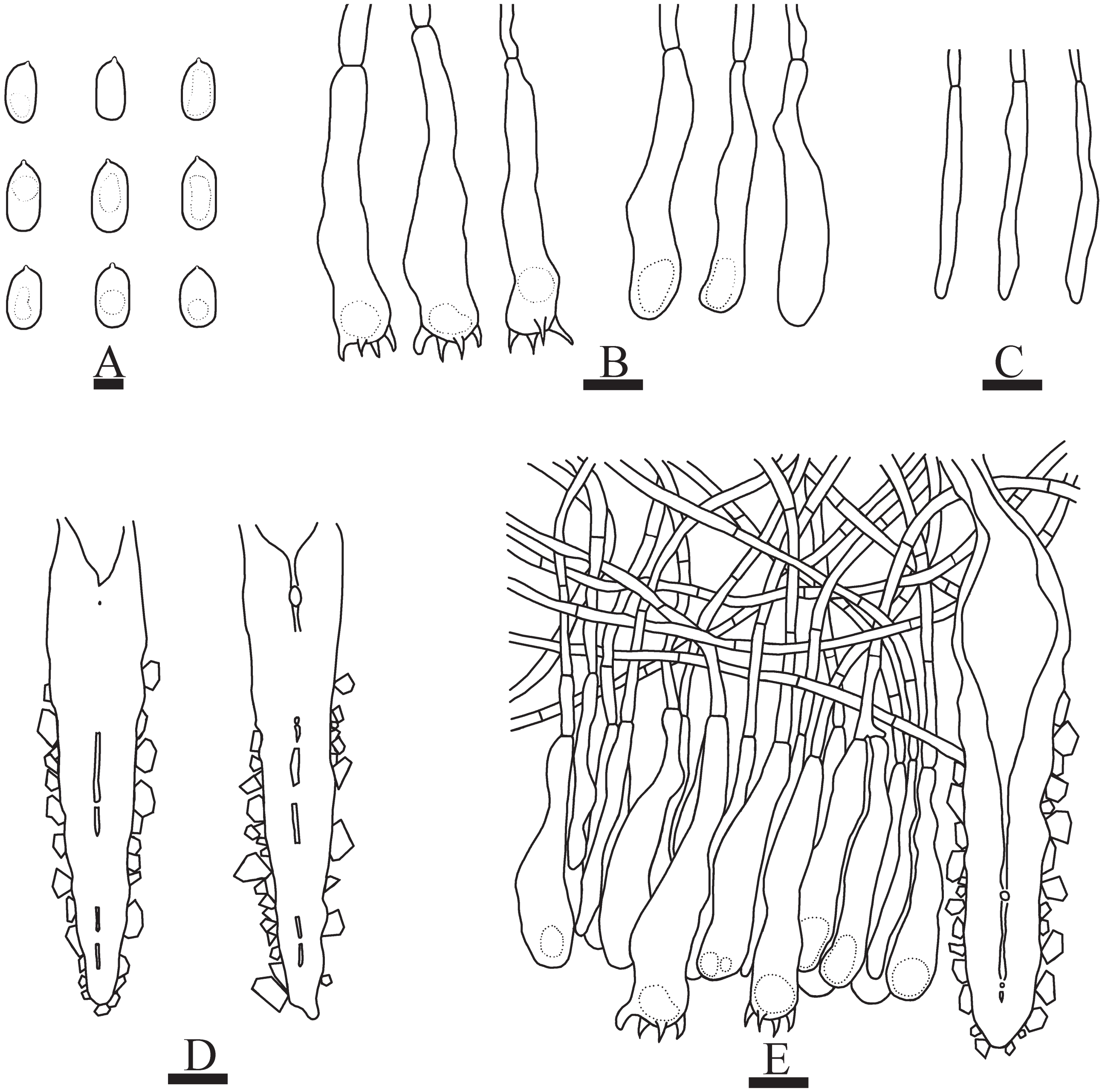

FIGURE 4. Microscopic structures of *Lopharia guangdongensis* (holotype, HMZhou 1163). (A) Basidiospores; (B) Basidia and basidioles; (C) Cystidia; (D) Lamprocystidia; (E) A section of the hymenium. Scale bars: A = 5 µm, B–E = 10 µm.

Discussion

Recently, many wood-inhabiting fungal taxa have been reported worldwide, including 18 *Lopharia* species (Liu *et al*. 2018, Wu *et al*. 2022, Gu *et al*. 2025, Liu *et al*. 2025). In the present study, a new species, *Lopharia guangdongensis*, is described based on phylogenetic analyses and morphological characteristics. A comparison of the morphology and type localities of *Lopharia* species is listed in Table 2.

TABLE 2. Main morphologies and type localities of *Lopharia* species.

