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Fungal diversity notes 1919–2016: taxonomic and phylogenetic contributions to fungal taxa

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Abstract
This article is the 18th contribution to the Fungal Diversity Notes series, in which we document 98 taxa across two phyla, eight classes, 21 orders, 46 families, and 59 genera. The represent samples of taxa were collected from a diverse range of regions, including Australia, Benin, Bolivia, Burkina Faso, Cameroon, Canada, China, Czechia, India, Japan, Madagascar, Mexico, New Zealand, Sri Lanka, Thailand, Togo, USA, Uzbekistan and Venezuela. Among these, we introduce one new genus, 59 new species, 13 new combinations, one new name and 24 new records, along with information on their hosts and geographic distributions. The newly introduced genus is *Fusicastoreum*, and the newly described species include: *Acrogenospora guangxiensis*, *Agaricus longistipitatus*, *A. sunanensis*, *Anthosulcatispora sichuanensis*, *Anthracoidea siccatae*, *Bjerkandera meridionalis*, *Camarophyllopsis brunnea*, *Candolleomyces analalavaensis*, *C. kely*, *C. macrosporus*, *Ceriporia yunnanensis*, *Choiromyces mongolicus*, *Colletotrichum duohuaense*, *Coprinus variicolor*, *Cystoderma alticola*, *C. microspore*, *C. yadongense*, *Cytospora lhaluensis*, *Diaporthe amberina*, *D. mangiferae*, *Elsinoe fuzhouensis*, *Epicocum maxima*, *Fulvifomes shailashikhara*, *Fusarium tuberculatum*, *Fusicastoreum arenarium*, *F. occidentale*, *F. pisiglareum*, *F. trappei*, *Gyalidea lluxitensis*, *Gymnopilus rimopileus*, *Hohenbuehelia triloba*, *Hymenagaricus ruber*, *Hypholoma darjeelingensis*, *Laccaria guizhouensis*, *Lactifluus aureoelephanti*, *L. croceivillus*, *Leucoagaricus ankarafantsikaensis*, *L. rutilus*, *Micropsalliota squamulosa*, *M. vinacea*, *Neomyrmecridium triseptatum*, *Niesslia wurfbainiae*, *Nigropunctata conspicosa*, *Ophiocordyceps jilinensis*, *Oxydothis dehongensis*, *Panaeolus ranwuensis*, *Pestalotiopsis buxicola*, *Pleurocordyceps puerensis*, *Pseudocercospora cunninghamia*, *Psilocybe zhushanensis*, *Remotididymella tachibana*, *Russula gaoligongensis*, *R. guilinensis*, *R. pseudovirescens*, *Sarocladium solani*, *Septoriella saviya-ramazanovaii*, *Seriascoma oblonga*, *Talaromyces pseudorugulosus* and *Tricholosporum madagascariense*. Additionally, species newly transferred from *Psilocybe* include *Deconica caespitosa*, *D. californica*, *D. goniospora*, *D. josecastilloi*, *D. latispora*, *D. novozoncuantlensis*, *D. oregonensis*, *D. venezuelana* and *D. vialis*. *Russula afroscrobiculata* is newly transferred from *Lactarius afroscrobiculatus*, and *Puccinia hamamelidis*, *P. hydrangeicola*, *P. philadelphi* are newly transferred from *Aecidium*. Furthermore, the new name *Puccinia shojiana* is proposed as a replacement for *Aecidium akebiae*. The 24 new records of hosts and geographical distributions include: *Agaricus pallidobrunneus*, *Bovista cretacea*, *Candolleomyces subsingeri*, *Clitopilus chichawatniensis*, *Collybiopsis gibbosa*, *C. subumbilicata*, *Curvularia geniculate*, *Cystoderma japonicum*, *Cytospora diatrypelloidea*, *C. schulzeri*, *Elsinoe leucospermi*, *Fulvifomes aurantiacus*, *Laccaria macrobasidia*, *Menisporopsis pandanicola*, *M. pirozynskii*, *Multifurca pseudofurcata*, *Musicillium elettariae*, *Myrmecridium pulvericola*, *Ophiocordyceps asiana*, *O. campes*, *Phellinus resupinatus*, *Phylloporia afrospathulata*, *Tropicoporus linteus* and *Typhula incarnate*. All taxa are supported by both morphological and phylogenetic analyses.

Keywords Ascomycota · Basidiomycota · New combination · New genus · New name · New record · New species

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1954. ***Agaricus pallidobrunneus*** R.L. Zhao, **new geographical record from India** (contributed by Arun Kumar Dutta and Pinaki Chattopadhyay)

1955. ***Agaricus sunanensis*** R.L. Zhao & B. Cao, **sp. nov.** (contributed by Bin Cao and Rui-Lin Zhao)

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1961. ***Micropsalliota vinacea*** Ralaiv., Liimat. & Niskanen, **sp. nov.** (contributed by Anna Ralaiveloarisoa, Kare Liimatainen and Tuula Niskanen)

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1967. ***Laccaria macrobasidia*** H.J. Cho & Y.W. Lim, **new geographical record from China** (contributed by Bin Cao and Rui-Lin Zhao)

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1970. ***Deconica goniospora*** (Berk. & Broome) Bradshaw, Ram.-Cruz & Dentinger, **comb. nov.** (contributed by Virginia Ramírez-Cruz, Alexander James Bradshaw, Bryn TM Dentinger, Florencia Ramírez-Guillén, Alonso Cortés-Pérez, Alma Rosa Villalobos-Arámbula, Oscar Castro-Jauregui, Paula Santos da Silva and Laura Guzmán-Dávalos)
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1973. ***Deconica novozoncuantlensis*** (Guzmán, Ram.-Cruz, Ram.-Guill. & E. Gándara) Bradshaw & Dentinger, **comb. nov.** (contributed by Virginia Ramírez-Cruz, Alexander James Bradshaw, Bryn TM Dentinger, Florencia Ramírez-Guillén, Alonso Cortés-Pérez, Alma Rosa Villalobos-Arámbula, Oscar Castro-Jauregui, Paula Santos da Silva and Laura Guzmán-Dávalos)
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1976. ***Deconica vialis*** (Murrill) Bradshaw, Ram.-Cruz & Dentinger, **comb. nov.** (contributed by Virginia Ramírez-Cruz, Alexander James Bradshaw, Bryn TM Dentinger, Florencia Ramírez-Guillén, Alonso Cortés-Pérez, Alma Rosa Villalobos-Arámbula, Oscar Castro-Jauregui, Paula Santos da Silva and Laura Guzmán-Dávalos)

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Phellinus Quél.
1995. ***Phellinus resupinatus*** M. Fisch., M. Cloete, L. Mostert & F. Halleen, **new geographical record from India** (contributed by Ramesh Murugadoss)

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Tropicoporus L.W. Zhou, Y.C. Dai & Sheng H. Wu
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Hysterangiales K. Hosaka & Castellano
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2002. ***Fusicastoreum trappei*** R.A. Day, Davoodian, T.W. May, T. Lebel & Castellano, **sp. nov.** (contributed by Rory Day, Naveed Davoodian, Tom W. May, Teresa Lebel and Michael Castellano)

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Russulaceae Lotsy
Lactifluus (Pers.) Roussel
2005. ***Lactifluus aureoelephanti*** T. Lebel, Nuytinck & Cooper, **sp. nov.** (contributed by Teresa Lebel, Jerry Cooper and Jorinde Nuytinck)
2006. ***Lactifluus croceivillus*** T. Lebel, Nuytinck & Cooper, **sp. nov.** (contributed by Teresa Lebel, Jerry Cooper and Jorinde Nuytinck)

Multifurca Buyck & V. Hofstetter.
2007. ***Multifurca pseudofurcata*** X.H. Wang, **new geographical record from India** (contributed by Arun Kumar Dutta, Bhaben Tanti and Niranjan Roy)

Russula Pers.
2008. ***Russula afroscrobiculata*** (Verbeken & Van Rooij) Tondeleir & Lagaet, **comb. nov.** (contributed by Phaedra Lagaet, Jorinde Nuytinck, Annemieke Verbeken, Lowie Tondeleir, Ruben De Lange, Felix Hampe and Cathrin Manz)
2009. ***Russula gaoligongensis*** R.L. Zhao, B. Cao & S.H. Wang, **sp. nov.** (contributed by Bin Cao, Shi-Hui Wang and Rui-Lin Zhao)
2010. ***Russula guilinensis*** R.L. Zhao, B. Cao & S.H. Wang, **sp. nov.** (contributed by Bin Cao, Shi-Hui Wang and Rui-Lin Zhao)
2011. ***Russula pseudovirescens*** N. Roy, A.K. Dutta & Tanti, **sp. nov.** (contributed by Arun Kumar Dutta, Bhaben Tanti and Niranjan Roy)

Pucciniomycetes R. Bauer, Begerow, J.P. Samp., M. Weiss & Oberw.
Pucciniales Caruel
Pucciniaceae Chevall., emend. Aime & McTaggart
Puccinia Pers.
2012. ***Puccinia hamamelidis*** (Dietel) Jing X. Ji & Kakish., **comb. nov.** (contributed by Jing-Xin Ji and Makoto Kakishima)
2013. ***Puccinia hydrangeicola*** (Henn.) Jing X. Ji & Kakish., **comb. nov.** (contributed by Jing-Xin Ji and Makoto Kakishima)
2014. ***Puccinia philadelphi*** (Dietel) Jing X. Ji & Kakish., **comb. nov.** (contributed by Jing-Xin Ji and Makoto Kakishima)
2015. ***Puccinia shojiana*** Jing X. Ji & Kakish., **nom. nov.** (contributed by Jing-Xin Ji and Makoto Kakishima)

Ustilaginomycetes Warm.
Ustilaginales Bek.
Anthracoideaceae Denchev
Anthracoidea Bref.
2016. ***Anthracoidea siccatae*** T. Denchev, Denchev, Lév.-Bourret & Kemler, **sp. nov.** (contributed by Teodor T. Denchev, Cvetomir M. Denchev, Étienne Léveillé-Bourret and Martin Kemler)

Introduction

Fungi represent one of the most diverse groups of organisms globally, playing essential roles in ecosystems as decomposers and symbionts. According to Fungal Names (FN, https://nmdc.cn/fungalnames/), over 150,000 fungal species have been described to date. However, estimates of the total number of fungal species vary widely, ranging from 2.2 to 3.8 million based on various estimation techniques

(Hawksworth and Lücking 2017) and from 11.7 to 13.2 million using high-throughput sequencing methods (Wu et al. 2019a). There is substantial evidence suggesting that fungal diversity may exceed even these estimates (Hyde 2022). As a result, many species remain undiscovered or undescribed. To tackle this challenge, initiatives such as *Fungal Diversity Notes* (Manawasinghe et al. 2024), *Fungal Planet* (Crous et al. 2023), and *Mycosphere Notes* series (Dong et al. 2023a) have established platforms for the introduction of numerous new fungal species.

To date, more than 1,900 entries have been published in the *Fungal Diversity Notes*, introducing new taxa, reference specimens, new data, and other taxonomic contributions, all supported by phylogenetic analyses (Liu et al. 2015a, 2024; Ariyawansa et al. 2015a; Li et al. 2016; Hyde et al. 2016, 2017a, 2019, 2020a; Tibpromma et al. 2017, 2018; Wanasinghe et al. 2018; Phookamsak et al. 2019; Yuan et al. 2020; Boonmee et al. 2021; Jayawardena et al. 2022; Senanayake et al. 2023; Manawasinghe et al. 2024). This paper constitutes the 18th installment in the series, detailing 98 taxa, including one new genus, 59 new species, 13 new combinations, one new name and 24 new records.

Materials and methods

The materials and methods employed in this study adhere to the protocols outlined in recent Fungal Diversity Notes (Liu et al. 2024; Manawasinghe et al. 2024). The taxa described were collected from various countries, including Australia, Benin, Bolivia, Burkina Faso, Cameroon, Canada, China, Czechia, India, Japan, Madagascar, Mexico, New Zealand, Sri Lanka, Thailand, Togo, USA, Uzbekistan, and Venezuela. This paper follows standard taxonomic protocols for the introduction of new taxa (Aime et al. 2021). The new taxa have been registered in databases such as Fungal Names (https://nmdc.cn/fungalnames/), Index Fungorum (https://www.indexfungorum.org/), Mycobank (https://www.mycobank.org/), and Faces of Fungi (https://www.facesoffungi.org/). The classification of Basidiomycota follows He et al. (2019, 2024a), while the classification of Ascomycota is based on Wijayawardene et al. (2018a, 2022).

Taxonomy

Ascomycota Caval.-Sm.
Dothideomycetes O.E. Erikss. & Winka.
Minutisphaerales Raja, Oberlies, Shearer & A.N. Mill.

Notes: Minutisphaerales was established by Raja (2015) based on phylogenetic analyses of combined SSU and LSU data. Members of the order include Acrogensporaceae and Minutisphaeraceae (Wijayawardene et al. 2022).

Acrogenosporaceae Jayasiri & K.D. Hyde.

Notes: The establishment of a monotypic family Acrogenosporaceae was supported by phylogenetic analysis of combined LSU, SSU, *rpb2* and *tef1* sequence data (Jayasiri et al. 2018) and classed in Minutisphaerales in Dothideomycetes incertae sedis (Hyde et al. 2023). Members of this family have been reported to be mostly from freshwater habitats (Raja et al. 2015; Hyde et al. 2019; Bao et al. 2020).

Acrogenospora M.B. Ellis.

Notes: *Acrogenospora* was introduced by Ellis (1971) to accommodate the type species *A. sphaerocephala* and *A. carmichaeliana* (asexual morphs), and it is classified in Acrogenosporaceae, Minutisphaerales, and Dothideomycetes. *Acrogenospora* has a total of 24 members; mostly of them are saprophytic on decaying submerge wood, with a worldwide distribution (Ellis 1971; Bao et al. 2020). The asexual morph is characterized by simple, unbranched conidiophores with regular septum-like markings formed during the serial release of single conidia followed by regrowth of the apical conidiogenous cell, a process known as acrogenous percurrent proliferation (Hughes 1978; Goh et al. 1998). The sexual morph is similar to *Farlowiella*, which is characterized by hysterothecial ascomata with thick-walls, a prominent sunken slit and 1-celled, pedicellate, hyaline or moderately pigmented ascospores (Hyde et al. 2019). However, Rossman et al. (2015) recommended protecting the name *Acrogenospora* over *Farlowiella*. At present, the important basis for the classification of species in this genus is the degree of pigmentation of the conidia and conidiophores, and conidial shape, size, color, guttules, basal cells, and position of conidial development (Bao et al. 2020; Li et al. 2024a). The genus has LSU, SSU, *tef1* and *rpb2* sequence data, and a few species contain ITS sequences. Available sequence data and phylogenetic analyses suggest that the *Acrogenospora* is monophyletic as circumscribed at the genus level by morphological traits, although data are limited (Harrington et al. 2022).

Acrogenospora guangxiensis Y.X. Shu & W. Dong, **sp. nov.**

Index Fungorum: IF 903081; *Facesoffungi*: FoF 17021; Figs. 1, 2

Etymology: Name refers to "Guangxi Zhuang Autonomous Region" where the holotype was collected.

Holotype: MHZU 24–0828.

Saprobic on submerged decaying wood. **Sexual morph**: Undetermined. **Asexual morph**: hyphomycetes. **Colonies** on the natural substratum sparse, effuse, dark black, glistening, hairy. **Mycelium** superficial and partially immersed, composed of septate, dark brown, smooth hyphae. **Conidiophores** 280–475 × 6–10 µm ($\bar{x}$ = 349 × 8 µm, n = 3), macronematous, mononematous, unbranched, erect, straight or slightly flexuous, septate, smooth, dark brown,

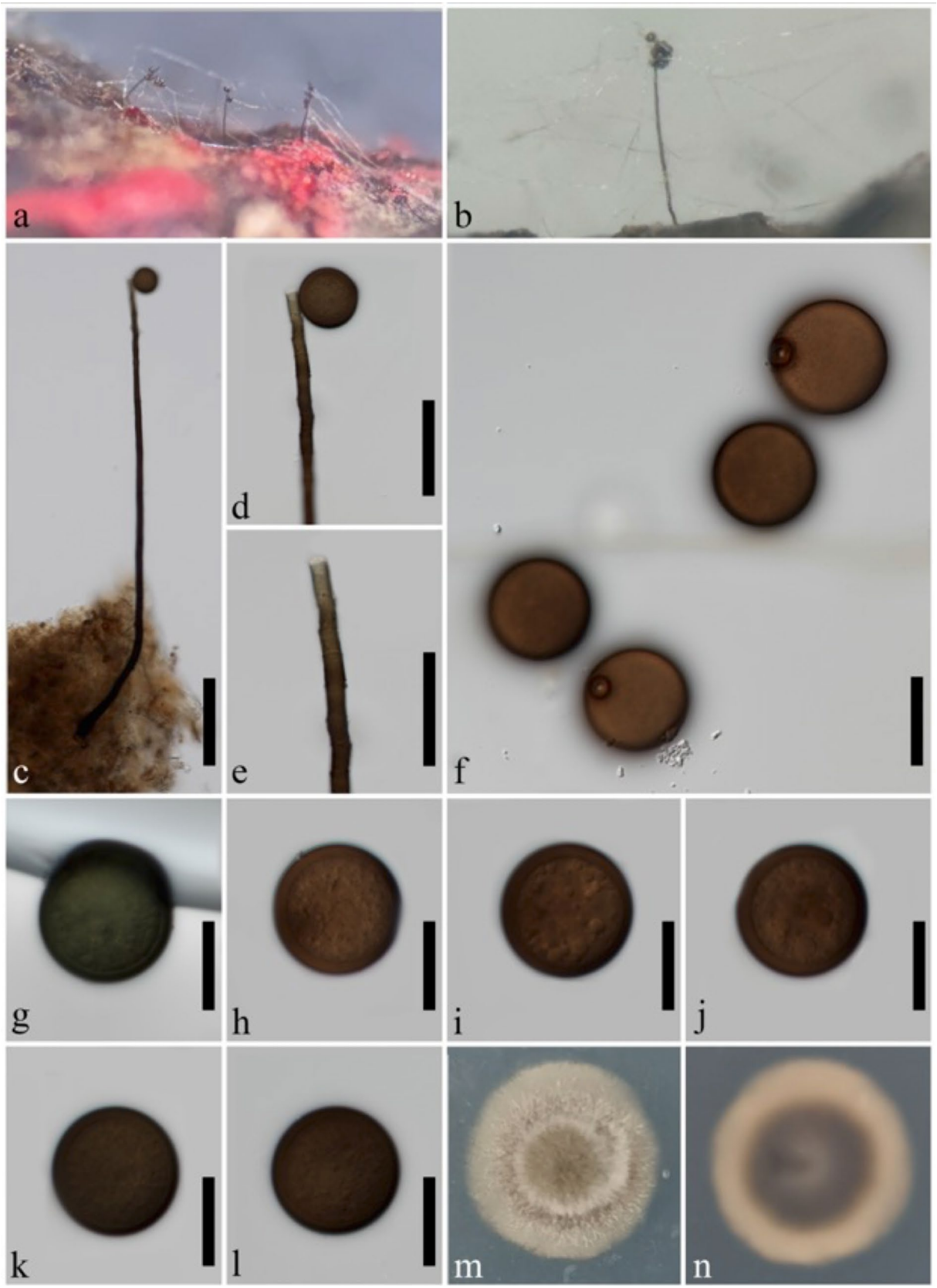


Fig. 1 ***Acrogenospora guangxiensis*** (MHZU 24–0828, **holotype**). **a, b** Colonies on wood. **c, d** Conidiophores and conidia. **e** Conidia growth location. **f–l** Conidia. **m, n** Colonies on PDA from above and reverse. Scale bars: **c** = 100 μm, **d, e** = 40 μm, **f–l** = 20 μm

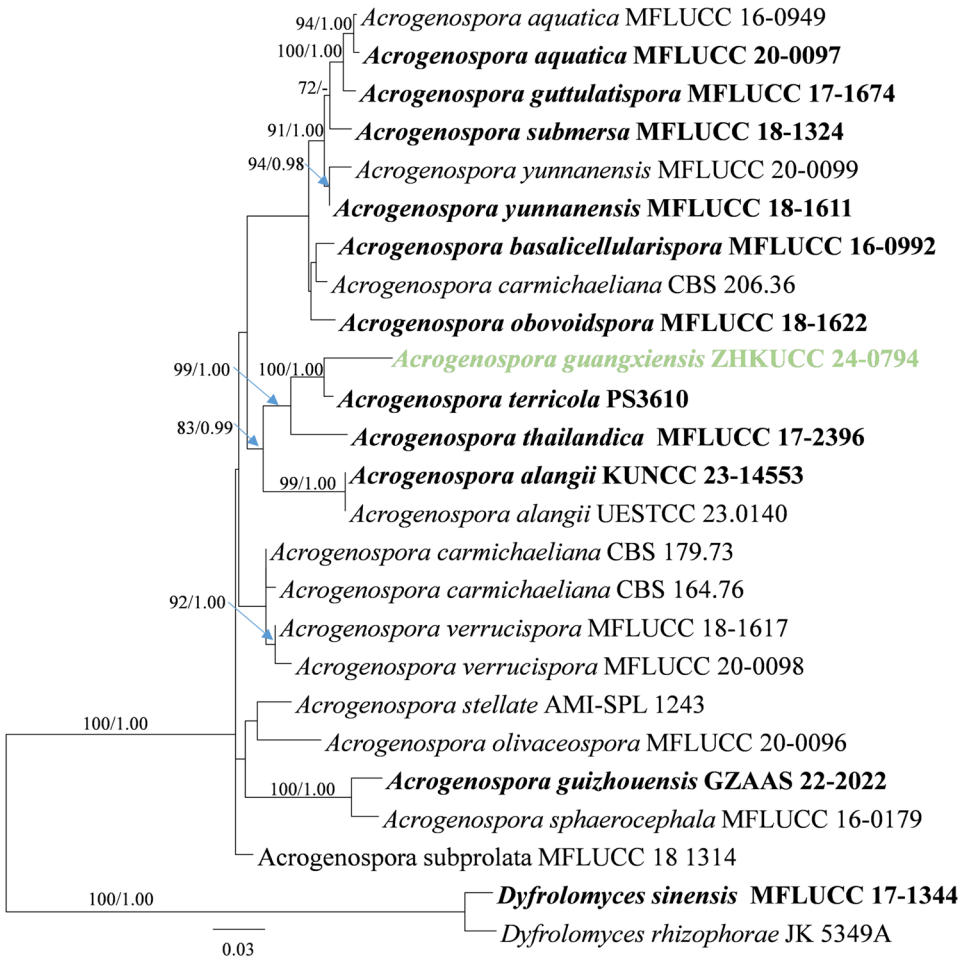


Fig. 2 Phylogenetic tree obtained from Maximum Likelihood analyses of a combined LSU, SSU, *tef1* and *rpb2* sequence data representing species of *Acrogenospora*. Twenty-five strains were included in the combined analyses. Bootstrap support values for ML equal to or greater than 70% and PP equal to greater than 0.95 are indicated at the nodes as ML/PP. The tree is rooted to *Dyfrolomyces rhizophorae* (JK 5349A) and *D. sinensis* (MFLUCC 17-1344) were used as the outgroup taxa. The ex-type strains are in bold, and the new isolates of this study are in green. Bar = 0.03 which represent the estimated number of nucleotide substitutions of site per branch

paler towards the apex. **Conidiogenous cells** monoblastic, cylindrical, initially inderterminate, later becoming intercalary, pale brown, smooth, percurrent proliferation. **Conidia** 23–29 µm, diameter ($\bar{x}$ = 26.5 µm, n = 15), acropleurogenous, solitary, spherical, truncate at base, aseptate, initially olive-green, later brown to dark brown, guttules, smooth.

Culture characteristics: Conidia germinating on PDA within 12 h; Colonies growing on PDA, reaching 12 mm in 15 days at 25 °C, circular, rough, dry, raised, edge entire, with dense, velvety, white to pale gray mycelium, in reverse dark brown in the middle and white in the periphery.

Material examined: CHINA, Guangxi Zhuang Autonomous Region, Qinzhou city, on decaying wood from freshwater habitat, 1 June 2023, *GX8.1* and *GX8.2* (MHZU 24–0828, **holotype**; ZHKUCC 24–0794, ex-type).

GenBank: ZHKUCC 24–0794: PP693395 (LSU), PP693396 (SSU), PP695182 (*tef1*), PP695182(*rpb2*).

Notes: In the phylogenetic analysis (Fig. 2), *Acrogenospora guangxiensis* ZHKUCC 24–0794 shares a sister relationship to *A. terricola* PS3610. Morphologically, *A. guangxiensis* ZHKUCC 24–0794 is most similar to *A. terricola* PS3610 with spherical conidium. But they can be distinguished by length of conidiophores and color of conidia. *Acrogenospora guangxiensis* ZHKUCC 24–0794 produces olive-green to dark brown spores on the conidiophores and conidiophores length up to 475 µm, the microscopic morphology of the colony could not be obtained, while the morphology of *A. terricola* PS3610 from pine needles in MEA medium and produce dark brown to black pores throughout the conidiophores, and the conidiophores length is up to 900 µm (Harrington et al. 2022). Regarding DNA sequence data comparison, there is a discrepancy of 1.97% (16 out of 813) and 0.30% (3 out of 1006) in nucleotide variations within the LSU and SSU sequence, respectively, between *A. guangxiensis* ZHKUCC 24–0794 and *A. terricola* PS3610. Unfortunately, *A. terricola* does not have a publicly available protein sequence and cannot be compared.

Mycosphaerellales P.F. Cannon.

Notes: Mycosphaerellales was introduced to accommodate Mycosphaerellaceae by Kirk et al. (2001), which was subsequently revised under the Capnodiales (Kirk et al. 2008). Lately, Abollahzadeh et al. (2020) revalidated

Mycosphaerellales as a separate order based on LSU, *tef1* and *rpb2* sequence data and analyses accommodating eight families Cystocoleaceae, Dissoconiaceae, Extremaceae, Mycosphaerellaceae, Neodevriesiaceae, Phaeothecoidiellaceae, Schizothyriaceae and Teratosphaeriaceae formerly treated in Capnodiales (Wijayawardene et al. 2022).

Mycosphaerellaceae Lindau.

Notes: Mycosphaerellaceae was introduced by Engler and Prantl (1897) with the family type Mycosphaerella Johanson, which was circumscribed as parasitic or saprobic on vascular plants or lichens, often forming pseudostroma or stroma and with developed hyphae in host tissue (von Arx and Müller 1975; Hyde et al. 2013). In total 129 genera have been assigned within Mycosphaerellaceae thus far (Wijayawardene et al. 2018b).

Pseudocercospora Speg.

Notes: *Pseudocercospora* was originally introduced by Spegazzini (1910) and was typified by *P. vitis*, a foliar pathogen of grapevines. The majority of *Pseudocercospora* species known to date are considered pathogens on a wide range of plants, mainly in tropical and sub-tropical regions, causing leaf spots, blights, fruit spots and fruit rot (Chupp 1954; Deighton 1976; von Arx 1983; Pons and Sutton 1988; Crous et al. 2013a).

Pseudocercospora cunninghamia Y. Zhang, Z.C. Liu & Z.P. Dou, **sp. nov.**

MycoBank: MB 856943; *Facesoffungi*: FoF 17087; Figs. 3, 4

Etymology: Refers to the host *Cunninghamia lanceolata*.

Holotype: BJFC LZC160120-57.

Needle leaves 3/4 wilted to fully wilted, sometimes a small branch of needles fully wilted, eventually turning brown. **Primary mycelia** within the substrate, secondary mycelium on the surface, subhyaline to pale brown, separated, branched, 3.0–5.0 µm wide. **Caespituli** amphigenous, punctiform, scattered, grayish-white to gray, mostly located on the underside of the leaves. **Pustule** pale brown, subspherical to spherical, 25.0–122.0 µm diam. **Conidiophores** tightly clustered, pale brown, occasionally with simple branched, upper part bluntly rounded or sometimes flexuous, 1–3 septate, 25.0–40.0 × 2.0–4.0 µm. **Conidiogenous cells** integrated, terminal or conidiophores reduced to conidiogenous cells, pale brown, unbranched, 12.0–20.0 × 3.0–4.0 µm, smooth, tapering to flat-tipped apical loci, unthickened, not darkened. **Conidia** solitary, narrowly subcylindrical, subhyaline to pale brown, apex rounded and obtuse, base nearly truncate to truncate, slightly thickened at the base, 0–7-septate, 23.0–75.0 × 2.0–3.0 µm.

Material examined: CHINA, Guangdong Province, Guangzhou City, South China Botanical Garden, Chinese Academy of Sciences, on needle leaves of *Cunninghamia lanceolata*, 23°18′N 113°37′E, 22 m asl, 20 Jan 2016, *Ying*

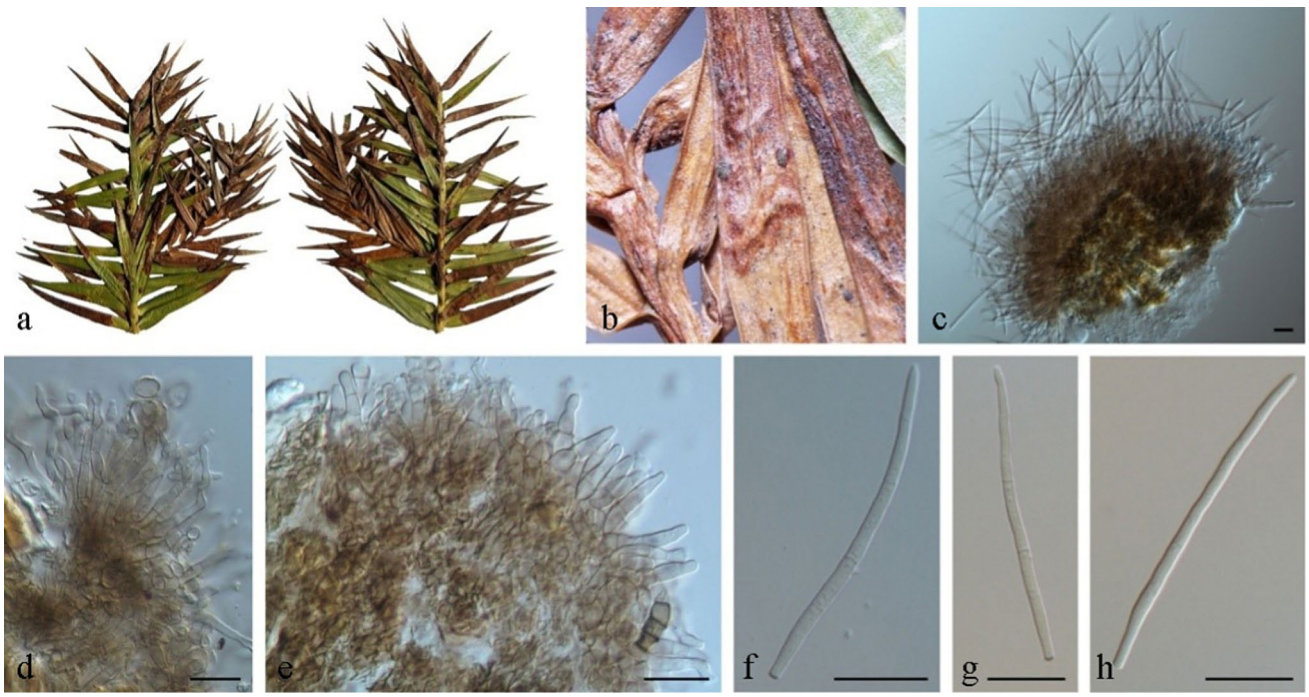


Fig. 3 ***Pseudocercospora cunninghamia*** (BJFC LZC160120-57, **holotype**). **a** Leaf spots on upper and lower leaf surface. **b** Close-up of leaf spot with fruiting. **c–f** Fascicles with conidiophores and conidiogenous cells. **g–h** Conidia. Scale bars = 10 µm

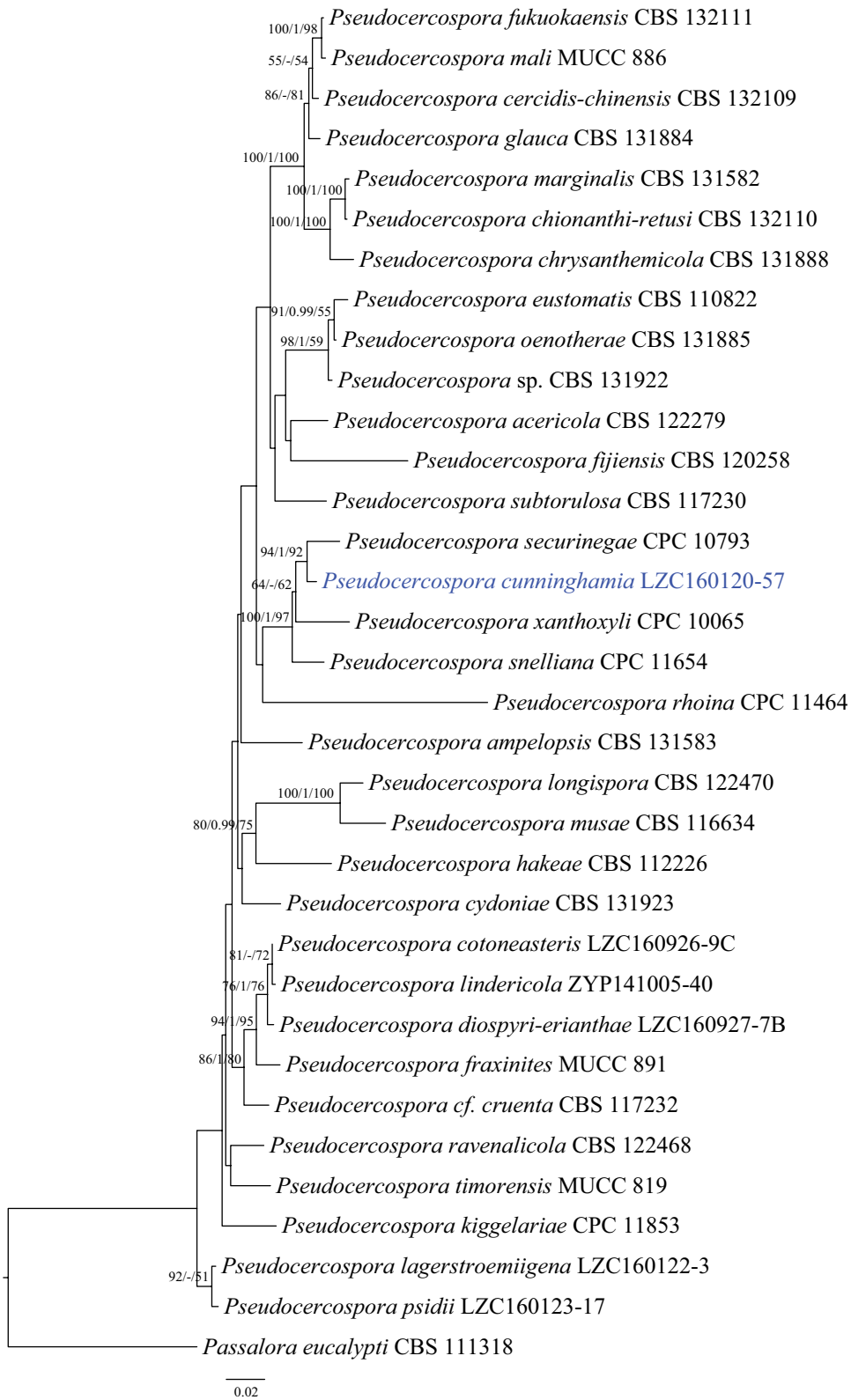


Fig. 4 Phylogenetic tree inferred from Maximum Likelihood analysis of *Pseudocercospora* based on a combined dataset of ITS, *tef1*, *act*, and *rpb2* genes. The outgroup taxon is *Passalora eucalypti* (CBS 111318). Support values are indicated at the nodes as follows: Maximum Likelihood bootstrap (ML ≥ 50%), Bayesian posterior probability (PP ≥ 0.90), and Maximum Parsimony bootstrap (MP ≥ 50%) (ML/PP/MP). The scale bar represents 0.02 substitutions per site

Zhang, *Zu-Chen Liu*, *Zhi-Peng Dou*, BJFC LZC160120-57 (**holotype**) and BJFC LZC160120-58.

GenBank: BJFC LZC160120-57: MH059728 (ITS), MH153937 (*tef1*), MH153896 (*act*), MH153850 (*rpb2*).

Notes: *Pseudocercospora cunninghamia* infects the needles of *Cunninghamia lanceolata*. *Pseudocercospora* is significantly affected by host range (Crous 2013). Except for this study, *Pseudocercospora* has not been known to infect

hosts of Taxodiaceae to date. Phylogenetic analysis showed that *Pseudocercospora cunninghamia* (BJFC LZC160120-57) differs from *P. securinegae* (CPC10793) by unique fixed alleles in three loci based on alignments of the separate loci deposited in the tree, by 4-bp in ITS (0.9%), 9-bp in *tef1* (3.5%) and 4 bp in *act* (2.7%). Morphologically, conidia of *P. securinegae* is hyaline, 2–7 septate, and spores larger than *Pseudocercospora cunninghamia* (3–4 × 25–l25 µm) (Deighton 1976). All the above reveal that *Pseudocercospora cunninghamia* is a new species.

Myriangiales Starbäck.

Notes: Myriangiales was erected by Starbäck in 1899 to accommodate species with crustose ascostromata and muriform ascospores. Fungi in this group are mostly pathogens, saprobes or epiphytes of plants. While four families were previously accepted in this order, only two families have been confirmed with DNA-based analyses to belong to this order – Elsinoaceae and Myriangiaceae (Jayawardena et al. 2015; Vinodhini et al. 2021).

Elsinoaceae Höhn. ex Sacc. & Trotter.

Notes: *Elsinoaceae* was established by Saccardo and Trotter (1913) with *Elsinoe* Racib. as its type genus. While it was subsequently proposed as a synonym of Myriangiaceae, these two families were ultimately separated through host range, morphological characters, and analyses of sequencing data (Jayawardena et al. 2015; Fan et al. 2017). Elsinoaceae is characterized by its production of erumpent or immersed pseudoascostromata comprised of pale hyphae or pseudoparenchymatous cells. Genera belonging to this family are predominatly plant pathogens, inducing spot and scab symptoms on many economically important hosts, including citrus, grapes and mango (Jayawardena et al. 2015).

Elsinoe Racib.

Notes: *Elsinoe* was introduced by Raciborski (1900) and is typified by *Elsinoe canavaliae*. Recent revisions of the genus (including its asexual morphological type *Sphaceloma*) have identified 84 species of *Elsinoe* (Fan et al. 2017; Marin-Felix et al. 2019; Ujat et al. 2023). *Elsinoe* species are plant pathogenic fungi that induce characteristic raised and cracked cork-like scabs or anthracnose spots on leaves and fruit. Most species in this genus are host-specific, with at least 77 of the 84 species affecting only a single host genus or species (Marin-Felix et al. 2019; Ujat et al. 2023). Some examples of hosts include *Anacardium, Citrus, Eucalyptus*, *Hovenia*, and *Vitis* (Ridley and Ramsfield 2005; Chung 2011; Fan et al. 2017; Marin-Felix et al. 2019; Pham et al. 2021; Roux et al. 2023). In most cases, *Elsinoe* species are not economically significant pathogens, affecting the appearance of the plants without causing significant crop loss (Holliday 1980).

The scab structures caused by *Elsinoe* contain pseudoascostromata, with 3 to 8 asci within each locule (Fan et al. 2017; Ujat et al. 2023). These asci are bitunicate, saccate to globose, and contain irregularly arranged ascospores that are oblong to fusiform with between 2 and 3 transverse septa (Marin-Felix et al. 2019; Ujat et al. 2023). In the asexual form, hyaline, ellipsoidal smooth-walled aseptate conidia are produced from polyphialidic conidiophores (Marin-Felix et al. 2019; Ujat et al. 2023). Full morphological analyses have been provided previously by Fan et al. (2017) and Ujat et al. (2023).

Elsinoe fuzhouensis J.Y. Su, Z.H. Wang & H.L. Hu, **sp. nov.**

Fungal Names: FN 571788; *Facesoffungi*: FoF 15309; Figs. 5, 6

Etymology: refers to Fuzhou City, the locality of the type specimen collected.

Holotype: CGMCC 3.25536.

Asexual morph: anthracnose on *Ficus microcarpa*. The leaves reddish-brown spots. **Conidiogenous cells** hyaline, ampulliform to doliiform, blastic. **Conidia** typically one celled, hyaline, round at the rear end, fusiform at the apical end, with one to three oil droplets, 5.47–7.12 × 2.2–3.13 µm, $\bar{x} = 6.34 \pm 0.43 \times 2.58 \pm 0.24$ µm, and n = 50. Sexual morph: not observed.

Cultural characteristics: colonies on MEA extremely slowly growing, reaching 18 mm at 25℃ after 21d in 12 h/12 h light/dark. Colony displayed red-brown, an irregular growth and wrinkled texture, no to little aerial hyphae.

Material examined: CHINA, Fujian Province, Fuzhou City, Gulou District, Yeshan Spring and Autumn Park, 26°10′20″N 119°29′15″E, 28.1 m asl, 03 May 2023, *Ji-Yu Su*, *Zong-Hua Wang*, *Hong-Li Hu*, FJ-R-1 (CGMCC 3.25536, **holotype**), FZ-R-1–2, FZ-R-1–3, FZ-R-1–4.

GenBank: CGMCC 3.25536: PP049023 (ITS), PP049250 (*rpb2*), PP049251 (*tef1*). FZ-R-1–2: PV130373 (ITS), PV166291 (*rpb2*), PV166294 (*tef1*); FZ-R-1–3: PV130374 (ITS), PV166292 (*rpb2*), PV166295 (*tef1*); FZ-R-1–4: PV130375 (ITS), PV166293 (*rpb2*), PV166296 (*tef1*).

Notes: *Elsinoe fuzhouensis* was isolated from diseased leaves of *Ficus microcarpa*. *Elsinoe fici* and *E. fici-caricae* are the two species reported on *Ficus* plants. However, they showed distant phylogenetic relationships with *E. fuzhouensis*. *Elsinoe citricola* and *E. fuzhouensis* were distributed in the same clade in the phylogenetic tree with high support (BS = 100%, PP = 1.00). While the *rpb2* sequences can separate the two species, because their sequence similarity differed by more than 3% while less than 7%. Morphologically, the colonies of *E. fuzhouensis* were red-brown, while *E. citricola*'s were yellow–brown on MEA. The spores of *E. fuzhouensis* are smaller than those of *E. citricola*

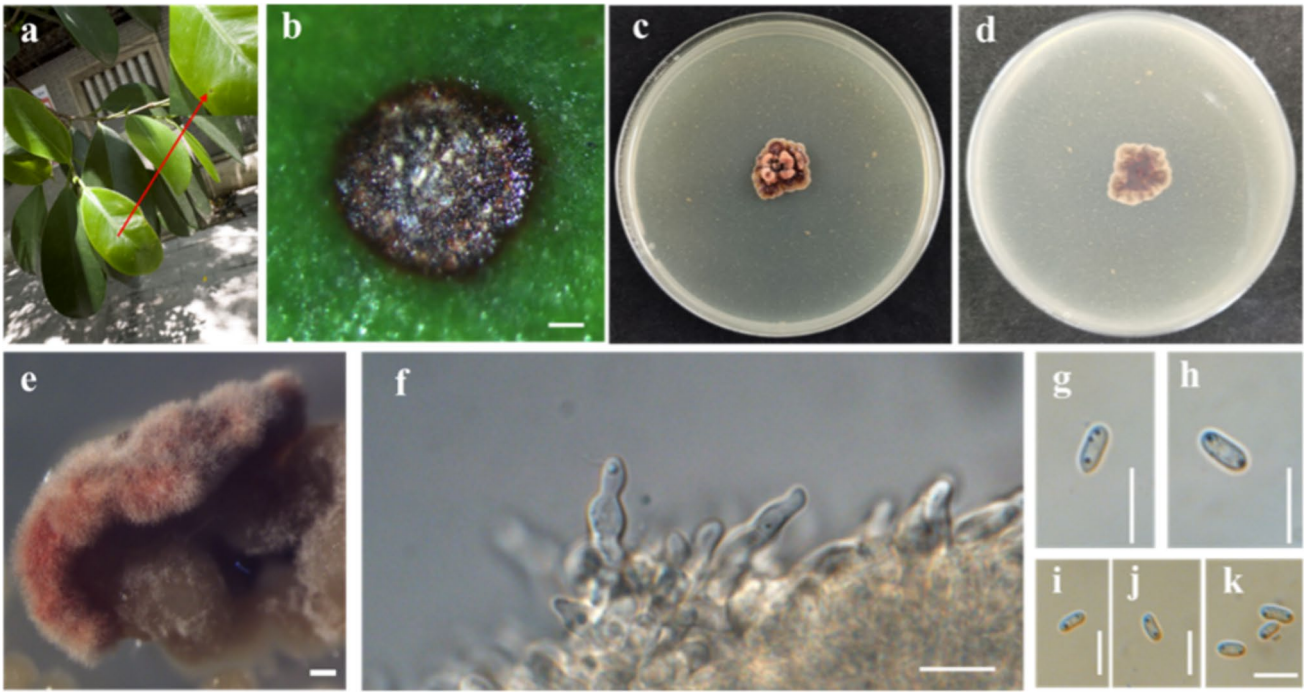


Fig. 5 ***Elsinoe fuzhouensis*** (CGMCC 3.23515, **holotype**). **a** Anthracnose on leaves of *Ficus microcarpa*. **b** Anthracnose under stereo-microscope. **c, d** Colony on MEA. **e** Conidial mass on MEA. **f** Conidiogenous cells on MEA. **g–k** Conidia on MEA. Scale bars: **b, e** = 100 µm, **f–k** = 10 µm

(5.47–7.12 × 2.2–3.13 vs. 5.5–9 × 2.5–4.5 µm) (Fan et al. 2017). Thus, *E. fuzhouensis* is recognized as a new species.