Species	Basidiomata	Size of Basidiospores	Hyphal System	Location	References
Lopharia albida	—	—	—	Brazil	Rick 1938
L. americana	—	—	—	Brazil	Rick 1928
L. avellanea	Ceraceous	6–7.3 × 2.3–3.4 µm	Monomitic	Spain	Larsson *et al.* 2025
L. ayresii	Membranous	9.5–12.5 × 6–8 µm	Monomitic	Mauritius	Maekawa *et al.* 2003
L. bambusae	—	—	—	Brazil	Rick 1960
L. cinerascens	Coriaceous	8–16 × 5–8 µm	Dimitic	USA	Chamuris 1988
L. cystidiosa	—	6.6–9.1 × 4.5–5.8 µm	Monomitic	India	Rehill & Bakshi 1965
L. erubescens	Ceraceous	5–6 × 1.5–2.5 µm	Monomitic	Brazil	Xavier de Lima *et al.* 2020
L. guangdongensis	**Coriaceous**	**8.8–11 × 5–6.5** µm	**Monomitic**	**China**	**Present study**
L. javanica	—	—	—	Indonesia	Hennings 1900
L. lilacina	—	—	—	Sri Lanka	Hjortstam 1989
L. minispora	Coriaceous	5.5–6.7 × 2.7–3.3 µm	Monomitic	China	Gu *et al.* 2025
L. mirabilis	Coriaceous	10–16 × 6–8 µm	Dimitic	Japan	Hjortstam & Ryvarden 2004
L. ochracea	Membranous	4–5 × 2.5–3 µm	—	New Zealand	Cunningham 1963
L. pilosiuscula	—	4.5–6.5 × 3.5–4 µm	—	Brazil	Welden 2010
L. pseudocinerascens	Ceraceous	8–13 × 4.5–6 µm	—	Central African Republic	Boidin & Gilles 2002
L. punctata	Membranous	9.5–12 × 7.5–10.1 µm	Monomitic	China	Gu *et al.* 2025
L. resupinata	Coriaceous	7–9 × 4–5 µm	Monomitic	China	Liu *et al.* 2018
L. rimosissima	—	—	—	Nicaragua	Welden 1975
L. sinensis	Coriaceous	11–14 × 6.5–8 µm	Dimitic	China	Liu *et al.* 2018

Phylogenetically, DNA sequence-based classification and identification have become the standard approach in fungal taxonomy (Hibbett *et al*. 2007, Xu 2020, Lücking *et al*. 2021, Zhou *et al*. 2023, Liu *et al*. 2025, Qin *et al*. 2025). In the present phylogeny, *Lopharia guangdongensis* is grouped with *L. ayresii* and is then closely related to *L. resupinata*. However, morphologically, *L. ayresii* can be distinguished from *L. guangdongensis* by its membranous basidiomata, larger basidia (45–75 × 9–12 µm *vs*. 36.5–50.5 × 8–10 µm) and wider basidiospores (6–8 µm *vs*. 5–6.5 µm (Boidin & Gilles 1991, Maekawa *et al*. 2003); *L. resupinata* can be separated from *L. guangdongensis* by its ceraceous basidiomata, pale orange, orange gray to grayish-orange hymenial surface, and smaller basidiospores (7–9 × 4–5 µm *vs*. 8.8–11 × 5–6.5 µm (Liu *et al*. 2018).

Morphologically, *Lopharia guangdongensis* resembles *L. cinerascens*, *L. minispora*, *L. mirabilis*, and *L. sinensis* in sharing the coriaceous basidiomata. However, *L. cinerascens* differs from *L. guangdongensis* by its matted-tomentose to strigose-hirsute basidiomata, a dimitic hyphal system, and longer basidia (50–80 × 6–11 µm *vs*. 36.5–50.5 × 8–10 µm (Cunningham 1956, Chamuris 1988). *L. minispora* can be distinguished from *L. guangdongensis* by its generative hyphae with clamp connections, and smaller basidiospores (5.5–6.7 × 2.7–3.3 µm *vs*. 8.8–11 × 5–6.5 µm (Gu *et al*. 2025). The taxon *L. mirabilis* differs from *L. guangdongensis* by its dimitic hyphae system, and larger basidiospores (10–16 × 6–8 µm *vs*. 8.8–11 × 5–6.5 µm (Hjortstam & Ryvarden 2004). *Lopharia sinensis* can be distinguished from *L. guangdongensis* by its dimitic hyphae system, larger basidiospores (11–14 × 6.5–8 µm *vs*. 8.8–11 × 5–6.5 µm (Liu *et al*. 2018).

To date, 18 species of *Lopharia* have been reported globally (Wu *et al*. 2022b). However, among the *Lopharia* species found in China, 50% were in tropical regions and 50% in temperate regions. In this study, we describe a new species from the subtropical regions of Guangdong Province, thereby enriching our understanding of *Lopharia* diversity in China. Further field investigations and molecular analyses are needed to reveal more new taxa of this genus.

Fungi secrete a spectacular array of bioactive chemical compounds and enzymes, playing crucial roles in the biosphere: from digesting organic matter and recycling nutrients from dead plant and animal tissues, to mediating intimate and mutually beneficial associations with the roots of almost all land plants (Case *et al*. 2025). Fungi are closer to humans than plants and can be treated as a strategic biological resource (Cui *et al*. 2023, Ming *et al*. 2023). They are of direct benefit to humanity and are estimated to contribute 54.57 trillion USD to the global economy through food, medicine production, and other products (He *et al*. 2024). The phylum Basidiomycota R.T. Moore is one of the major branches in the fungal tree of life, with global estimates of 1.4–4.2 million species in the phylum and latest estimates of 0.7 to 1 million species, which represents about 28–40% of all fungal diversity (Dai *et al*. 2021, He *et al*. 2024, Yang *et al*. 2025). Therefore, for future utilization, it is now urgent to recognize and conserve fungi (Dong *et al*. 2025).

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