Elsinoe leucospermi L. Swart & Crous, **new geographical record from New Zealand.**

Index Fungorum: IF 627343; *Facesoffungi*: FoF 15302; Figs. 7, 8

Pathogenic on *Leucadendron* sp., causing scab on stems and leaves. Scab lesions on leaves are brown to gray, mostly abaxial, circular, raised, 10–15 mm in diameter, sometimes surrounded by a reddish halo. *Sexual morph:* No spores or spore bearing structures found on plant material. *Asexual morph:* No spores or spore bearing structures found on plant material or in culture.

Culture characteristics: Very slow growth on PDA at 21 °C under black light, with colonies reaching 10 mm in diameter after 30 days of growth. Colonies well raised above agar surface, folded, with smooth, lobate margins and short white aerial hyphae in tufts. Surface black, light-brown to coral, reverse scarlet or coral. Hyphae densely septate, hyaline to pigmented, branched, smooth-walled.

Material examined: NEW ZEALAND, Wanganui, from scab on *Leucadendron* sp. leaves, June 2023, *L. Braithwaite*, *PHEL T23_02700*. Culture stored at the International Collection of Microorganisms from Plants (ICMP 25035) and dried specimen voucher at the New Zealand Fungarium (PDD 120167).

Hosts and distribution: AUSTRALIA, on *Leucadendron chamelaea-pubibracteolatum, Leucad. laureolum and Leucad. thymifoloum, Leucad.* sp., *Leucospermum cordifolium, Leucos.* sp., and *Serruria florida*; CANARY ISLANDS, on *Leucos. cordifolium;* NEW ZEALAND, *Leucad.* sp.; USA, on *Leucad. chamelaea-pubibracteolatum, Leucad. laureolum, Leucad. pubibracteolatum, Leucad. thymifoloum, Leucad.* sp., *Leucos. cordifolium, Leucos.* sp.; SPAIN, on *Leucos.* sp.; SOUTH AFRICA, on *Leucad. pubibracteolatum, Leucad.* sp., *Leucos. cordifolium, Leucos. cordifolium*, *Leucos.* sp., and *Serruria florida*; ZIMBABWE, on *Leucos.* sp., *Leucos. glabrum*, *Leucos. reflexum*, *Leucad.* sp., and *Leucos.* sp. (Swart et al. 2001; Fan et al. 2017; Farr et al. 2021; this study).

GenBank: ICMP 25035: OR807180 (ITS), OR814104 (*rpb2*).

Notes: The identification of *Elsinoe* is often difficult due to their slow-growing nature, and the lack of fertile structure production in nature. This can make the detection of *Elsinoe* fruiting structures and spores challenging, as was observed in this instance. Both sectioning of symptomatic leaf and stem material and examining the pure culture did not result in finding spores or spore bearing structures. However, the symptoms clearly indicated that the disease could be caused by an infection with *Elsinoe* and DNA sequence analysis confirmed the identity of the obtained culture as *E. leucospermi*. Multi-gene

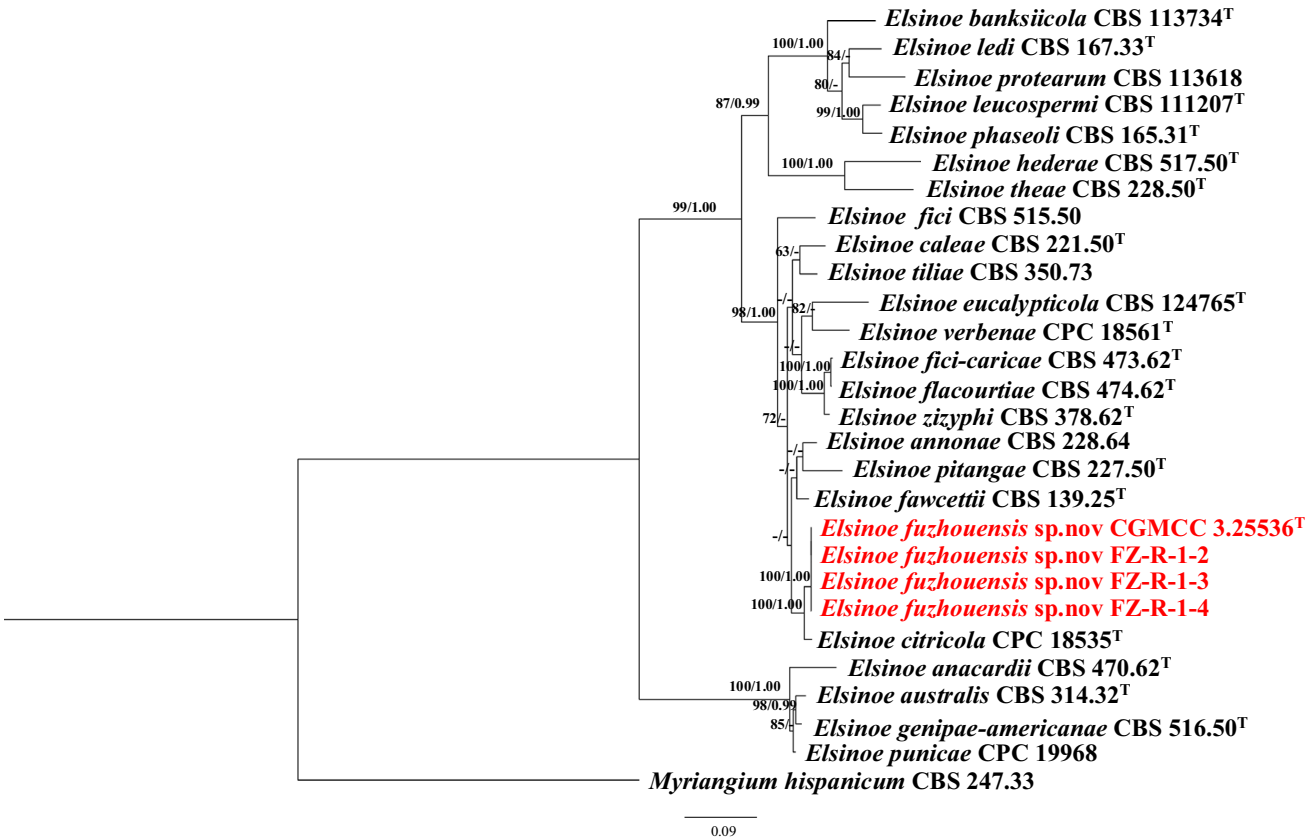


Fig. 6 Maximum Likelihood phylogram of *Elsinoe* species based on a combined matrix of ITS, *rpb2* and *tef1* genes [*Myriangium hispanicum* (CBS 247.33) is the outgroup]. Numbers in front of slash stand for the Maximum Likelihood bootstrap values, and numbers behind the slash stand for the Bayesian posterior probabilities. "-" indicates that the given branches were supported less than 50% by Maximum Likelihood bootstrap or 0.93 by Bayesian analyses. The new species are in red. "T" refers to a type specimen

phylogenetic analysis using the combined ITS and *rpb2* regions demonstrated that isolate ICMP 25035 groups in a well-supported clade with other isolates of *E. leucospermi*, including the type strain CBS 11207 (Fig. 8). The sequences of the ITS and *rpb2* regions were 100% identical to the sequences of CBS 11207. This is the first record of *E. leucospermi* from New Zealand.

Pleosporales Luttr. ex M.E. Barr.

Notes: The order Pleosporales established by Luttrell (1955), is the largest order in the class Dothideomycetes, comprising more than 90 families and 650 genera (Wijayawardene et al. 2022). In recent years, numerous new pleosporalean families, genera and species were introduced based on molecular studies and morphological diagnosis (Wanasinghe et al. 2020, 2022; Xie et al. 2022; Yang et al. 2022). Although some pleosporalean occur as endophytes (Knapp et al. 2015), parasites (Ariyawansa et al. 2020) and lichenicolous (Etayo and Pino-Bodas 2021), most pleosporalean taxa are saprobic (Brahmanage et al. 2020).

Didymellaceae Gruyter, Aveskamp & Verkley.

Notes: *Didymellaceae* comprises diverse fungal species which has a wide host range. These species are important plant pathogens as well as they are reported as endophytes and saprobes (Chen et al. 2015).

Epicoccum Link.

Notes: Epicoccum is a cosmopolitan genus in Didymellaceae which is a well-known phytopathogenic genus (Chen et al. 2025). Currently there are 18 recognized species within this genus (Index Fungorum 2024). These fungi are known for producing secondary metabolites, such as pigments, antimicrobial compounds, and nanoparticles (Taguiam et al. 2021). *Epicoccum* species play significant roles as biocontrol agents against plant pathogens and have potential biotechnological applications (Del Frari et al. 2019).

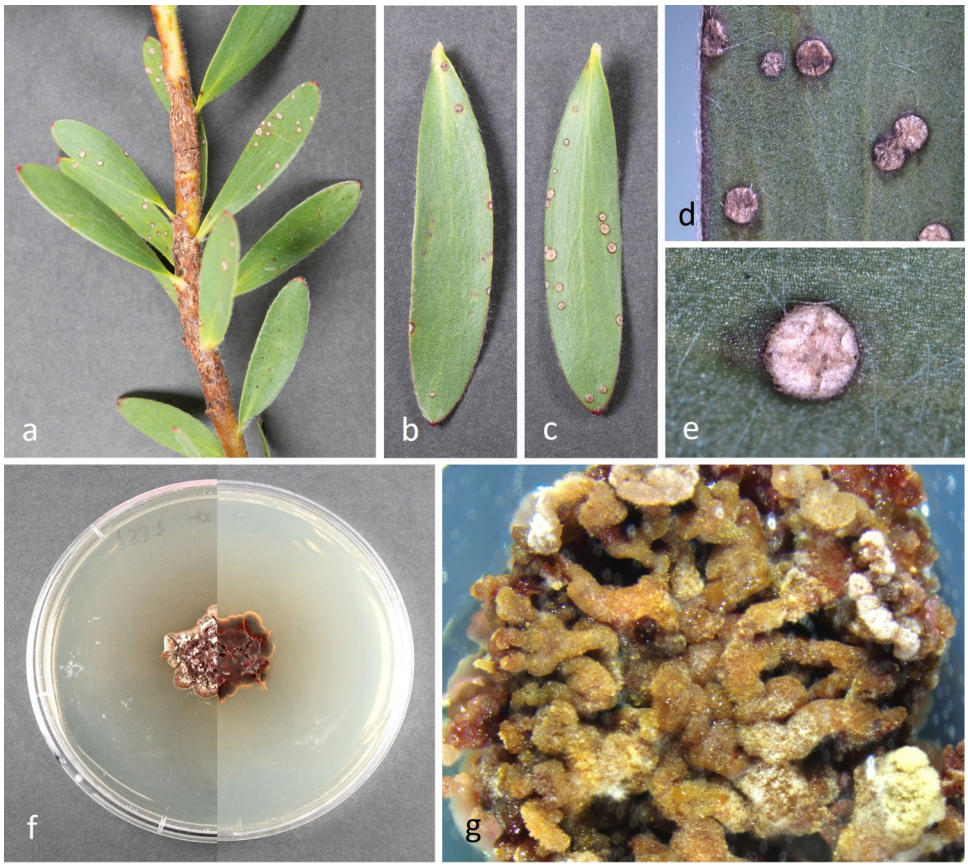


Fig. 7 ***Elsinoe leucospermi*** (PDD 120167; ICMP 25035, living culture). **a** Scab symptom on *Leucadendron* sp. stem and leaves. **b** Scab symptoms on adaxial leaf surface. **c** Scab symptoms on abaxial leaf surface. **d, e** Appearance of characteristic raised and cracked cork-like structures on infected leaves. **f** Growth on PDA media after 60 days. **g** Closer view of the raised folded colony forming on PDA

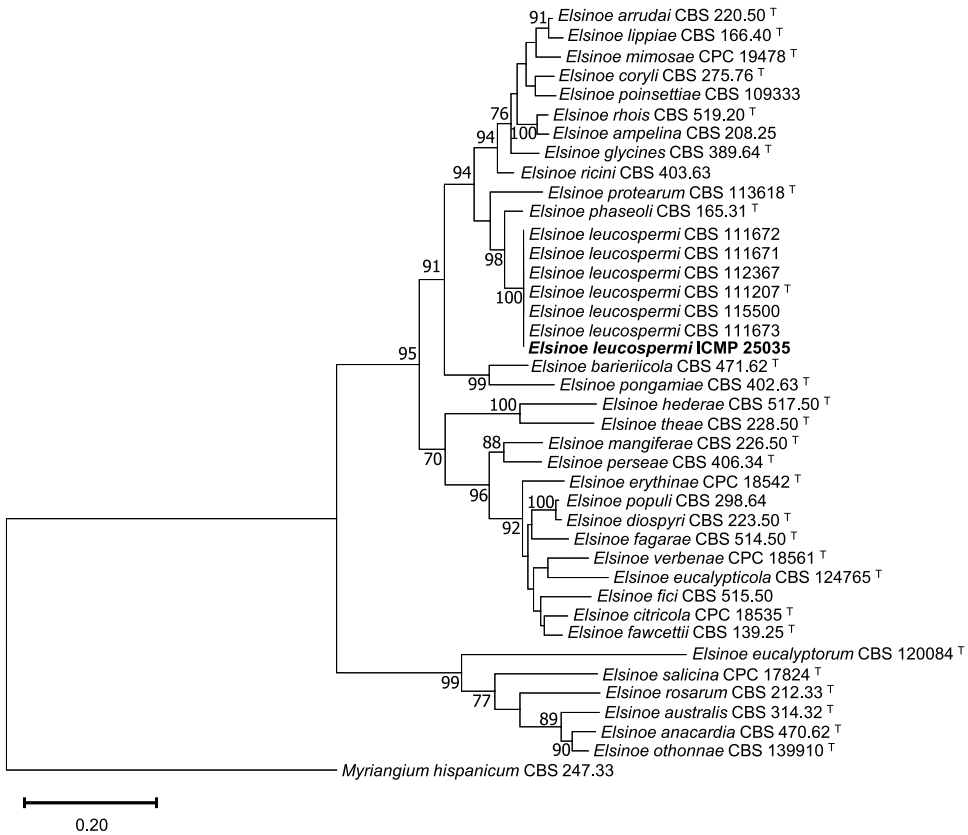


Fig. 8 Maximum Likelihood (GTR + G + I) tree illustrating the phylogenetic placement of the *Elsinoe leucospermi* isolate ICMP 25035 from New Zealand (in bold). The phylogram is based on the analysis of concatenated ITS and *rpb2* sequences. Branches are labelled with bootstrap probabilities ≥ 70% across 10,000 bootstrapping replicates, and type specimens are denoted by a superscript "T". *Myriangium hispanicum* CBS 247.33 was used as an outgroup

Epicocum maxima Manawas., Q.L. Tan & Y.X. Zhang, **sp. nov.**

Index Fungorum: IF 903595; *Facesoffungi*: FoF 17681; Figs. 9, 10

Etymology: epithet refers to the host, *Citrus maxima* from which the fungus was isolated.

Holotype: ZHKUCC 24–1069.

Endophytic on *Citrus maxima*, sexual morph: not observed. Asexual morph: after 4 weeks on OA medium, **Pycnidia** 80–152 × 70–125(–140) µm (mean = 125 × 110 µm, n = 30), transparent to black, solitary or aggregated, ovoid or subspherical, sometimes pear-shaped, surface or semi-buried in the medium. The walls of pycnidium are composed of elongated and equal diameter cells, with 3–4 layers of cell layers, including 2–3 layers of brown outer layer, with a thickness of 17–22 µm. Conidiophore: not observed. Conidiogenus cells: not observed. **Conidia** ellipsoid to cylindrical, smooth, hyaline, 7.2–9.3 × 3.2–5.0 µm (mean = 8 × 4.1 µm, n = 50).

Culture characteristics: Cultivate on OA medium for 7 days, with a colony diameter of 72 mm (n = 5). The edge of the colony is regular, the hyphae are closely attached, and the colony is white to gray in the center, white to gray on the back, with a slight yellow color. Cultivate on PDA medium for 7 days and cover the plate with mycelium. The white mycelium is lush, dense, with regular edges, and the back is white to slightly orange yellow. Cultivate on MEA medium for 7 days with a colony diameter of 75 mm (n = 5). The edge of the colony is regular, with dense white hyphae, slightly orange in the middle, radiating, and white to orange on the back.

Material examined: CHINA, Guangdong Province, Guangzhou, Shaoguan City, Renhua County, Renhua County, Daqiao Town, Changba Village, Jin Zhe Yuan Ecological Agriculture Co. LTD. On *Citrus maxima*, 25 August 2021, *Ishara S. Manawasinghe*, ZHKUCC 24–1069 (**holotype**), living cultures ZHKUCC 24–1070, ZHKUCC 24–1071 and ZHKUCC 24–1072.

GenBank: ZHKUCC 24–1069: PV486802 (ITS), PV486804 (LSU), PV494564 (*rpb2*), PV494562 (*tub2*).

Notes: In the multigene phylogenetic analysis constructed by ITS, LSU and *rpb2* and *tub2* (Fig. 10), the species in this study formed an independent branch, with a particular sister relationship to *E. poaceicola*, with 99% ML bootstrap support and 1.0 BYPP value. In terms of morphological identification, the PDA culture medium of the strain in this study covered the plate at 25 ℃, and the growth rate was faster than the *E. poaceicola* 51 mm

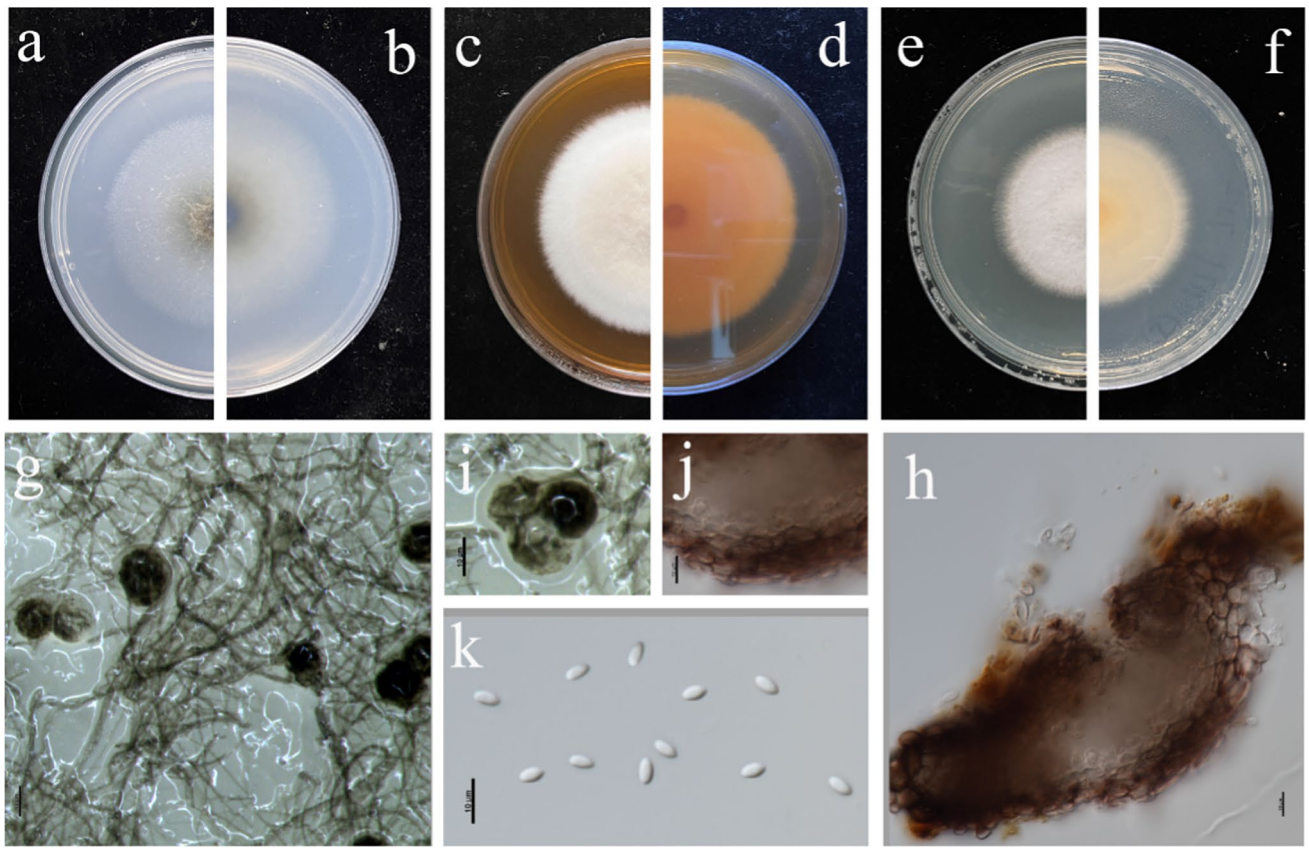


Fig. 9 ***Epicocum maxima*** *(*ZHKUCC 24–1069, **holotype). a**, **b** Colony on OA (front and reverse). **c**, **d** Colony on MEA (front and reverse). **e**, **f** Colony on PDA (front and reverse). **g**, **i** Pycnidium forming on OA. **j**, **h** Section of pycnidium. **k** Conidia. Scale bars: **g**–**k** = 10 µm

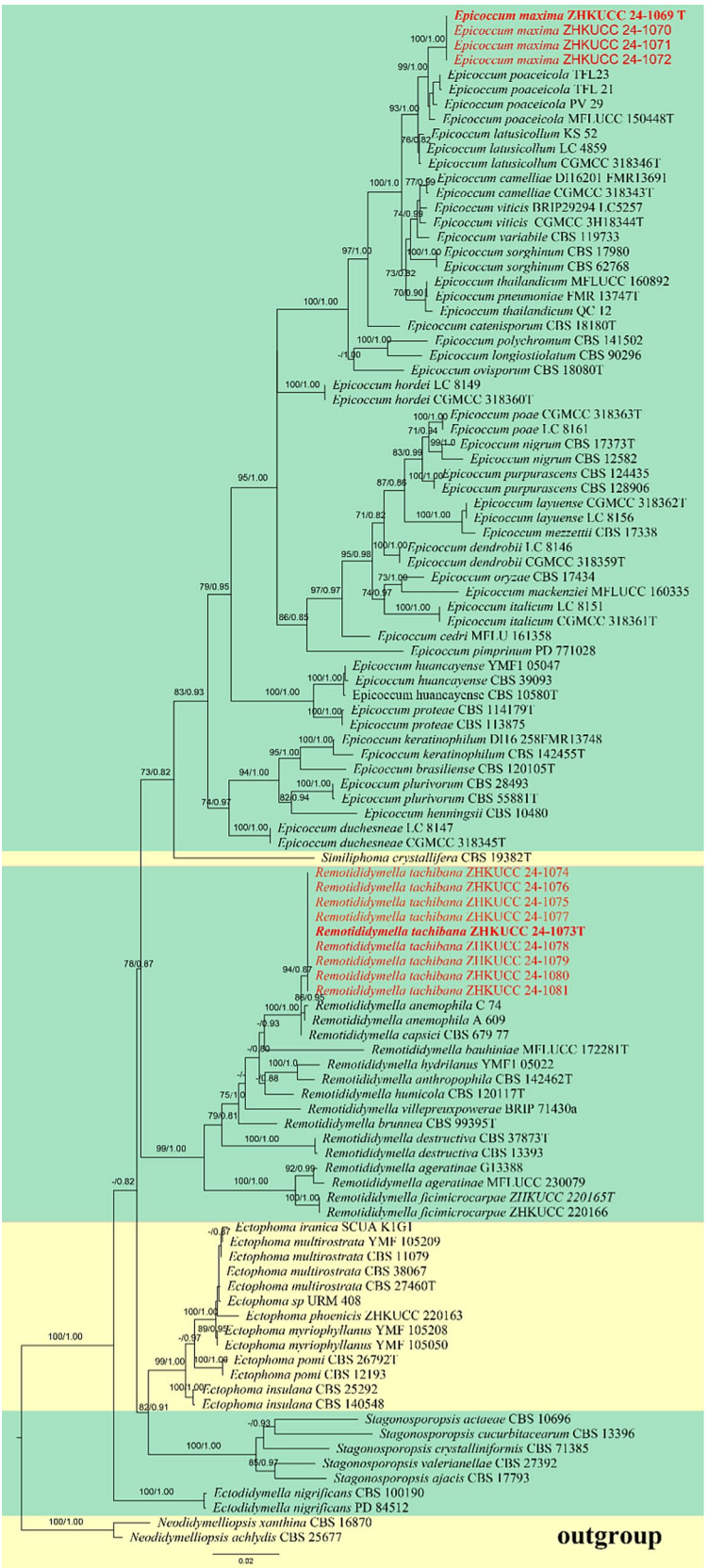


Fig. 10 The Maximum Likelihood consensus tree inferred from the combined ITS, LSU, *rpb2* and *tub2* sequences of *Epicoccum*, *Remotididymella* and other closely related genera in Didymellaceae. Bootstrap support values for Maximum Likelihood (ML, first value) equal to or greater than 75% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Neodidymelliopsis xanthina* (CBS 168.70) and *Neodidymelliopsis achlydis* (CBS 256.77). Type strains are indicated with "[T]". The newly generated sequences are indicated in red

(Thambugala et al. 2017). The conidia in this study ranged from 7.2–9.3 × 3.2–5.0 µm (mean = 8 × 4.1 µm) compared to *E. poaceicola* (2–)3–5.7 × 1.8–3 µm (mean = 4 × 2.2) µm larger. Based on morphological characteristics and multigene phylogenetic analysis, the strain in this study was identified as a new species.

Remotididymella Valenz.-Lopez, Crous, Cano, Guarro & Stchigel.

Notes: Remotididymella was introduced by Valenzuela-Lopez et al. (2018) based on ITS, LSU, *rpb2* and *tub2* sequence data in Didymellaceae. They are associated with plant and animals mostly as saprobic and pathogenic fungi. Currently there are 11 species epithets available for this genus in Index Fungorum (2024, November).

Remotididymella tachibana Manawas., Q.L. Tan & Y.X. Zhang, **sp. nov.**

Index Fungorum: IF 903596; *Facesoffungi*: FoF 17682; Figs. 10, 11

Etymology: epithet refers to the host, *Citrus tachibana* a from which the fungus was isolated.

Holotype: ZHKUCC 24–1073.

Endophytic on *C. tachibana* and *C. nobilis*. Sexual morph: develop after 4 weeks OA medium. **Ascomata** is black, nearly spherical to inverted pear-shaped, solitary, with a pore opening, semi buried or surface grown on OA medium, 70–150 × 75–140(–160) µm (mean = 125 × 110 µm, n = 30). **Asci** cylindrical to rod-shaped, hyaline, gradually becoming thinner at the base and top, containing eight ascospores with sizes ranging from 74–97 × 8.7–11.6 µm (mean = 87 × 10 µm, n = 50). **Ascospores** hyaline, straight or slightly curved, with a blunt top and a wide blunt bottom, septate, septa slightly contracted, upper cell is usually wider than the lower cell, transparent and smooth, 14–17 × 4–5 µm (mean = 16 × 4 µm, n = 50). Asexual morph: not observed.

Culture characteristics: Cultivate on OA medium for 7 days, with a colony diameter of 70 mm (n = 5). The colony is gray, with regular edges and white aerial hyphae. The back is gray to dark gray, radiating. Cultivate on PDA medium for 7 days with a colony diameter of 60 mm (n = 5). The colony is white gray with lush hyphae, with a gray center and a white circular edge. The center of the back is gray to lead black, with regular edges. Cultivate on MEA medium

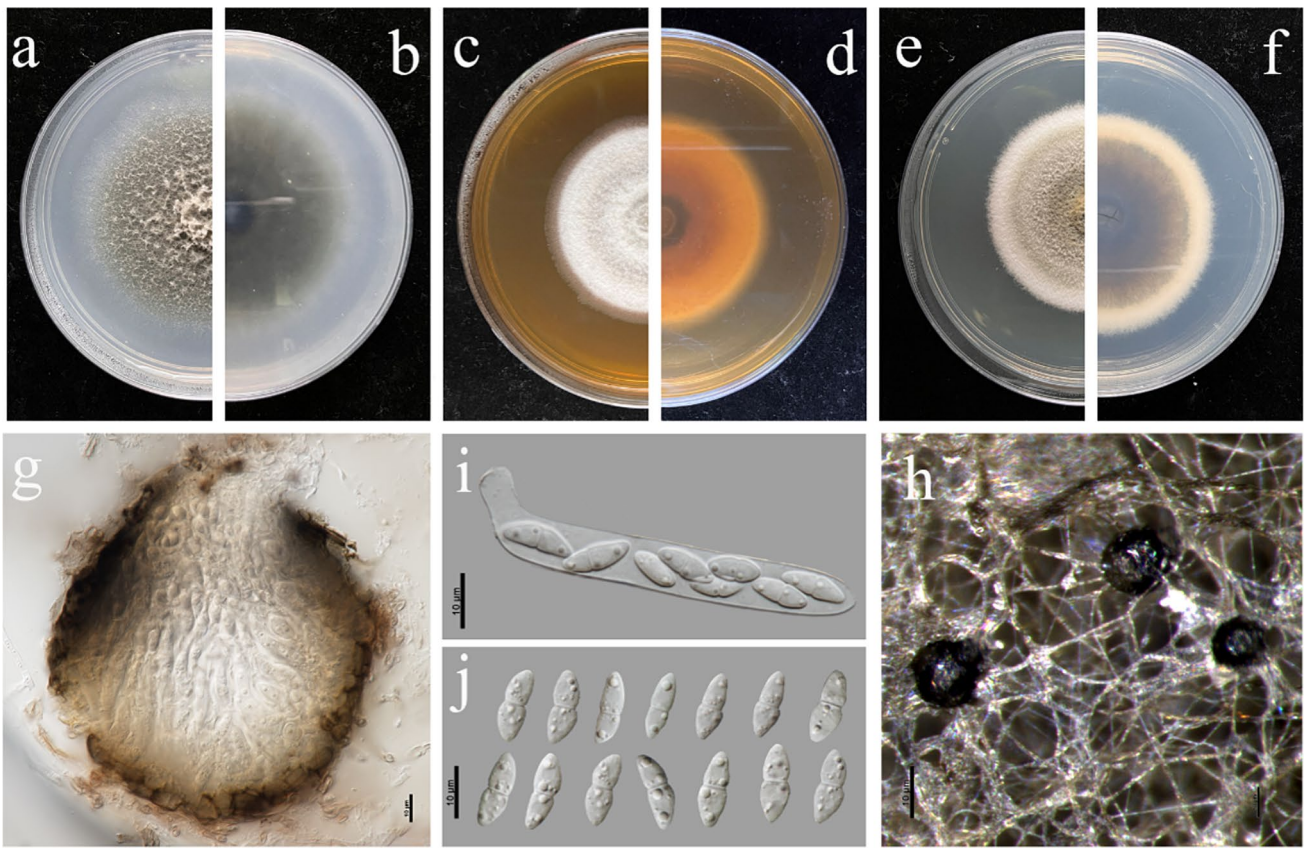


Fig. 11 ***Remotididymella tachibana*** *(*ZHKUCC 24–1073, **holotype**). **a**, **b** Colony on OA (front and reverse, 5 d). **c**, **d** Colony on MEA (front and reverse, 5 d). **e**, **f** Colony on PDA (front and reverse, 5 d). **g** Ascomata. **i** Asci. **j** Ascospores. **h** Aggregated ascomata on OA. Scale bars: **g**–**j** = 10 µm

for 7 days, with a colony diameter of 54 mm (n = 5). The colony is white, the hyphae are dense and tightly adhered, with regular edges, white on the back, and a slight orange color in the middle.

Material examined: CHINA, Guangdong Province, Guangzhou, Shaoguan City. On *Citrus tachibana,* 25 August 2021, *Ishara S. Manawasinghe*, ZHKUCC 24–1073 (**holotype**), living cultures ZHKUCC 24–1074, ZHKUCC 24–1075, ZHKUCC 24–1076, ZHKUCC 24–1077, ZHKUCC 24–1078, ZHKUCC 24–1079, ZHKUCC 24–1080 and ZHKUCC 24–1081.

GenBank: ZHKUCC 24–1073: PV486803 (ITS), PV486805 (LSU), PV494565 (*rpb2*), PV494563 (*tub2*).

Notes: In the multigene phylogenetic analysis constructed by ITS, LSU, *rpb2* and *tub2* (Fig. 10), the species in this study formed an independent branch, with a particular sister relationship to *R. anemophila*, with 94% ML bootstrap support and 0.87 BYPP value. Morphologically, the ascomata of our isolates 70–150 × 75–140(–160) µm (mean = 125 × 110 µm) is bigger than that of *R. anemophila* 91–121 × 84–86 µm. There is a difference in the size of the asci between 74–97 × 8.7–11.6 µm and *R. anemophila* 35–102 × 9–11 µm. Based on morphological characteristics and multigene phylogenetic analysis, the strain in this study was identified as a new species.

Occultibambusaceae D.Q. Dai & K.D. Hyde.

Notes: Occultibambusaceae was established by Dai et al. (2017) based on *Occultibambusa* as type genus. The family accommodates five genera viz. *Brunneofusispor*, *Neooccultibambusa*, *Occultibambusa*, *Seriascoma*, and *Versicolorisporium* based on morphology and phylogeny (Hatakeyama et al. 2008; Dai et al. 2017; Doilom et al. 2017; Phookamsak et al. 2019).

Seriascoma Phook., D.Q. Dai & K.D. Hyde.

Notes: The genus *Seriascoma* was introduced by Dai et al. (2017) and accommodate *S. didymospora* as the type species from decaying bamboo culms. The genus *Seriascoma* records 5 species in Index Fungorum (https://www.indexfungorum.org/Names/Names.asp). The sexual morph of *Seriascoma* is characterized by gregarious, with slit-like opening, multiloculate, ostiolar ascostromata, immersed beneath clypeus, thick-walled peridium composed of dark brown pseudoparenchymatous cells of *textura angularis*, clavate, long pedicellate, apically rounded, with well-developed, ocular chamber, bitunicate, fissitunicate asci, and clavate to fusiform, with rounded ends, hyaline, 1-septate, slightly constricted at the septum, straight to curved, smooth-walled, with guttulate ascospore (Dai et al. 2017). The sexual morph of *Seriascoma* is characterized by solitary to gregarious, immersed in cortex layers, raised, black, eustromatic conidiomata, conidiomata wall composed of dark brown to black pseudoparenchymatous cells of *textura angularis*, holoblastic, phialidic, determinate, discrete, cylindrical to ampulliform or lageniform, hyaline, aseptate, apically attenuated, with distinct periclinal thickening, smooth-walled conidiogenous cells, oblong, hyaline, aseptate, smooth-walled conidia with rounded to obtuse ends (Dai et al. 2017).

Seriascoma oblonga H.J. Zhao & W. Dong, **sp. nov.**

Index Fungorum: IF 902893; *Facesoffungi*: FoF 16780; Figs. 12, 13

Etymology: refers to oblong conidia.

Holotype: MHZU 24–0622.

Asexual morph: coelomycetous. **Conidiomata** 160–200 µm high, 315–400 µm diam., coriaceous, erumpent, semi-immersed in cortex layers, solitary to gregarious, subglobose, dark gray, uni-loculate, glabrous. **Wall of conidiomata** 15–80 µm thick, thin- to thick-walled, of unequal thickness, thick at the sides, comprised of host and fungi tissue, with several layers of brown to dark brown, pseudoparenchymatous cells of textura angularis. **Conidiophores** arising from the base of the cavity reduced to conidiogenous cells. **Conidiogenous cells** 4–9.5 × 2–4.5 µm ($\bar{x}$ = 6.0 × 3.1 µm, n = 30), enteroblastic, phialidic, determinate, discrete, ampulliform or lageniform, hyaline, aseptate, apically attenuated, with distinct periclinal thickening, smooth-walled. **Conidia** 5.5–8 × 2.2–3.2 µm ($\bar{x}$ = 6.4 × 2.8 µm, n = 30), oblong, with rounded to obtuse ends, hyaline, aseptate, guttulate, verrucose, smooth-walled.

Culture characters: Conidia germinating on PDA within 12 h, colonies growing on PDA, reaching 20–26 mm diam. in 4 weeks at 25–28 °C, circular, dense, flat, slightly raised, smooth with entire white edge, velvety to floccose, slightly radiating, aspect smooth, slightly raised at the center, pale brown from above, dark green from below.

Material examined: CHINA, Sichuan Province, Weiyuan County, Zhenxi Town, Huaci Village. Isolated from decaying bamboo, 31 January 2023, *J. Hu*, *SC024* and *SC025* (MHZU 24–0622, **holotype**; ZHKUCC 24–1168, ex-type).

GenBank: ZHKUCC 24–1168: PQ475789 (ITS), PQ475790 (LSU), PQ474276 (*tef1*).

Notes: In the phylogenetic analysis, *Seriascoma oblonga* forms a sister branch with *S. yunnanense* (Fig. 13). Regarding DNA sequence data comparison, there is a discrepancy of 2.1% (10 out of 476, 3gaps) and 0.2% (1 out of 424, no gaps) in nucleotide variations within the ITS and *tef1* sequence, respectively, between *S. oblonga* ZHKUCC 24–1168 and *S. yunnanense* SICAU 22–0059. However, morphologically, *S. yunnanense* have no asexual morph (Rathnayaka et al. 2019; Zeng et al. 2022). *Seriascoma oblonga* fit in the asexual morph of *Seriascoma*. *Seriascoma*

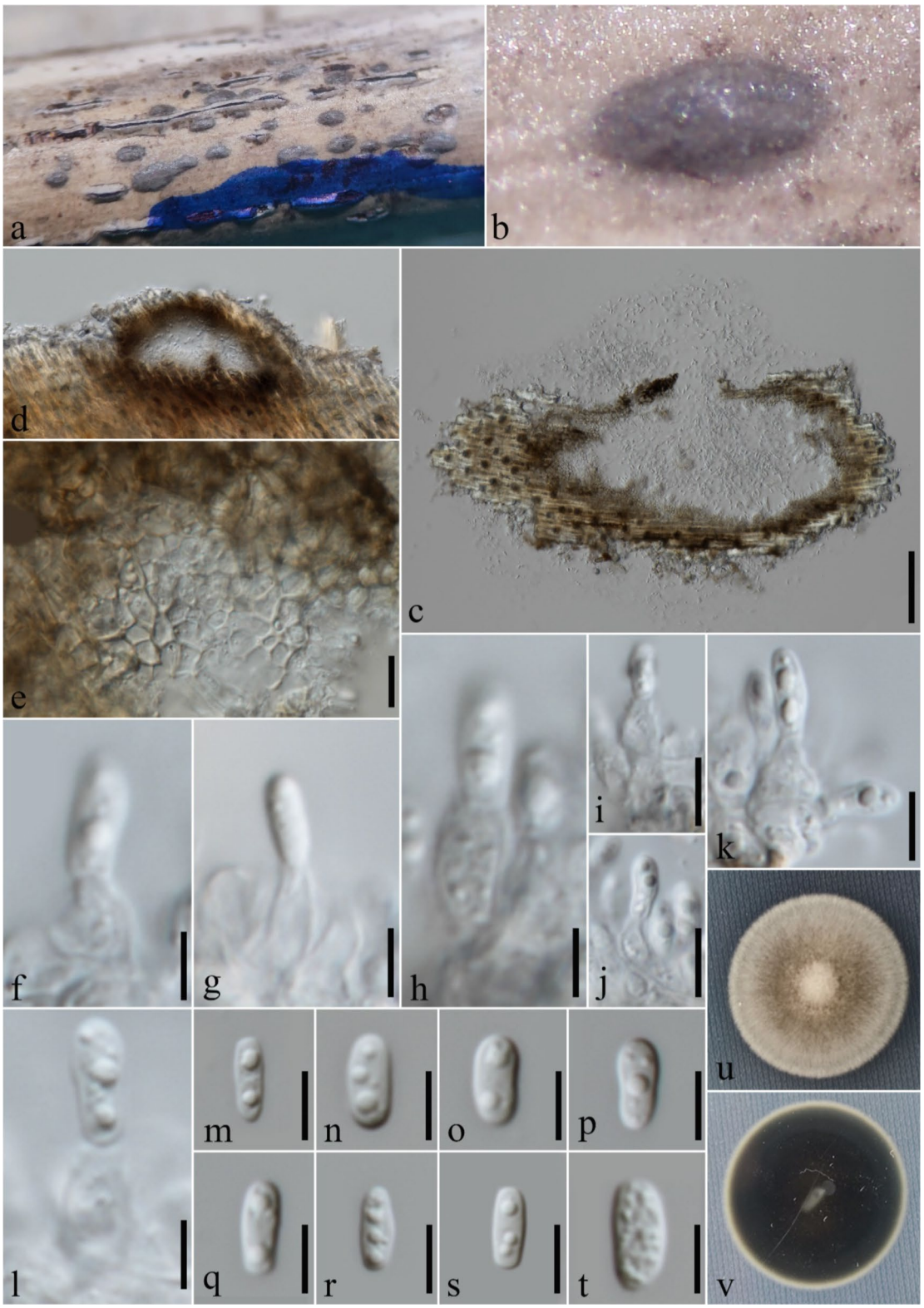


Fig. 12 ***Seriascoma oblonga*** (MHZU 24–0622**, holotype**). **a, b** Conidiomata on host surface. **c, d** Section through conidiomata. **e** Conidiomata wall. **f–l** Conidiogenous cells. **m–t** Conidia. **u, v** Colonies on PDA fromabove and reverse. Scale bars: **c** = 100 µm, **e** = 20 µm, **f–t** = 10 µm

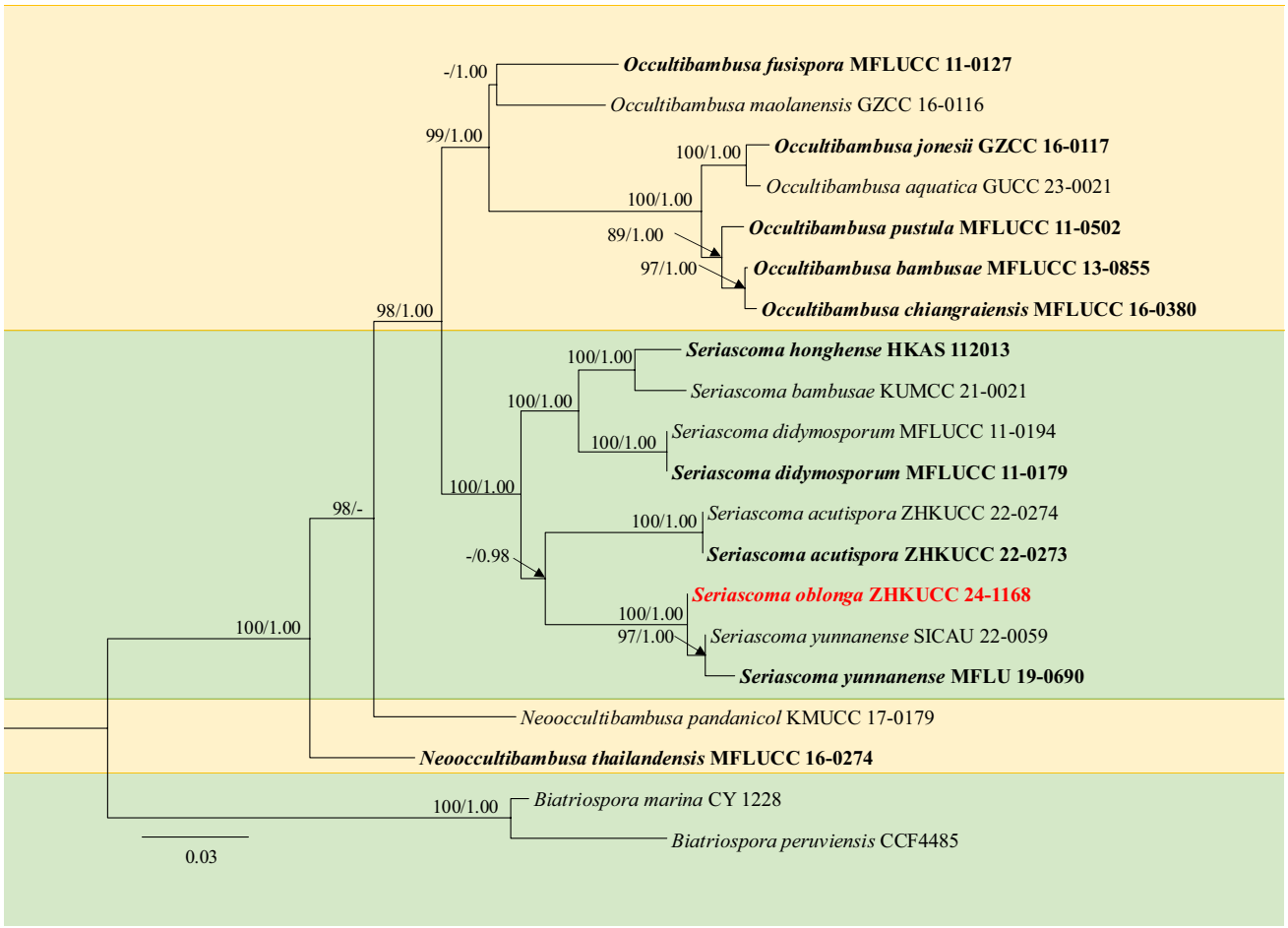


Fig. 13 Maximum Likelihood tree based on ITS sequences, bootstrap support values for ML equal to or greater than·75% and PP equal to greater than 0.95 are indicated at the nodes as ML/PP. New species are shown in red. The ex-type strains are in bold

oblonga was isolated from decaying bamboo. *Seriascoma didymospora* was found from on bamboo pieces on WA culture. *Seriascoma oblonga* can be distinguished from *S. didymospora* by differences in the shape of conidiogenous cells. *Seriascoma oblonga* lacks of the cylindric conidiogenous cells than *S. didymospora*. In addition, *S. oblonga* has conidia that are larger (5.5–8 × 2.2–3.2 µm) compared to those of *S. didymospora* (4–5.5 × 1.5– 2 µm). *Seriascoma oblonga* has conidiomata that are higher and wider (160–200 µm high, 315–400 µm diam.) compared to those of *S. didymospora* (110–170 µm high, 250– 470 µm diam.) (Dai et al. 2017).

Phaeosphaeriaceae M.E. Barr.

Notes: The Phaeosphaeriaceae is a family of fungi within the class Dothideomycetes, order Pleosporales, comprising genera that inhabit various environments such as plant debris, soil, and aquatic habitats. These fungi are characterized by darkly pigmented spores and septate hyphae. Recent research has focused on their taxonomy and phylogeny, utilizing molecular techniques to clarify relationships and discover new species (Wanasinghe and Maharachchikumbura 2023). Currently, the family consists of 84 genera (Wijayawardene et al. 2022). Studies have identified several Phaeosphaeriaceae species as significant plant pathogens affecting crops like cereals and legumes, focusing on their lifecycle and disease management (Guarnaccia et al. 2018; Dong et al. 2023b). There is also growing interest in their secondary metabolites, which show potential in pharmaceutical applications such as antimicrobial and anticancer activities (Zhang et al. 2021; Li et al. 2022b). Additionally, research has explored their ecological roles, including nutrient cycling and acting as endophytes in plants, contributing to organic matter decomposition and influencing plant health and soil ecosystems (Hyde et al. 2016; Tennakoon et al. 2020).

Septoriella Oudem.

Notes: *Septoriella* was first described by Oudemans (1889). The genus was reported as saprobic or pathogenic

causing leaf spots on several host plants in terrestrial habitats (Marin-Felix et al. 2019; Wanasinghe and Maharachchikumbura 2023). Based on molecular phylogenies, many genera, i.e., *Allophaeosphaeria*, *Dactylidina*, *Hydeopsis*, *Naemostroma*, *Phaeopoacea*, *Poaceicola* and *Vagicola* were considered as synonyms of *Septoriella* (Marin-Felix et al. 2019; Wanasinghe and Maharachchikumbura 2023). There are 59 epithets of *Septoriella* listed in Species Fungurum, however, only 41 species were confirmed by molecular data. In this study, we follow the latest treatment and updated accounts of Wanasinghe and Maharachchikumbura (2023) for *Septoriella*.

Septoriella saviya-ramazanovaii Senwanna, N. Suwannar. & Gafforov, **sp. nov.**

Index Fungorum: IF 902282; *Facesoffungi*: FoF 17093; Figs. 14, 15

Etymology: "*saviya-ramazanovaii*" in honor of Uzbekistan scientist, Prof. Ramazanova Saviya Sulaymanovna (1929–2022) for her contribution to the mycological research of Uzbekistan.

Holotype: TASM 6172.

Saprobic on dead branches of *Ferula foetida* (Bunge) Regel (Apiaceae). Sexual morph: **Ascomata** 260–360 µm high, 210–460 µm diam., dark brown to black, scattered, solitary, semi-immersed to erumpent through the host

Fig. 14 ***Septoriella saviya-ramazanovaii*** (TASM 6172, **holotype**). **a–c** Appearance of ascomata on host. **d** Cross section of ascomata. **e** Peridium. **f** Pseudoparaphyses in ddH_2O. **g** Group of ascospores in ddH_2O. **h–j** Ascospores in 3% KOH. **k** Asci in ddH_2O. **l–n** Asci in 3% KOH. Scale bars: **a** = 500 µm, **b–d** = 100 µm, **e, f** = 15 µm, **g–n** = 50 µm

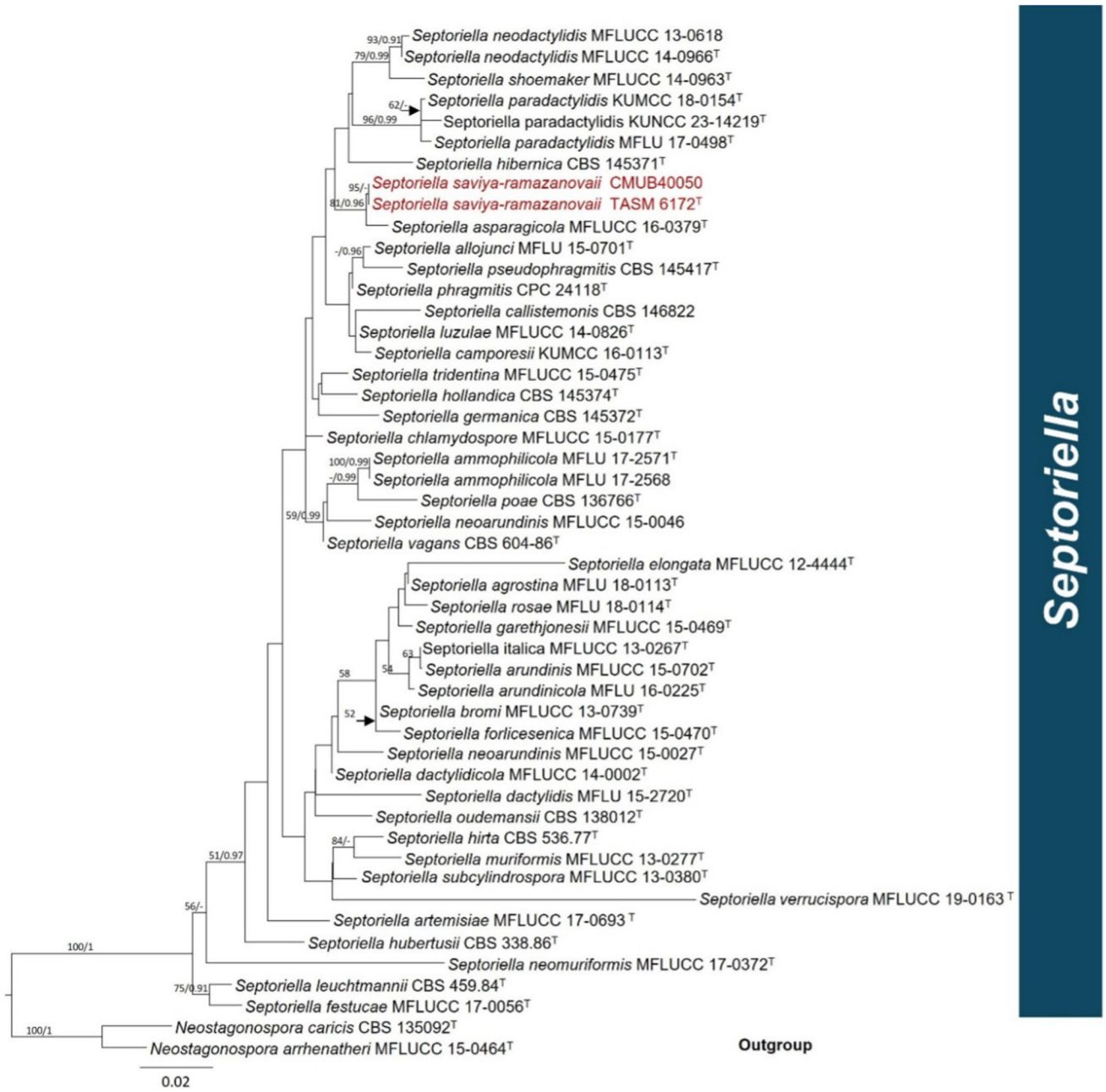


Fig. 15 Maximum Likelihood consensus tree inferred from the combined SSU, LSU, ITS, *tef1* and *rpb2* multiple sequence alignments. Bootstrap support values for Maximum Likelihood (ML, first value) equal to or greater than 50% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.90 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Neostagonospora arrhenatheri* MFLUCC 15–0464 and *N. caricis* CBS 135092. Ex-type strains are indicated with "^{T}". The newly generated sequences are indicated in red

epidermis, subglobose to ampulliform, or irregular in shape, uni-loculate, glabrous, ostiolate. **Peridium** 25–50 µm wide, composed of thick-walled, light brown to dark brown cells of textura angularis. **Hamathecium** numerous, 2.5–11 µm wide, broadly cellular pseudoparaphyses, narrower towards the apex, septate, deeply constricted at the septa near the base, embedded in a hyaline gelatinous matrix. **Asci** (178–)190–235(–284) × 16–20(–23) µm ($\bar{x}$ = 215 × 19 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded. **Ascospores** (115–)124–208(–215) × 4–7(–9) µm ($\bar{x}$ = 163 × 6 µm, n = 40), multi-seriate, overlapping, scolecosporous, filiform to subcylindrical, brown to yellowish brown, with rounded ends, slightly tapered towards the lower cell, euseptate,

4–8-septate, not constricted at the septa, smooth-walled. Asexual morph: undetermined.

Material examined: UZBEKISTAN, Jizzakh Region, Forish District, Yangiqishloq village, dead branches of *Ferula foetida*, 05 May 2021, *Y. Gafforov*, **holotype** TASM 6172, **paratype** CMUB40050.

GenBank: TASM 6172: PP915981 (ITS), PP915979 (LSU), PP920636 (*tef1*); CMUB40050: PP915982 (ITS), PP915980 (LSU), PP920637 (*tef1*).

Notes: In the present phylogenetic analyses, *Septoriella saviya-ramazanovaii* clusters with the sister taxon *S. asparagicola* (MFLUCC 16–0379) with 81% ML and 0.96 PP statistical support (Fig. 15). However, *Septoriella saviya-ramazanovaii* differs from *S. asparagicola* in shapes and sizes of asci and ascospores. Due to the diverse morphological characteristics of sexual and asexual morphs of *Septoriella* species, it is difficult to distinguish the species solely on morphological examination. *Septoriella saviya-ramazanovaii* differs from other sexual morph members in having filiform to subcylindrical ascospores which are similar to the conidia of *S. allojunci*, *S. artemisiae*, *S. arundinicola*, *S. arundinis*, *S. callistemonis*, *S. germanica*, *S. phragmitis* (type species), *S. poae* (Leuchtmann 1984; Crous et al. 2014, 2015a, 2021a; Li et al. 2015; Wanasinghe et al. 2018; Marin-Felix et al. 2019). *Septoriella arundinis*, *S. dactylidis*, *S. leuchtmannii*, *S. muriformis*, *S. neodactylidis*, *S. neomuriformis*, *S. shoemaker*, and *S. vagans*, have fusiform ascospores with transverse and vertical septate (Ariyawansa et al. 2015a; Crous et al. 2015a; Jayasiri et al. 2015; Li et al. 2015; Liu et al. 2015a; Hyde et al. 2017a; Wanasinghe et al. 2018). *Septoriella ammophilicola*, *S. asparagicola*, *S. chlamydospore*, *S. dactylidicola*, *S. forlicesenica*, *S. hollandica*, *S. luzulae*, *S. neoarundinis*, *S. paradactylidis*, *S. tridentina*, and *S. verrucispora* present fusiform ascospores with transversely septa (Ariyawansa et al. 2015a; Hyde et al. 2017a, 2019; Thambugala et al. 2017; Marin-Felix et al. 2019; Zhang et al. 2019b; Dayarathne et al. 2020). *Septoriella allojunci*, *S. atrata*, *S. artemisiae*, *S. arundinicola*, *S. bromi*, *S. callistemonis*, *S. camporesii*, *S. canadensis*, *S. caroliniana*, *S. festucae*, *S. germanica*, *S. halensis*, *S. hirta*, *S. huberti*, *S. junci*, *S. mexicana*, *S. oudemansii*, *S. philippinensis*, *S. phragmitis*, *S. poae*, *S. pseudophragmitis*, *S. restionis*, *S. rockiana*, *S. romuleae*, *S. subcylindrospora*, *S. thalassica*, *S. trachycarpa*, *S. trachycarpi*, *S. unigalerita*, and *S. viciae* are known only by its asexual morph (Oudemans 1889; Saccardo 1892, 1907, 1913, 1916; Saccardo et al. 1931; Nag Raj 1933; Sutton 1980; Sutton and Melnik 1999; Kohlmeyer and Volkmann-Kohlmeyer 2000; Lee and Crous 2003; Taylor and Hyde 2003; Andrianova and Minter 2007; Crous et al. 2014, 2015a, 2021a; Ariyawansa et al. 2015a; Li et al. 2015; Thambugala et al. 2017; Wanasinghe et al. 2018; Marin-Felix et al. 2019; Hyde et al. 2020a). *Septoriella hibernica* remained sterile on all media tested (Marin-Felix et al. 2019). Presently, *Septoriella ammophilicola*, *S. arundinis*, and *S. neoarundinis* have demonstrated the connection between sexual and asexual morphs through sequence data and culture studies (Thambugala et al. 2017; Dayarathne et al. 2020). Based on our phylogenetic analyses and morphological analyses, herein we introduce a new species, *Septoriella saviya-ramazanovaii* from dead branches of *Ferula foetida* in Uzbekistan. In addition, this genus is new to the mycobiota of Central Asia and first time discovered on genus *Ferula* of the Apiaceae plant family, and may also reveal many new ascomycete and basidiomycete fungal species from arid and semi-arid regions (Gafforov and Hoshino 2015; Yatsiuk et al. 2016; Antonín et al. 2017; Gafforov 2017; Gafforov et al. 2017, 2019, 2020, 2023; Gafforov and Rakhimov 2017; Kan et al. 2017; Yuan et al. 2017a; Pem et al. 2018, 2019a, b; Samarakoon et al. 2018; Abdurazakov et al. 2021; Appadoo et al. 2021; Htet et al. 2021; Lestari et al. 2021; Aluthmuhandiram et al. 2022; Dong et al. 2023c; Senwanna et al. 2024).

Pleosporaceae Nitschke.

Notes: *Pleosporaceae* was introduced based on the immersed ascomata and pseudoparaphyses by Nitschke (1869). Luttrell (1955) assigned *Pleosporaceae* under Pleosporales and treated Pseudosphaeriales as a synonym of Pleosporales. *Alternaria*, *Bipolaris*, *phoma-like* and *Stemphylium* are more common asexual morphs in *Pleosporaceae*, which are saprophytes or parasites on various hosts. Its sexual morph is characterized by black, sometimes hairy or setose ascomata. Ostiole papillate or apapillate, occasionally with a pore-like ostiole, ostiolar canal filled with or without periphyses (Ariyawansa et al. 2015b). Its asexual morph is coelomycetous or hyphomycetous, and the conidiogenous cells can be phialidic, annellidic or sympodial blastic (Ariyawansa et al. 2015b). *Pleosporaceae* accepts 24 genera (Wijayawardene et al. 2022).

Curvularia Boedijn.

Notes: *Curvularia* was established by Boedjin (1933), currently classified in the family *Pleosporaceae* (order Pleosporales, class Dothidiomycetes) together with *Alternaria*, *Bipolaris*, *Exserohilum*, *Stemphylium* and others (Ferdinandez et al. 2021). There are 247 epithets listed in Index Fungorum (Aug 2024). *Curvularia* species mostly can be saprophytes, endophytes, or human pathogens, and are found in a variety of habitats including air, indoor environments, soil, water, or plant material (Almaguer et al. 2013; Marin-Felix et al. 2020). In this study, we introduce a new host species *Curvularia geniculata* isolated from *Citrus reticulata*.

Curvularia geniculata (Tracy & Earle) Boedijn, **new host record.**

Index Fungorum: IF 317565; *Facesoffungi:* FoF 16747; Figs. 16, 17

Endophytes on *Citrus reticulata*. Sexual morph: not observed. Asexual morph: **Colonies** on PDA, the hyphae were 2.3–3.2 µm wide, septate, transparent, and branched. **Conidiophores** macronematous, mostly arising from creeping hyphae, brown, septate, simple or branched, erect or curved, with a knee-shaped top, smooth walls, 115–250 × 4–5.5 µm ($\bar{x}$ = 170 × 4.5 µm, n = 10). **Conidiogenous cells** light to medium brown, with smooth walls, subcylindrical or cylindrical, occasionally swollen, terminal or intercalary, 6–14 × 3.5–5.5 µm ($\bar{x}$ = 9 × 5 µm, n = 20). **Conidia** apical and basal cells transparent to light brown, mature conidia middle medium brown to dark brown and swollen, straight or slightly curved, ovate or pear-shaped or fusiform, mostly 4-septate, a few 3-septate, smooth-walled, 15–27 × 7–12 µm ($\bar{x}$ = 22 × 9.5 µm, n = 30). **Hilum** obvious, prominent, 1–2 µm wide, black.

Culture characteristics: colonies on PDA reaching 66–76 mm diam., at 25 °C after 7 days, the colony is round, with complete edges and cottony hyphae; from above, medium gray-green; from below, gray-black, and there are white hyphae circles in the middle and edges. Colonies on MEA reaching 59–69 mm diam., at 25 °C after 7 days, the colony is round, with complete edges and flat; from above, light yellow, the middle part is white and has abundant hyphae, the edge hyphae is sparse and white; from below, brown.

Material examined: CHINA, Guangdong Province, Shaoguan City, on *Citrus reticulata*, July 2021, *Z. Zheng & I.S. Manawasinghe*, MHZU 24–1190, living cultures ZHKUCC 24–1818, ZHKUCC 24–1819.

GenBank: ZHKUCC 24–1818: PV290841 (ITS); ZHKUCC 24–1819: PV290842 (ITS).

Notes: The phylogenetic results showed that our isolate clustered with *C. geniculata* (Fig. 17). Conidia of our isolate strain are similar to *C. geniculate* (USJCC-0073) with 3–4 septate, smooth-walled (Boedijn 1933). Therefore, we

Fig. 16 ***Curvularia geniculata*** (ZHKUCC 24–1818). **a** Upper and reverse side of cultures on PDA after seven days. **b** Upper and reverse side of cultures on MEA after seven days. **c** conidioma. **d** Stromata. **e**–**g** Conidiophores. **h**–**m** Conidia. Scale bars: **e**–**m** = 10 µm

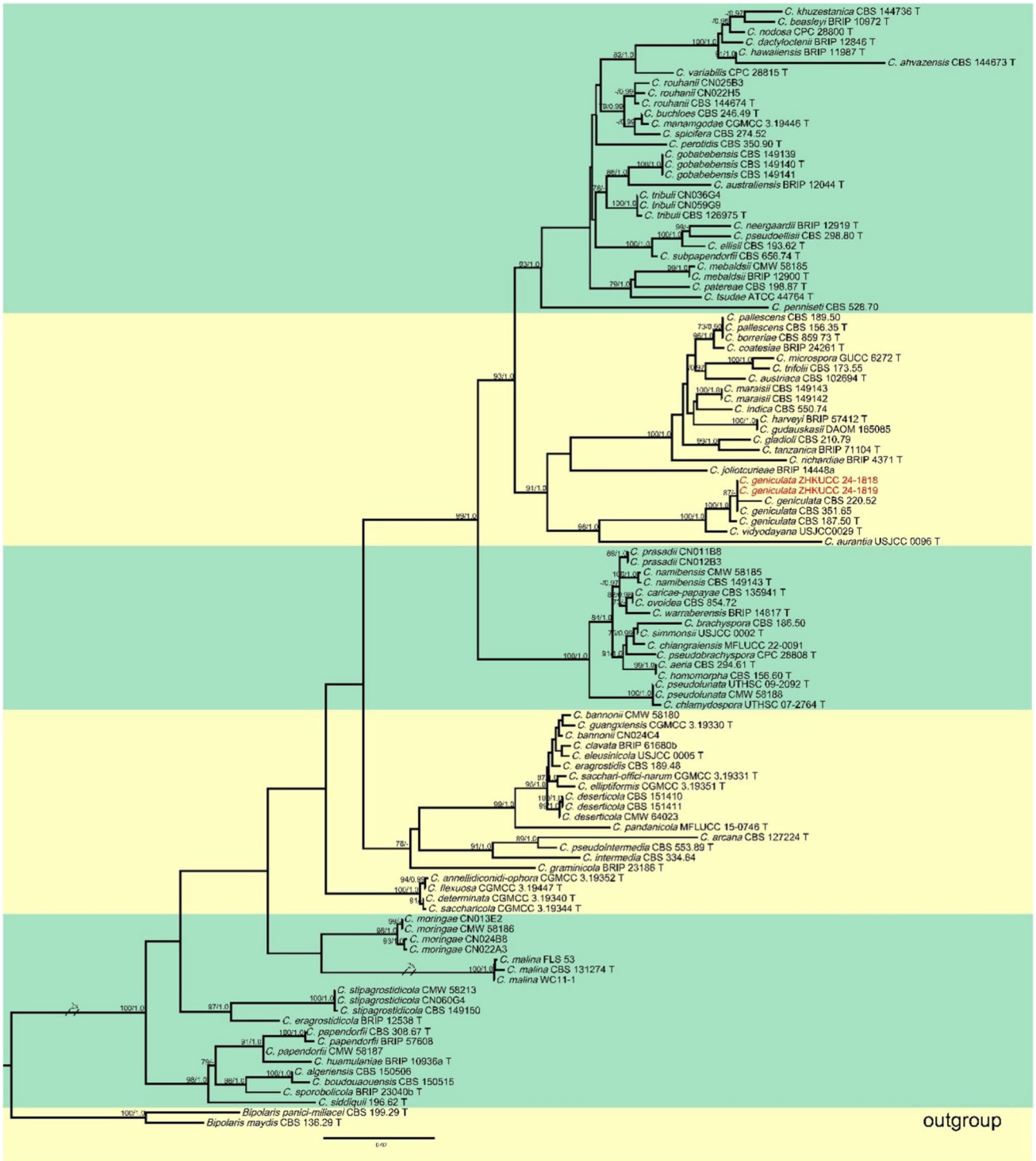


Fig. 17 Maximum Likelihood consensus tree inferred from the combined ITS, *gapdh* and *tef1* multiple sequence alignments. Bootstrap support values for Maximum Likelihood (ML, first value) equal to or greater than 80% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted in *Bipolaris maydis* (CBS 136.29) and *B. panici-miliacei* (CBS 199.29). Ex-type strains are indicated with "[T]". The newly generated sequences are indicated in red

identified our isolate as *C. geniculata*. In this study, *C. geniculata* was reported on *Citrus reticulata* for the first time.

Sulcatisporaceae Kaz. Tanaka & K. Hiray.

Notes: Based on the phylogeny, The family Sulcatisporaceae was initially established for accommodating the genera *Magnicamarosporium*, *Sulcatispora* and *Neobambusicola* (Tanaka et al. 2015). Becide these three genera, to date there are 9 genera with in the family, including *Anthosulcatispora*, *Kazuakitanaka*, *Loculosulcatispora*, *Parasulcatispora*, *Pseudobambusicola* and *Uniappendiculata* (Wijayawardene et al. 2022). The sexual morphs of the family are characterized by subglobose ascomata with a short ostiolar neck, trabeculate pseudoparaphyses, clavate asci, broadly fusiform ascospores, whereas the asexual morphs are described by ellipsoid to subglobose conidia with or without striate ornamentation (Tanaka et al. 2015).

Anthosulcatispora Phukhams. & K.D. Hyde.

Notes: The genus *Anthosulcatispora* was introduced by Phukhamsakda et al. (2020) based on morphological comparisons and phylogeneic analysis. The sexual morph was initially characterized as *Neobambusicola brunnea* (Phookamsak et al. 2019). The asexual morph is characterized by subglobose conidiomata, elongated cylindrical or truncate conidiogenous cells and oblong and aseptate conidia. Currently, *Anthosulcatispora* comprises 3 species including the introduced species in this study.

Anthosulcatispora sichuanensis Y.P. Chen & Maharachch., **sp. nov.**

MycoBank: MB 851952; *Facesoffungi*: FoF 15499; Figs. 18, 19

Etymology: refers to the province "Sichuan", where the holotype was collected.

Holotype: HUEST 23.0585.

Sexual morph: **Ascomata** 521–735 µm high, 457–614 µm width ($\bar{x}$ = 625 × 522 µm, n = 10); immersed on the branches; dark brown to black; inner chamber empty with hyaline ascus adhered to the inner wall; multilayer wall composed of brown, irregular elliptical cells. **Ostiole** open in mature ascomata for releasing ascospores but invisible in immature ascomata. **Asci** 87.8–161.5 µm long, 5.4–7.2 µm width ($\bar{x}$ = 127.6 × 6.4 µm, n = 30); 8-spored; hyaline. **Ascospores** 13.8–17.6 µm long, 4.3–6.1 µm width ($\bar{x}$ = 15.8 × 5.2 µm, n = 40); hyaline; 2-septate with 3 divisions; uniform in shape and smooth with rounded ends. **Paraphyses** hyaline, interspersed among the asci. Asexual morph: undetermined.

Culture characteristics: Conidia germinated on PDA within 12 h at 25 °C in darkness. Colonies grayish-tan color overall with a more intense brown at the centers, velvety especially towards the edges with slightly raised and more condensed central region on the front side; dark brown to black in the center and fading to a lighter brown at the edges on the reverse side.

Material examined: CHINA, Sichuan Province, Chengdu City, Pengzhou City, Huilonggou, 31°17'N, 103°47'E, 2300 m asl, from decaying stems of an unidentified woody plant, 28 Jul 2021, *Yanpeng Chen* & *Yaobin Guo*, *HLG13.2* (HUEST 23.0585, **holotype**; UESTCC 23.0583, ex-type) and *HLG13.3*.

GenBank: UESTCC 23.0583: PP262634 (SSU), PP262632 (ITS), PP262633 (LSU), PP234626 (*tef1*), PP234625 (*rpb2*).

Notes: The phylogenetic tree reveals that strain UESTCC 23.0583 clusters closely with the ex-type strains *Anthosulcatispora subglobosa* (MFLUCC 17–2065) and *A. brunnea* (MFLU 18–1393), with strong support (100/1.00/100) (Fig. 19). Online BLASTn analyses of barcode sequences from strain UESTCC 23.0583 demonstrate sequence identities of 87% (447/514, 24 gaps), 98% (800/813, 2 gaps), 93% (695/756, no gap), and 94% (630/669, 1 gap) with *A. subglobosa* MFLUCC 17–2065, using ITS, LSU, *rpb2*, and *tef1* sequences, respectively. Morphologically, *A. subglobosa* is characterized by its asexual morphology, with aseptate conidia (Phukhamsakda et al. 2020). In contrast, collection HUEST 23.0585 exhibits sexual morphology with septate ascospores. *A. brunnea* is distinguished by its sexual morphology, featuring brown and 1-septate ascospores (Phookamsak et al. 2019), which differs from HUEST 23.0585, with hyaline and 2-septate ascospores. Considering the BLASTn results, phylogenetic analysis, and morphology, we propose introducing our collection as a new species within the genus *Anthosulcatispora*, designated as *A. sichuanensis*.

Eurotiomycetes O.E. Erikss. & Winka.

Eurotiales G.W. Martin ex Benny & Kimbr.

Notes: Eurotiales is a large order in Ascomycota that contains ca. 1300 species, 28 genera and 5 families (Houbraken et al. 2020; Visagie et al. 2024). The concept of Eurotiales was proposed by Benny and Kimbrough (1980) and accepted and emended by Kirk et al. (2001), including members of common green and blue moulds, when present, producing nonostiolate ascocarps containing irregularly disposed, evanescent asci. Eurotiales members are mainly saprothrophic, but some are oppotunistic pathogens for animals and humans (e.g., Houbraken et al. 2020). Molecular analyses have been carried out to clarify the evolutionary relationships (Houbraken et al. 2020; Visagie et al. 2024).

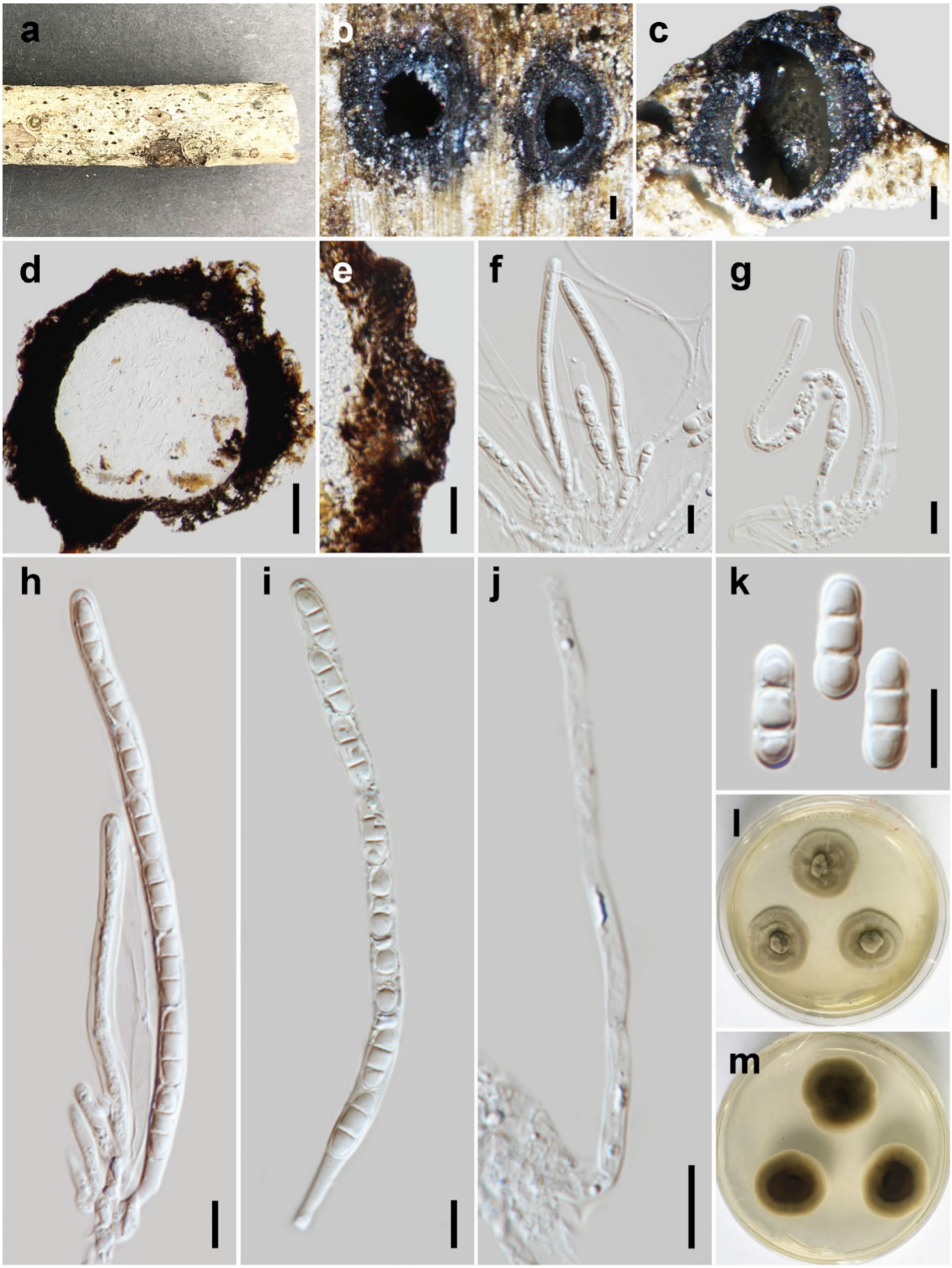


Fig. 18 *Anthosulcatispora sichuanensis* (HUEST 23.0585, **holotype**). **a** Natural substrate. **b** Close-up of ascomata. **c, d** Vertical section of ascomata. **e** Wall of an ascoma. **f–i** Ascus. **j** Paraphysis. **k** Ascospores. **l, m** Cultures on PDA after 4 weeks (front and back view). Scale bar: **c, d** = 100 µm, e = 20 µm, **f–k** = 10 µm

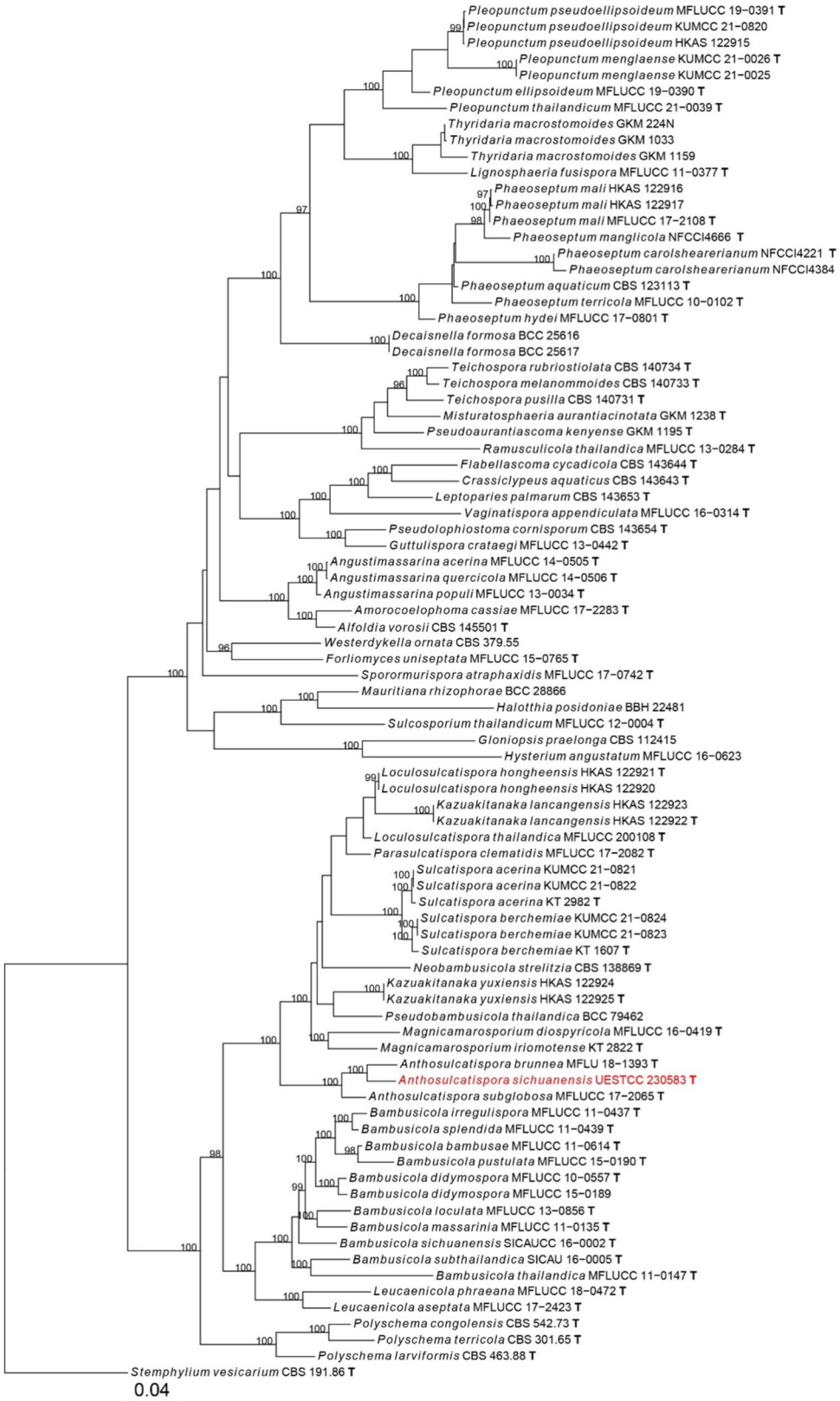


Fig. 19 Maximum Likelihood tree based on combined SSU, ITS, LSU, *tef1* and *rpb2* sequences. UFBoot values greater than 95% are shown around nodes. New species is shown in red. "T" refers to an ex-type strain

Trichocomaceae E. Fisch.

Notes: Trichocomaceae was introduced by Engler and Prantl (1898) based on the teleomorphic genus *Trichocoma*. Subsequently, the members of Trichocomaceae have been revised for several times based on morphology (Malloch and Cain 1972; Malloch 1985a, b), and this family has been reclassified as the development of molecular phylogeny (Houbraken and Samson 2011; Houbraken et al. 2020). This family contains species producing typical Eurotiales-type teleomorphs and phialidic conidium-producing cells bearing conidia in basipetal chains (e.g., Raper and Thom 1949; Pitt 1979). Although Houbraken and Samson (2011) and Houbraken et al. (2020) presented systematic analyses of Trichocomaceae at subgenus level based on sequences from ITS, *BenA*, *CaM*, *rpb2* genes, comprehensive studies on the relationship of genera in this family are still lacking.

Talaromyces C.R. Benj.

Notes: The genus *Talaromyces* was described by Benjamin (1955) and is the largest genus in Trichocomaceae with ca. 203 species (Houbraken et al. 2020; Visagie et al. 2024). Phylogenetic relationships of infrageneric taxa have been more objectively elucidated. The latest classification system shows that the genus comprises eight sections, *Bacillispori* Yilmaz et al., *Helici* Yilmaz et al., *Islandici* Yilmaz et al., *Purpurei* Stolk & Samson, *Subinflati* Yilmaz et al., *Talaromyces*, *Trachispermi* Yaguchi & Udagawa, and *Tenues* Sun et al. (Yilmaz et al. 2014; Sun et al. 2020).

Talaromyces pseudorugulosus Q.M. Wang, Z.X. Feng & L. Wang, **sp. nov.**

MycoBank: MB 844827; *Facesoffungi*: FoF 17094; Figs. 20, 21

Etymology: the species epithet referring to its similarity with *Talaromyces rugulosus*.

Holotype: HMAS 351923.

Colony characters: **CYA** 25 °C, 7d: Colonies moderately deep, margins low, entire; texture velvety; mycelium light yellow; sporulation sparse, conidia *en masse* grayish green (30B, Kornerup and Wanscher 1978); exudates absent, soluble pigments absent; reserve light yellow. **MEA** 25 °C, 7d: Colonies moderately deep, dented at centers, margins low, entire; radially sulcate; texture velvety; mycelium yellow and white; sporulation moderately sparse, conidia *en masse* grayish green (30B); exudates absent, soluble pigments absent; reserve light orange-red. **YES** 25 °C, 7d: Colonies moderately deep, dented at centers, margins low, entire; texture velvety; mycelium yellow and white; sporulation limited, conidia *en masse* grayish green (30B); exudates limited, in minute clear droplets, soluble pigments absent; reserve brownish-yellow. **OA** 25 °C, 7d: Colonies restricted, margins low, entire; texture velvety; mycelium yellow and white; sporulation absent; exudates absent, soluble pigments absent; reverse light yellow. **DG18** 25 °C, 7d: Colonies restricted, margins low, entire; texture velvety; mycelium white; sporulation moderate, conidia *en masse* pastel green (26A4); exudates absent, soluble pigments absent; reserve brownish-yellow. **CREA** 25 °C, 7d: Abundant acid produced.

Micromorphology: **conidiophores** arising from surface hyphae; **stipes** 68.7–438 × 1.8–3.5 µm, smooth-walled; **penicilli** biverticillate; **metulae** 2–5 per verticil, 9–13 × 2.5–3 µm; phialides 4–6 per verticil, acerose to ampulliform, 7–11 × 2–3 µm; **conidia** ellipsoid, 2.5–3.4 × 1.5–2.5 µm, thick-walled. Ascomata not observed.

Material examined: CHINA, Xizang Autonomous Region, soil, Sep 2021, *Q.M. Wang*, *Z.X. Feng*, *SCDG35t* (HMAS 351923, **holotype**; CGMCC 3.16296, ex-type); Xizang Autonomous Region, soil, Sep 2021, *Q.M. Wang*, *Z.X. Feng*, *SCDG35tA*; Hainan Province, Qionghai Area, Boao Town Yudai Road coconut coast, Tidal flats, Feb 2022, *Q.M. Wang*, *Z.X. Feng*, *YTHS14-100*.

GenBank: HMAS 351923: ON427037 (ITS), ON667682 (*BenA*), ON703619 (*CaM*), ON703699 (*rpb2*); YTHS14-100: ON427053 (ITS), ON982464 (*BenA*), ON982465 (*CaM*), ON703710 (*rpb2*); SCDG35tA: ON942225 (ITS), ON961790 (*BenA*), ON961797 (*CaM*), ON961801 (*rpb2*).

Notes: *Talaromyces pseudorugulosus* phylogenetically related to *T. acaricola* (Fig. 21). It is characterized by slow growth and colonies with yellowish mycelium and abundant acid production on CREA. In the multigene phylogeny, it is closely related to *T. acaricola*. But *T. acaricola* bears biverticillate and irregular penicilli and fusiform conidia.

Lecanoromycetes O.E. Erikss. & Winka.

Graphidales Bessey.

Notes: Graphidales is a large order of lichen-forming fungi most closely related to Spirographaceae and containing about 2000 species distributed within six families: Diploschistaceae, Fissurinaceae, Gomphillaceae, Graphidaceae, Redonographaceae and Thelotremataceae (Rivas Plata et al. 2013; Lücking et al. 2014; Kraichak et al. 2018; Flakus et al. 2019; Wijayawardene et al. 2020). The order comprises crustose species growing mainly on bark in the tropics.

Gomphillaceae Walt. Watson.

Notes: Gomphillaceae is composed of 46 genera and is characterized by thin, mostly anastomosing paraphyses, non-amyloid asci with a ring structure in the apex, and mostly hyaline, transversely septate to muriform ascospores (e.g., Lücking et al. 2005; Xavier-Leite et al. 2022, 2023). The first modern revision of the lichenized family Gomphillaceae

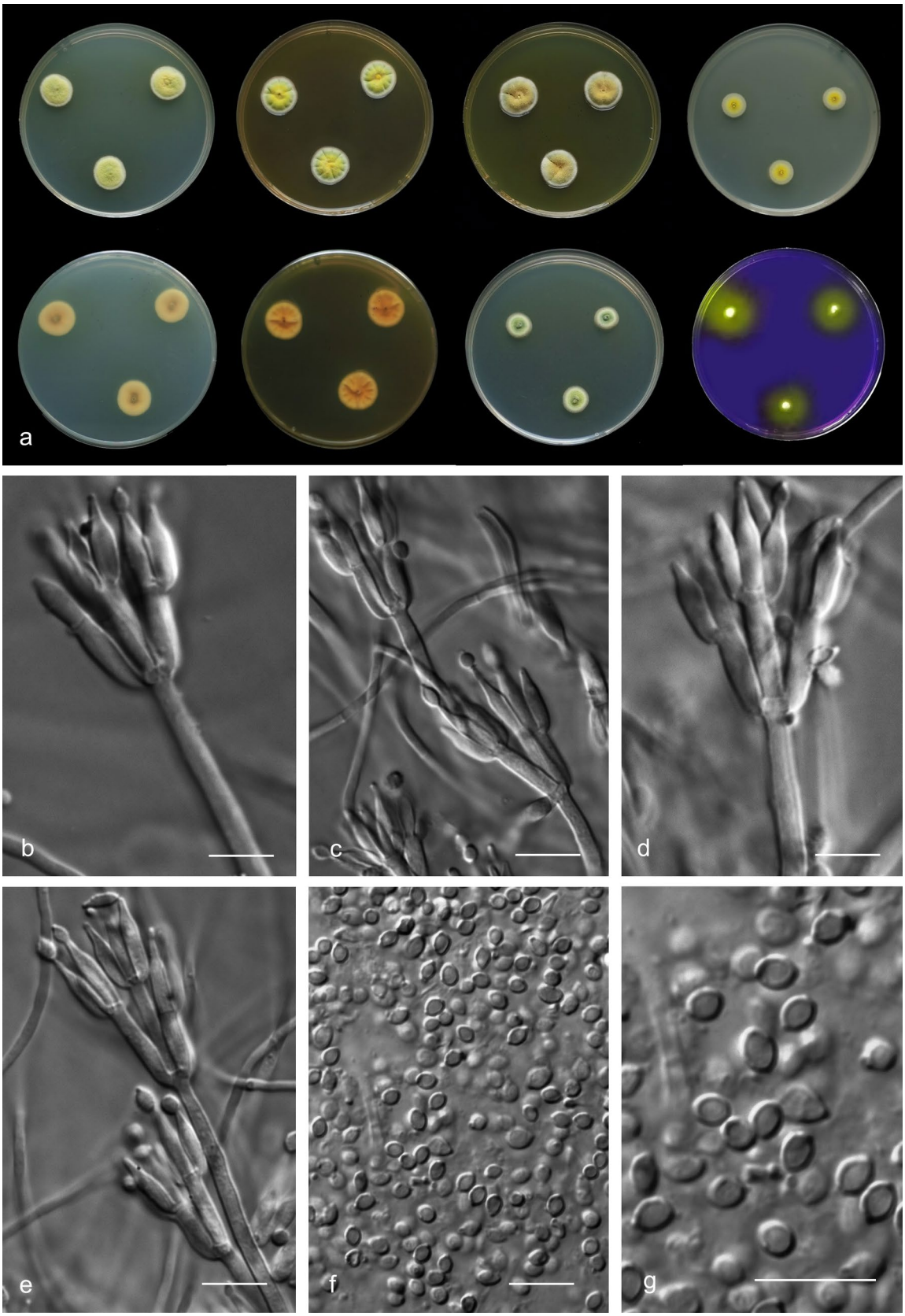
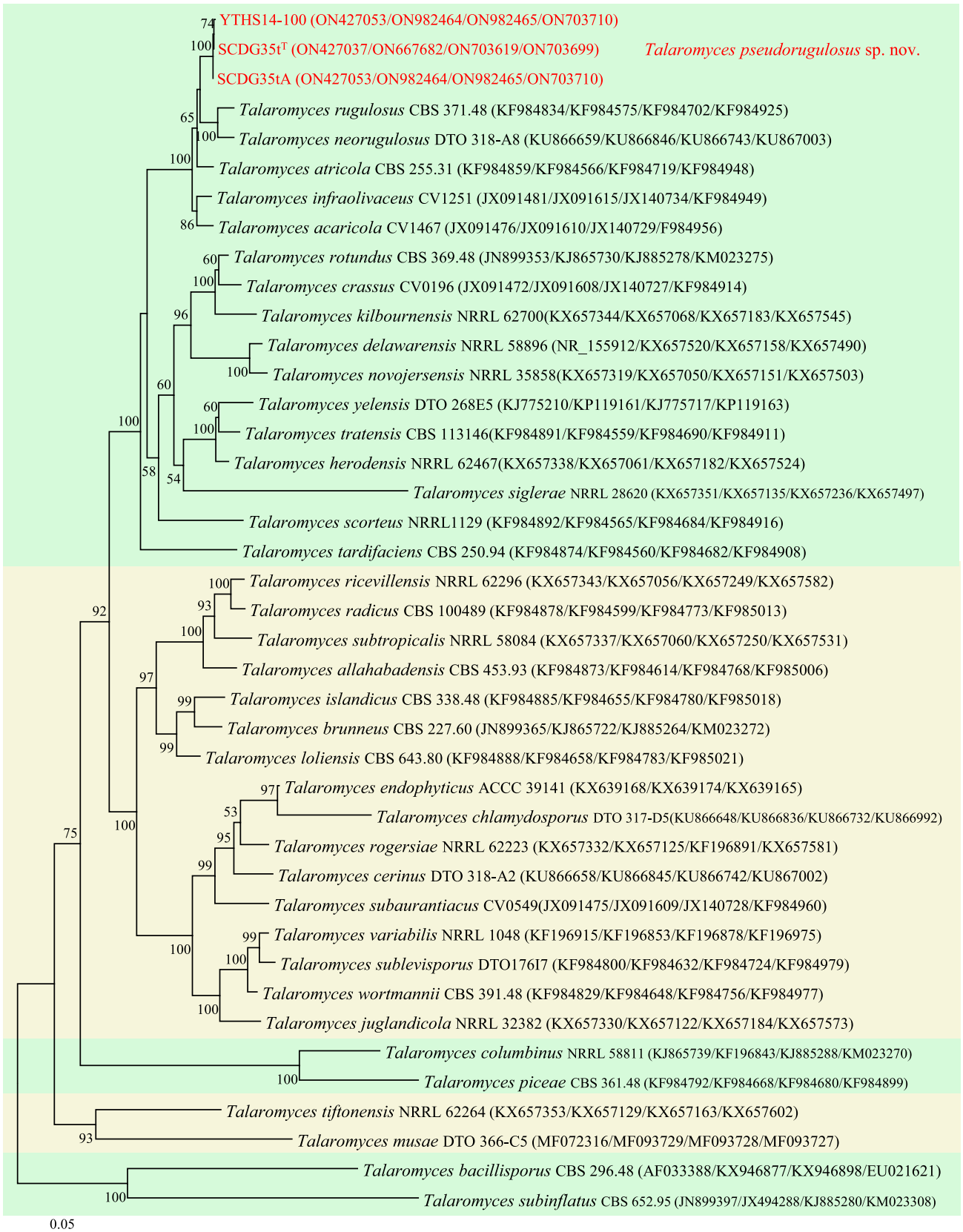


Fig. 20 ***Talaromyces pseudorugulosus*** (CGMCC 3.16296, ex-type). **a** Colonies from left to right (top row) CYA, MEA, YES, and OA; (bottom row) CYA reverse, MEA reverse, DG18 and CREA. **b–e** Conidiophores. **f–g** Conidia. Scale bar = 10 µm


YTHS14-100 (ON427053/ON982464/ON982465/ON703710)
SCDG35t[T] (ON427037/ON667682/ON703619/ON703699)
SCDG35tA (ON427053/ON982464/ON982465/ON703710)
Talaromyces pseudorugulosus sp. nov.
Talaromyces rugulosus CBS 371.48 (KF984834/KF984575/KF984702/KF984925)
Talaromyces neorugulosus DTO 318-A8 (KU866659/KU866846/KU866743/KU867003)
Talaromyces atricola CBS 255.31 (KF984859/KF984566/KF984719/KF984948)
Talaromyces infraolivaceus CV1251 (JX091481/JX091615/JX140734/KF984949)
Talaromyces acaricola CV1467 (JX091476/JX091610/JX140729/F984956)
Talaromyces rotundus CBS 369.48 (JN899353/KJ865730/KJ885278/KM023275)
Talaromyces crassus CV0196 (JX091472/JX091608/JX140727/KF984914)
Talaromyces kilbournensis NRRL 62700(KX657344/KX657068/KX657183/KX657545)
Talaromyces delawarensis NRRL 58896 (NR_155912/KX657520/KX657158/KX657490)
Talaromyces novojersensis NRRL 35858(KX657319/KX657050/KX657151/KX657503)
Talaromyces yelensis DTO 268E5 (KJ775210/KP119161/KJ775717/KP119163)
Talaromyces tratensis CBS 113146(KF984891/KF984559/KF984690/KF984911)
Talaromyces herodensis NRRL 62467(KX657338/KX657061/KX657182/KX657524)
Talaromyces siglerae NRRL 28620 (KX657351/KX657135/KX657236/KX657497)
Talaromyces scorteus NRRL1129 (KF984892/KF984565/KF984684/KF984916)
Talaromyces tardifaciens CBS 250.94 (KF984874/KF984560/KF984682/KF984908)
Talaromyces ricevillensis NRRL 62296 (KX657343/KX657056/KX657249/KX657582)
Talaromyces radicus CBS 100489 (KF984878/KF984599/KF984773/KF985013)
Talaromyces subtropicalis NRRL 58084 (KX657337/KX657060/KX657250/KX657531)
Talaromyces allahabadensis CBS 453.93 (KF984873/KF984614/KF984768/KF985006)
Talaromyces islandicus CBS 338.48 (KF984885/KF984655/KF984780/KF985018)
Talaromyces brunneus CBS 227.60 (JN899365/KJ865722/KJ885264/KM023272)
Talaromyces loliensis CBS 643.80 (KF984888/KF984658/KF984783/KF985021)
Talaromyces endophyticus ACCC 39141 (KX639168/KX639174/KX639165)
Talaromyces chlamydosporus DTO 317-D5(KU866648/KU866836/KU866732/KU866992)
Talaromyces rogersiae NRRL 62223 (KX657332/KX657125/KF196891/KX657581)
Talaromyces cerinus DTO 318-A2 (KU866658/KU866845/KU866742/KU867002)
Talaromyces subaurantiacus CV0549(JX091475/JX091609/JX140728/KF984960)
Talaromyces variabilis NRRL 1048 (KF196915/KF196853/KF196878/KF196975)
Talaromyces sublevisporus DTO176I7 (KF984800/KF984632/KF984724/KF984979)
Talaromyces wortmannii CBS 391.48 (KF984829/KF984648/KF984756/KF984977)
Talaromyces juglandicola NRRL 32382 (KX657330/KX657122/KX657184/KX657573)
Talaromyces columbinus NRRL 58811 (KJ865739/KF196843/KJ885288/KM023270)
Talaromyces piceae CBS 361.48 (KF984792/KF984668/KF984680/KF984899)
Talaromyces tiftonensis NRRL 62264 (KX657353/KX657129/KX657163/KX657602)
Talaromyces musae DTO 366-C5 (MF072316/MF093729/MF093728/MF093727)
Talaromyces bacillisporus CBS 296.48 (AF033388/KX946877/KX946898/EU021621)
Talaromyces subinflatus CBS 652.95 (JN899397/JX494288/KJ885280/KM023308)
0.05

◂**Fig. 21** Maximum Likelihood phylogenetic tree inferred using the combined sequences of ITS, *BenA*, *CaM* and *rpb2* depicting the phylogenetic positions of new taxa within section *Islandici* of *Talaromyces*. Bootstrap percentages over 50% from 1000 bootstrap replicates are shown on the major branches. Bar = 0.05 substitutions per nucleotide position. The new taxa are in red

based on molecular phylogeny was provided by Xavier-Leite et al. (2022).

Gyalidea Lettau ex Vězda.

Notes: *Gyalidea* is a cosmopolitan genus with about 60 saxicolous, corticolous, bryophilous or terricolous species, mainly distributed in tropical and subtropical regions. It is characterized by a crustose thallus, zeorine apothecia, with mostly well-developed thalline margin, non-amyloid hymenium composed of simple to sparsely branched and anastomosed paraphyses, cylindrical to clavate, thin-walled asci with thickened apical tholus, and a small ocular chamber, and hyaline transversely septate or submuriform to muriform ascospores (e.g., Vězda 1966; Vězda and Poelt 1991; Etayo and Vězda 1994; Harada and Vězda 1996; Aptroot and Lücking 2003; Nordin et al. 2007; Lumbsch et al. 2009; Svensson 2012; Harada and Sakata 2016; Kondratyuk et al. 2019; McCarthy 2020, 2021).

Gyalidea lluxitensis Flakus, Suchan, Plata & Rodr. Flakus, **sp. nov.**

MycoBank: MB 855029; *Facesoffungi*: FoF 17095; Figs. 22, 23

Etymology: the epithet refers to Mt. Wila Lluxita, the locality of the type specimen.

Holotype: KRAM-L 75069.

Thallus crustose, epilithic, 0.5–7 cm wide, continuous to sparsely fissured, not areolate, pale greenish gray with a pinkish tinge, pale to dark grayish brown or almost black, dull, 30–80 µm thick, smooth, composed of hyaline, vertically oriented hyphae. **Cortical layer** 5–9 µm thick, paraplectenchymatous, consisting of dark pigmented hyphae. **Photobiont** chlorococcoid, cells broadly ellipsoid to subglobose, 5–10 µm diam.

Apothecia orange-brown to dark-brown, sometimes pale brown-orange with rose tinge, scattered, usually solitary or in small groups of 2–3, immersed in the thallus (when young) to sessile and constricted at the base (when mature), 0.3–0.8 mm diam., 200–500 µm tall, rounded; in a section usually with a pinkish pigment (dissolving in K). **Margin** thick to evanescent, pale to dark brown. **Disc** concave to flat, pale brown-orange with rose tinge, pale do dark brown, usually paler than margin, smooth, epruinose, sometimes translucent when wet. **Exciple** laterally 70–150 µm thick, 100–300 µm thick at the base, composed of radiating hyphae, inner portion proso- to paraplectenchymatous of hyaline, thick-walled hyphae (hyphal lumina 1–3 × 2–6 µm), outer portion of thin-walled, grayish brown pigmented hyphae (hyphal lumina 0.5–2 × 2–7 µm), mixed with photobiont cells. **Epihymenium** 5–15 µm thick, pale yellowish to grayish brown, K–. **Hymenium** 110–150 µm thick, hyaline, not inspersed, non-amyloid, K–. **Subhymenium** hyaline or very pale yellowish/pinkish, 30–40 µm thick, K–, K/I–; hyphae variously orientated. **Hypothecium** hyaline to very pale yellowish/pinkish, 100–150 µm thick, K–, composed of short-celled, thick-walled hyphae. **Paraphyses** simple to sparsely branches and anastomoses, 1–1.5 µm thick, apices slightly swollen, 2–3 µm wide. **Asci** narrowly clavate to cylindrical or broadly clavate, multi-spored (≥ 60-spored), 75–160 × 9–22 µm, wall and contents non-amyloid; ascoplasm K/I + orange; apex rounded at maturity, with an evident tholus (7–18 µm tall), with or without apical apparatus. **Ascospores** colorless, 0(–1)-septate, broadly to narrowly ellipsoid, sometimes slightly bent or tapering to one end, with a gelatine perispore when immature, (6–)7–11(–12.5) × (2–)3.5–5.5(–7) µm (n = 60); 1-septate slightly constricted at the septa. **Pycnidia** immersed, opening irregularly, hole- or crack-like, usually marginal. **Conidiogenous cells** hyaline, narrowing upwards, 4–10 × 1–2 µm. **Conidia** hyaline, simple, narrowly ellipsoid, 2.5–4.5 × 1–1.5 µm (n = 40).

Material examined: BOLIVIA, Dept. La Paz, Prov. Los Andes, near road Lipichi-Peñas, above Laguna Jankho Kkota, 16°03′20″S, 68°18′12″W, 4898 m, Mt. Wila Lluxita, subnival vegetation of Humid Puna, small stream below glacier, on submerged granite rock, 5 Dec 2016, *A. Flakus 28,919 & P. Rodriguez-Flakus* (KRAM-L 75069, **holotype**; LPB, **isotype**), *28,929* (KRAM-L 75070, LPB), *28,925* (KRAM-L 75071, LPB), *28,916* (KRAM-L 75072, LPB); below Mt. Wila Lluxita, 16°03′19.51″S, 68°18′07.13″W, 4877 m, subnival vegetation of Humid Puna, small stream below glacier, on submerged granite rock, 5 Dec 2023, *A. Flakus 30,029, T. Suchan & O. Plata* (KRAM-L 75073, LPB), *30,035* (KRAM-L 75074, LPB).

GenBank: KRAM-L 75069: PQ654506 (ITS), PQ619019 (nucLSU), PQ619023 (mitSSU); KRAM-L 75070: PQ654508 (ITS), PQ619021 (nucLSU), PQ619025 (mitSSU); KRAM-L 75071: PQ654507 (ITS), PQ619020 (nucLSU), PQ619024 (mitSSU); KRAM-L 75072: PQ654505 (ITS), PQ619018 (nucLSU), PQ619022 (mitSSU).

Notes: *Gyalidea lluxitensis* is an epilithic, fresh-water lichen, characterized by large, sitting to constricted apothecia, thin, sparsely fissured thallus, multispored (≥ 60-spored) asci and predominantly simple ascospores, (6–)7–11(–12.5) × (2–)3.5–5.5(–7) µm. Although the morphology of the new species does not fully fit the concept of *Gyalidea* (especially the simple ascospores), our ML and BI phylogenetic analyses (Fig. 23) strongly supported its generic placement

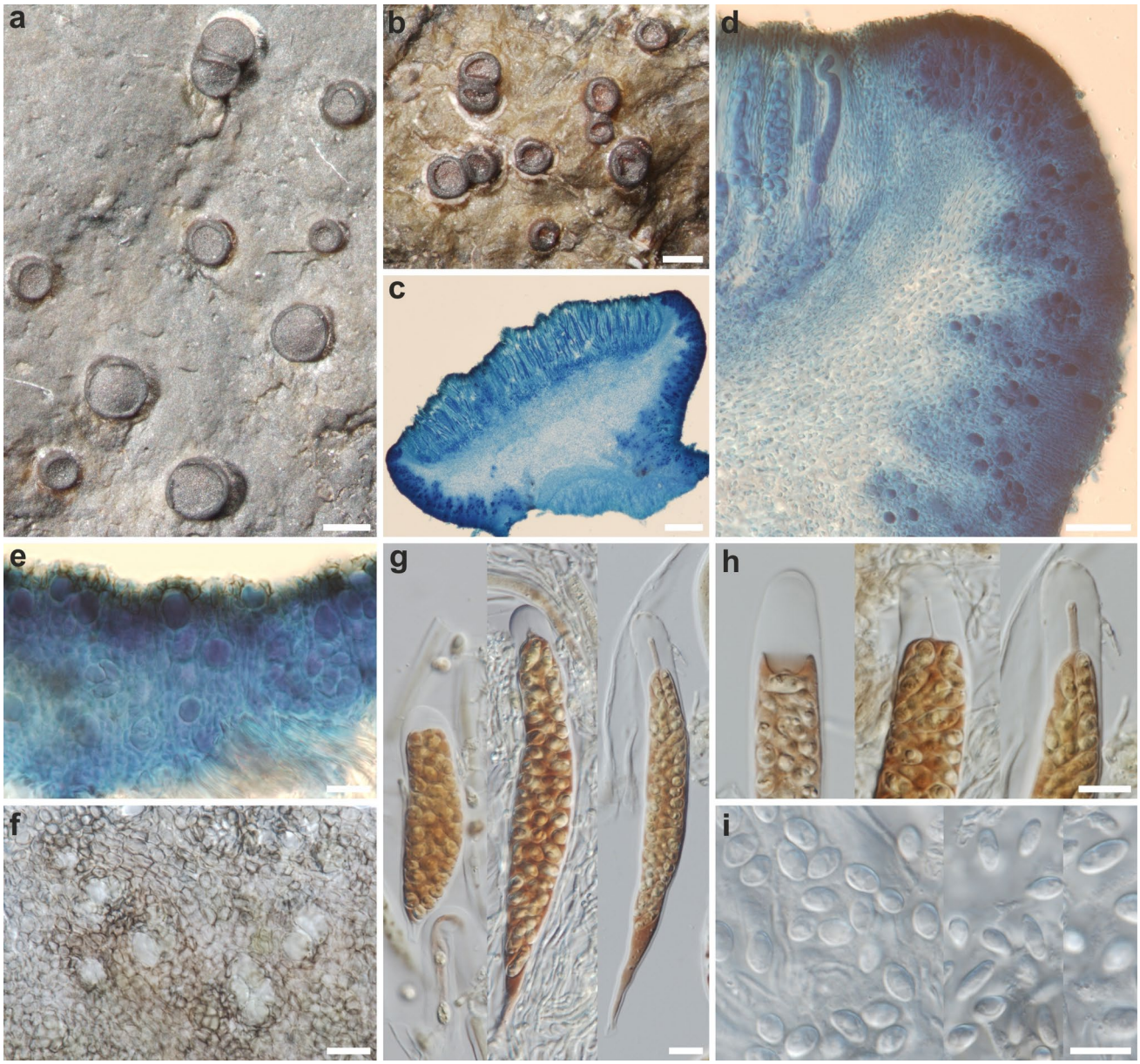


Fig. 22 ***Gyalidea lluxitensis*** (KRAM-L 75069, **holotype**). **a, b** Habit of ascomata growing on granite. **c** Transversal section of ascoma in LPCB. **d** Transversal section of exciple in LPCB. **e** Transversal section of thallus composed of vertically oriented hyphae mixed with photobiont cells and dark-pigmented cortical layer in LPCB. **f** External view of thallus showing cells of cortical layer (large opening caused by protruding photobiont cells). **g** Asci mounted in Lugol's solution pretreated by 10% KOH. **h** Ascus apical apparatus mounted in Lugol's solution pretreated by 10% KOH. **i** Ascospores in distilled water. Scale bars: **a, b** = 500 µm, **c** = 100 µm, **d** = 25 µm, **e–i** = 10 µm

within this genus. *Gyalidea* contains only six species developing multispored asci: *Gyalidea asteriscus* (Anzi) Aptroot & Lücking, *G. luzonensis* (Kalb & Vězda) Aptroot & Lücking, *G. multispora* Lumbsch & Vězda, *G. polyspora* R. Sant., *G. vezdae* S. Y. Kondr., Lőkös, J. P. Halda & Hur and *G. vonkonratii* Lumbsch & Papong (Vězda and Poelt 1991; Aptroot and Lücking 2003; Nordin et al. 2007; Lumbsch et al. 2009; Kondratyuk et al. 2019). All of them, however, can be distinguished by having constantly 1- to multiseptate or sub- to muriform ascospores, and different sizes, colors and morphology of apothecia.

Pezizomycetes O.E. Erikss. & Winka.
Pezizales J. Schröt.

Notes: Pezizales is the only order of Pezizomycetes in Ascomycota, which consists of 22 families, with 200 genera and 2000 species (Pfister and Healy 2021). The system for the Pezizales was mainly based on that proposed by Korf

in 1973, and the phylogenetic concept of the Pezizales was expanded considerably when Trappe (1979) abandoned the Tuberales and transferred 30 hypogeous genera to the Pezizales. Most Pezizales taxa are saprobic, mutualistic, endophytes, or parasitic on plants (Hansen and Pfister 2006; Arnold 2007; Kumar et al. 2017; Pfister and Healy 2021). The ascomata of this order are epigeous (above ground), or hypogeous (below ground). Epigeous taxa have exposed spore-bearing structures (most of them with a cup or a sponge-like morphology) that possess a forcible mode of spore discharge, while hypogeous taxa are characterized by enclosed, underground fruit bodies in which spore dispersal is mediated by dehiscence or animal mycophagy (Trappe 1979). The truffles of commerce belong to this latter group.

Tuberaceae F. Berchtold & J. Presl.

Notes: Tuberaceae is one of the most diverse lineages of symbiotic truffle-forming fungi (Hansen and Pfister 2006; Kirk et al. 2008; Murat et al. 2018). Bonito et al. (2013) produced the first comprehensive molecular phylogeny for the Tuberaceae and there are no true epigeous taxa known in the family. Tuberaceae currently consists of six genera: *Choiromyces*, *Dingleya*, *Labyrinthomyces*, *Loculotuber*, *Nothojafnea*, *Reddellomyces* and *Tuber* (Pfister and Healy 2021). The two common genera, *Choiromyces* and *Tuber*, produce sizable and aromatic fruiting bodies that are highly valued in some European and Asian countries (Bonito and Smith 2016; Wang et al. 2022). Despite their ecological importance and a long history as a gourmet food, there are still many unanswered questions concerning the molecular system, biology, genetics and ecology of Tuberaceae (Murat et al. 2018).

Choiromyces Vittad.

Notes: The genus *Choiromyces* with *C. meandriformis* Vittad. as the type species was first described in 1831 (Vittadini 1831). It is interesting that species of *Tuber* are incredibly diverse across the Northern Hemisphere, and yet, in contrast, the genus *Choiromyces* includes just a few relatively rare but geographically widespread species (Bonito and Smith 2016; Wang et al. 2022). The latest Phylogenetic analysis showed that the genus has at least nine species, six of which have been described and accepted, including *C. cerebriformis* T.J. Yuan, S.H. Li & Y. Wang, *C. helanshanensis* Juan Chen & P.G. Liu, *C. sichuanensis* S.P. Wan, R. Wang, *C. alveolatus* (Harkn.) Trappe, *C. venosus* (Fr.) Th. Fr (= *C. meandriformis* Vittad.), and *C. magnusii* (Mattir.) Paol. (Trappe 1975; Pegler et al. 1993; McNeill 2012; Moreno et al. 2012; Chen et al. 2016; Yuan et al. 2021; Wang et al. 2022). Although wang et al. (2022) presented systematic analyses of *Choiromyces* based on sequences from ITS genes, comprehensive studies on this genus are still lacking.

Choiromyces mongolicus S.P. Wan & F.Q. Yu, **sp. nov.**

Mycobank: MB 852605; *Facesoffungi*: FoF 15541; Figs. 24, 25

Etymology: refers to Inner Mongolia Autonomous Region, the locality of the type specimen.

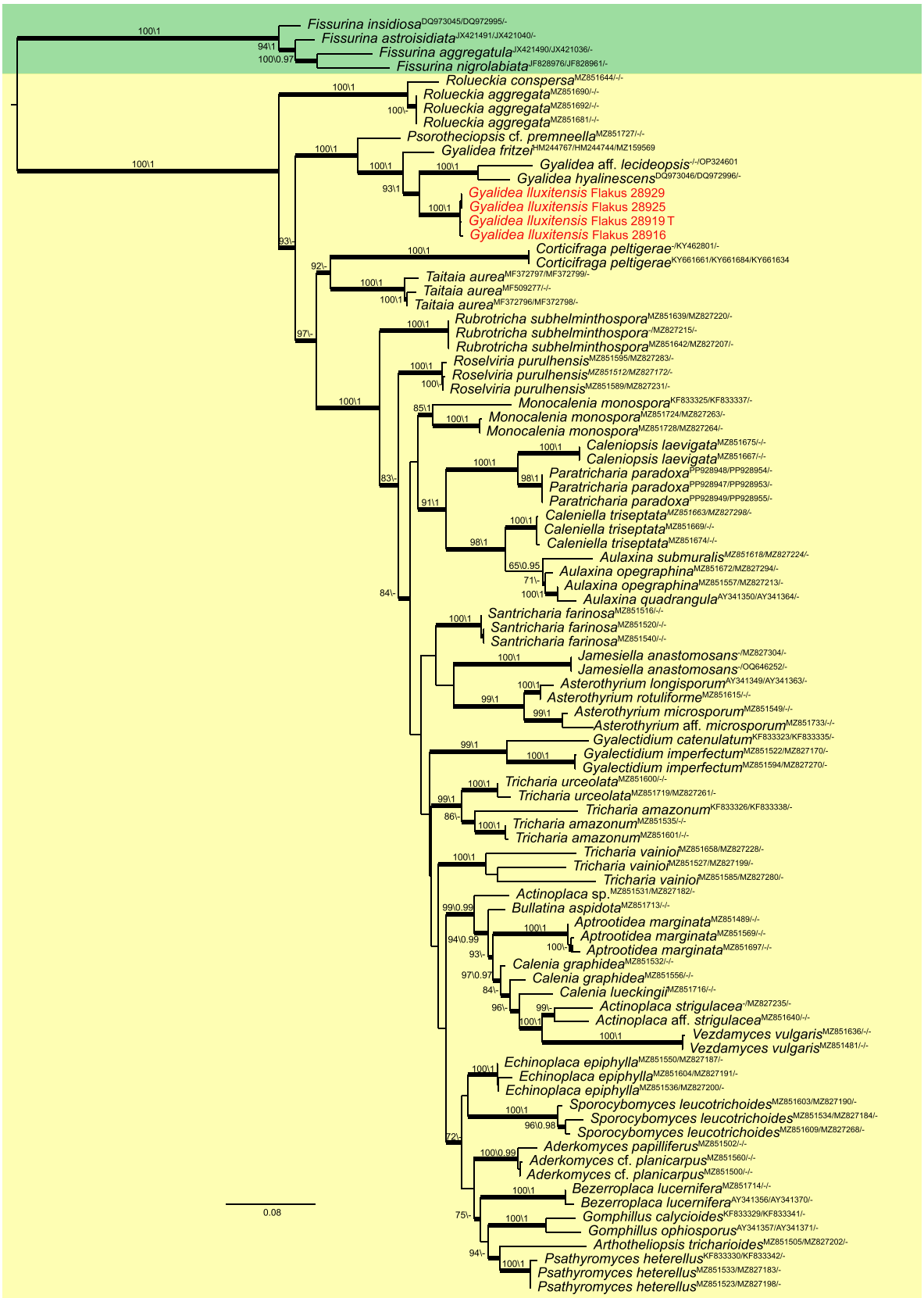
Holotype: YNAU1853.

Ascomata 2.4–10.5 cm in diam, hypogeous, subglobose or tuberiform, knobby with deep lobes, partially cracked, surface smooth, white, pale yellow to reddish-brown with white crackles when fresh, then becoming reddish-brown when dry. **Peridium** 252–552 µm thick, not clearly differentiated, prosenchymatous, composed of subglobose to subangular cells, 4.3–15.2 × 3.9–11.9 µm, light brown or hyaline, and composed of intricately interwoven, hyaline and thin-walled hyphae, 4.0–6.4 in diam. Dermatocystidia, multi-septate, multinodal, branched, blunt-tipped, intertwining and forming dense and friable superficial layer, 0.7–10 µm at septa in diam, hyaline to whitish. **Gleba** solid, milky white, pale yellow to reddish brown with a light brown tinge, marbled with white veins, consisting of interwoven thin-walled hyphae. **Odor** strong mushroom flavor, pleasant. **Asci** hyaline, clavate to saccate, 8-spored, (62.5–)70.9–99.6(–101.8) × (37.4–)37.5–56.0(–57.9) µm (n = 30). **Ascospores** spherical, pale yellow–brown at maturity, (16.9–)17.5–22.0(–23.1) × (16.5–)17.3–21.4(–22.6) µm in diam (n = 80), (Q = 1.00–1.06), ornamented with straight or slightly curved stick-like sparse spines, 1.20–1.96 µm tall, with irregularly blunt or rounded tips.

Material examined: CHINA, Inner Mongolia Autonomous Region, Xing'an League, 46°77′N 120°31′E, 1100 m asl, 7 Oct 2023, *WSP2645* (YNAU1853, **holotype**); Xing'an League, 46°76′N 120°33′E, 1108 m asl, 7 Oct 2023, *WSP2641* (YNAU1849); Xing'an League, 46°80′N 120°33′E, 1108 m asl, 7 Oct 2023, *WSP2642* (YNAU1850); Xing'an League, 46°80′N 120°41′E, 1204 m asl, 7 Oct 2023, *WSP2643* (YNAU1851); Xing'an League, 46°80′N 120°44′E, 1211 m asl, 7 Oct 2023, *WSP2644* (YNAU1852); Liaoning Province, Dalian City, Pulandian District, 39°38′N 122°03′E, 876 m asl, 14 Sep 2023, *WSP2613* (YNAU1821).

GenBank: YNAU1853: OR840536 (ITS); YNAU1849: OR840532 (ITS); YNAU1850: OR840533 (ITS); YNAU1851: OR840534 (ITS); YNAU1852: OR840535 (ITS); YNAU1821: OR840531 (ITS).

Notes: *Choiromyces mongolicus* belongs to the Heilanshanensis group (Fig. 25). This group includes all Chinese species, and has been distinguished from other European, American and Asian taxa. Phylogenetically, *C. mongolicus* is clearly separated from the other three reported Chinese species, *C. cerebriformis*, *C. helanshanensis* and *C. sichuanensis* (Fig. 25). Moreover, there are distinct morphological differences, with *C. mongolicus* having typical one-layer peridium, and smaller spores up to 22.6 µm (Chen et al. 2016; Yuan et al. 2021; Wang et al. 2022).


Fissurina insidiosa DQ973045/DQ972995/-
Fissurina astroisidiata JX421491/JX421040/-
Fissurina aggregatula JX421490/JX421036/-
Fissurina nigrolabiata JF828976/JF828961/-
Rolueckia conspersa MZ851644/-/-
Rolueckia aggregata MZ851690/-/-
Rolueckia aggregata MZ851692/-/-
Rolueckia aggregata MZ851681/-/-
Psorotheciopsis cf. premneella MZ851727/-/-
Gyalidea fritzei HM244767/HM244744/MZ159569
Gyalidea aff. lecideopsis -/-/OP324601
Gyalidea hyalinescens DQ973046/DQ972996/-
Gyalidea lluxitensis Flakus 28929
Gyalidea lluxitensis Flakus 28925
Gyalidea lluxitensis Flakus 28919 T
Gyalidea lluxitensis Flakus 28916
Corticifraga peltigerae -/KY462801/-
Corticifraga peltigerae KY661661/KY661684/KY661634
Taitaia aurea MF372797/MF372799/-
Taitaia aurea MF509277/-/-
Taitaia aurea MF372796/MF372798/-
Rubrotricha subhelminthospora MZ851639/MZ827220/-
Rubrotricha subhelminthospora -/MZ827215/-
Rubrotricha subhelminthospora MZ851642/MZ827207/-
Roselviria purulhensis MZ851595/MZ827283/-
Roselviria purulhensis MZ851512/MZ827172/-
Roselviria purulhensis MZ851589/MZ827231/-
Monocalenia monospora KF833325/KF833337/-
Monocalenia monospora MZ851724/MZ827263/-
Monocalenia monospora MZ851728/MZ827264/-
Caleniopsis laevigata MZ851675/-/-
Caleniopsis laevigata MZ851667/-/-
Paratricharia paradoxa PP928948/PP928954/-
Paratricharia paradoxa PP928947/PP928953/-
Paratricharia paradoxa PP928949/PP928955/-
Caleniella triseptata MZ851663/MZ827298/-
Caleniella triseptata MZ851669/-/-
Caleniella triseptata MZ851674/-/-
Aulaxina submuralis MZ851618/MZ827224/-
Aulaxina opegraphina MZ851672/MZ827294/-
Aulaxina opegraphina MZ851557/MZ827213/-
Aulaxina quadrangula AY341350/AY341364/-
Santricharia farinosa MZ851516/-/-
Santricharia farinosa MZ851520/-/-
Santricharia farinosa MZ851540/-/-
Jamesiella anastomosans -/MZ827304/-
Jamesiella anastomosans -/OQ646252/-
Asterothyrium longisporum AY341349/AY341363/-
Asterothyrium rotuliforme MZ851615/-/-
Asterothyrium microsporum MZ851549/-/-
Asterothyrium aff. microsporum MZ851733/-/-
Gyalectidium catenulatum KF833323/KF833335/-
Gyalectidium imperfectum MZ851522/MZ827170/-
Gyalectidium imperfectum MZ851594/MZ827270/-
Tricharia urceolata MZ851600/-/-
Tricharia urceolata MZ851719/MZ827261/-
Tricharia amazonum KF833326/KF833338/-
Tricharia amazonum MZ851535/-/-
Tricharia amazonum MZ851601/-/-
Tricharia vainioi MZ851658/MZ827228/-
Tricharia vainioi MZ851527/MZ827199/-
Tricharia vainioi MZ851585/MZ827280/-
Actinoplaca sp. MZ851531/MZ827182/-
Bullatina aspidota MZ851713/-/-
Aptrootidea marginata MZ851489/-/-
Aptrootidea marginata MZ851569/-/-
Aptrootidea marginata MZ851697/-/-
Calenia graphidea MZ851532/-/-
Calenia graphidea MZ851556/-/-
Calenia lueckingii MZ851716/-/-
Actinoplaca strigulacea -/MZ827235/-
Actinoplaca aff. strigulacea MZ851640/-/-
Vezdamyces vulgaris MZ851636/-/-
Vezdamyces vulgaris MZ851481/-/-
Echinoplaca epiphylla MZ851550/MZ827187/-
Echinoplaca epiphylla MZ851604/MZ827191/-
Echinoplaca epiphylla MZ851536/MZ827200/-
Sporocybomyces leucotrichoides MZ851603/MZ827190/-
Sporocybomyces leucotrichoides MZ851534/MZ827184/-
Sporocybomyces leucotrichoides MZ851609/MZ827268/-
Aderkomyces papilliferus MZ851502/-/-
Aderkomyces cf. planicarpus MZ851560/-/-
Aderkomyces cf. planicarpus MZ851500/-/-
Bezerroplaca lucernifera MZ851714/-/-
Bezerroplaca lucernifera AY341356/AY341370/-
Gomphillus calycioides KF833329/KF833341/-
Gomphillus ophiosporus AY341357/AY341371/-
Arthotheliopsis trichariodes MZ851505/MZ827202/-
Psathyromyces heterellus KF833330/KF833342/-
Psathyromyces heterellus MZ851533/MZ827183/-
Psathyromyces heterellus MZ851523/MZ827198/-
0.08

◂**Fig. 23** Phylogenetic reconstruction of the systematic position of *Gyalidea lluxitensis* inferred from ML analyses of combined dataset of nucLSU, ITS and mitSSU. Bold branches represent either bootstrap values ≥ than 70 and/or Bayesian posterior probabilities ≥ than 0.95. New species is shown in red. "T" refers to a type specimen

Sordariomycetes O.E. Erikss. & Winka.

Amphisphaeriales D. Hawksw. & O.E. Erikss.

Notes: Amphisphaeriales in Ascomycota that contains ca. 1243 species, 87 genera and 15 families (Wijayawardene et al. 2022). The concept of Amphisphaeriales has been accepted in consecutive studies using multigene phylogenies in the subclass Xylariomycetidae (Senanayake et al. 2015; Crous et al. 2018). However, based on the previous study, Wijayawardene et al. (2018b) accepted 11 families in Amphisphaeriales. Subsequently, Hyde et al. (2020b) reported that Amphisphaeriales is a moderately supported clade sister to Xylariales and comprises 17 families. However, Wijayawardene et al. (2022) only mentioned 15 families viz. Amphisphaeriaceae, Apiosporaceae, Beltraniaceae, Castanediellaceae, Clypeophysalosporaceae, Hyponectriaceae, Iodosphaeriaceae, Melogrammataceae, Oxydothidaceae, Phlogicylindriaceae, Pseudomassariaceae, Pseudosporidesmiaceae, Pseudotruncatellacea, Sporocadaceae, Vialaeaceae.

Oxydothidaceae S. Konta & K.D. Hyde.

Notes: Oxydothidaceae was established to accommodate the genus *Oxydothis* (Konta et al. 2016). Hyde et al. (2017b) evaluate the ranking of taxa of Sordariomycetes by providing a molecular clock, that proved Oxydothidaceae is a well-supported family. Members of Oxydothidaceae play a significant impact on ecology and economy (Hyde et al. 2020b). Species of this family having a J + (rarely J-) asci in sexual, and with mononematous conidiophores in Asexual morph. Hyde et al. (2020b) indicate that it is vital to identify species and study their biotrophic nature, which may provide resources for biological control and protect plants during planting.

Oxydothis Penz. & Sacc.

Notes: *Oxydothis* was initially established by Penzig and Saccardo (1897) to accommodate three species *Oxydothis grisea*, *O. nigricans* and *O. maculosa*, within Oxydothidaceae, Amphisphaeriales in Sordariomycetes as type species *Oxydothis grisea*. *Oxydothis* was considersied as one of the most common genera encountered in monocotyledons (Tibpromma et al. 2018). There are two types of ascomata of this genus, one is developed singly or in clusters, in darkened, ellipsoidal raised areas on the host surface, and have distinctive eccentric ostioles; whereas another is developed below a raised sheet of host epidermis, and usually not darkened (Fröhlich and Hyde 2000). However, many species in this genus are still lack of DNA sequence data for most species and potential species complexes.

Oxydothis dehongensis G.Q. Zhang, D.Q. Dai & L.S. Han, **sp. nov.**

Index Fungorum: IF 901554; *Facesoffungi*: FoF 15291; Figs. 26, 27

Etymology: refers to Dehong prefecture, the locality of the type specimen.

Holotype: MHZU 23–0267.

Sexual morph: **Ascomata** 550–850 µm diam., 340–550 µm high, forming slightly raised domes, solitary or clustered in groups (mostly 2–3), immersed, subglobosa, truncated at the base, conical in section, coriaceous, papilla at one end curving upwards to the host surface. **Peridium** 15–20 µm wide, composed of 2–3 layers of pale brown to hyaline cells with *textura prismatica*. **Paraphyses** seems to dissolve during maturation. **Asci** 190–250 µm × 13–20 µm ($\bar{x}$ = 232 × 16 µm, n = 20), 8-spored, cylindrical, straight to curve, pedicellate, unitunicate, with a wedge-shaped, J +, apical ring, 2–4 µm diam, bluing in Melzer's reagent, truncated at the top. **Ascospores** 45–95 × 4.5–9 µm ($\bar{x}$ = 72 × 6.5 µm, n = 30), fusiform, initially hyaline, becoming brown when overmatured, obliquely 1-seriate, tapering gradually from a constricted central or seldom upper central septum to short, pointed processes, smooth walled, guttulate, pointed at ends. Asexual morph: undetermined.

Material examined: CHINA, Yunnan Province, Dehong Dai and Jingpo autonomous prefecture, Mang city, Xuangang village, 24°45′N 98°43′E, 919.77 m, 22 Jul 2023, *Gui-Qing Zhang*, *Dong-Qin Dai*, *Li-Su Han*, *HLS67* (MHZU 23–0267, **holotype**), ex-type ZHKUCC 23–0986, culture ZHKUCC 23–0987; Ibid. *HLS58* (MHZU 23–0269), culture ZHKUCC 23–0988.

GenBank: ZHKUCC 23–0986: PP580831 (ITS), PP002130 (*nucLSU*), PP002127 (*nucSSU*), PP001172 (*tef1*); ZHKUCC 23–0987: PP580832 (ITS), PP002131 (*nucLSU*), PP002128 (*nucSSU*), PP001173 (*tef1*); ZHKUCC 23–0988: PP598863 (ITS), PP002132 (*nucLSU*), PP002129 (*nucSSU*), PP001174 (*tef1*).

Notes: Combined ITS, LSU and *tef1* gene analysis (Fig. 27) showed that our isolate (ZHKUCC 23–0986, ZHKUCC 23–0987, ZHKUCC 23–0988) grouped with *Oxydothis inaequalis*, *Oxydothis yunnanensis* and *O. fortunei*, forming a distinct clade with ML/BP = 100%/1 statistical support. Our collection differs from *Oxydothis inaequalis* by it has larger asci and ascospores while *O. inaequalis* with narrower (11.25–13.75 µm) asci and narrower (5–6.25 µm) ascospores (Hidayat et al. 2006). Our collection differs from *Oxydothis fortunei* by its wide asci with J +, apical ring and *O. fortunei* has small, solitary or aggregated ascomata (200–315 µm diam.), smaller-sized asci (9–14 µm), J- subapical ring and smaller ascospores (56–72 µm) (Hu et al. 2022a). Our collection differs from *Oxydothis yunnanensis* in having wide asci with J +, apical ring, 1-seriate, large-sized asci and ascospores while *Oxydothis yunnanensis* with

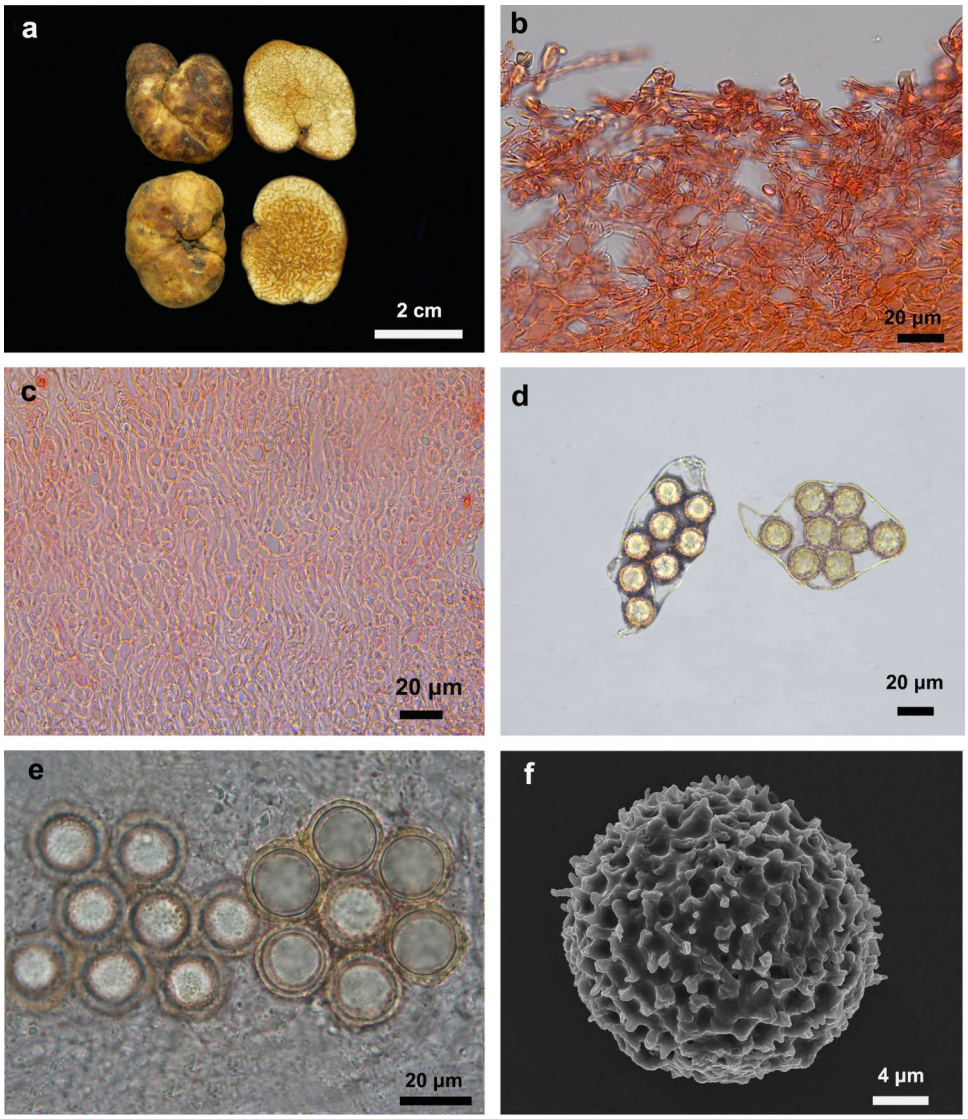


Fig. 24 ***Choiromyces mongolicus*** (YNAU1853, **holotype**). **a** Ascoma. **b** Dermatocystidia. **c** Peridium section. **d, e** light micrograph (LM) of ascospores. **f** SEM image of an ascospore

2-seriate, smaller-sized asci (108–152 × 6.5–13.5 µm) and ascospores (54–69 × 2.5–4 µm) (Senanayake et al. 2023). Our collection does not fit with any exist species and thus, we introduce our collection as a new species, *Oxydothis dehongensis.*

Sporocadaceae Corda.

Notes: Sporocadaceae is also known as pestalotioid fungi, contains a typical group of appendaged coelomycetes. Taxa in this family are defined as having multi-septate and more or less fusiform conidia with appendages at one or both ends, frequently with some melanised cells, resembling those taxa having affinities with *Pestalotia* (Nag Raj 1993; Liu et al. 2019). Spodocadaceae taxa are ecologically important as they occur as saprobes, endophytes or pathogens, on leaves, twigs, branches and fruits on a wide range of host plants (Nag Raj 1993; Liu et al. 2019; Jiang et al. 2023).

Pestalotiopsis Steyaert.

Notes: *Pestalotiopsis* was separated from *Pestalotia* based on 5-celled conidia, while species with 4-celled conidia were transferred to *Monochaetia* and species with 6-celled conidia kept in *Pestalotia* (Steyaert 1949). Recently, part species were removed to *Neopestalotiopsis* and *Pseudopestalotiopsis* based on the molecular data of ITS, *tef1* and *tub2* (Maharachchikumbura et al. 2014). Several species of this genus are important phytopathogens, while the others are saprobes or endophytes (Jiang et al. 2022).

Pestalotiopsis buxicola N. Jiang & B. Cao, **sp. nov.**

Fungal Names: FN 571957; *Facesoffungi*: FoF 17096; Fig. 28

Etymology: "*buxi*" refers to the host genus *Buxus* and "*-cola*" means inhabiting.

Holotype: CAF800090.

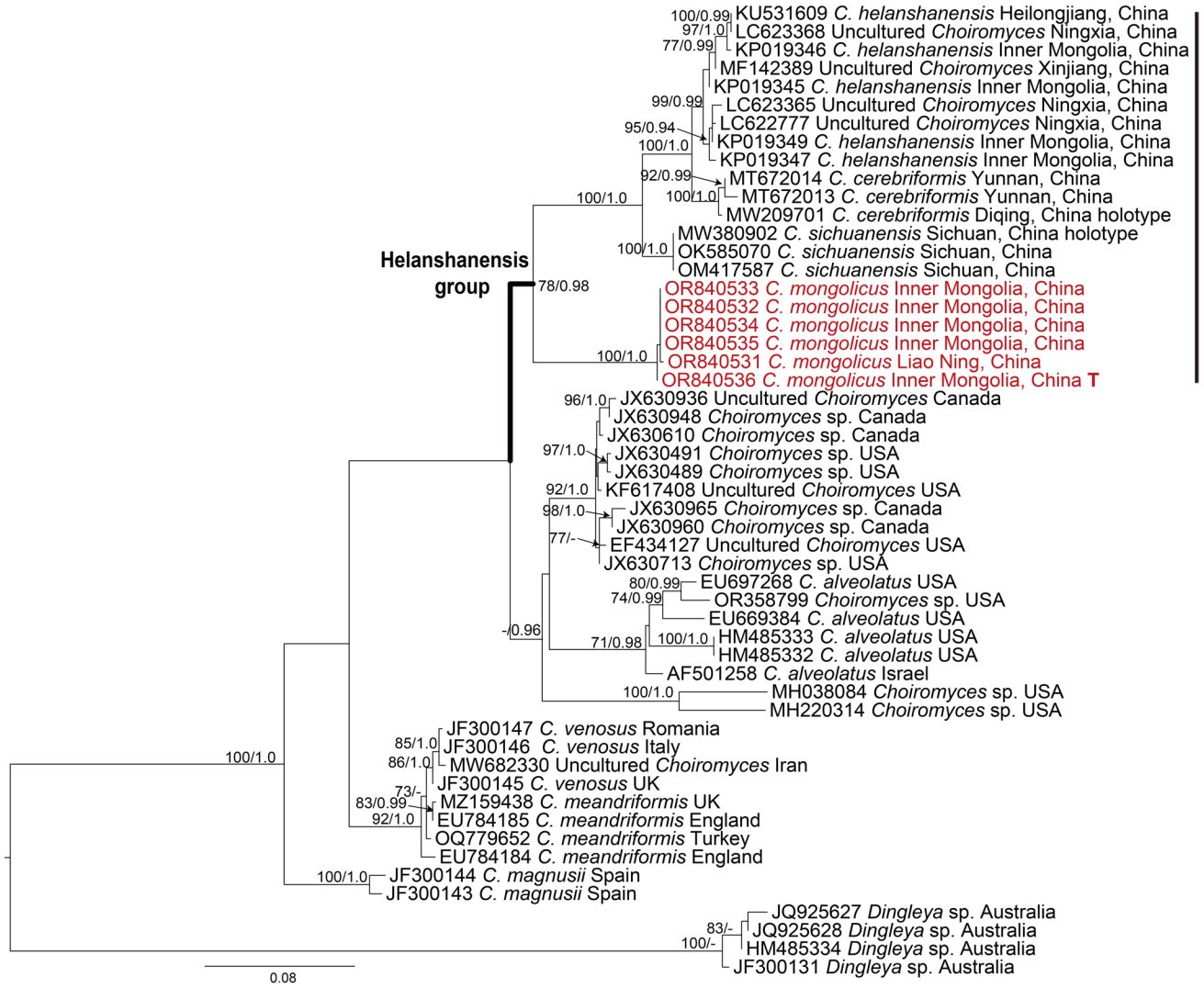
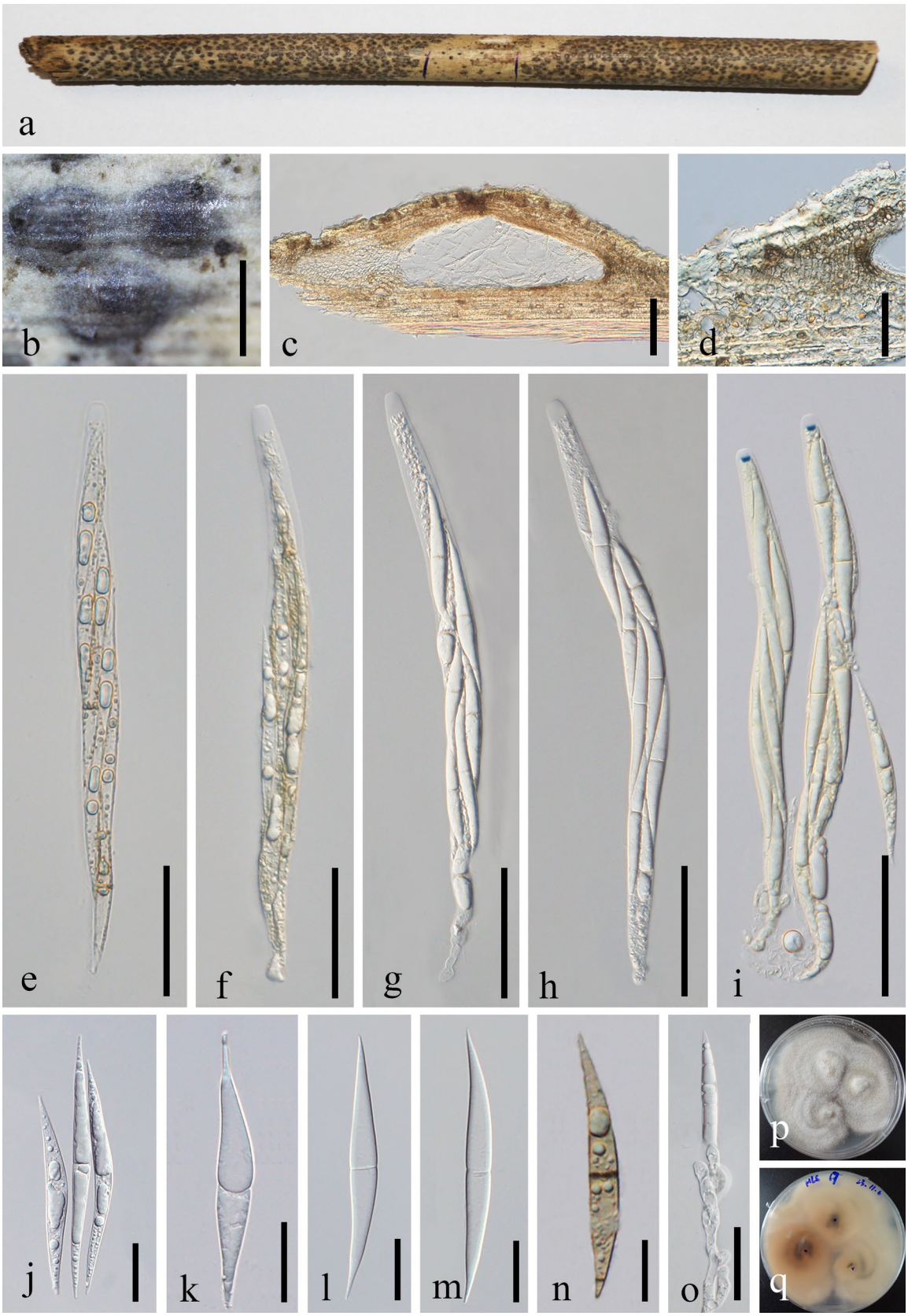


Fig. 25 Maximum Likelihood tree based on ITS sequences, bootstrap values greater than 50% and posterior probabilities greater than 0.90 are shown around nodes. New species are shown in red. "T" refers to a type specimen

Conidiomata in culture sporodochial, aggregated or solitary, erumpent, pulvinate, black, 100–250 µm diam., exuding black conidial masses. **Conidiophores** indistinct, usually reduced to conidiogenous cells. **Conidiogenous cells** hyaline, smooth, cylindrical to spherical, annelidic, 8.5–26 × 2.5–4.5 µm. **Conidia** fusoid, straight or slightly curved, 4-septate, smooth, slightly constricted at the septa, (14.5–)16–20.5(–22.5) × (5.5–)6–7(–8) µm; **basal cell** obconic with a truncate base, thin-walled, hyaline or pale brown, 3.5–5.5 µm; **median cells** 3, trapezoid or subcylindrical, concolorous, brown, thick-walled, the first median cell from base 3.5–5 µm long, the second cell 4–5 µm long, the third cell 4–5.5 µm long, together 11.5–15.5 µm long; **apical cell** conic with an acute apex, thin-walled, hyaline, 2.5–4 µm long; **basal appendage** single, unbranched, tubular, centric, straight or slightly bent, 4–6.5 µm long; **apical appendages** 2–3, unbranched, tubular, centric, straight or bent, 6–15.5 µm long. **Colonies** on MEA flat, spreading, with flocculent aerial mycelium and entire edge, white, reaching 70 mm diam. after 7 d at 25 °C, forming black conidiomata; on PDA flat, spreading, with flocculent aerial mycelium and entire edge, white, reaching 70 mm diam. after 7 d at 25 °C, forming black conidiomata.

Material examined: CHINA, Shaanxi Province, Ankang City, Xiangxidong Park, 32°40′32″N 109°18′57″E, 2504 m asl, on leaf spots of *Buxus bodinieri*, 8 Jul 2017, *Ning Jiang*, *JN17.245* (CAF800090, **holotype**; CFCC 57357, ex-type) and *JN17.246* (living culture CFCC 57358).

GenBank: CFCC 57357: PP965518 (ITS), PP957899 (*tef1*), PP957901 (*tub2*); CFCC 57358: PP965519 (ITS), PP957900 (*tef1*), PP957902 (*tub2*).


a
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◂**Fig. 26** ***Oxydothis dehongensis*** (MHZU 23–0267, **holotype**). **a** Bamboo specimen. **b** Appearance of fruiting bodies on host substrate. **c** Section of ascoma. **d** Peridium. **e–h** Asci in water. **i** Reaction of apical ring in Melzer's reagent. **j–n** Ascospores. **o** Germinating ascospores. **p**, **q** Cultures on PDA from above and below. Scale bars: **b** = 500 µm, **c** = 1000 µm, **d** = 50 µm, **e–i** = 50 µm, **j–o** = 20 µm

Notes: Two isolates from leaf spots of *Buxus bodinieri* cluster a distinct clade from all known species of *Pestalotiopsis* (Supplementary data, Online Resource 1), representing a new species named *P. buxicola*. *Pestalotiopsis buxicola* is phylogenetically close to *P. photiniicola* from *Photinia serrulate*, but has wider conidia (6–7 µm vs. 4–5 µm) (Chen et al. 2017b).

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández.

Notes: Chaetosphaeriales was introduced in Sordariomycetidae by Huhndorf et al. (2004) based on ITS sequence data. This order currently comprises four families including Chaetosphaeriaceae (Wijayawardene et al. 2022).

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels.

Notes: Chaetosphaeriaceae was introduced without any description by Locquin (1984) to accommodate five genera including *Chaetosphaeria*, *Loramyces*, *Niesslia*, *Rhagadostoma*, and *Zignöella*. These species are mostly associated as saprobic fungi on wood or decaying plant parts including leaves, and fruits in terrestrial and aquatic habitats, sometimes isolated from soil and fresh plant parts such as leaves, less commonly pathogens (Zhang et al. 2022a, b).

Menisporopsis S. Hughes.

Notes: *Menisporopsis* was established by Hughes (1952) to accommodate *M. theobromae*. Liu et al. (2015a, b) provided a detailed description of *M. theobromae* along with DNA sequence data and phylogeny for the first time for this genus. There are 17 epithets listed in Index Fungorum (July 2024). Keys to the *Menisporopsis* species were provided by Tsui et al. (1999) and Castañeda Ruíz et al. (2001). In this study, we introduce a new host species *Menisporopsis pirozynskii* isolated from dead stems of *Cyclosorus interruptus*.

Menisporopsis pandanicola Tibpromma & K.D. Hyde, **new host record.**

Index Fungorum: IF 554522; *Facesoffungi*: FoF 04533; Figs. 29, 30

Saprobic on dead stems of *Dypsis lutescens*. Sexual morph: undetermined. Asexual morph: Hyphomycetous, scattered, brown to dark. **Setae** 390–420 × 8–9 µm, central, solitary, erect, straight or slightly flexuous, unbranched, dark brown, septate, smooth, thick-walled, brown to dark brown at the base, pale brown towards the apex. **Conidiophores** 75–80 × 15–20 µm, closely compacted into synnemata, brown, straight or slightly flexuous, pale to medium brown, septate, smooth- and thick-walled. **Conidiogenous cells** 20–28 × 3–3.7 µm, polyphialidic, terminal, integrated, lageniform at apex, erect, straight, smooth. **Conidia** 16–18 × 2.2–3.8 µm, aggregated into a slimy mass, hyaline, aseptate, smooth- and thin-walled, lunate, curved, conical at both ends, guttulate, with (1–)2 setula of the different length at each end, sparsely three at one side, setulae situated on different planes, 3–11.5 µm long.

Culture characteristics: colonies on PDA reaching 25 mm diam. at 25 °C after 6 days, hypophyllous, effuse, thick, inconspicuous, mycelium partly immersed and partly superficial, composed of pale brown, septate hyphae, raised on surface media.

Material examined: CHINA, Yunnan Province, Xishuangbanna City, on dead inflorescences of *Dypsis lutescens* (Arecaceae), 6 February 2023, *Y.R. Xiong & L. Lu*, *DZY-SWK-4* (MHZU 24–0473, new host record).

GenBank: MHZU 24-0473a: PQ764965 (ITS), PQ764971 (LSU); MHZU 24-0473b: PQ764966 (ITS), PQ764972 (LSU).

Note: *Menisporopsis pandanicola* was first introduced on dead leaf of *Pandanus* sp. in Hong Kong, China by Tibpromma & K.D. Hyde (Tibpromma et al. 2018). Subsequently, it also be reported on dead leaves of unidentified tree from Guangdong, Guangxi and Yunnan, China (Wu and Diao 2022). The phylogenetic results showed that our isolates clustered with *M. pandanicola* with 100% ML and 1.00 BIPP bootstrap support (Fig. 30). Morphologically, our collection fit well with *M. pandanicola* description (Tibpromma et al. 2018; Wu and Diao 2022). In addition, our collection supplement morphology characteristics about conidia setulae sparsely have three at one side and situated on different planes. Based on phylogenetic analysis and morphology, we introduce our isolation as new host record of *M. pandanicola* on *Dypsis lutescens.*

Menisporopsis pirozynskii Varghese & V.G. Rao, **new host record.**

Index Fungorum: IF 317565; *Facesoffungi*: FoF 17089; Fig. 30, 31

Saprobic on dead stems of *Cyclosorus interruptus*. Sexual morph: undetermined. Asexual morph: **Colonies** on plant substrate effuse, scattered, white to pale brown. **Mycelium** partly immersed, composed of brown hyphae. **Setae** central, solitary, erect, straight, unbranched, dark brown, septate, smooth, thick-walled, subulate, the lower part of each seta encased by tightly compacted conidiophores (170–280 × 5–10.5 µm) at the base. **Synemata** 75–150 × 8.5–22.5 µm. **Conidiophores** 147 × 5.5–16 µm, macronematous, synnematous, encasing lower part of setae; separate filaments unbranched, straight or slightly flexuous,

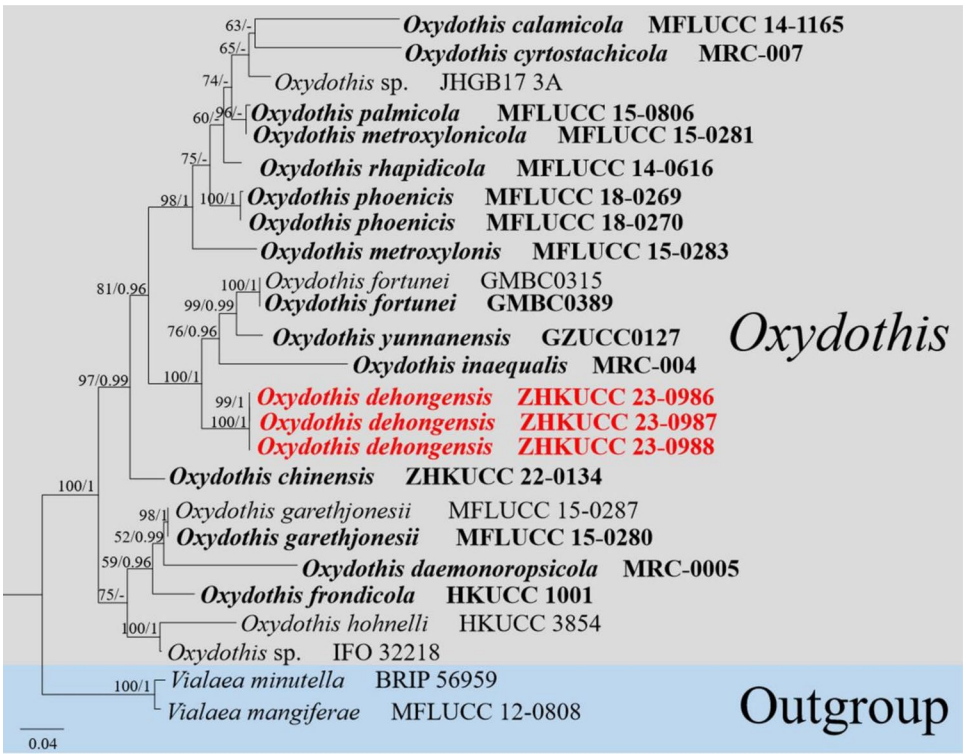


Fig. 27 Phylogram generated from Maximum Likelihood analysis based on combined ITS, LSU and *tef1* sequence data of 24 taxa. Bootstrap support for ML equal to or greater than 50% and clade credibility values greater than 0.95 (the rounding of values to 2 decimal proportions) from Bayesian inference analysis are labelled at each node. Ex-type strains are in bold, while the new isolate is indicated in red bold. The tree is rooted to *Vialaea minutella* (BRIP 56959) and *V. mangiferae* (MFLUCC 12–0808)

lower part narrow, upper part wider, pale brown, smooth. **Conidiogenous** cells monophialidic, integrated, terminal, cylindrical, with collarettes. **Conidia** 16.0–22 × 3–4 µm ($\bar{x}$ = 20.0 × 3.0 µm, n = 30), aggregated in slimy heads, acrogenous, semi-endogenous, appendiculate with one or two setulae at each end, setulae 3–11 µm long, aseptate, curved, cylindrical or fusiform, hyaline, smooth.

Culture characteristics: colonies on PDA reaching 25 mm diam. at 25 °C after 6 days, full, moist, rough, felty, with margin undulate and irregular; from above, creamy white at the margin and white in the middle; from below, creamy white edges and dark brown in the middle with a circle of yellow between the two colors; no pigmentation is produced in culture.

Material examined: CHINA, Yunnan Province, Xishuangbanna City, on dead stems of *Cyclosorus interruptus* (Thelypteridaceae), January 2024, *H. Li & I.S. Manawasinghe*, *YX5-008* (MHZU 24–0584), living cultures ZHKUCC 24–1063, ZHKUCC 24–1064.

GenBank: ZHKUCC 24–1063: PQ203229 (ITS), PQ206193 (LSU); ZHKUCC 24–1064: PQ203230 (ITS), PQ206194 (LSU).

Note: The phylogenetic results showed that our isolate clustered with *Menisporopsis pirozynskii* with 98% ML bootstrap values (Fig. 30). Conidia of our isolation is similar to *M. pirozynskii* (MFC-SK082-02) type description, which is aseptate, lunate, hyaline conidia with 1–2 setula at each end, and small differences sizes in Conidia (Tsui et al. 1999). Based on these, we identified our isolate as *M. pirozynskii*. This is the first report of *M. pirozynskii* associated with of *Cyclosorus interruptus.*

Diaporthales Nannf.

Notes: The Diaporthales is a distinct order in the subclass Diaporthomycetidae (Sordariomycetes) and it includes pathogens, saprobes and endophytes, with no known coprophilous, hypersaprobes or mycophylic species (Barr 1978; Rossman et al. 2007; Vasilyeva et al. 2007; Maharachchikumbura et al. 2015, 2016). Taxa of this order inhabit a wide diversity of hosts and substrates, including most economically and ecologically important trees and crops, soil and living animal and human tissues (Barr 1978; Gryzenhout et al. 2006).

Cytosporaceae Fr.

Notes: Cytosporaceae was established by Fries (1825) as *Cytisporei* with *Cytospora* Ehrenb. as its type genus. The family has been revised several times, temporarily including up to 13 genera (Maharachchikumbura et al. 2016). Senanayake et al. (2017) provide a comprehensive morphological description of Cytosporaceae and accepted five genera. Senanayake et al. (2018) accepted seven genera (*Cryptascoma, Cytospora*, *Hypophloeda, Pachytrype, Paravalsa*, *Waydora*, and *Xenotypa*), based on morphological characters. Only three of them (*Cytospora, Pachytrype* and *Waydora*) have been confirmed to belong to this family using DNA sequence data (Senanayake et al. 2018), hence further

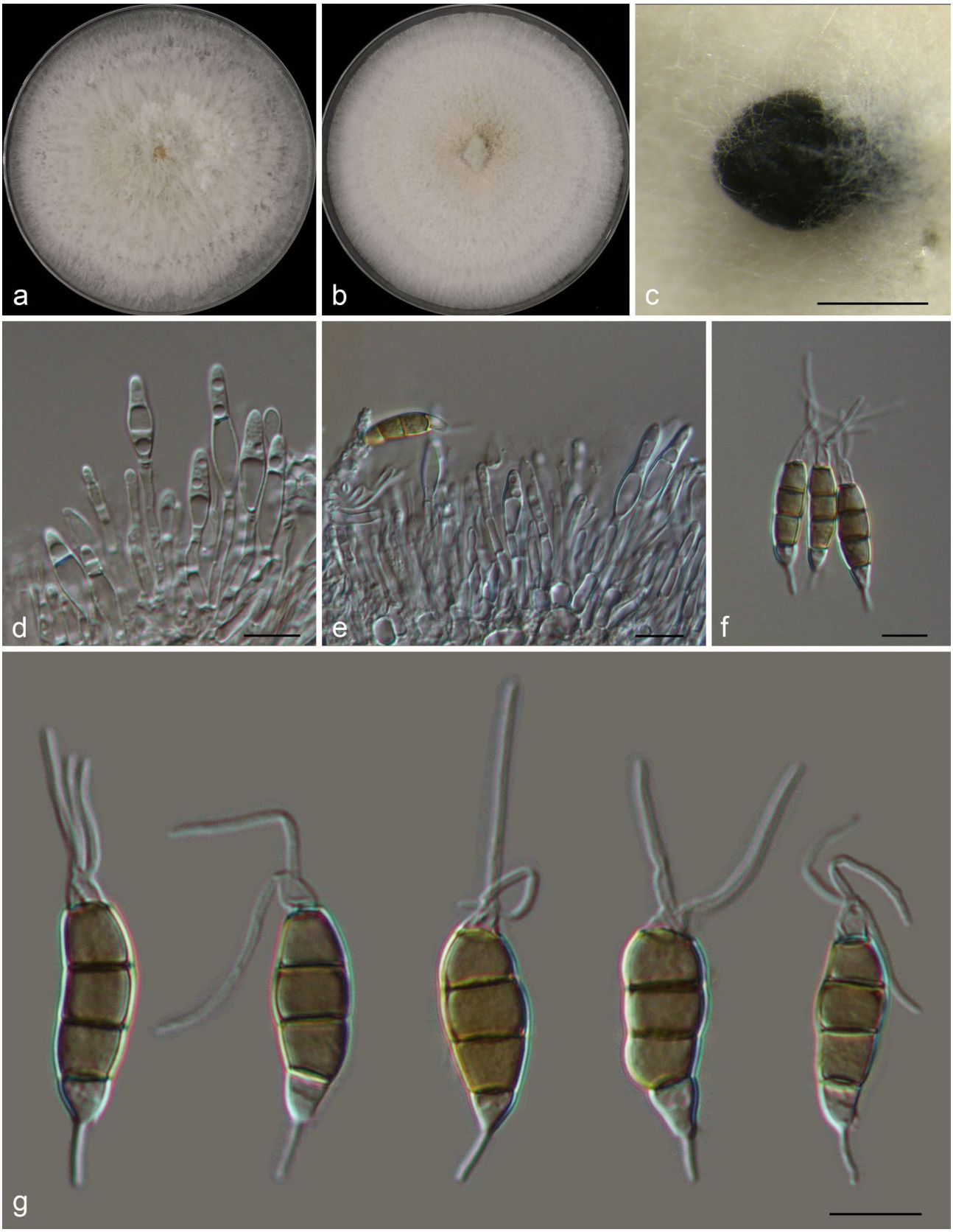


Fig. 28 ***Pestalotiopsis buxicola*** (CFCC 57357, ex-type). **a** Colony on PDA after 10 d at 25 °C. **b** Colony on MEA after 10 d at 25 °C. **c** Conidioma formed on PDA. **d**, **e** Conidiogenous cells giving rise to conidia. **f**, **g** Conidia. Scale bars: **c** = 200 µm, **d**–**g** = 10 µm

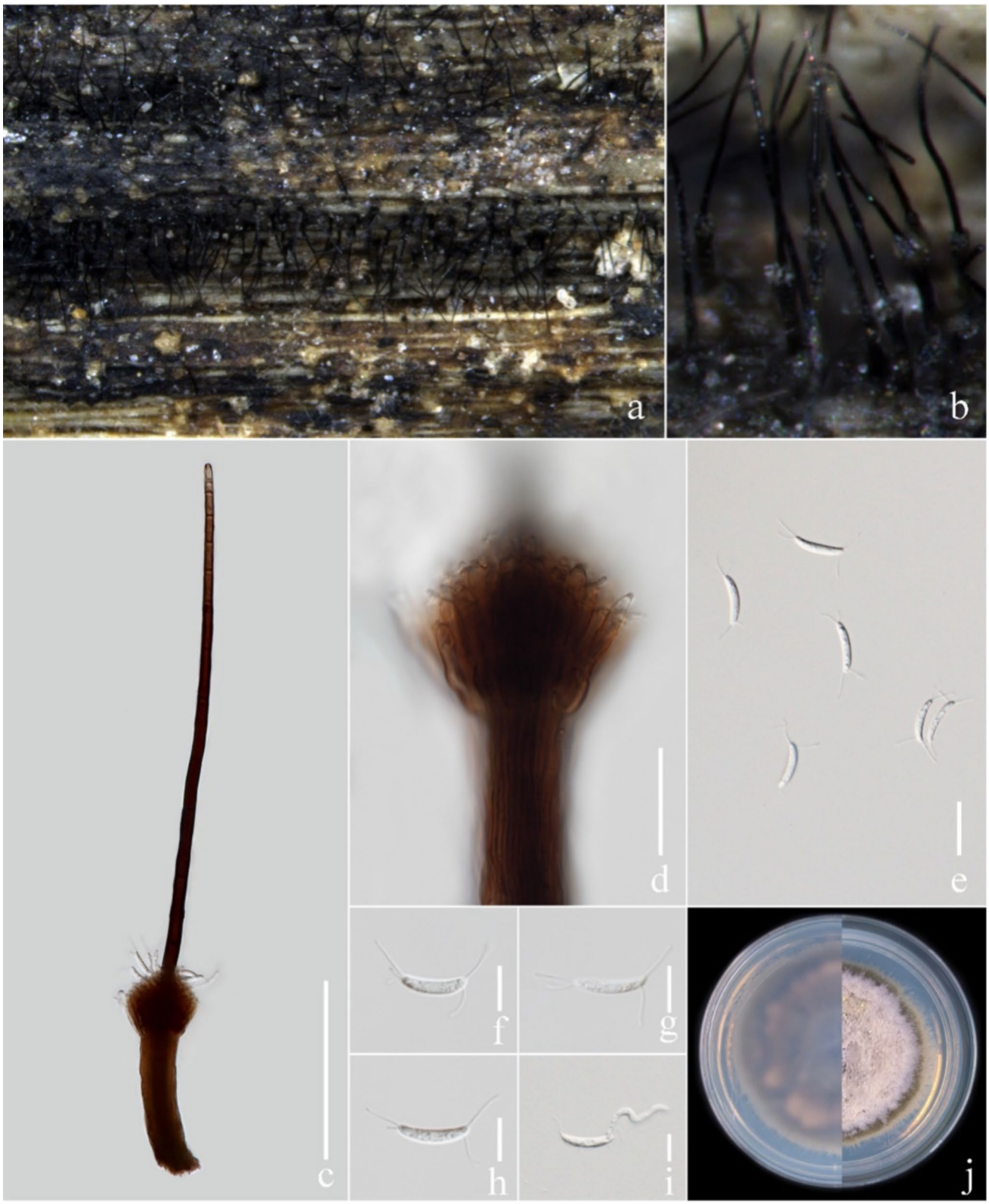


Fig. 29 ***Menisporopsis pandanicola*** (MHZU 24–0473). **a, b** Colonies on natural substrate. **c** Setae with conidiophores, conidiogenous cells and conidia. **d** Conidiogenous cells with conidia. **e**–**h** Conidia. **i** Germinated conidium. **j** Colony on PDA (front and below). Scale bars: **c** = 100 µm, **d, e** = 20 µm, **f**–**i** = 10 µm

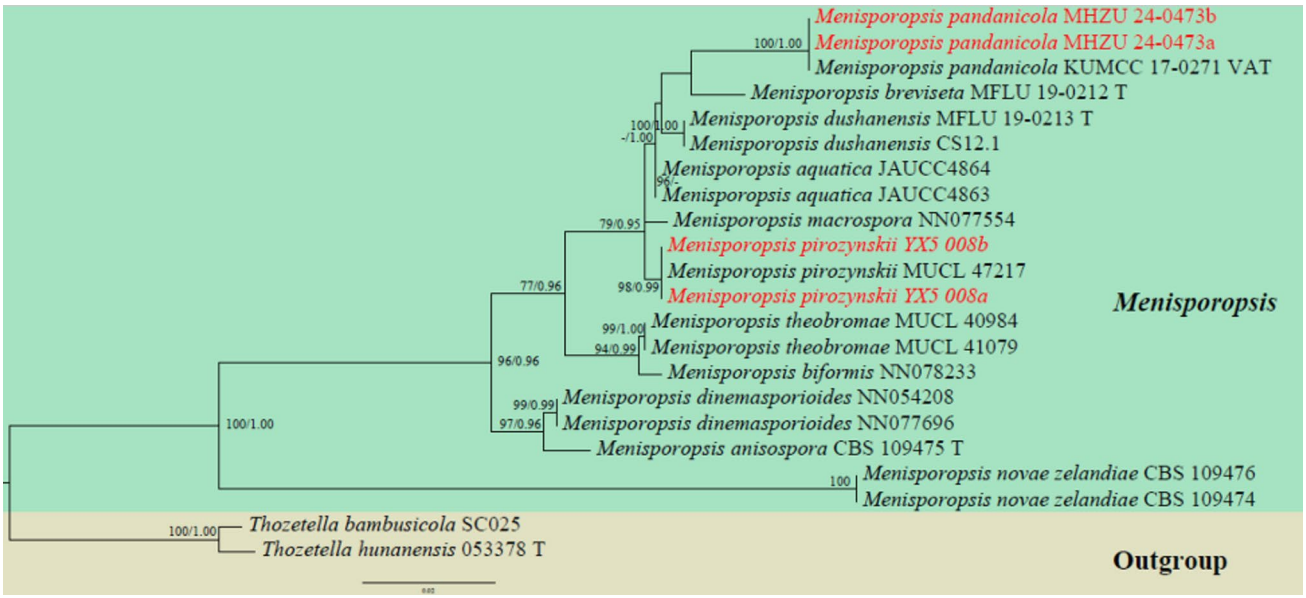


Fig. 30 Maximum Likelihood consensus tree inferred from the combined ITS and LSU sequence alignments. Bootstrap support values for Maximum Likelihood (ML, first value) equal to or greater than 75% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Thozetella bambusicola* (SC025) and *T. hunanensis* (053378). Ex-type strains are indicated with "[T]". The newly generated sequences are indicated in red

collections and molecular studies are required to confirm the placement of the remaining four genera. Cytosporaceae includes saprobes and plant pathogens that mostly cause cankers and dieback of hardwood and coniferous trees.

Cytospora Ehrenb.

Notes: *Cytospora* was first introduced by Ehrenberg in 1818 with the description of four species; *C. betulina*, *C. epimyces*, *C. resinae*, and *C. ribis* (Ehrenberg 1818; Norphanphoun et al. 2017). *Cytospora chrysosperma* is the type species of the genus, as clarified by Donk (1964). There are over 120 accepted species of *Cytospora*, with 695 names recorded on Index Fungorum (http://www.indexfungorum.org/Names/Names.asp; Wijayawardene et al. 2017a). In 2015, five genera previously used for the sexual stages of *Cytospora* species (i.e., *Leucocytospora*, *Leucostoma, Valsa*, *Valsella*, and *Valseutypella*) were synonymised with *Cytospora* (Rossman et al. 2015).

Cytospora species have been associated with infections in over 100 different plant species, being important canker and dieback pathogens of a wide range of plants including *Malus* spp., *Eucalyptus* spp., and *Olea europea* (Norphanphoun et al. 2017; Senanayake et al. 2017; Ma et al. 2018; Zhang et al. 2019a; Liu et al. 2020; Petrović et al. 2023). These fungi have been reported as saprobic opportunists or mild to severe pathogens, causing necrosis of plant tissue leading to loss in tree productivity (Fan et al. 2020; Pan et al. 2020, 2021; Monkai et al. 2021; Gulnaz et al. 2024).

Full morphological descriptions have been provided by previous studies (Adams et al. 2004; Norphanphoun et al. 2017). The asexual fruiting structures produced by *Cytospora* are often characterized by conidiomata with complex or labyrinthine locules/chambers, branched filamentous conidiophores, and hyaline allantoid conidia (Adams et al. 2004; Norphanphoun et al. 2017; Wijayawardene et al. 2017a). The sexual stage is characterized by stromatic or pseudostromatic, erumpent ascostromata (Adams et al. 2004; Wijayawardene et al. 2017a; Fan et al. 2020).

Cytospora diatrypelloidea G.C. Adams & M.J. Wingf., **new geographical record from New Zealand and a new host record.**

Index Fungorum: IF 500223; *Facesoffungi*: FoF 15305; Figs. 32, 33

Associated with leaf spots and necrosis, debris and dead branches of Myrtaceae species.

Sexual morph: not observed.

Asexual morph: **Conidiomata** pycnidial, aggregated and abundant with pale yellow cirrhi in ten-day old cultures. **Conidiophores** hyaline, branched or unbranched. **Conidiogenous cells** phialidic, narrowing at the apices, 6.9–8.9–9.8 × 1.5–1.7–2.0 µm

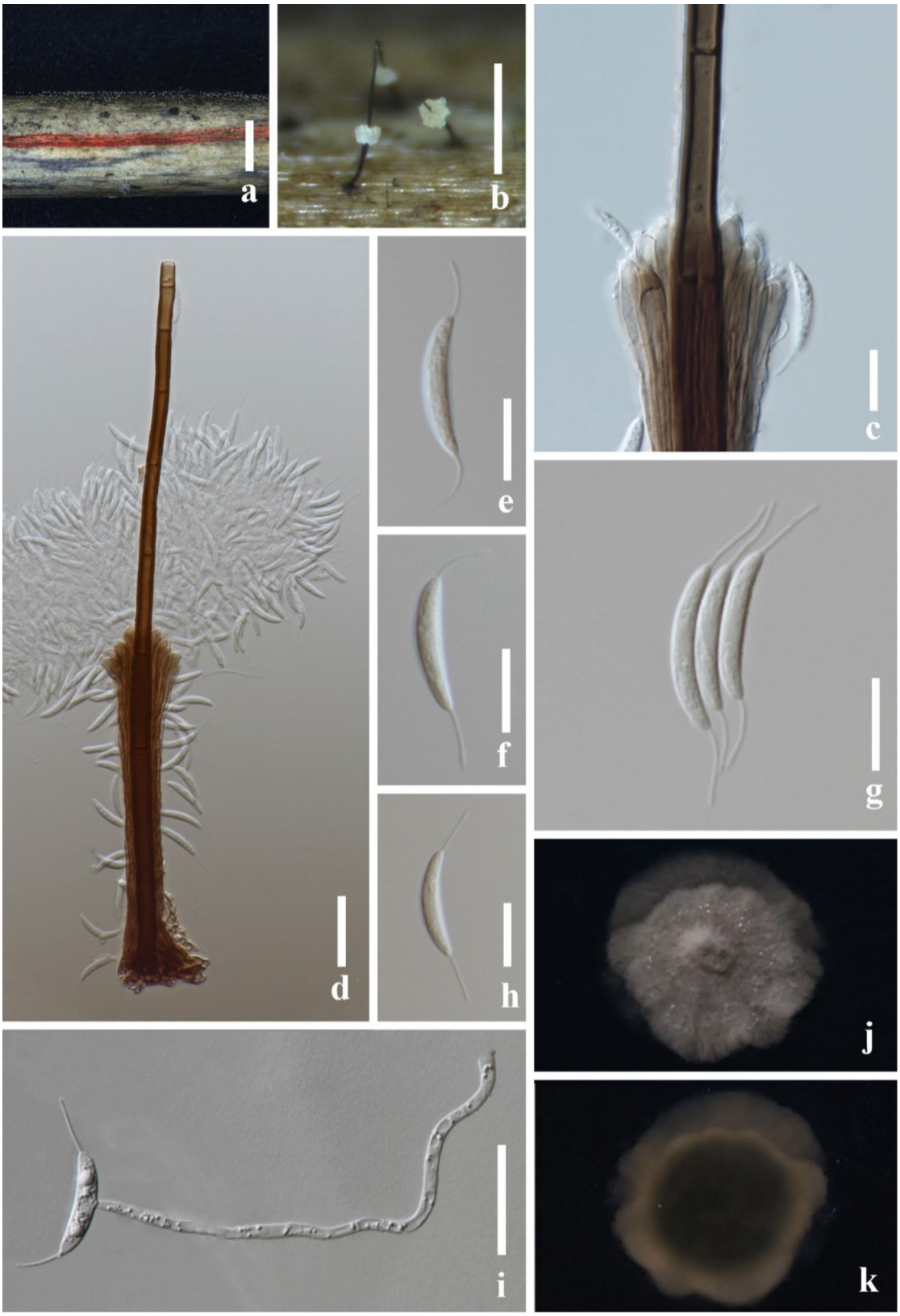


Fig. 31 ***Menisporopsis pirozynskii*** (MHZU 24–0584). **a** Decaying branch of host. **b** Colonies on natural substrate. **c, d** Conidiophores, conidiogenous cells and conidia. **e**–**g** Conidia. **i** Germinated conidium. **j, k** Colony on PDA (front and below). Scale bars: **a** = 2 mm, **b** = 0.2 mm **c**, **d, i** = 25 µm, **e**–**g** = 10 µm

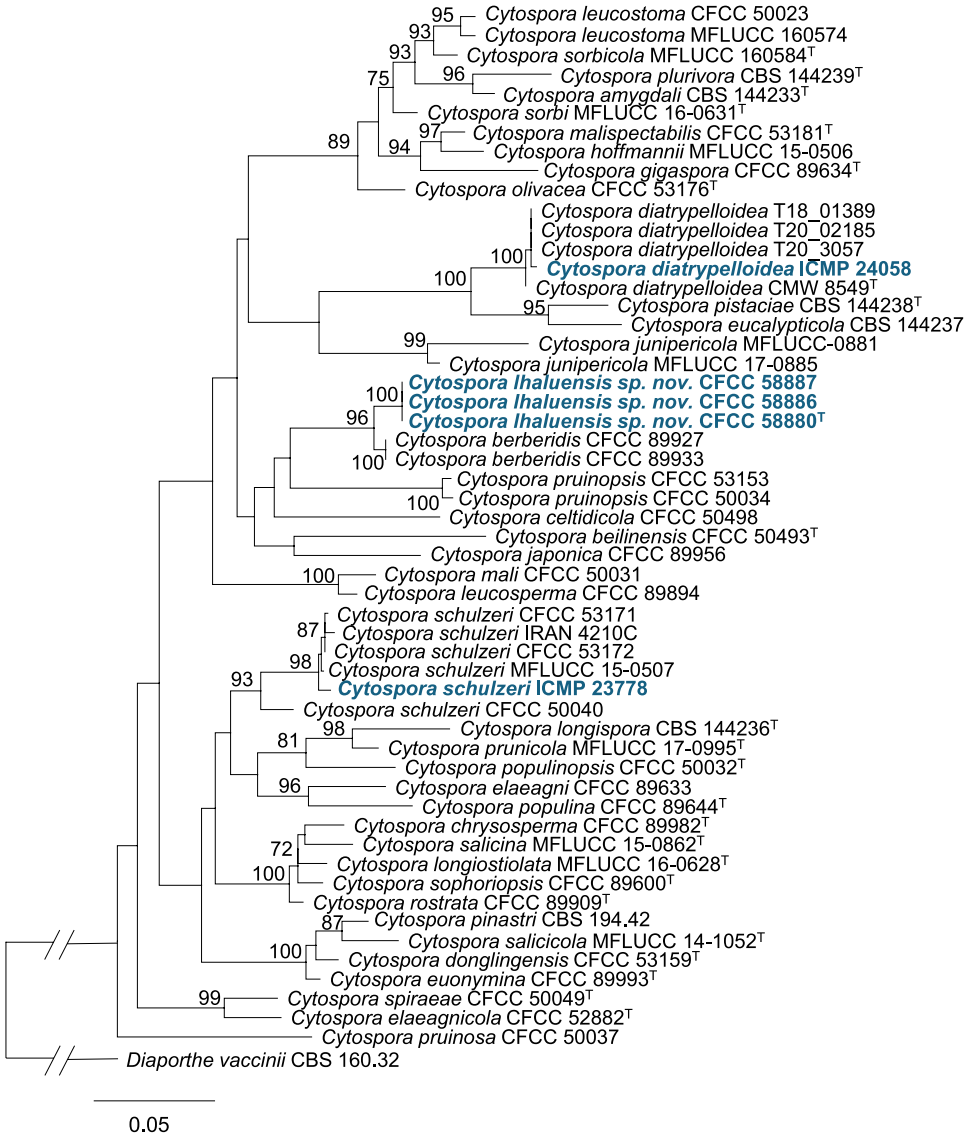


Fig. 32 Maximum likelihood (GTR + G + I) tree illustrating the phylogenetic placement of the *Cytospora* species discussed in-text (in bold) within the genus. This phylogenetic tree is based on the alignment of concatenated ITS, *act* and *rpb2* sequences. Branches are labelled with bootstrap probabilities ≥ 70% across 1,000 bootstrapping replicates, and type specimens are denoted by a superscript "T". *Diaporthe vaccinii* CBS 160.32 was used as an outgroup

(n = 20). **Conidia** hyaline, aseptate, allantoid, eguttulate, 4.9–5.4–8.9 × 1.0–1.5–2.5 µm (n = 20).

Culture characteristics: Colonies on PDA at 21 °C and incubated under black light were slow growing, 10–12 mm in diameter after three days and 15–25 mm in diameter after seven days; with uneven margin expansion, raised, pale olive-gray to olive-black on the surface with a greenish irregular margin, olive-black on reverse.

Material examined: NEW ZEALAND, from leaf spots on *Eucalyptus leucoxylon*, August 2016, *R. Thangavel*, PHEL T16_01761A. Culture stored at the International Collection of Microorganisms from Plants (ICMP24058); Pauatahanui, from leaf necrosis on *Eucalyptus* sp., April 2018, *R. Thangavel*, PHEL T18_01389; Lower Hutt, from leaf necrosis on *Corymbia ficifolia*, September 2020, *K. Hofer*, PHEL T20_02185; and Auckland, from leaf spot on *Eucalyptus nitens*, December 2020, *R. Thangavel*, PHEL T20_03057.

Known hosts and distribution: AUSTRALIA, on *Eucalyptus* sp. (Summerell et al. 2006) and *E. globulus* (Adams et al. 2004); NEW ZEALAND, on *Eucalyptus* sp., *E. nitens*, *E. leucoxylon*, and *Corymbia ficifolia* (this study).

GenBank: OR807322, PP068838, PP068839, PP068840 (ITS), OR808084 (LSU), OR814105 (*act*), OR814109 (*rpb2*), OR814113 (*tef1*), OR814117 (*tub2*).

Notes: Multi-gene phylogeny using combined ITS, LSU, *rpb2* and *act* sequences demonstrated that our isolate and the type strain of *C. diatrypelloidea* (CMW8549) clustered into a well-supported clade (Fig. 32). There is limited sequence data available for the type strain of *C. diatrypelloidea,* but only a single nucleotide difference in the ITS region was found to our isolate. Additional DNA regions were sequenced in this study to provide additional reference sequence data.

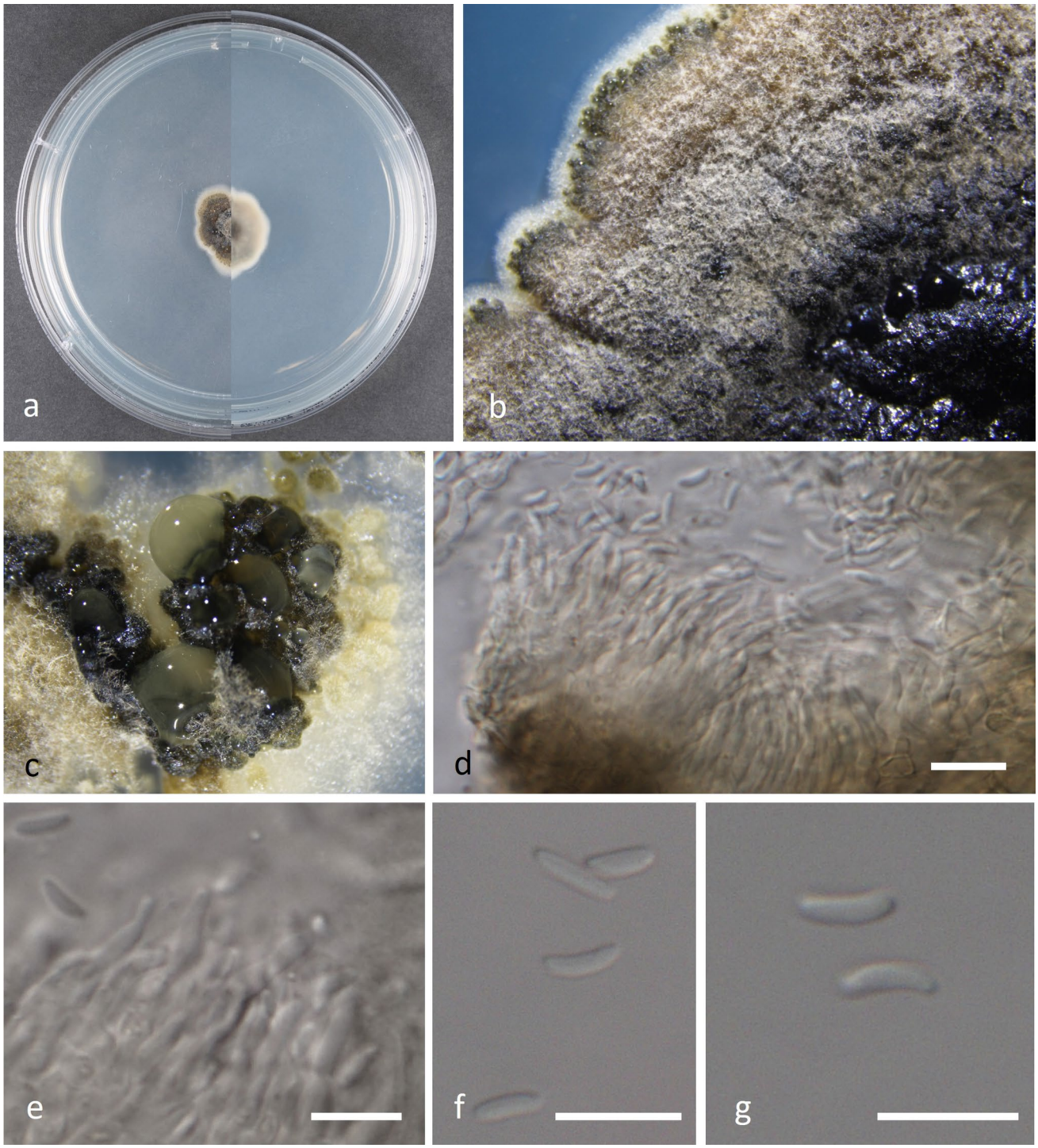


Fig. 33 ***Cytospora diatrypelloidea*** (ICMP24058). **a** Colony on PDA media after 7 days. **b** Close up of colony edge. **c** Conidiomata on colony surface with pale yellow cirrhi. **d, e** Conidiogenous cells. **f, g** Conidia. Scale bars = 10 µm

Since the first find of *C. diatrypelloidea* in New Zealand in 2016, the fungus has been associated with leaf necrosis on *Eucalyptus* sp., leaf necrosis on *Corymbia ficifolia* and leaf spot on *Eucalyptus nitens*. While Australian records of *C. diatrypelloidea* are from dead branches (Adams et al. 2004) and leaf litter (Summerell et al. 2006), the New Zealand detections are from fresh symptomatic leaf material indicating that *C. diatrypelloidea* could be plant pathogenic. However, further studies are needed to confirm pathogenicity of *C. diatrypelloidea*.

This is the first published record of *C. diatrypelloidea* form New Zealand and first report from a non-*Eucalyptus* host. *Corymbia ficifolia* belongs to Myrtaceae, suggesting that *C. diatrypelloidea* could be present in a wider range of hosts in Australia and New Zealand, where this plant family is wide-spread and species-rich.

Cytospora lhaluensis N. Jiang & B. Cao, **sp. nov.**

Fungal Names: FN 571958; *Facesoffungi*: FoF 17097; Figs. 32, 34

Etymology: refers to Lhalu Wetland National Nature Reserve, the locality of the type specimen.

Holotype: CAF800091.

Conidiomata Pycnidial, ostiolated, semi-immersed in the host bark, scattered, pulvinate, with multiple locules. **Conceptacle** absent. **Ectostromatic disc** brown, circular to ovoid, (120–)150–220(–320) µm diam., with one ostiole per disc. **Ostioles** dark, at the same level as the disc, (25–)40–70(–90) µm diam. **Locule** numerous, arranged circularly or elliptically with independent walls, 120–200 µm diam. **Peridium** comprising few layers of cells of textura angularis, brown to dark brown. **Conidiophores** hyaline, unbranched, thin walled, filamentous. **Conidiogenous cells** enteroblastic polyphialidic, 7–12.47–17.5 × 1.5–2.21–3 µm (n = 20). **Conidia** hyaline, allantoid, smooth, aseptate, thin-walled, 5.5–6.5–7.5 × 1.5–2.16–2.5 µm (n = 20). **Colonies** on PDA flat, spreading, with flocculent mycelium and entire edge, initially white, becoming brown after 10 days, reaching a 90 mm diameter after 25 days at 25 °C in the dark.

Material examined: CHINA, Xizang Autonomous Region, Lhasa City, Lhalu Wetland National Nature Reserve, on dead branches of *Prunus davidiana*, 28 Jul 2022, *Peng Jin*, *Yuanyuan Liu*, *Ning Jiang*, *Min Liu*, *JN22.149* (CAF800091, **holotype**; CFCC 58880, ex-type), *JN22.150* (living culture CFCC 58886) and *JN22.151* (living culture CFCC 58887).

GenBank: CFCC 58880: PP965509 (ITS), PP957867 (*act*), PP957874 (*rpb2*), PP957881 (*tef1*), PP957888 (*tub2*); CFCC 58886: PP965510 (ITS), PP957868 (*act*), PP957875 (*rpb2*), PP957882 (*tef1*), PP957889 (*tub2*); CFCC 58887: PP965511 (ITS), PP957869 (*act*), PP957876 (*rpb2*), PP957883 (*tef1*), PP957890 (*tub2*).

Notes: *Cytospora lhaluensis* from *Prunus davidiana* in the present study is phylogenetically close to *C. berberidis* from *Berberis dasystachya* (Fig. 32). These two species share similar conidial shape and size, but differs in the locule number in the conidiomata (Liu et al. 2015a).

Cytospora schulzeri Sacc. & P. Syd., **new geographical record from New Zealand.**

Mycobank: MB 551378; *Facesoffungi*: FoF 01022; Figs. 32, 35

Associated with branch canker and dieback of *Malus* species.

Sexual morph: not observed.

Asexual morph: **Conidiomata** pycnidial, forming within 10 days, irregularly scattered on the surface of the colonies in culture. **Conidiophores** hyaline, reduced to conidiogenous cells. **Conidiogenous cells** hyaline, phialidic, 9.8–11.5–12.8 × 1.0–1.4–2.0 µm (n = 20). **Conidia** hyaline, aseptate, allantoid to slightly curved, eguttulate, 3.0–5.2–6.9 × 1.0–1.5–2.0 µm (n = 20).

Culture characteristics: Colonies on PDA at 21 °C and incubated under black light reached 14–19 mm in diameter after three days, covering the 9 cm Petri dish in seven days; with even margin expansion, flat, without aerial mycelium, white to buff on the surface, white to light brown on reverse.

Material examined: NEW ZEALAND, Ettrick, Roxburgh, from branch canker of *Malus domestica*, August 2020, *M. Braithwaite*, *PDL3791*, PHEL T20_01779. Culture stored at the International Collection of Microorganisms from Plants (ICMP23778).

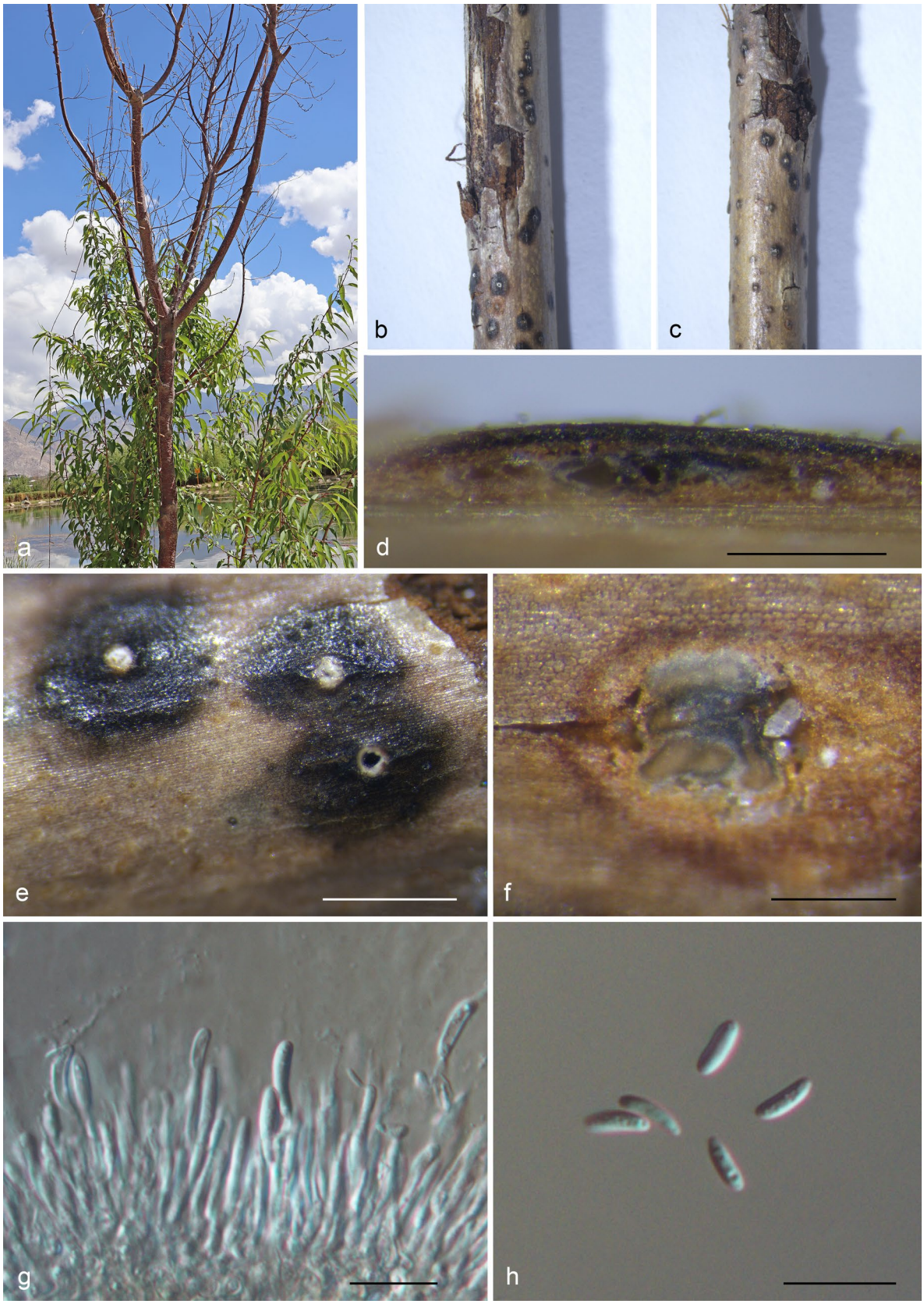
Known hosts and distribution: RUSSIA, on *Malus domestica* (Ariyawansa et al. 2015a); CHINA, on *Malus sieversii* (Ma et al. 2018); IRAN, on *Malus domestica* (Hanifeh et al. 2022); NEW ZEALAND, on *Malus domestica* (this study).

GenBank: ICMP23778: OR807323 (ITS), OR808085 (LSU), OR814106 (*act*), OR814110 (*rpb2*), OR814114 (*tef1*), OR814118 (*tub2*).

Notes: In phylogenetic analysis, ICMP23778 grouped in a strongly supported monophyletic clade with other *C. schulzeri* sequences. Pathogenicity testing with isolate ICMP23778 showed some pathogenicity towards *Malus domestica*. Approximately a third of infected detached apple shoots developed internal necrosis after inoculation with *C. schulzeri*, confirming earlier reports of this species being an opportunistic plant pathogen. Previously, *C. leucostoma* of *Cytospora* sp. have been reported from *Malus* sp. in New Zealand, dating back to as early as 1926 (Landcare Research 2023). No cultures have been stored for these finds and therefore their identity cannot be verified. This is the first record of *C. schulzeri* from New Zealand. Note that this organism was first identified as *Cytospora parasitica* but has been amended to *Cytospora schulzeri* given the taxonomic revisions of Lin et al. (2024).

Diaporthaceae Höhn. ex Wehm.

Notes: The family *Diaporthaceae* comprises many endophytic and phytopathogenic fungal species (Udayanga et al. 2011). Wehmeyer (1975) confined this family to *Diaporthe* and *Mazzantia*. Barr (1978) synonymised Diaporthaceae under Valsaceae. Castlebury et al. (2002) analysed LSU nrDNA sequence data of diaporthoid taxa and showed the distinct placement of Diaporthaceae in Diaporthales, forming a well-supported clade.


a
b
c
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e
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h

◂**Fig. 34** ***Cytospora lhaluensis*** from *Prunus davidiana* (CAF800091, **holotype**). **a** Symptoms of canker disease on the host. **b**, **c**, **e** Conidiomata formed on branches. **d** Longitudinal section through the conidioma. **f** Transverse section through the conidioma. **g** Conidiophores and conidiogenous cells. **h** Conidia. Scale bars: **d**–**f** = 200 µm, **g**, **h** = 10 µm

Diaporthe Nitschke.

Notes: The genus *Diaporthe* (syn. *Phomopsis*) was established by Nitschke (1870) with *D. eres* as the type species. Species in this genus have a cosmopolitan distribution and broad host range, occurring as endophytes, saprobes and plant pathogens (Santos and Phillips 2009; Santos et al. 2010; Udayanga et al. 2011, 2014; Gomes et al. 2013; Dissanayake et al. 2017; Yang et al. 2018; Hu et al. 2024). Previous studies have identified more than 2000 species names as belonging to *Diaporthe* and *Phomopsis* (Index Fungorum, http://www.indexfungorum.org/, accessed 25 April 2024).

Diaporthe amberina A.L. Jia & X.L. Fan, **sp. nov.**

Fungal names: FN 571934; *Facesoffungi*: FoF 17098; Fig. 36

Etymology: named after the color of colony amber.

Holotype: CFCC 70615.

Description: Culture sterile. On PDA, hyphae septate. Colonies covering the Petri dish after 21 d at 25 °C. Cultures on PDA initially white, irregular. Colonies thin with a uniform texture, lacking aerial mycelium, growing slowly up to 3 cm after 3 d and becoming amber after 7 d, entirely covering the 6 cm Petri dish after 21 d. Colonies flat with a uniform texture, colony margin irregular. Conidiomata not observed on medium surface after 30 d.

Materials examined: CHINA, Guangxi Zhuang Autonomous Region, Baise City, isolated from fruits of *Mangifera indica*, Aug. 2022, living culture CFCC 70615 (**holotype**), living culture CFCC 70616.

GenBank: CFCC 70615: PP741456 (ITS), PP741960 (*cal*), PP741965 (*his3*), PP741970 (*tef1*), PP741975 (*tub2*); CFCC 70616: PP741457 (ITS), PP741961 (*cal*), PP741966 (*his3*), PP741971 (*tef1*), PP741976 (*tub2*); Supplementary data, Online Resource 2.

Notes: *Diaporthe amberina* was isolated from fruits of *Mangifera indica* with symptoms in China. Phylogenetically (Supplementary data, Online Resource 1), *Diaporthe amberina* is close to *D. acuta* but it can be distinguished from *D. acuta* by the difference of sequences: 28/531 in ITS, 8/456 in *cal*, 11/440 in *his3*, 20/253 in *tef1* and 18/387 in *tub2* (Guo et al. 2020). The isolates CFCC 70615 and 70,616 form a distinct clade with high support value (ML/BI = 100/1). Therefore, we introduce it here as a new species.

Diaporthe mangiferae A.L. Jia & X.L. Fan, **sp. nov.**

Fungal names: FN 571935; *Facesoffungi*: FoF 17099; Fig. 37

Etymology: named after the host genus on which it was collected, *Mangifera indica*.

Holotype: CFCC 70614.

Description: Culture sterile. On PDA, hyphae septate. Colonies covering the Petri dish after 7 d at 25 °C. Cultures on PDA initially white, growing fast up to cover the 5.5 cm Petri dish after 3 d. Colonies flat with a uniform texture, lacking aerial mycelium, entirely covering the 6 cm Petri dish after 7 d, becoming buff after 14 d. Colony margin regular. Conidiomata not observed on medium surface after 30 d.

Materials examined: CHINA, Guangxi Zhuang Autonomous Region, Baise City, isolated from fruits of *Mangifera indica*, Aug. 2022, living culture CFCC 70614 (**holotype**), living cultures CFCC 70617 and CFCC 70618.

GenBank: CFCC 70614: PP741458 (ITS), PP741962 (*cal*), PP741967 (*his3*), PP741972 (*tef1*), PP741977 (*tub2*); CFCC 70617: PP741459 (ITS), PP741963 (*cal*), PP741968 (*his3*), PP741973 (*tef1*), PP741978 (*tub2*); CFCC 70618: PP741460 (ITS), PP741964 (*cal*), PP741969 (*his3*), PP741974 (*tef1*), PP741979 (*tub2*); Supplementary data, Online Resource 2.

Notes: *Diaporthe mangiferae* was isolated from fruits of *Mangiferam indica* with symptoms in China. The three isolates are phylogenetically separated from all other available isolates included in this study (Supplementary data, Online Resource 1). The clear multi-gene phylogram place it in a distinct clade with high support (ML/BI = 100/1). Therefore, the current three isolates (CFCC 70614, 70,617 and 70,618) are identified as a new species, *D. mangiferae.*

Glomerellales Chadef. ex Réblová, W. Gams & Seifert.

Notes: Glomerellales, an order Latin name, was validly published in 2011, to accommodate three families: Australiascaceae, Glomerellaceae and Reticulascaceae (Réblová et al. 2011). Recently, it has expanded to encompass five families and one incertae sedis genus (Wijayawardene et al. 2022). Glomerellales forms a monophyletic clade basal to Hypocreomycetidae and is estimated to have originated around 274 million years ago (Bao et al. 2023). Species within this order have adapted to various ecological niches and are distributed in both terrestrial and aquatic environments (Réblová et al. 2011).

Glomerellaceae Locq. ex Seifert & W. Gams.

Notes: The family Glomerellaceae accommodates the teleomorph *Glomerella* and its anamorph *Colletotrichum*. Zhang et al (2006) excluded Glomerellaceae from the Phyllachorales and placed in Hypocreomycetidae incertae sedis. While Réblová et al. (2011) included Glomerellaceae in newly established Glomerellales.

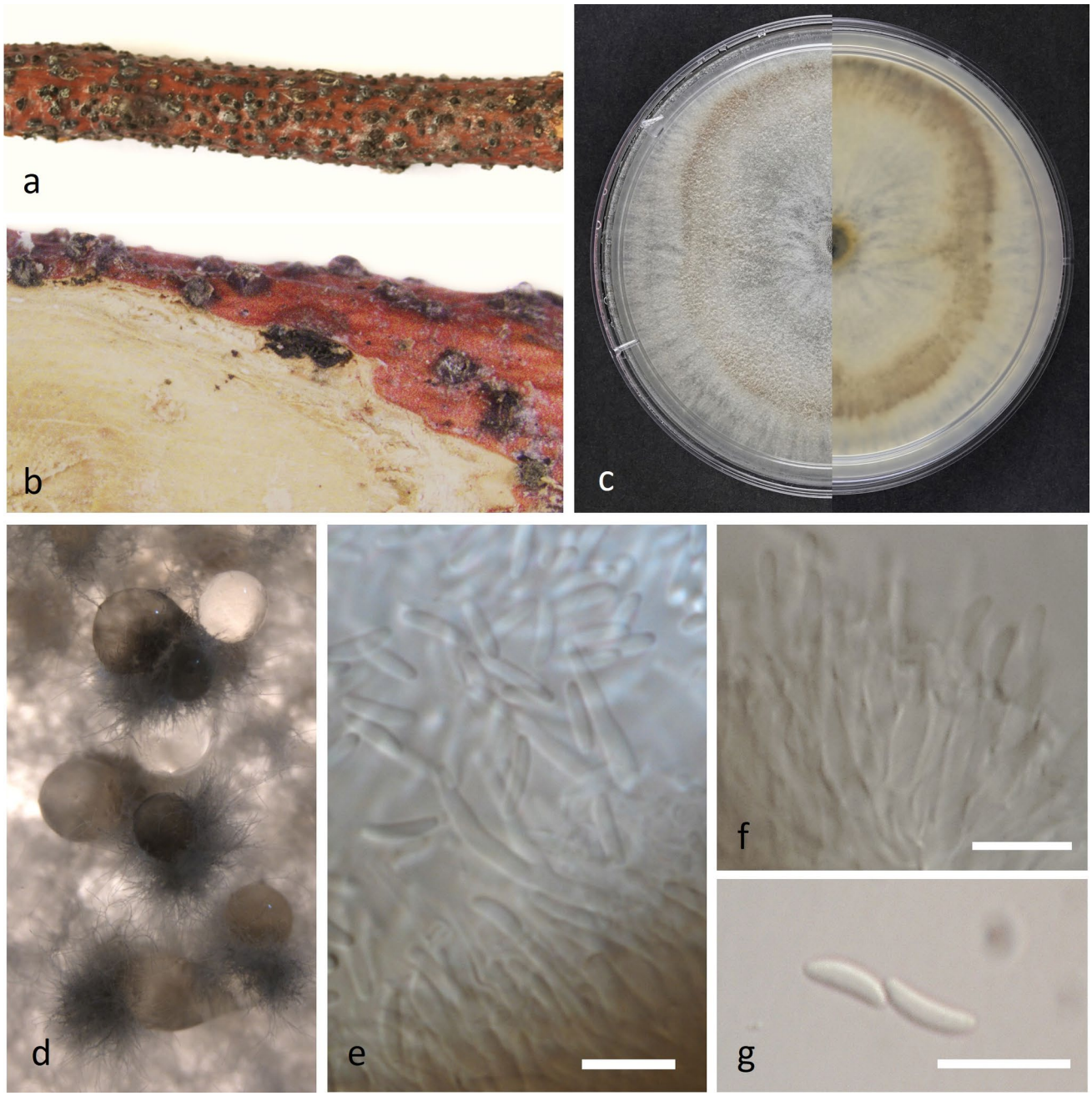


Fig. 35 ***Cytospora schulzeri*** (ICMP23778). **a** Symptoms found on host. **b** across section of a conidiomata. **c** Colony on PDA media after 7 days. **d** Conidiomata on a colony in pure culture. **e, f** Conidiogenous cells. **g** Conidia. Scale bars = 10 µm

Colletotrichum Corda.

Notes: The genus *Colletotrichum* was described by Corda (1831) to accommodate the species with setae in acervulus. The species number of this genus varied from 11 to around 750 (von Arx 1957). Cannon et al (2012) discussed the classification status and future directions of *Colletotrichum* and proposed 9 species complex and several independent units for different *Colletotrichum* groups. The number of *Colletotrichum* was updated to 16 species complex and 15 independent species (Talhinhas and Baroncelli 2021; Liu et al. 2022). Many species of *Colletotrichum* are plant pathogens (Li et al. 2023; Sun et al. 2023; Yao et al. 2023; Ding et al. 2024; Lu et al. 2024; Wang et al. 2024a).

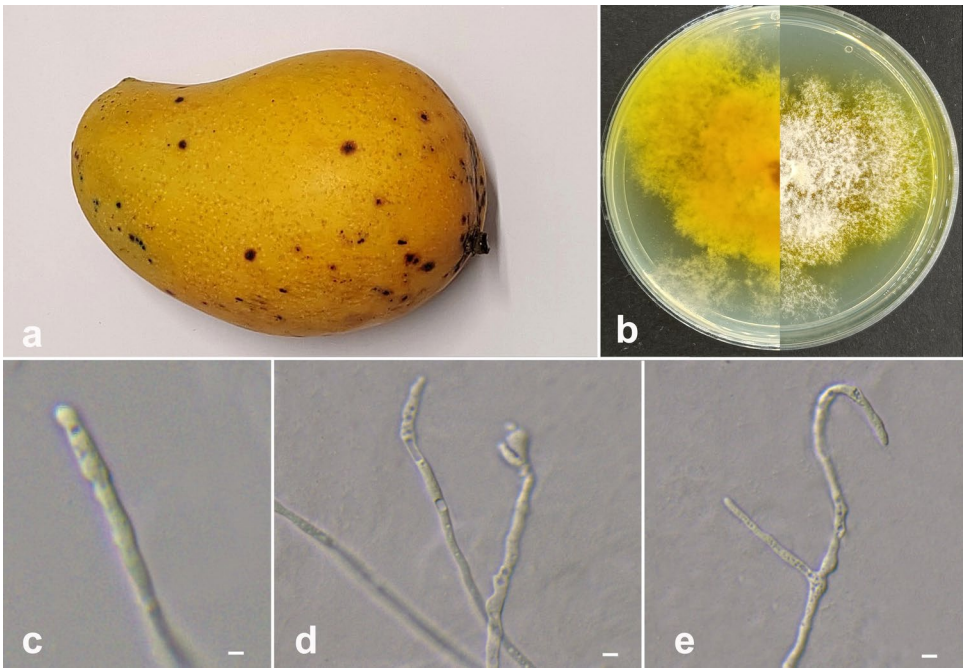


Fig. 36 *Diaporthe amberina* (CFCC 70615, **holotype**). **b** Culture on PDA. **c–e** Hyphae. Scale bars = 10 µm

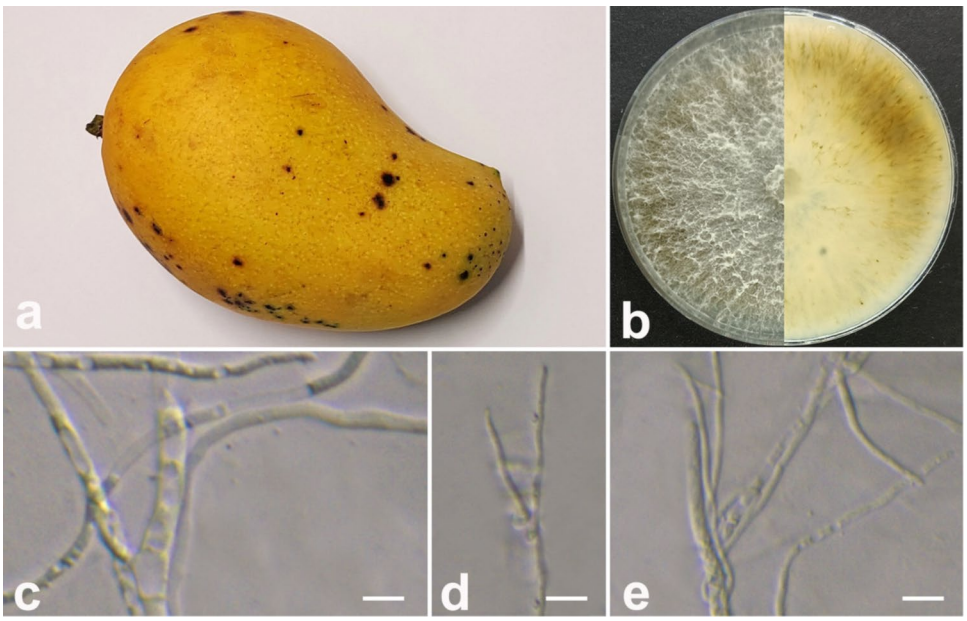


Fig. 37 *Diaporthe mangiferae* (CFCC 70614, **holotype**). **b** Culture on PDA. **c–d** Hyphae. Scale bars = 10 µm

Colletotrichum duohuaense H.L. Hu, Y.P. Hu, H. Yu & X.Z. Zhou, **sp. nov.**

Fungal Names: FN 571818; *Facesoffungi*: FoF 17241; Figs. 38, 39

Etymology: refers to the Chinese specific epithet of the host *Polygonatum cyrtonema* Hua, means multiflowers.

Holotype: CGMCC 3.24303.

Asexual morph: the leaves first with reddish-brown anthracnose on *Polygonatum cyrtonema*, later the spots expanded irregularly, the center part became yellow gray, the out part kept reddish-brown. The Koch's postulates confirmed its pathogenicity. **Acervulus** light brown. **Conidiophores** hyaline, straight or lightly curved, fence-like formed along the acervulus. **Conidiogenous cells** hyaline, ampulliform to doliiform, blastic. **Conidia** typically one celled, hyaline, long ellipsoid, with several droplets, 13.8–17.2 × 4.9–6.2 µm, $\bar{x}$ = 15.3 ± 0.9 × 5.5 ± 0.3 µm, and n = 50. Sexual morph: not observed.

Cultural characteristics: Colonies on PDA reaching 7.3 cm at 26℃ after 7 d in dark. Colony gray-white to white, with plenty of aerial hyphae, velvet texture. Orange conidial mass formed after cultured on OA for 15 d at 26℃ in dark.

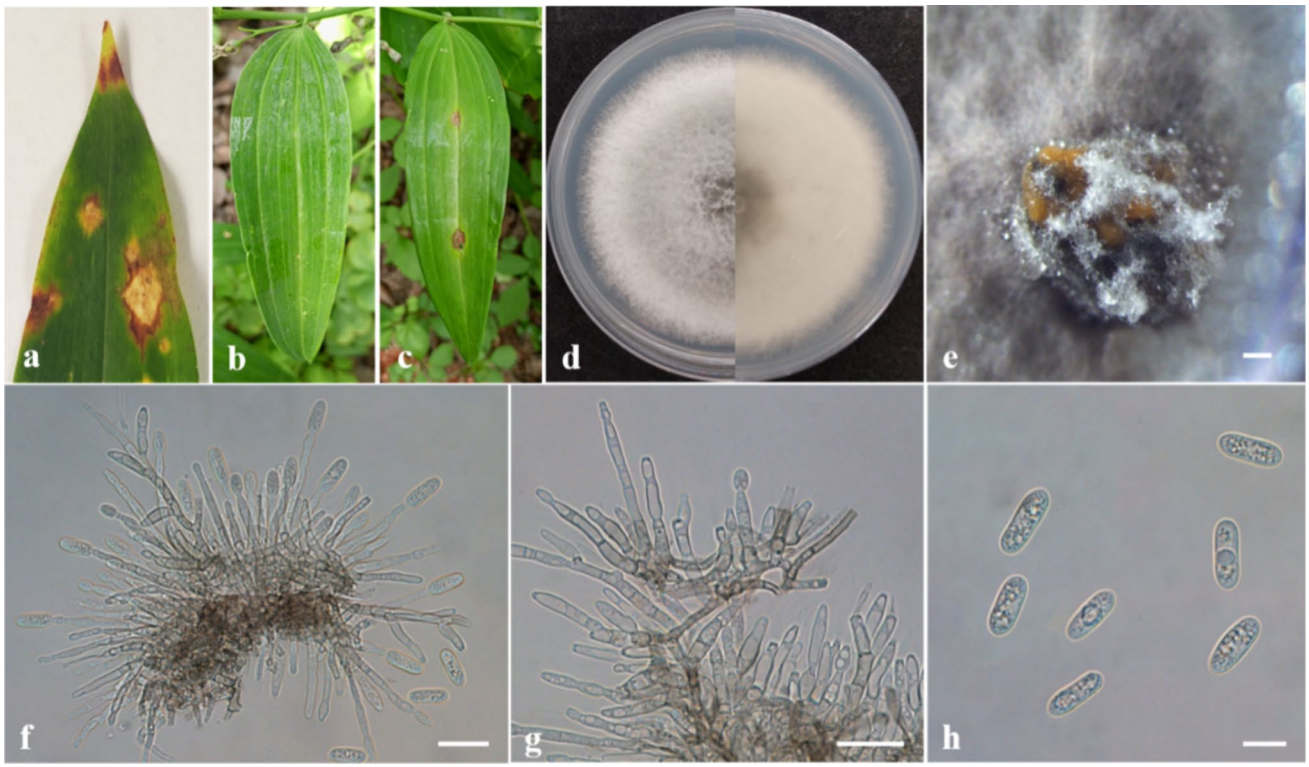


Fig. 38 ***Colletotrichum duohuaense*** (CGMCC 3.24303, **holotype**). **a** Infected leave. **b** CK for Koch's postulates. **c** Leave inoculated with *C. duohuaense*. **d** Colony cultured on PDA for 7d. **e** Conidial mass (cultured on OA for 15d). **f** Acervulus and conidiophores. **g** Conidiogenous cells. **h** Conidia. Scale bars: **e** = 100 μm, **f**–**g** = 20 μm, **h** = 10 μm

Material examined: CHINA, Fujian Province, Jian'ou City, Yushan Town, Dingdun Village, 27°01′29″N 118°33′36″E, 720 m asl, 22 Jul. 2021, *Hong-Li Hu*, *Yan-Ping Hu*, *Hao Yu* and *Xian-Zhi Zhou*, D1_DY1_C1 (CGMCC 3.24303, **holotype**), D1-DY3-A, D1-DY5-A, D1-DY6-A, D1-DY7-C-2.

GenBank: CGMCC 3.24303: PP095136 (ITS), PP092234 (*gapdh*), PP092229 (*chs-1*), PP092219 (*act*), PP092224 (*cal*); D1-DY3-A: PP095137 (ITS), PP092235 (*gapdh*), PP092230 (*chs-1*), PP092220 (*act*), PP092225 (*cal*); D1-DY5-A: PP095138 (ITS), PP092238 (*gapdh*), PP092233 (*chs-1*), PP092221 (*act*), PP092226 (*cal*); D1-DY6-A: PP095139 (ITS), PP092236 (*gapdh*), PP092231 (*chs-1*), PP092222 (*act*), PP092227 (*cal*); D1-DY7-C-2: P095140 (ITS), PP092237 (*gapdh*), PP092232 (*chs-1*), PP092223 (*act*), PP092228 (*cal*).

Notes: *Colletotrichum duohuaense* was isolated from diseased leaves of *Polygonatum cyrtonema*. There have been five *Colletotrichum* species reported on *P. cyrtonema*, and two are in *Colletotrichum gloeosporioides* species complex, i.e., *C. fructicola* and *C. gloeosporioides* (Dan et al. 2023a, b). However, they didn't cluster with *C. duohuaense* in the phylogenetic tree. *Colletotrichum duohuaense*, *C. henanense* and *C. yulongense* were distributed in the same clade with high support (BS = 100%, PP = 1.00). But the spores of *C. duohuaense* is obviously larger than *C. henanense* (8–17 × 3–5.5 μm, av ± SD = 12.5 ± 1.8 × 4.5 ± 0.6 μm) and *C. yulongense* (11–13 × 4–5 μm, mean ± SD = 12.0 ± 1 × 4 .5 ± 0.5 μm) (Liu et al. 2015b; Wang et al. 2019). Thus, *C. duohuaense* is reported as a new species.

Plectosphaerellaceae W. Gams, Summerb. & Zare.

Note: The family Plectosphaerellaceae was established by Zare et al. (2007), with *Plectosphaerella* as the type genus, and includes 23 other accepted genera (Tibpromma et al. 2018; Wijayawardene 2020). Members of Plectosphaerellaceae are fungicolous, insecticolous, plant pathogens, and saprobic (Phukhamsakda et al. 2020). Morphologically, the ascomata are subglobose to globose or pyriform, with a paler, elongated neck. The asci are 8-spored, cylindrical, clavate, or saccate. Ascospores are ellipsoidal to ovoid, 1- or 2-celled, hyaline or pigmented. Conidiophores can be simple or branched, with mono- or polyphialidic conidiogenous cells. Conidia vary in shape, are 1- or 2-celled, hyaline or pigmented, and are arranged in slimy heads or chains (Giraldo and Crous 2019).

Musicillium Zare & W. Gams.

Note: Musicillium was separated from *Verticillium* Nees., based on molecular data. Morphologically, *Musicillium* is similar to species in the Plectosphaerellaceae, which are

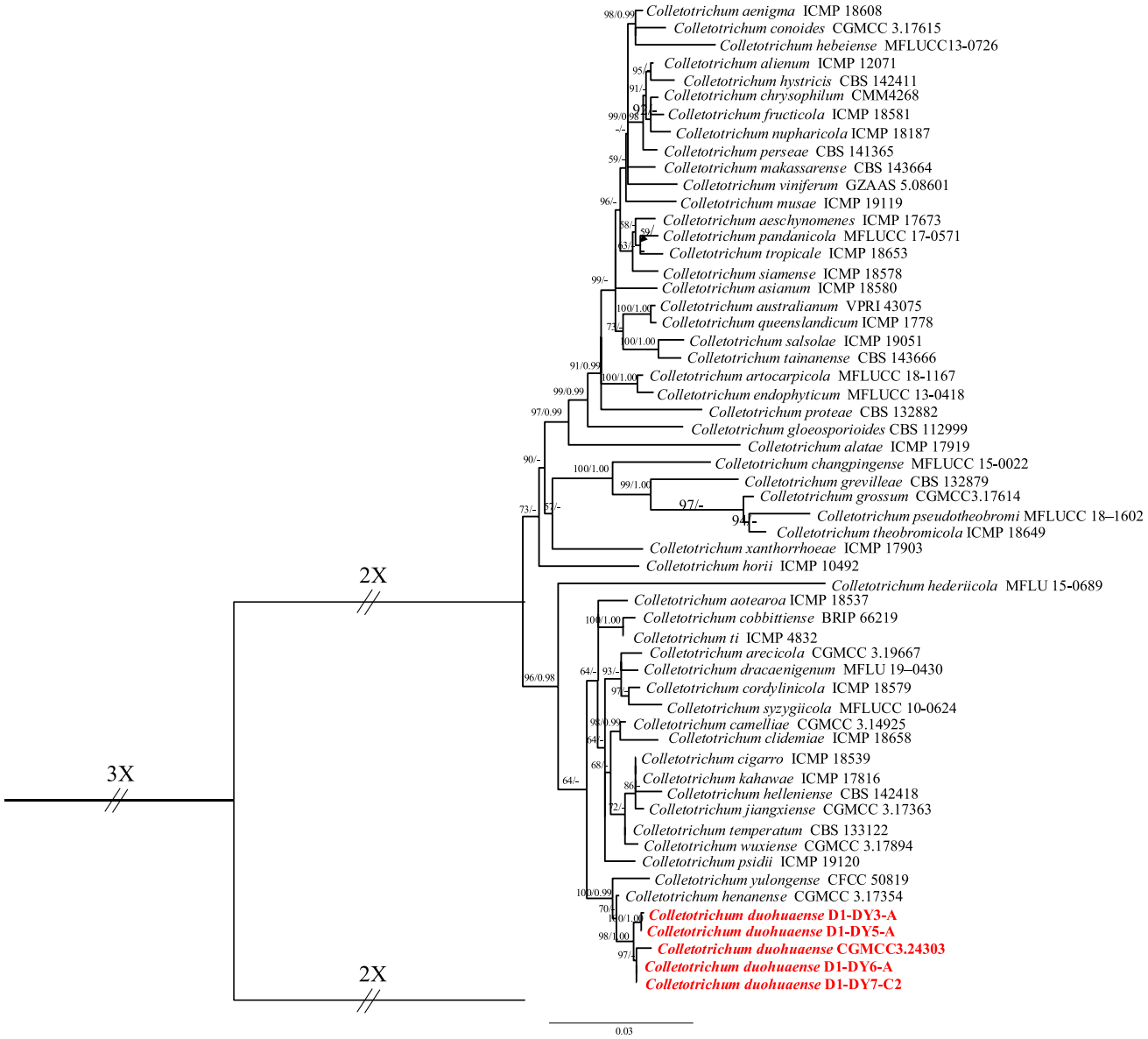


Fig. 39 Maximum Likelihood phylogram of *Colletotrichum gloeosporioides* species complex based on a combined matrix of ITS, *gadpd*, *chs-1*, *act* and *cal* genes [*Colletotrichum boninense* (CBS 123755) is the outgroup]. Numbers in front of slash stand for the Maximum Likelihood bootstrap values, and numbers behind the slash stand for the Bayesian posterior probabilities. "-" indicates that the given branches were supported less than 50% by Maximum Likelihood bootstrap or 0.93 by Bayesian analyses. The new species are in red

typified with long, brown conidiophores, bearing whorls, aculeate phialides, produced moniliform hyphae (Zare et al. 2007). The type species, *M. theobromae* (= *Verticillium theobromae*) is known as the causal agent of cigar-end rot, and has caused serious disease in bananas (*Musa* spp.) in Iran, Finland, Jamaica, Morocco and the Netherlands (Zare et al. 2007; Youssef et al. 2020). Tibpromma et al. (2018) introduced the second species, *M. pandanicola* from *Pandanus* in Thailand. Later, *M. elettariae* and *M. tropicale* were introduced simultaneously. *Musicillium elettariae* has a wide distribution in Iran, Rwanda and Thailand, whereas, *M. tropicale* seems to have a mostly tropical distribution (Lindau and Crous 2019).

Musicillium elettariae Giraldo López & Crous, **new geographical record from China and a new host record.**

MycoBank: MB 828065; *Facesoffungi*: FoF 15207; Figs. 40, 41

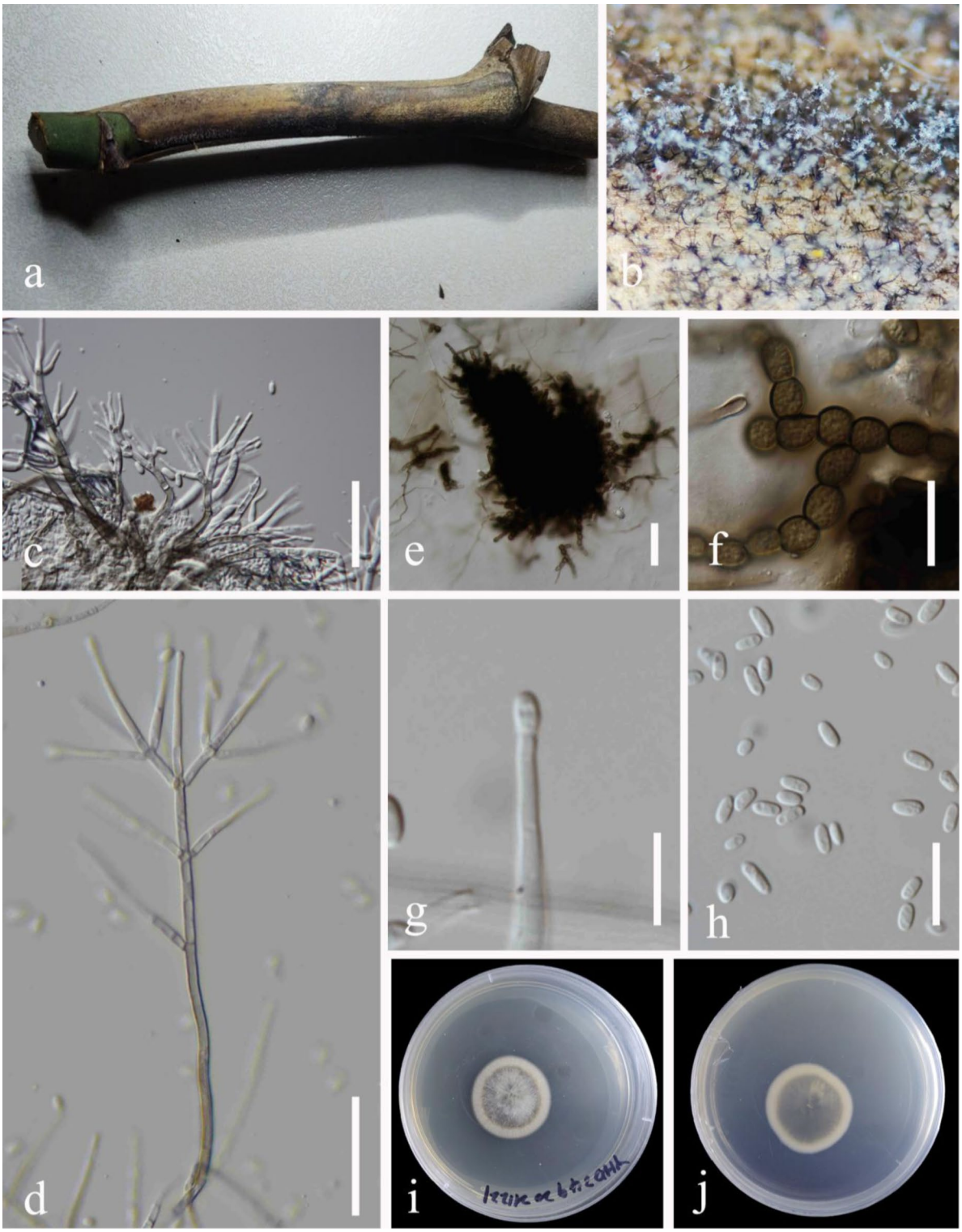


Fig. 40 ***Musicillium elettariae*** (KUNCC23-14,819). **a** Host. **b** Appearance of colonies on host. **c** Conidiophores from host. **d** Conidiophores from PDA. **e, f** Moniliform hyphae. **g** Phialides. **h** Conidia. **i, j** Colony on PDA. Scale bars: **c** = 50 μm, **d** = 20 μm, **e** = 50 μm, **f** = 20 μm, **g** = 5 μm, **h** = 10 μm

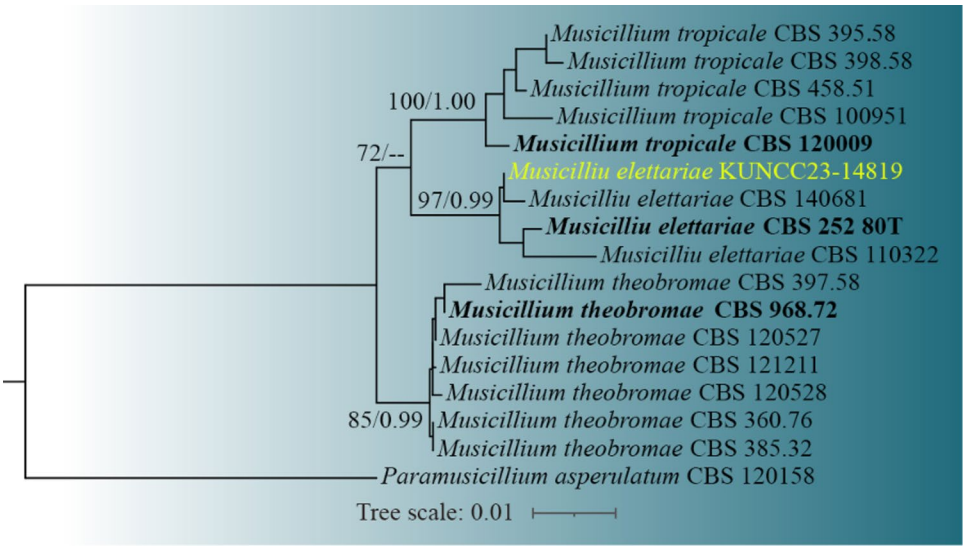


Fig. 41 Phylogram generated from the Maximum Likelihood analysis based on the combined LSU, ITS, *tef1* and *tub2* sequence data of the genus *Musicillium*. The tree topology of the Maximum Likelihood analysis is similar to the Bayesian analysis. The best RAxML tree is presented. Bootstrap support values for ML greater than 50% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Paramusicillium asperulatum* (CBS 120158). Ex-type strains are bold. The newly generated sequences are indicated in yellow

On twig of *Smilax elegantissima*. **Colonies** superficial, numerous, black at the base, upper white. **Conidiophores** 115–446 µm long, arising from immersed hyphae, smooth, septate, erect, simple or verticillate towards the apex, pale to dark brown, hyaline at the tip, bearing 2–3 whorls of 2–5 phialides, lateral branches sometimes. **Phialides** 17–34 µm long × 1–2.7 µm diam ($\bar{x}$ = 23 × 2.1 µm, L/W = 10.9, n = 20), hyaline, terminal, lateral. **Conidiogenous cells** enteroblastic, monophialidic, with minute collarette and periclinal thickening visible. **Conidia** 3.0–7.7 × 1.4–2.6 ($\bar{x}$ = 5.2 × 2.1 µm, L/W = 2.4, n = 30), cylindrical, hyaline, aseptate, round ends. **Moniliform hyphae** 6–10 µm, globose to subglobose, verruculose, thick-walled, brown, commonly aggregating into microsclerotium-like structures. **Culture characteristics**: mycelium reaching 27 mm diam within 14 days on PDA, slightly flat, raised at the center, woolly, margin entire, mouse gray at the center, white margin, reverse dark mouse gray, aerial mycelium white.

Material examined: CHINA, Yunnan Province, Kunming City, Panlong District, 25°8′15.65″ N 102°47′13.70″ E, altitude 1918 m, on twig of *Smilax elegantissima*, 15 December 2021, *Hongde Yang*, KUNCC23-14,819.

GenBank: KUNCC23-14,819: OR922577 (ITS), OR922583 (SSU), OR922581 (LSU), PQ453869 (*tub2*), PQ453871 (*tef1*).

Known hosts: *Carex pendula*, *Elettaria cardomomum*, *Musa acuminata* (Giraldo and Crous 2019), *Smilax elegantissima* (this study).

Notes: Our collection was morphologically and phylogenetically fitted with the holotype of *M. elettariae* (CBS 252.80). Its sexual morph was reported recently, as saprobic on dead leaves of *Musa* sp, and was recognized by superficial, perithecial ascomata with setae, ascospores cylindrical with acute ends with one septum (Samarakoon et al. 2024). *Musicillium elettariae* has been found distribution in Iran, Rwanda, Thailand (Giraldo and Crous 2019). In this study, *M. elettariae* was recorded for the first time from China on *Smilax elegantissima*.

Hypocreales Lindau.

Notes: Hypocreales was established by Lindau (1897) to accommodate the single family Hypocreaceae. Following the updated accounts of Hypocreales in Bao et al. (2023), the order comprises eighteen families based on morphological, phylogenetic and evolutionary evidence. Numerous newly taxonomic studies of this order were reported over the past decade (Quandt et al. 2014; Maharachchikumbura et al. 2016; Hongsanan et al. 2017; Crous et al. 2018; Hyde et al. 2020b; Ou et al. 2020; Wijayawardene et al. 2022; Bao et al. 2023; Perera et al. 2023; Xiao et al. 2023a, b; Zhang et al. 2023a, b, c). Some families, such as Clavicipitaceae, Cordycipitaceae, and Ophiocordycipitaceae, members of these families have significant medicinal, economic and ecological value (Kepler et al. 2012, 2013, 2017; Quandt et al. 2014).

Nectriaceae Tul. & C. Tul.

Notes: Nectriaceae is a family of fungi within the order Hypocreales, described by the brothers Charles and Louis René Tulasne in 1865. This highly diverse group of fungi is found throughout the world, with great diversity in warm and tropical regions (Rossman et al. 1999; Schroers et al. 2011; Lombard et al. 2015). Then, 70 genera and around 1,336 species were listed in 2020 (Wijayawardene et al. 2020).

Fusarium Link.

Notes: *Fusarium* is a large genus with hundreds of species (Crous et al. 2021a, b). The sexual forms of some species are known and belong to several genera in the class

Ascomycetes and order Hypocreales, such as *Gibberella*, *Nectria*, or *Neocosmopora*. However, the sexual state of many species remains unknown (Gordon 2017; Crous et al. 2021a, b). This genus has a worldwide distribution and is found in tropical, temperate, and even desert regions (Dignani and Anaissie 2004). Several species of this genus are able of causing plant, animal, and even human diseases (O'Donnell et al. 2000; Stępień et al. 2019; Zhao et al. 2023a; Yang et al. 2024a). Phytopathogenic *Fusarium* species attack various plants including cereals that are important for human and animal nutrition, in particular by infecting specific parts: grains, seedlings, crowns, roots, or stems, causing numerous diseases (commonly known as fusariosis). The term fusariosis is less specific as it refers to any syndrome caused by any species of *Fusarium* on a crop. These infections cause huge economic losses due to a significant reduction in commercial yield and a decrease in product quality (Nganje et al. 2004; Wang et al. 2023a; Qin et al. 2024; Wei et al. 2024).

Fusarium tuberculatum Tiendrebeogo, Decock, Somda & Legrève, **sp. nov.**

MycoBank: MB 856637; *Facesoffungi*: FoF 17100; Figs. 42, 43

Etymology: refers to chlamydospores ornamented with tubercules.

Holotype: MUCL58421.

Culture characteristics: On PDA in the dark at 27 °C, average growth of 7.2 mm/day, for 7 days of incubation; aerial mycelium cottony and often grazing, the colony surface grayish brown to dark Ruby with whitish features above, cottony some time dotted with floccose aerial mycelium; reverse violet brown to ruby, lacking diffusible pigment; odor absent. On synthetic nutrient agar (SNA), aerial mycelium absents, colony translucid, with abundant sporulation on the medium surface. On CLA, aerial mycelium sparse with bright orange sporodochia forming on the carnation leaves.

Microscopic characteristics: On carnations leaf agar (CLA). **Aerial mycelia** made of unbranched or sparingly branched hyphae; **conidiophores** bearing intercalary or terminal phialides, monophialidic, subulate to subcylindrical, smooth- and thin-walled; **microconidia**, with 0–2 septate (uni or bicellular): 0-septate 4.7–7 × 1.5–2.3 (av. 5.3 × 1.7 µm); 1-septate 6–8 × 1.6–2.3 (av. 7.2 × 2.2 µm); 2-septate, 8–10 × 2–3.2 (av. 8.8 × 2.8 µm); **macroconidia** conidia born on conidiogenous cells solitary or densely gathered into sporodochia; **sporodochia** on carnation leaves globulose, with conidia accumulating into a pale orange mucilaginous drop; **sporodochial conidiophores** verticillately branched and densely packed, consisting of a smooth- and thin-walled stipe, bearing apical whorls of monophialides, subulate to subcylindrical; **sporodochial macroconidia** smooth- and thin-walled, hyaline, falcate, curved dorsiventrally with almost parallel sides tapering slightly towards both ends, a blunt to foot-like basal cell and a blunt to papillate, curved apical cell, 3–5 septate: 3-septate 32–38 × 4–4.6 µm (av. 35.8 × 4.2 µm); 4-septate 37–40 × 4–5.5 µm (av. 38 × 4.5 µm); 5-septate 41.3–43 × 4–5.6 µm (av. 41.5 × 4.5 µm); **chlamydospores** terminal or intercalary, single or bicellular, averaging

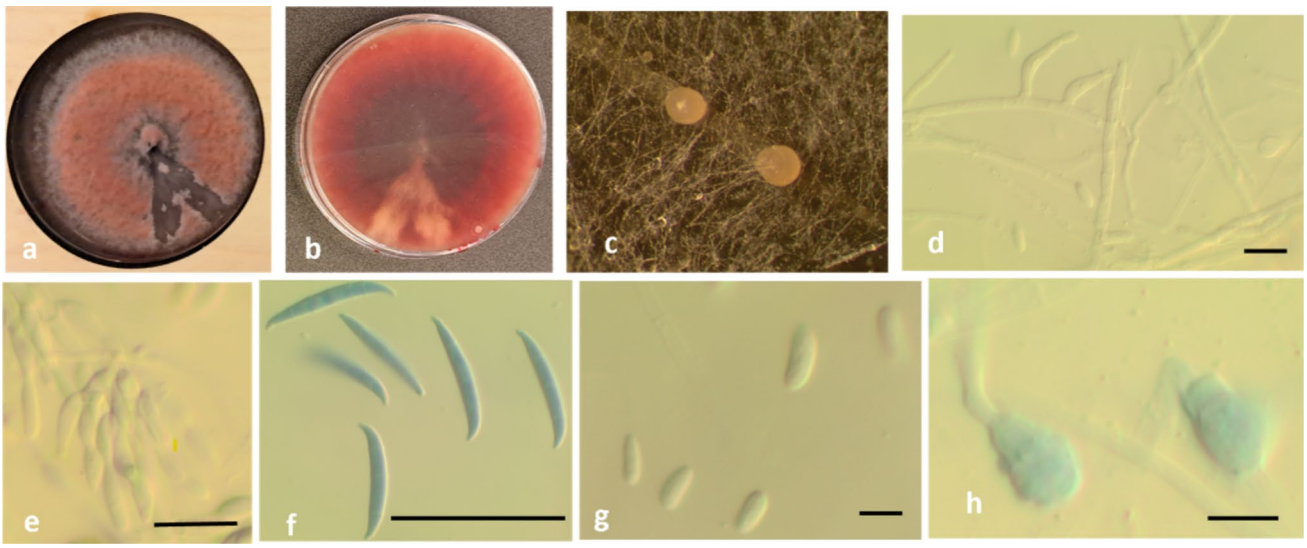


Fig. 42 ***Fusarium tuberculatum. a, b*** Colony on PDA. **c** Sporodochia with a drop of conidia. **d** Microphialides. **e** Conidiogenous cellular with monophialide. **f** Macroconidia. **g** Microconidia. **h** Tuberculate chlamydospore. Scale bars: **d** = 7 µm, **e** = 12 µm, **f** = 40 µm, **g** = 7 µm, **h** = 10 µm. Credit: Tiendrebeogo and Decock

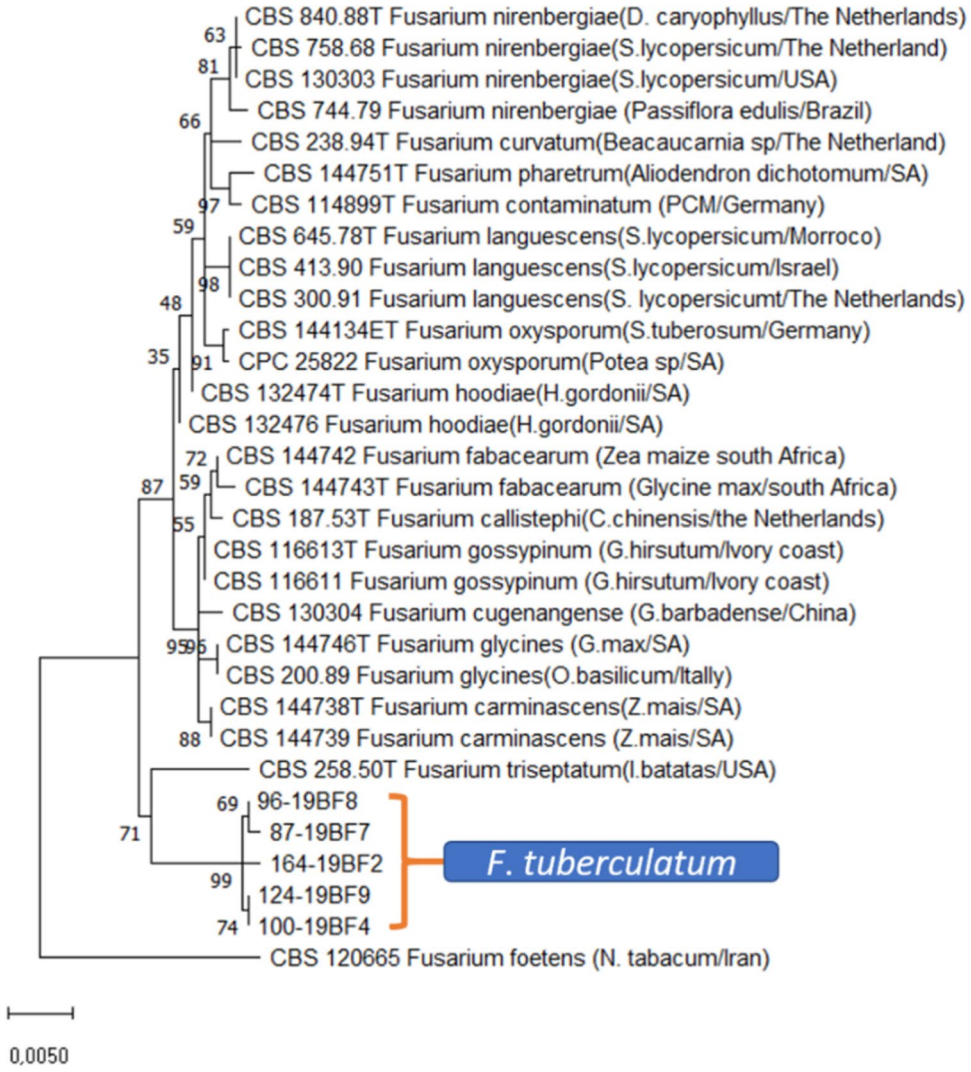


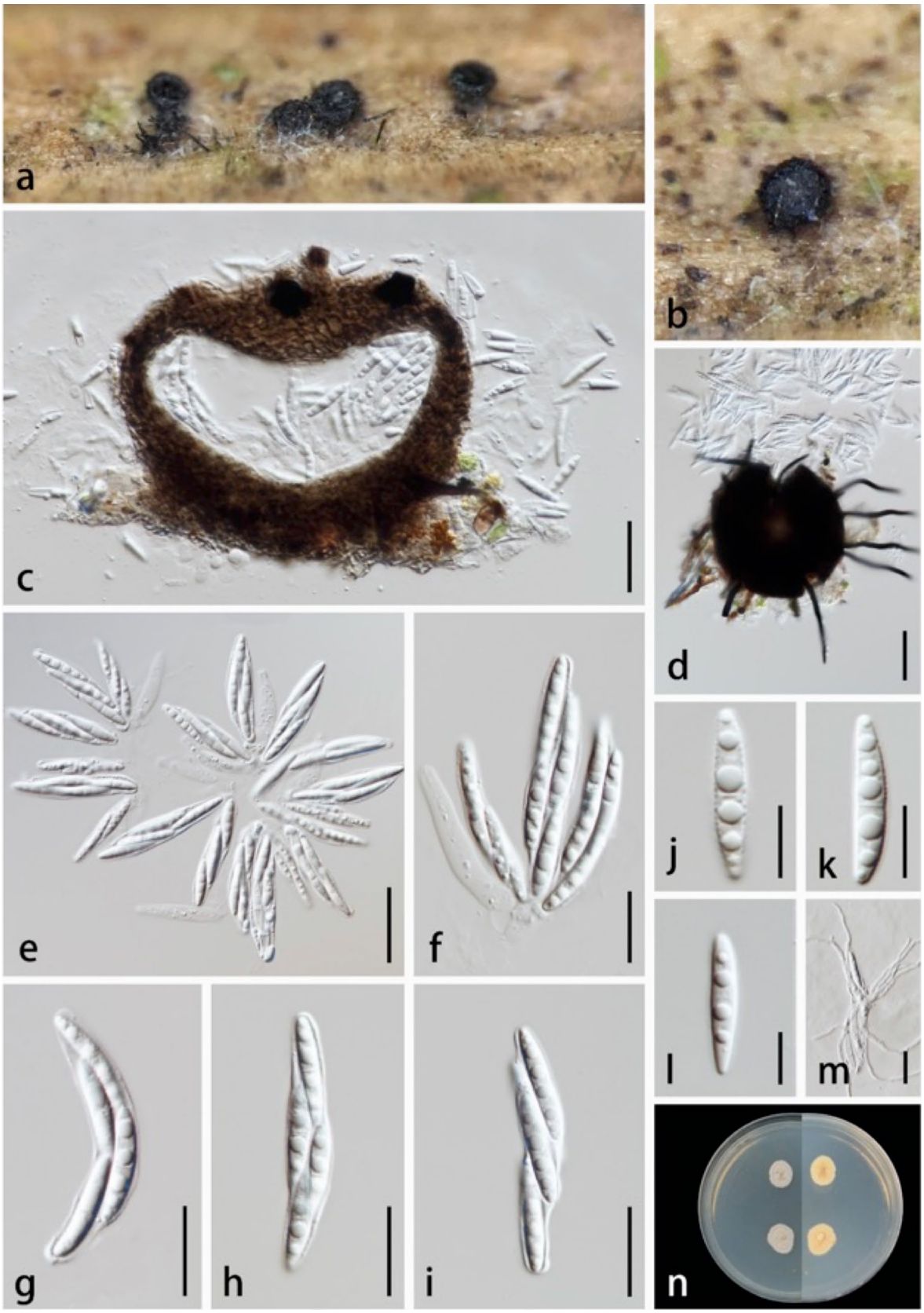
Fig. 43 Phylogenetic tree constructed by the Maximum Likelihood method with a bootstrap of 1000 replicates, representing the evolution of the relationships between a combined dataset of four-locus sequences, namely, *tef1*, *cmdA*, *rpb2*, and IGS from 31 strains isolated from tomatoes with 26 sequences recovered from Lombard et al. (2019)

7.3 × 6.3 µm, thick-walled, the wall tuberculate, with blunt tubercles (Fig. 42).

Material examined: BURKINA FASO, Boucle du Mouhoun region, 11°51′21"N 4°17′55"W, isolated from the root of *Solanum lycopersicum* (Solanaceae) with wilt symptoms, March 2019, *A. Tiendrebeogo*, *100/19BF4* (MUCL58421, **holotype**); Mouhoun region, 13°7′27"N 3°25′31"W, isolated from *Solanum lycopersicum* (Solanaceae) root with wilt symptoms, Avril 2019, *124/19BF4* (MUCL58422); South-West region, 10°53′18"N 3°16′36"W, root of *Solanum lycopersicum* (Solanaceae) with wilt symptoms, March 2019, *096/19BF8* (MUCL58423); Cascades region, 10°41′20"N 4°45′31"W, isolated from *Solanum lycopersicum* (Solanaceae) root with wilt symptoms, March 2019, *087/19BF7* (MUCL58424); Central Plateau region, 12°30′27"N 1°22′14"W, isolated from *Solanum lycopersicum* (Solanaceae) root with wilt symptoms, December 2019, *164/19BF2* (MUCL58425).

GenBank: MUCL58421: OP272543 (*tef1*), OQ221746 (IGS), PP938436 (*cmdA*), PQ036167 (*rpb2*).

Notes: *Fusarium tuberculatum* is phylogenetically closely related to *F. triseptatum* L. Lombard & Crous, described from the USA, and which is known to infect *Ipomoea batatas* (Lombard et al. 2019). It is also known from Ivory Coast. *Fusarium tuberculatum* differs in having rough-walled, tuberculate chlamydospores (Fig. 42) and abundance of macroconidia, curved, 3–5-septate, with less production of microconidia. Based on a Megablast search of NCBIs GenBank nucleotide database, the closest hits using the *tef1* sequence (–700 bp long) corresponds to *Fusarium oxysporum* strain SEMAF0043, GenBank MN539104 (identities = 691/692, 99.72%, one gap). This strain has been isolated in Mali, a country neighboring Burkina Faso, from an unidentified host. Comparison of the sequences (*tef1*) of the 4 other strains of *F. tuberculatum* also showed a high similarity with SEMAF0043,


a
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◂**Fig. 44** *Niesslia wurfbainiae* (MHZU 24–0032, **holotype**). **a, b** Appearance of ascostromata on host surface. **c** Section through ascoma. **d** Ascoma with spines. **e–i** Asci. **j–l** Ascospores. **m** Germinated ascospore. **n** Colony on PDA (front and below). Scale bars: **c–e** = 100 µm, **f, g–i** = 50 µm, **j–l** = 10 µm, **m** = 20 µm

GenBank MN539104, with an identity of 99.86 to 100%. Phylogenetic analysis based on the four loci (*tef1*, *cmdA*, *rpb2*, and IGS) was carried out in order to ensure the correct identification of these strains. The phylogenetic tree obtained highlighted a distinct clade (Fig. 43).

Niessliaceae Kirschst.

Notes: *Niessliaceae* was proposed to accommodate a group of saprobic and parasitic fungi that are commonly found in decaying wood, leaf, soil, as well as occasionally on fungicolous and lichenicolous (Huang et al. 2021). The sexual morphs are characterized by perithecial ascomata with setae or irregular appendages, unitunicate, ellipsoidal to fusiform asci with inamyloid apical ring and hyaline, ellipsoidal to fusiform ascospores. Niessliaceae has both coelomycetous and hyphomycetous asexual morphs. The hyphomycetous is characterized by mononematous, macronematous, hyaline conidiophores, oval to ellipsoidal, aseptate, hyaline conidia (Gams et al. 2019; Huang et al. 2021). The coelomycetous are globose to subglobose conidiomata, hyaline, septate, cylindrical to subcylindrical conidiophores, oval to ellipsoidal, guttulate conidia (Samuels and Barr 1997; Gams et al. 2019; Huang et al. 2021). Currently, the family includes 21 genera, of which only 8 genera have available molecular data (Huang et al. 2021).

Niesslia Auersw.

Notes: *Niesslia* was introduced by Auerswald (1869) with *N. chaetomium* as the type species. The genus has tiny, spiny, mostly dark brown, shiny ascomata and acremonium-like asexual morph (Gams et al. 2019). In this study, we introduce a novel species *N. wurfbainiae* isolated from dead stems of *Wurfbainia villosa*.

Niesslia wurfbainiae C.F. Liao, Doilom & K.D. Hyde, **sp. nov.**

Index Fungorum: IF 903222; *Facesoffungi*: FoF 17091; Figs. 44, 45

Etymology: in reference to the host *Wurfbainia villosa* from which it was isolated.

Holotype: MHZU 24–0032.

Saprobic on dead stems of *Wurfbainia villosa*. Sexual morph: **Ascomata** 125–155 µm (av. 142 µm), superficial, solitary to aggregated, black, globose, sessile, collapsing cup-like when dry, with a central ostiole, setose. **Setae** 70–110 × 4–9 µm (av. 95 × 7 µm), acute, with a wide base, simple, dark or gold brown, light twisted, thick-walled. **Exciple** 10–15 mm wide, dark brown cells of textura angularis epidermoid in transversal section. **Paraphyses** not observed in mature perithecia. **Asci** 35–50 × 6–11 µm (av. 45 × 10 µm), cylindric-clavate to clavate, with a short foot at the base and a truncate apex, unitunicate, 4-spored, I–, K/I–. **Ascospores** 16–22 × 3–5 µm (av. 20.5 × 4 µm), uniseriate or biseriate, elongate ellipsoid to fusiform, tapers from the middle to the sides overlapping, verrucous, without perispore, with round ends, hyaline, 1-septate with 2–3-guttules in each cell. Aexual morph: undetermined.

Culture characteristics: colonies on PDA reaching 15 mm diam. at 25 °C after two weeks, flat, dry, rough, felty, margin undulate and irregular; gray both from above and below; not producing pigmentation in the culture.

Material examined: CHINA, Guangdong Province, Yangchun City, on dead stems of *Wurfbainia villosa* (Lour.) Škorničk. & A.D. Poulsen. (Zingiberaceae), 10 April 2022, *C.F. Liao* & *Y.H. Yang*, *YAM26* (MHZU 24–0032, **holotype**; ZHKUCC 24–0225, ex-type) and *YAM27*.

GenBank: ZHKUCC 24–0225: PQ773318 (ITS), PQ773319 (LSU), PQ778211 (SSU).

Notes: The morphological characteristics of *Niesslia wurfbainiae*, such as dark brown ascomata with setose and tendency to collapse into a cup-like shape when dry, align well with the generic concept of *Niesslia*. However, *N. wurfbainiae* differs from other species in having four ascospores in its asci, whereas most species typically have eight ascospores and *N. robusta* occasionally has four to eight ascospores. *Niesslia wurfbainiae* has longer spine (130–200 µm vs. 25–35 µm) as compared to *N. robusta* (Gams et al. 2019). Phylogenetically, *N. wurfbainiae* (ZHKUCC 24–0225) form a distinct subclade which is basal to *N. fusiformis* (CBS 325.77) and *N. indica* (CBS 313.74) with 81% ML (Fig. 45). The morphological comparison of *N. wurfbainiae* with those of *N. fusiformis* (CBS 325.77) and *N. indica* cannot be conducted as *N. fusiformis* (CBS 325.77) and *N. indica* (CBS 313.74) have been reported as asexual morph while *N. wurfbainiae* is present in its sexual morph. Based on the phylogenetic and morphological evidence, *N. wurfbainiae* is proposed as a new species. It is unique in having 4-spored, elongate ellipsoidal to fusiform ascospores, verrucous, 1-septate with 2–3-guttules in each cell.

Ophiocordycipitaceae G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora.

Notes: Sung et al. (2007) proposed a new family Ophiocordycipitaceae based on them revised *Ophiocordyceps* through analysis of seven loci composition. Move phylogenetically distinct species from Cordycipitaceae and Clavicipitaceae s.str. to Ophiocordycipitaceae. According to the comprehensive phylogenetic analysis, Quandt et al. (2014) identify six genera within the Ophiocordycipitaceae: *Ophiocordyceps*, *Tolypocladium*, *Purpureocillium*, *Harposporium*,

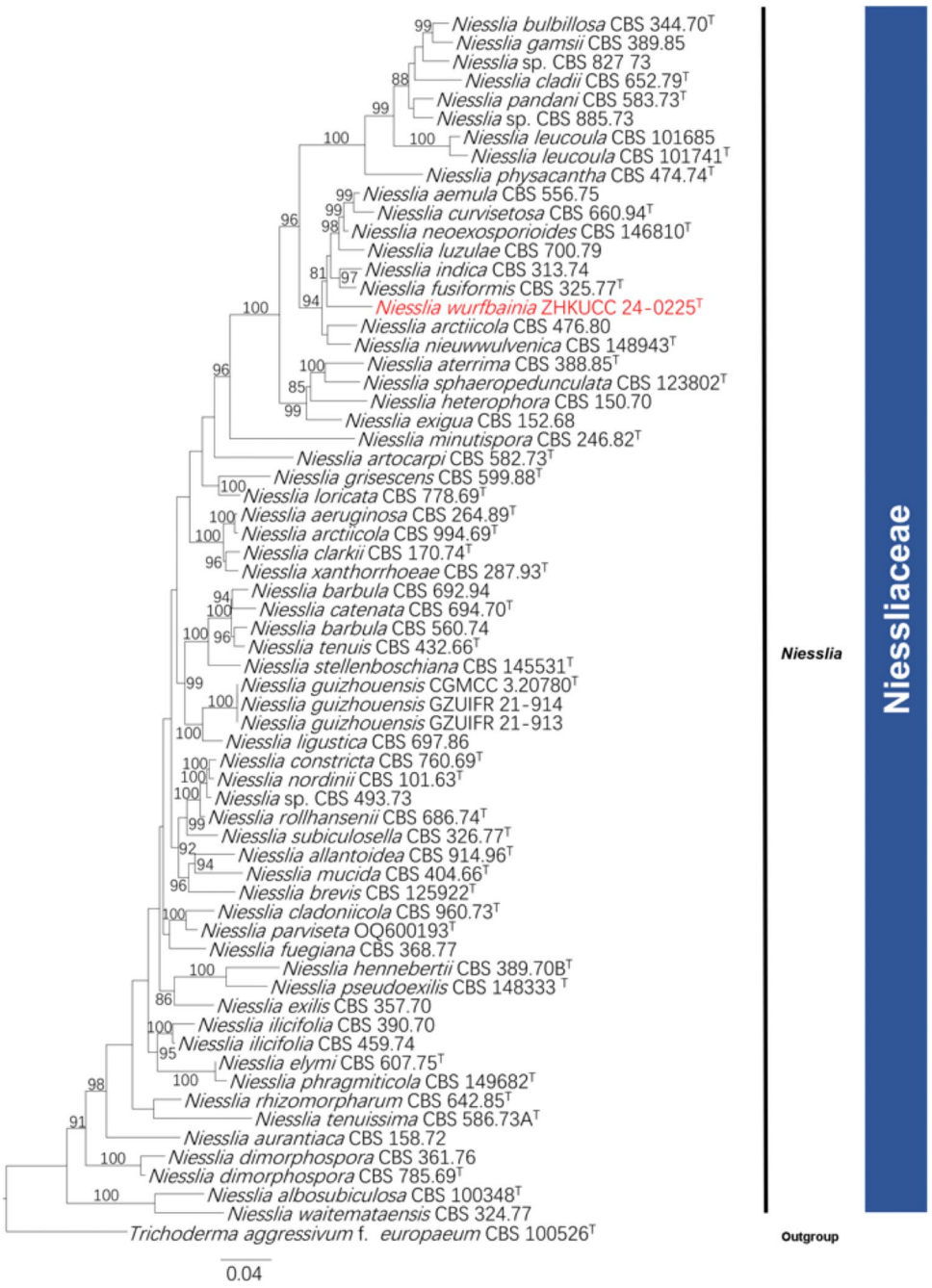


Fig. 45 Maximum Likelihood consensus tree inferred from the combined ITS, LSU and *tef1* multiple sequence alignments. Bootstrap support values for Maximum Likelihood (ML) equal to or greater than 80%. The scale bar indicates expected changes per site. The tree is rooted to *Trichoderma aggressivum* f. *europaeum* CBS 100526. Ex-type strains are indicated with "[T]". The newly generated sequences are indicated in red

Drechmeria, and *Polycephalomyces*. Spatafora et al. (2015) confirmed this classification of Ophiocordycipitaceae and introduced 10 new combinations into *Drechmeria*, four new combinations into *Harposporium*, 23 new combinations and 15 synonymies in *Ophiocordyceps*, and one new combination into *Purpureocillium*.

Ophiocordyceps Petch.

Notes: Petch (1932) proposed that the *Ophiocordyceps* refers to *Cordyceps* that produce non-dissociating ascospores. Sung et al. (2007) described *Ophiocordyceps* as the type genus of the Ophiocordycipitaceae. The species belonging to the *Ophiocordyceps* are identified based on either molecular phylogeny or morphological characteristics. Most species produce dark, tough and flexible stromata. The morphology of the stromata is varied, ranging from filiform and wiry to clavate and fibrous, superficial to completely immersed perithecia. Quandt et al. (2014) and Yang et al. (2024b) revised this genus through morphological observations and phylogenetic analyses. Some species of *Ophiocordyceps* are an important Chinese medicine (Xiao et al. 2023a; Li et al. 2024d).

Ophiocordyceps asiana Mongkols., Khao-ngam, Himaman, Rungjind. & Luangsa-ard, **new host record from China.**

MycoBank: MB 838742; *Facesoffungi*: FoF 15773; Figs. 46, 47

Sexual morph: **Host** 20.9 × 12.7 mm, adult of *Tessaratoma* sp., peltate, dark brown. **Stromata** arising from the thorax of the host, paired, unbranched, cylindrical, black to red–orange, 93.36–112.8 × 0.97–3.12 mm, without sterile apical. **Stipes** 73.7–85.2 × 0.97–1.52 mm, cylindrical, smooth, black to light orang, with a fertile part. **Fertile parts** 11–23.6 × 2.64–3.12 mm, cylindrical, yellow to orange. **Perithecia** (702–)712–869–979(–994) × (144–)196–224–263(–266) µm, elongated ovoid, completely immersed, inclined close arrangement. **Asci** (235–)256–367–501(–515) × (4.3–)4.7–6.0–7.8(–12.8) µm, hyaline, filiform, with a hemispheric apical cap of (4.0–)5.8–7.6–9.6(–10.0) × (4.2–)4.3–6.6–7.9(–8.8) µm. **Ascospores** easily breaking into part-spores. **Secondary ascospores** (9.25–)10.1–11.5–13.1(–14.1) × (1.0–)1.1–1.9–2.4(–2.8) µm, cylindrical, smooth.

Material examined: CHINA, Guizhou Province, Libo County, 25°15′N 100°97′E, 12 Jul 2022, *Xian Zhang*, *Xing-Can Peng*, *LB22071254* (HKAS 125846).

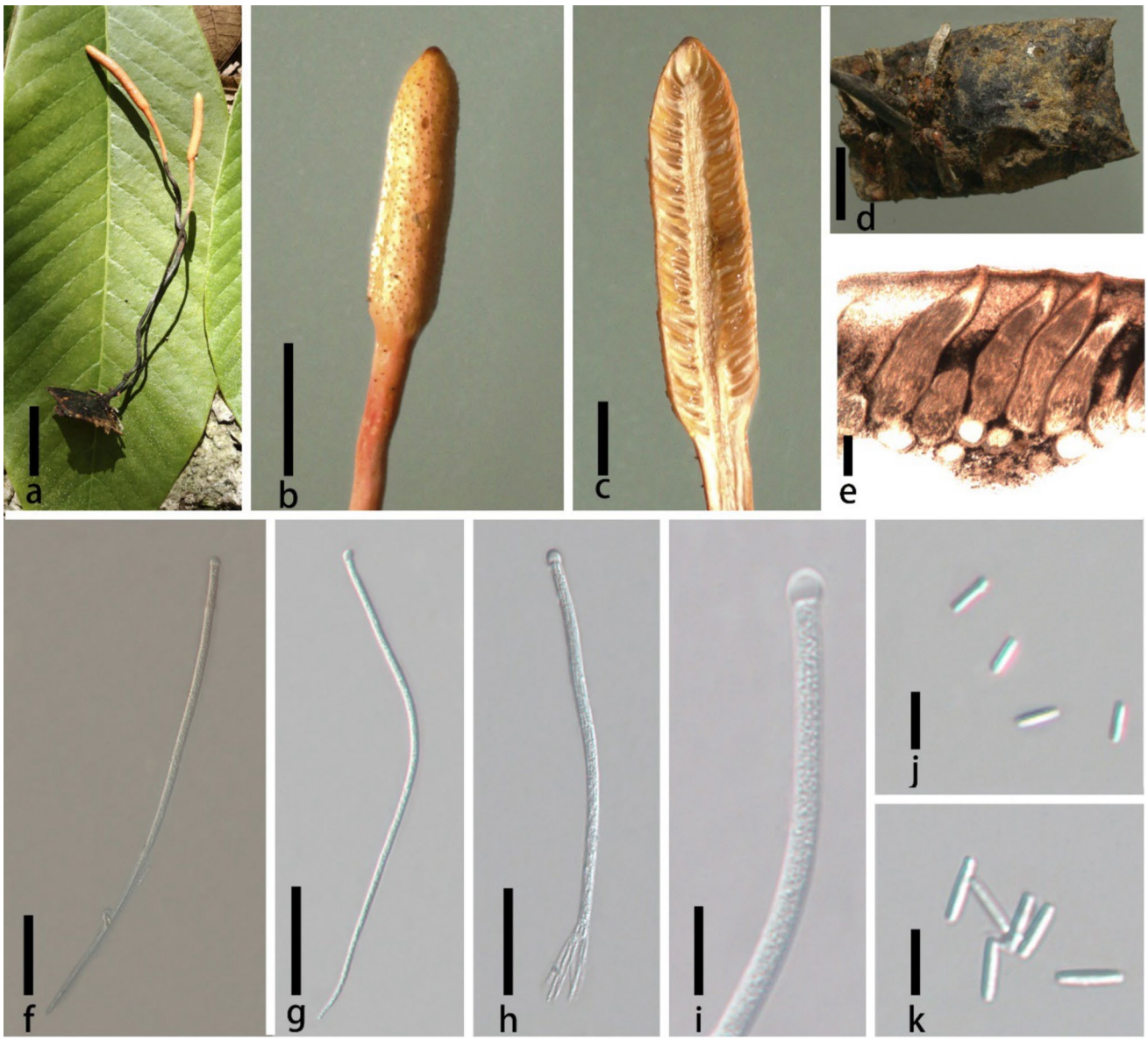


Fig. 46 ***Ophiocordyceps asiana*** (HKAS 125846) **a** Stroma arising from host. **b** Fertile part. **c** Cross-section through part of stroma with perithecia. **d** Host. **e** Perithecia. **f–h** Ascospores. **i** Apical cap of asci. **j–k** Secondary ascospores. Scale bars: **a** = 10 mm, **b–c** = 5 mm, **d** = 2 mm, **e** = 200 µm, **f** = 50 µm, **g** = 100 µm, **h** = 50 µm, **i** = 20 µm, **j** = 10 µm, **k** = 20 µm

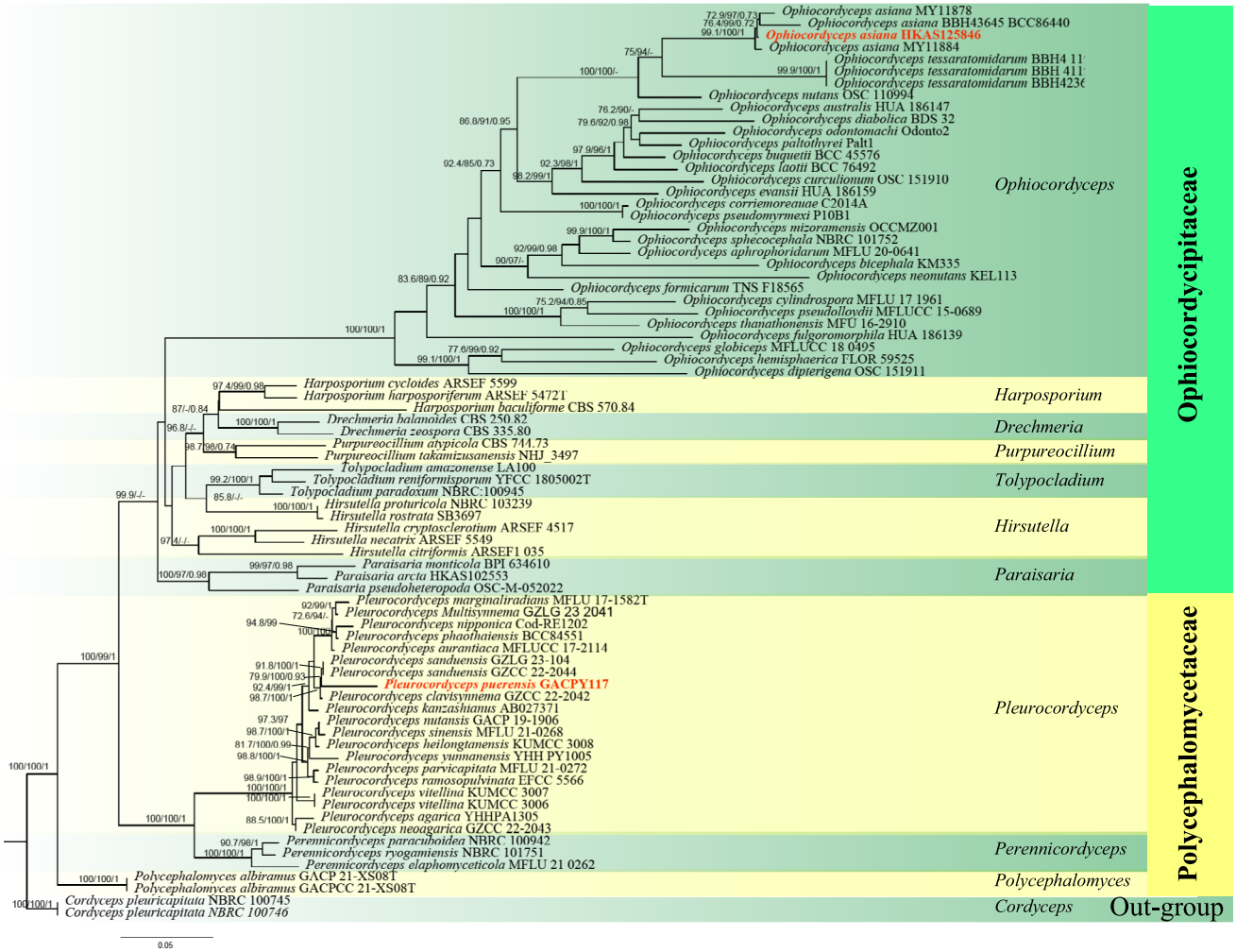


Fig. 47 Maximum Likelihood phylogenetic tree based on concatenation of ITS, LSU, SSU, *tef1* and *rpb1* sequence data. The phylogeny was inferred using IQ-tree. The number of SH-aLRT > 75% / UFB > 85% / PP > 0.90 are indicated above the nodes. My data are indicated in red bold font

GenBank: HKAS 125846: PP627513 (ITS), PP616710 (LSU), PP707760 (SSU), PP654215 (*tef1*), PP654217 (*rpb1*).

Notes: Among samples of *Ophiocordyceps nutans* complex, Khao-ngam et al. (2021) confirmed that Thai materials formed two independent branches through the multi-loci phylogeny analysis, which were obviously separated from *O. nutans*, including a new *Ophiocordyceps asiana* (Ophiocordycipitaceae, Hypocreales). And the *O. asiana* from China, Japan and Thailand was summarized and recorded. The host of *O. asiana* from Thailand are proposed as Pentatomidae and Coreidae. The host of *O. asiana* from Japan are Coreidae, Pentatomidae and Acanthosomatidae. In this study, *O. asiana* parasitic on *Tessaratoma* sp. is a new host.

Ophiocordyceps campes Tasan., Thanakitp. & Luangsa-ard, **new geographical record from China.**

Index Fungorum: IF 835588; *Facesoffungi*: FoF 16987; Figs. 48, 49

Parasitic on larvae of Lepidoptera, collected in leaf litter in forests, without mycelium cover on host. **Sexual morph** not observed. **Asexual morph** Hirsutella-like. **Synnemata** 3–5.5 cm long, 0.5–1.5 mm wide, cylindrical with tapering tip, stipitate, gradually become white or grayish white to the upper portion, scattered on the insect body, without fertile head. **Phialides** hyaline, smooth, with an inflated base, 9.7–13.5 × 2.5–4.2 µm ($\bar{x}$ = 11.6 × 3.4 µm, n = 40), tapering to a thin neck, 4.2–7.4 um long, 1.3 µm wide. **Conidia** hyaline, smooth, ellipsoid or fusiform, 4.8–6.7 × 1.2–2.3 µm ($\bar{x}$ = 5.7 × 1.8 µm, n = 40).

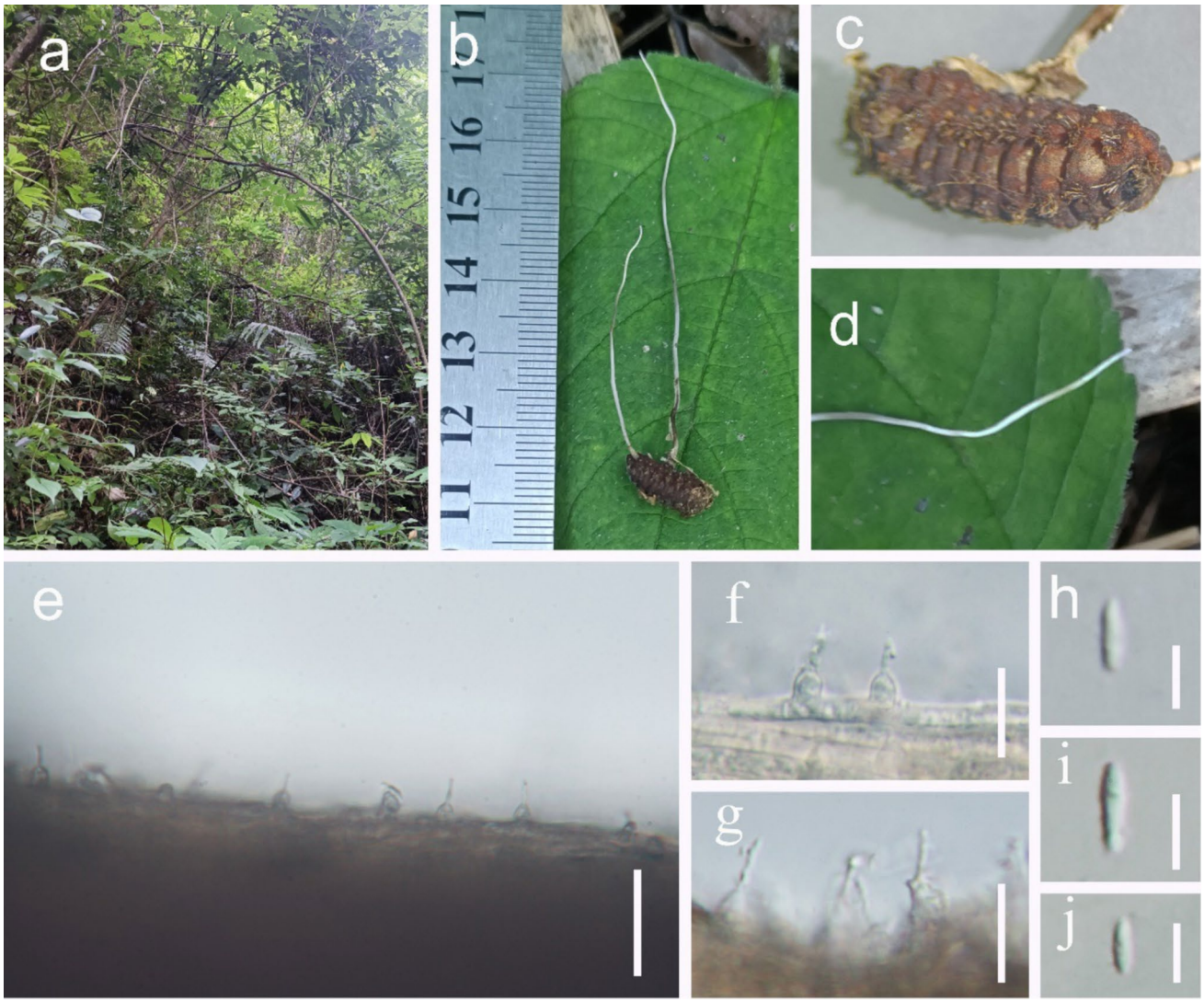


Fig. 48 ***Ophiocordyceps campes*** (HKAS 132243). **a** Habitat. **b** Synnemata on host. **c** Host. **d** Synnemata. **e–g** Phialides. **h–j** Conidia. Scale bars: **e** = 30 µm, **f–g** = 10 µm, **h–j** = 5 µm

Material examined: CHINA, Guizhou Province, Qiandongnan Miao and Dong Autonomous Prefecture, Zhenyuan County, 27°6′N 108°24′E, 583 m asl, 26 Jun 2023, *Yuan-Pin Xiao*, *Yu Yang*, *TX23100* (HKAS 132243).

GenBank numbers: HKAS 132243: PQ528947 (ITS), PQ528945 (LSU), PQ528942 (SSU), PQ522477(*rpb1*), PQ569913 (*rpb2*), PQ522480 (*tef1*).

Notes: *Ophiocordyceps campes* was introduced by Tasanathai et al. (2020), which was found on the larva of Lepidoptera in Thailand. Phylogenetic analysis showed that our new isolation TX23100 is a sister taxon to *O. campes* (BCC36938) (Fig. 49). Morphologically, our new isolate is almost identical to *O. campes* except for the conidia (Tasanathai et al. 2020). Our new isolate has smaller conidia than the holotype of *O. campes* (Tasanathai et al. 2020). Molecularly, our new isolate (HKAS 132168) is not significantly different from *O. campes* (BCC36938). Thus, we identified our new isolate as *O. campes*, marking the first report of this species collected from China.

Ophiocordyceps jilinensis Y.P. Xiao & Y. Yang, **sp. nov.**

Index Fungorum: IF 903017; *Facesoffungi*: FoF 16977; Figs. 49, 50

Etymology: refers to Jilin Province, the locality of the type specimen.

Holotype: HKAS 144583.

Parasitic on adult Orthoptera, which is found on the abaxial side of fern fronds, where a light brown mycelium envelops the entire host, without the presence of synnemata. **Sexual morph** not observed. **Asexual morph** Hirsutella-like. **Hyphae** hyaline and initially smooth, developing warts on older; septate, 3.2 µm to 4.8 µm in

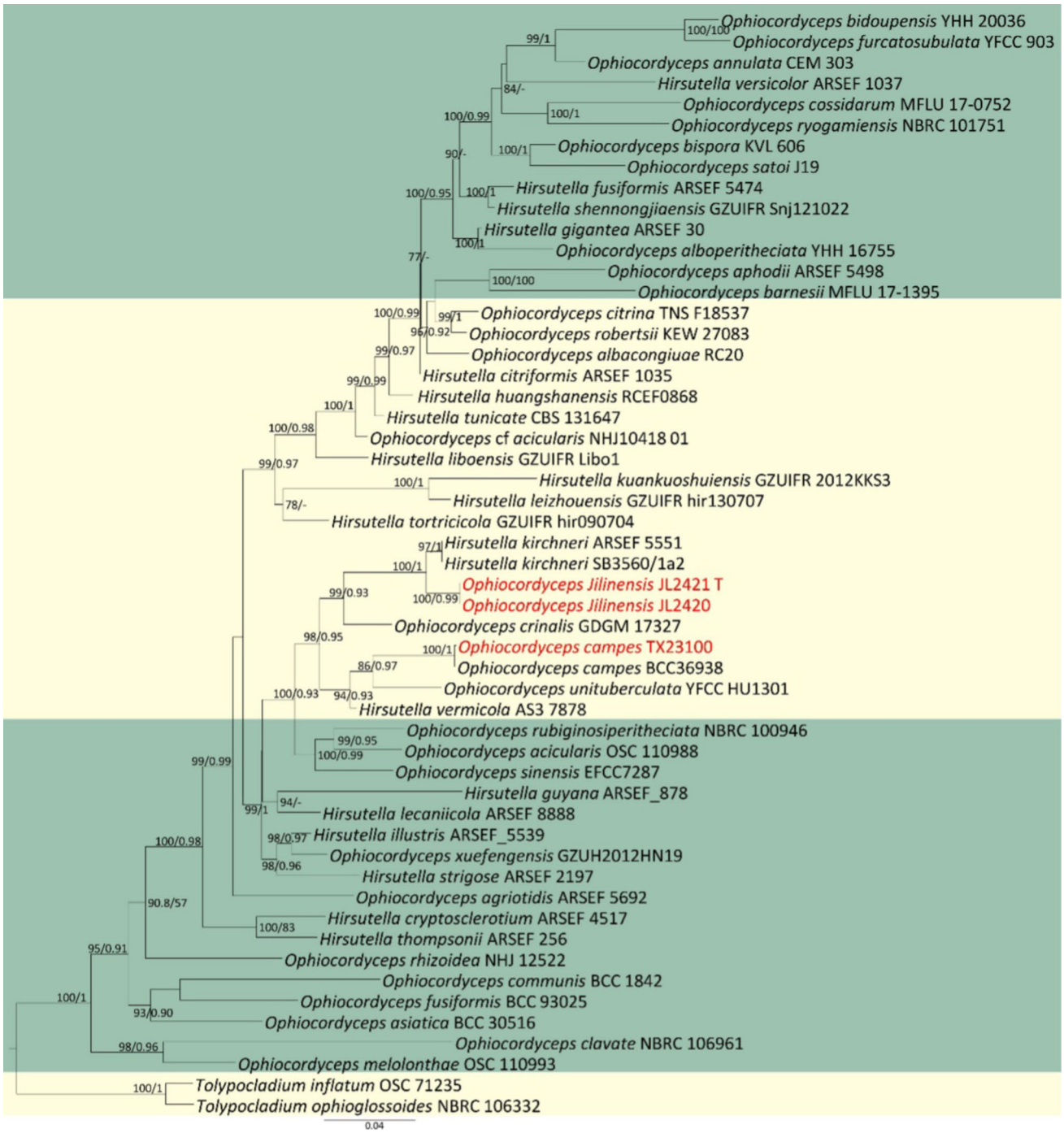


Fig. 49 A phylogram was constructed using Maximum Likelihood analysis with RAxML based on sequence data from six gene regions: LSU, ITS, SSU, *tef1*, *rpb1* and *rpb2* sequence data. *Tolypocladium inflatum* and *T. ophioglossoides* were employed as outgroup taxa. Nodes with Maximum Likelihood bootstrap values exceeding 75% and Bayesian posterior probabilities higher than 0.90 are indicated on the phylogram. Newly generated sequences are highlighted in bold red. "T" refers to a type specimen

width. **Phialides**, mono- or polyphialidic, emerging from the hyphae laterally or at the ends, hyaline, cylindrical, adorned with small warts, are inflated at the base, with 2–3 arranged in a whorl, 19.2–35.7 × 3.2–4.5 µm ($\bar{x}$ = 27.5 × 3.8 µm, n = 50), tapering to a slender, verruculose, with narrow neck 8.2–14.6 µm long, 1.5 µm wide. **Conidia** hyaline, smooth, ellipsoid or lemon-shaped, arising from the apex of the neck singly, 5.3–7.8 × 4.2–5.3 µm ($\bar{x}$ = 6.5 × 4.8 µm, n = 50), surrounded by mucous sheath.

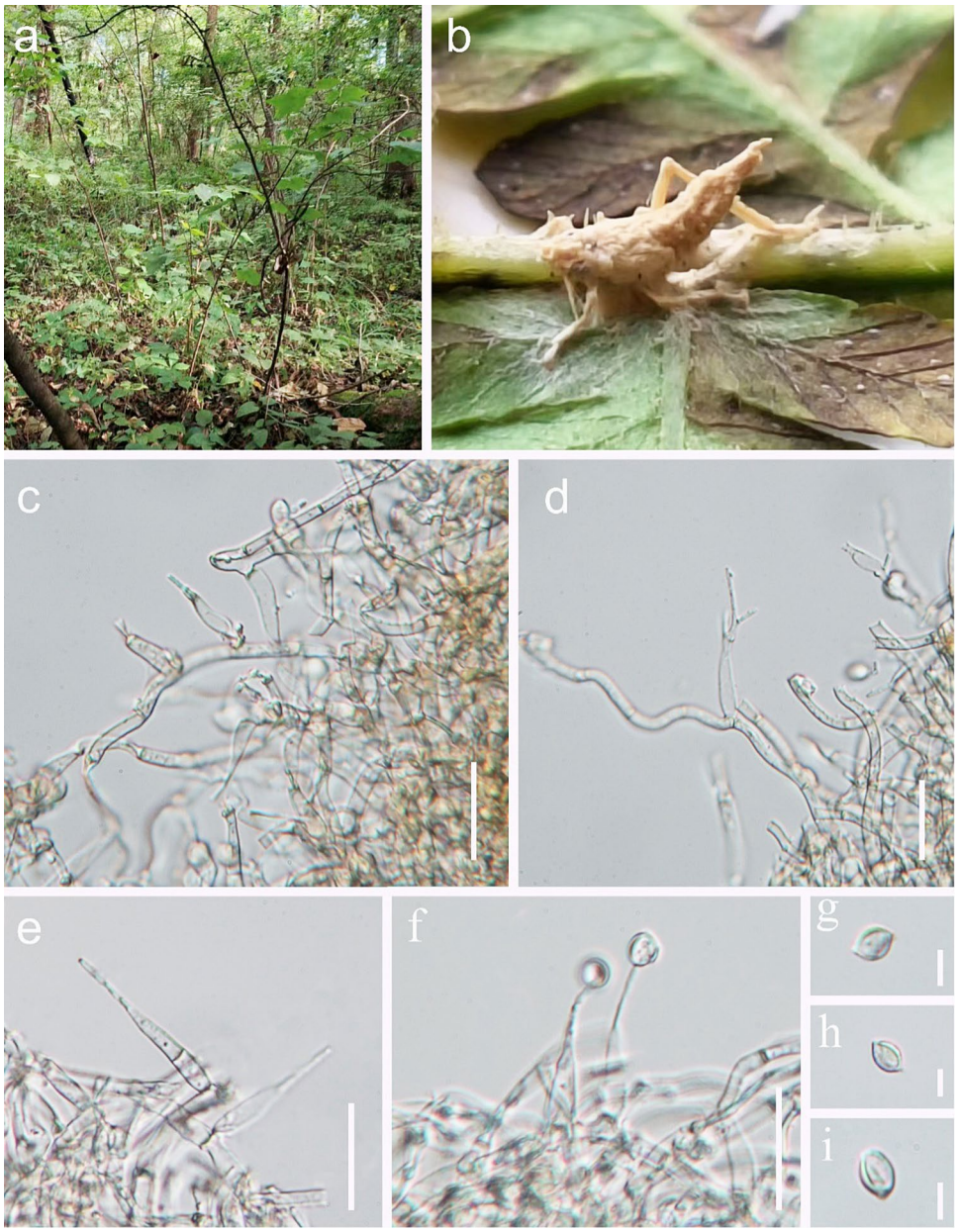


Fig. 50 *Ophiocordyceps jilinensis* (HKAS 144583, **holotype**). **a** Habitat. **b** Mycelium on host. **c–e** Phialides. **f** Phialides with conidia. **g–i** Conidia. Scale bars: **c–f** = 20 µm, **g–i** = 5 µm

Material examined: CHINA, Jilin Province, Baishan City, Fusong County, 42°25′N 127°27′E, 781 m asl, 10 Aug 2024, *Yuan-Pin Xiao*, *Yu Yang*, *JL2421* (HKAS 144583, **holotype**); *JL2420* (HKAS 144584, **Paratype**).

GenBank numbers: JL2421: PQ528946 (ITS), PQ528943 (LSU), PQ528940 (SSU), PQ522476 (*rpb1*), PQ569911 (*rpb2*), PQ522478 (*tef1*); JL2420: PQ528947 (ITS), PQ528944 (LSU), PQ528941 (SSU), PQ569912 (*rpb2*), PQ522479 (*tef1*).

Notes: *Ophiocordyceps jilinensis* clustered with *Hirsutella kirchneri* and *O. crinalis* in the phylogenetic tree with support (100% MLBP, 1.00 PP) (Fig. 49). Comparing the ITS and *tef1* sequences of *O. jilinensis* and *H. kirchneri* revealed 97.23% (13 bp differences), 96.91% (24 bp differences) sequence similarities, respectively. Comparing the LSU, *tef1* and *rpb1* sequences of *O. jilinensis* and *O. crinalis* revealed 97.27% (21 bp differences), 92.15% (51 bp differences) and 90.33% (61 bp differences), separately. Morphologically, *O. jilinensis* parasitizing the adult Orthoptera and have longer phialides (19.2–35.7 µm vs. 15–24 µm) and bigger conidia (5.3–7.8 × 4.2–5.3 µm vs. 4.5–6 × 2.5–3.5 µm) (Minter et al. 1983). Thus, we would like to introduce *O. jilinensis* as a new species based on phylogenetic and morphological analyses.

Polycephalomycetaceae Y.P. Xiao, Y.B. Wang, T.C. Wen, H. Yu & K.D. Hyde.

Notes: Polycephalomycetaceae was delineated by Xiao et al. (2023a, b) and is distinctly separate from Ophiocordycipitaceae. They also establish *Polycephalomyces* as the type genus of Polycephalaceae and recognize three genera within the Polycephalomycetaceae (*Perennicordyceps*, *Pleurocordyceps*, and *Polycephalomyces*) forming a clade sister to the Ophiocordycipitaceae. Additionally, Johnston and Park (2023) introduced *Dingleyomyces* as a novel genus for an endemic New Zealand fungus, which parasitizes the stromata of *O. robertsii* and *O. hauturu*. The majority of species in this family exhibit a wide range of insect and fungal hosts.

Pleurocordyceps Y.J. Yao, Y.H. Wang, S. Ban, W.J. Wang, Yi Li, Ke Wang & P.M. Kirk.

Notes: Wang et al. (2021a) established a novel genus named *Pleurocordyceps* within the Polycephalomycetaceae through a combination of phylogenetic analysis and morphological characteristics. They introduced ten species belonging to the *Pleurocordyceps*. *Pleurocordyceps*, with its type species *Pleurocordyceps sinensis*, was first described by Wang et al. (2021a) based on its association with *Paecilomyces sinensis* (Chen et al. 1984). Xiao et al. (2023a, b) further enriched the diversity of the genus and its associated families by adding new species of *Pleurocordyceps*. Additionally, Xiao et al. (2024) identified four new species of *Pleurocordyceps* through systematic analysis utilizing sequences of ITS, LSU, SSU, *rpb1*, *rpb2*, and *tef1*.

Pleurocordyceps puerensis X. Zhang, Z.L. Liu & T.C. Wen, **sp. nov.**

Index Fungorum: IF 902009; *Facesoffungi*: FoF 15772; Figs. 47, 51

Etymology: '*puerensis*' in reference to the city where the species was found.

Holotype: GACPY117.

Sexual morph: **Host** 37.4 × 2.8–4.9 mm, a larva of Coleoptera, slender, cylindrical, brown. **Stromata** arising from the head and tail of the host, paired, branched, cylindrical, yellow to brown, 19.6–27.0 × 0.6–4.0 mm, with sterile apical (9.8–11.4 × 0.5–0.7 mm). **Stipes** 17.2–22.5 × 0.6–1.6 mm, clavate, the color gradually becoming lighter towards the apex, yellow to brown, with a fertile part. **Fertile parts** 1.9–4.1 × 2.2–4.0 mm, subglobose or hemispherical, yellowish. **Perithecia** (791–)796–829–852(–997) × (171–)217–272–325(–371) µm, ovoid, immersed, yellow to hyaline, the color gradually becomes lighter towards the inner layer. **Asci** (225–)317–442–597(–600) × 3.4–4.1–4.5(–4.9) µm, hyaline, cylindrical, with a hemispheric apical cap of (2.3–)3.6–4.2–4.7(–5.6) × (3.6–)4.3–4.8–5.1(–5.2) µm. **Ascospores** (143–)173–224–265(–270) × (0.9–)1–1.2–1.4(–1.5) µm, filiform, hyaline, irregular multiseptate. **Secondary ascospores** (3.9–)4–5.2–5.6(–5.8) × (1.1–)1.2–1.5–1.6(–1.8) µm, cylindrical, smooth.

Material examined: CHINA, Yunnan Province, Puer City, 22°72′N 100°96′E, 1339.4 m asl, 22 Oct 2022, *Xian Zhang*, *Zhong-liang Liu*, *Y20231022117* (GACPY117, **holotype**).

GenBank: GACPY117: PP627512 (ITS), PP616709 (LSU), PP707759 (SSU), PP654214 (*tef1*), PP654216 (*rpb1*).

Notes: The new species is sister to *P. sanduensis* with nearly maximum support (SH-aLRT 79.9% / UFB 100% / PP 0.93, Fig. 47). Due to the lack of sexual morph of *P. sanduensis* and *P. puerensis*, it is impossible to compare them in morphological characteristics. However, the new species differs from *P. sanduensis* by 2 bp (including 1 gap) in ITS, 22 bp (including 7 gap) in SSU, 6 bp in *tef1* and 1 bp (including 1 gap) in *rpb1*. Thus, we introduce *P. puerensis* as a new species of the *Pleurocordyceps*.

Sarocladiaceae L. Lombard.

Notes: Crous et al. (2018) introduced Sarocladiaceae to accommodate the distinctive lineage of *Parasarocladium* and *Sarocladium* based on phylogenetic evidence (Crous et al. 2018; Hyde et al. 2020b), and *Sarocladium*, the type genus of the family (Hyde et al. 2020b). Sarocladiaceae is characterized by elongated phialides rising solitary on vegetative hyphae or on conidiophores that are sparsely or repeatedly branched, with elongated conidia (Giraldo López et al. 2015). Some species of Sarocladiaceae are reported as plant pathogens causing sheath-rot of rice and bamboo (Sawada 1922; Gams and Hawksworth 1975; Sakthivel et al. 2002; Ayyadurai et al. 2005), or as human pathogens from calf tissue of legs, sputum and clinical wash fluid (Giraldo López et al. 2015), and some species are recorded as saprobes on monocotyledons and dicotyledons (Giraldo López et al. 2015; Liu et al. 2017; Crous et al. 2018; Phukhamsakda et al. 2020).

Sarocladium W. Gams & D. Hawksw.

Notes: *Sarocladium* was established by Gams and Hawksworth (1975) and reviewed the taxonomy by Summerbell et al. (2011) with *S. oryzae* as the type species. As previously reported, *Sarocladium* was formed a complex phylogenetic affinity with *Acremonium* (Summerbell et al. 2011; Giraldo López et al. 2015; Maharachchikumbura et al. 2015, 2016; Wijayawardene et al. 2017b). Subsequently, the phylogenetic placement of *Acremonium* and *Sarocladium* was confirmed since the type species of *Acremonium* (*A. alternatum*) formed a well-supported lineage in Bionectriaceae (Crous et al. 2018; Hyde et al. 2020b). The genus is characterized by cylindrical, phialidic conidiogenous cells and elongated phialides rising solitary on vegetative hyphae or on conidiophores that are sparsely or repeatedly branched,

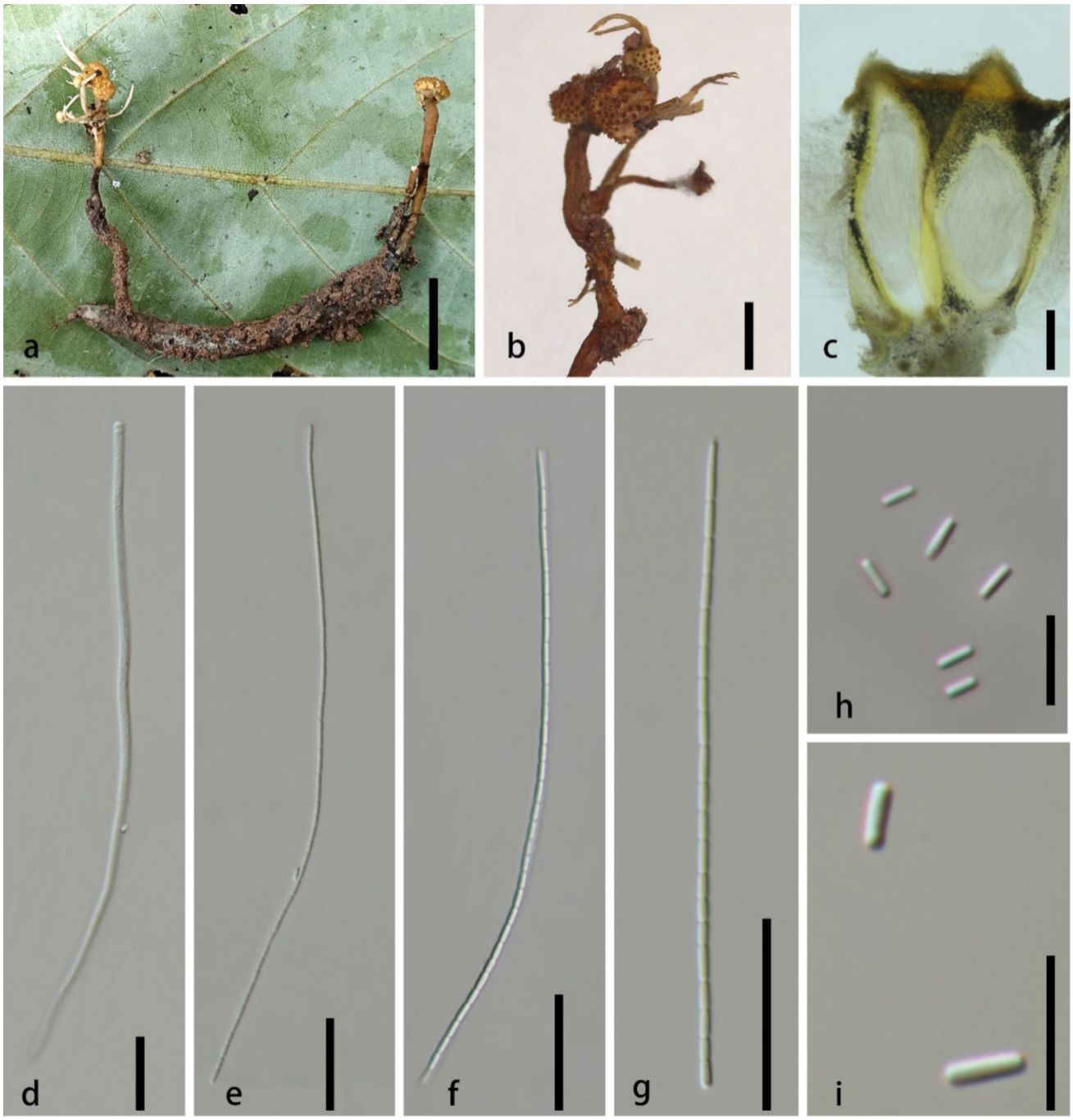


Fig. 51 ***Pleurocordyceps puerensis*** (GACPY117, **holotype**). **a** Stroma arising from host. **b** Fertile part. **c** Perithecia. **d** Asci. **e**–**f** Ascospores. **g** Part of ascospores. **h**–**i** Secondary ascospores. Scale bars: **a** = 10 mm, **b** = 1 mm, **c** = 200 µm, **d**–**g** = 25 µm, **h**–**i** = 10 µm

and the production of cylindrical conidia (Summerbell et al. 2011; Ou et al. 2020). Recently, Members of *Sarocladium* are being discovered as plant pathogens, endophytes, mycoparasites (Rivera-Varas et al. 2007), saprobes and a few are opportunistic human pathogens (Rivera-Varas et al. 2007; Yeh and Kirschner 2014; Giraldo López et al. 2015; Liu et al. 2017; Crous et al. 2018; Ou et al. 2020), and distributed worldwide, such as China, Egypt, Germany, India, Kenya, Solomon, Sri Lanka et al. (Summerbell et al. 2011; Liu et al. 2017; Crous et al. 2018; Xiao et al. 2023a, b; Zhang et al. 2023a, b, c). Currently, 36 species epithets are registered under *Sarocladium* in Index Fungorum.

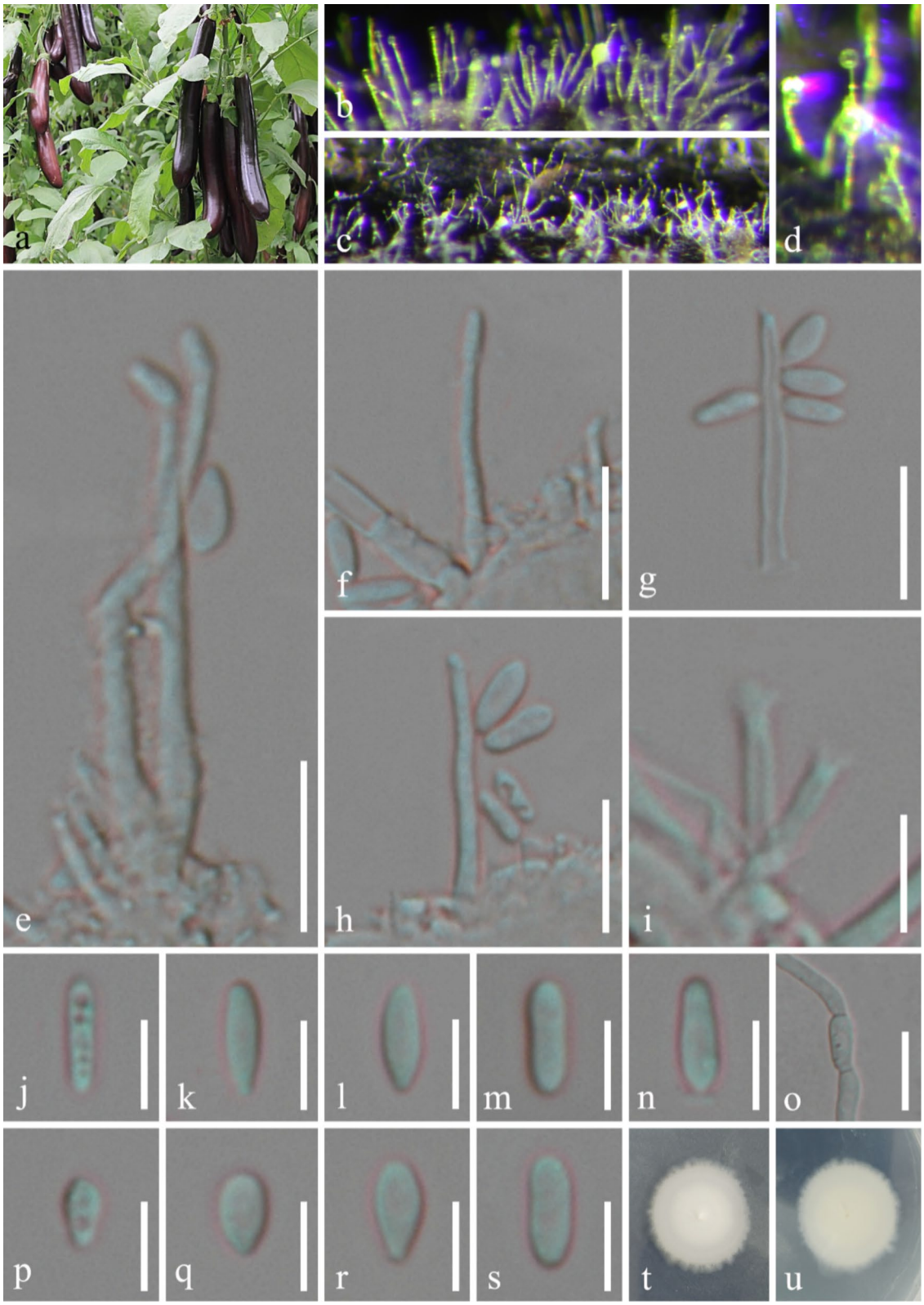


Fig. 52 ***Sarocladium solani*** (HKAS 132482, **holotype**). **a** *Solanum melongena*. **b – d** Colony on host surface. **e – h** Conidiophores with conidia. **i** Conidiophores. **j – n, p – s** Conidia **o** Germinated conidium. **t – u** Colony on PDA (t from above, u from below). Scale bars: **e – i, o** = 10 µm, **j – n, p – s** = 5 µm

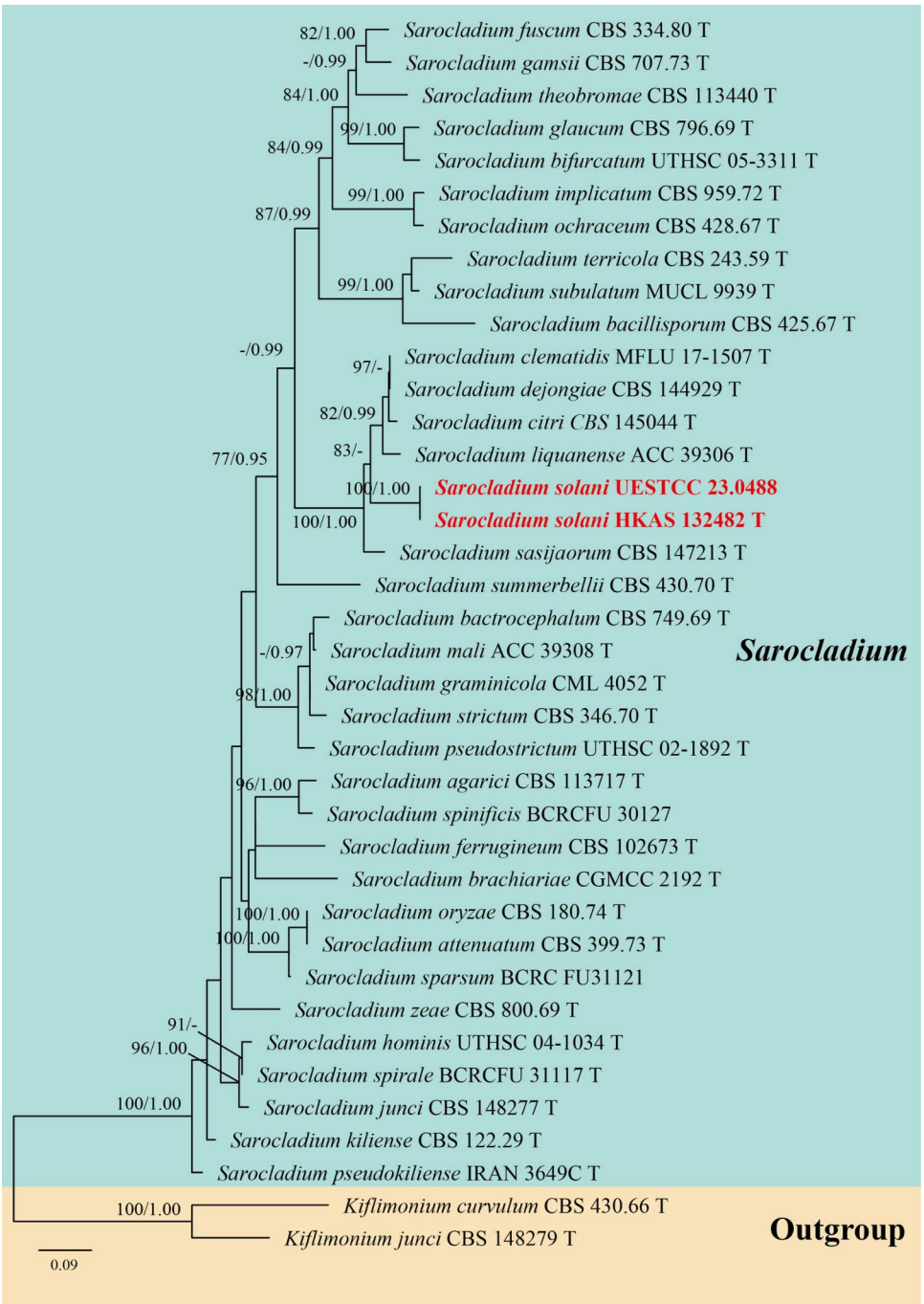


Fig. 53 Phylogenetic tree from Maximum Likelihood analysis based on the combined ITS and *rpb2* sequences data. Branches support for ML ≥ 75% and Bayesian inference posterior probabilities (BIPP) ≥ 0.95 are marked above or below branches as MLBS/BIPP. Thickened branches indicate branch support with MLBS = 100% and BIPP = 1.00. The tree was rooted with *Kiflimonium curvulum* (CBS 430.66, ex-type) and *K. junci* (CBS 148279, ex-type). The abbreviation T indicate the ex-type strain. Names in red are newly collected taxa

Sarocladium solani H.Z. Du & Jian K. Liu, **sp. nov**.

MycoBank: MB 854032; *Facesoffungi*: FoF 15873; Figs. 52, 53

Etymology: The epithet '*solani*' refers to the host genus *Solanum* on which the holotype was collected.

Holotype: HKAS 132482.

Saprobic on dead fruits of *Solanum melongena* (Solanaceae), Sexual morph: Undetermined. Asexual morph: **Conidiomata** sporodochial, superficial, solitary to gregarious, scattered, sporodochia globose, thin- and smooth-walled, shiny, glistening, hyaline to subhyaline. **Mycelium** partly immersed, partly superficial on host surface, and hyaline to subhyaline, unseptate, branched, up to 1–2 µm wide in culture, sometimes bound together into ropes, could produce hyphal coil and net form structure. **Conidiophores** 16–29 µm ($\bar{x}$ = 23 µm, n = 20) long, 1–2 µm ($\bar{x}$ = 1.5 µm, n = 20) wide, cylindrical, micronematous, solitary, erect, hyaline to subhyaline, short, smooth-walled, unbranched, aseptate, straight or slightly curved. **Conidiogenous cells** indistinct, short, hyaline, smooth-walled. **Conidia** 4–7 µm

($\bar{x}$ = 5 µm, n = 30) long, 1.5–2.5 µm ($\bar{x}$ = 2 µm, n = 30) wide, unicellular, narrower cylindrical, clavate, with round ends, aseptate, hyaline to subhyaline, thin- and smooth-walled.

Culture characteristics: Conidia germinated on PDA within 24 h, and germ tubes produced from basal cell. Colonies growing on PDA reached 15–18 mm in diameter after three weeks at 25℃. Colonies circular, margin entire, dense, surface smooth, white in the whole colony from above and reverse, no pigmentation on PDA.

Material examined: CHINA, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, 106°41′48″E 26°32′18″N, elevation 1127 m, 20 January 2021, *H.Z. Du*, cultivated samples, on dead fruits of medicinal plant *Solanum melongena* L. (Solanaceae). *S69* (HKAS 132482, **holotype**), ex-type living culture CGMCC 3.27460; *ibid.*, on dead stems of *Solanum melongena*, *S69-1* (HUEST 23.0489, **paratype**), living culture UESTCC 23.0488.

GenBank: HKAS 132482: PP811630 (ITS), PP816294 (*rpb2*); UESTCC 23.0488: PP811631 (ITS), PP816295 (*rpb2*).

Notes: Sarocladium solani has close phylogenetic relationship with *S. liquanense* based on ITS and *rpb2* sequence data, and formed a distinct lineage in *Sarocladium* (Fig. 53). The nucleotide base pair comparison between *S. solani* (ex-type, CGMCC 3.27460) and *S. liquanense* (ex-type, ACC 39306) revealed 40/518 bp (7.7%) of ITS differences. Morphologically, *S. solani* resembles *S. liquanense* in having cylindrical, solitary, erect conidiophores and unicellular, ellipsoidal to cylindrical conidia (Hou et al. 2019), but *S. liquanense* differs from *S. solani* in having branched and septate *Conidiophores*. Therefore, based on morphological comparison and phylogenetic analyses, *S. solani* associated with medicinal plant *Solani melongena* (Solanaceae) is introduced as a new species in China.

Myrmecridiales Crous.

Notes: The monotypic order Myrmecridiales was introduced by Crous et al. (2015b). Currently, only the type family Myrmecridiaceae is accepted in this order.

Myrmecridiaceae Crous.

Notes: Myrmecridiaceae was established by Crous et al. (2015b), with *Myrmecridium* as the type. Crous et al. (2018) introduced the second genus *Neomyrmecridium* in this family.

Myrmecridium Crous.

Notes: *Myrmecridium* was introduced by Arzanlou et al. (2007), with *M. schulzeri* as the type species. Asexual morph of *Myrmecridium* is characterized by erect, unbranched, septate conidiophores, polyblastic, terminal and intercalary conidiogenous cells, and solitary, obovoidal or fusiform, smooth or finely verrucose-walled conidia (Arzanlou et al. 2007; Crous et al. 2013b, 2015b, 2018; Xu et al. 2023; Yang et al. 2023a). Sexual species of *Myrmecridium* is only known for *M. montsegurinum*, it is characterized by immersed, subglobose to conical, hyaline to pale brown ascomata, cylindrical paraphyses longer than asci, cylindrical asci with long stipe and broadly rounded apical, and ellipsoidal, 3-septate, delicately verrucose ascospores (Réblová et al. 2016). Twenty-four species are accepted in *Myrmecridium*, most these species are isolated from living or dead plant tissues, and a few species isolated from soil and house dust (Jie et al. 2013; Crous et al. 2013b, 2016a, 2018; Yang et al. 2023a). All *Myrmecridium* species have sequence date in GenBank, but *M. mexiae* was no morphological corresponding description (Tan and Steinrucken 2024).

Myrmecridium pulvericola Koppel, Visagie, Hirooka & Seifert, **new geographical record from China.**

Fungal Names: FN 815486; *Facesoffungi*: FoF 16385; Figs. 54, 55

Saprobic on submerged decaying wood. Asexual morph: **Colonies** on natural substrate superficial, scattered, solitary or gathered, brown, hairy. **Mycelium** partly immersed, partly superficial, composed of septate, smooth-walled, pale brown to hyaline hyphae. **Conidiophores** 74–135 × 2.1–3.2 µm ($\bar{x}$ = 104.1 × 2.7 µm, n = 20), macronematous, mononematous, erect, unbranched, mostly straight, cylindrical, sometimes inflated at the basal cells, sparse septate, brown, slightly paler towards the apex, subhyaline to pale brown at the apex, with multiple denticulate conidiogenous loci. **Conidiogenous cells** integrated, polyblastic, terminal, becoming intercalary, sympodial, short, pimple-like denticles. **Conidia** 3.6–6.9 × 2.3–3.6 µm ($\bar{x}$ = 5.2 × 2.8 µm, n = 30), solitary, ellipsoidal to obovoid, pale brown, thin-walled, finely verrucose, aseptate, rounded apical and tapering to the base, with a small hilum. Sexual morph: Undetermined.

Culture characteristics: Conidia germinating on PDA within 12 h, and germ tubes produced from the apex. Colonies growing on PDA, and after 3 weeks of incubation at room temperature, the diameter reaches about 15 mm. Mycelia damp, dense, colonies on the surface of PDA, slightly raised but concave in the center, surface pucker, with regular edges, pale pink. Reverse white to pale pink, smooth.

Material examined: CHINA, Guangxi Zhuang Autonomous Region, Nanning City (22°59′48.12″N 108°13′32.30″E), on unknow species submerged decaying wood, 17 November 2023, *Qiu-Xia Yang*, *S-5965* (HKAS 136941), living culture KUNCC 23–17,553.

GenBank: PQ143312 (ITS), PQ143314 (LSU).

Notes: Phylogenetic analysis showed that the new collection (KUNCC 23–17,553) clustered with the ex-type strain of *Myrmecridium pulvericola* (DAOMC 21694) with

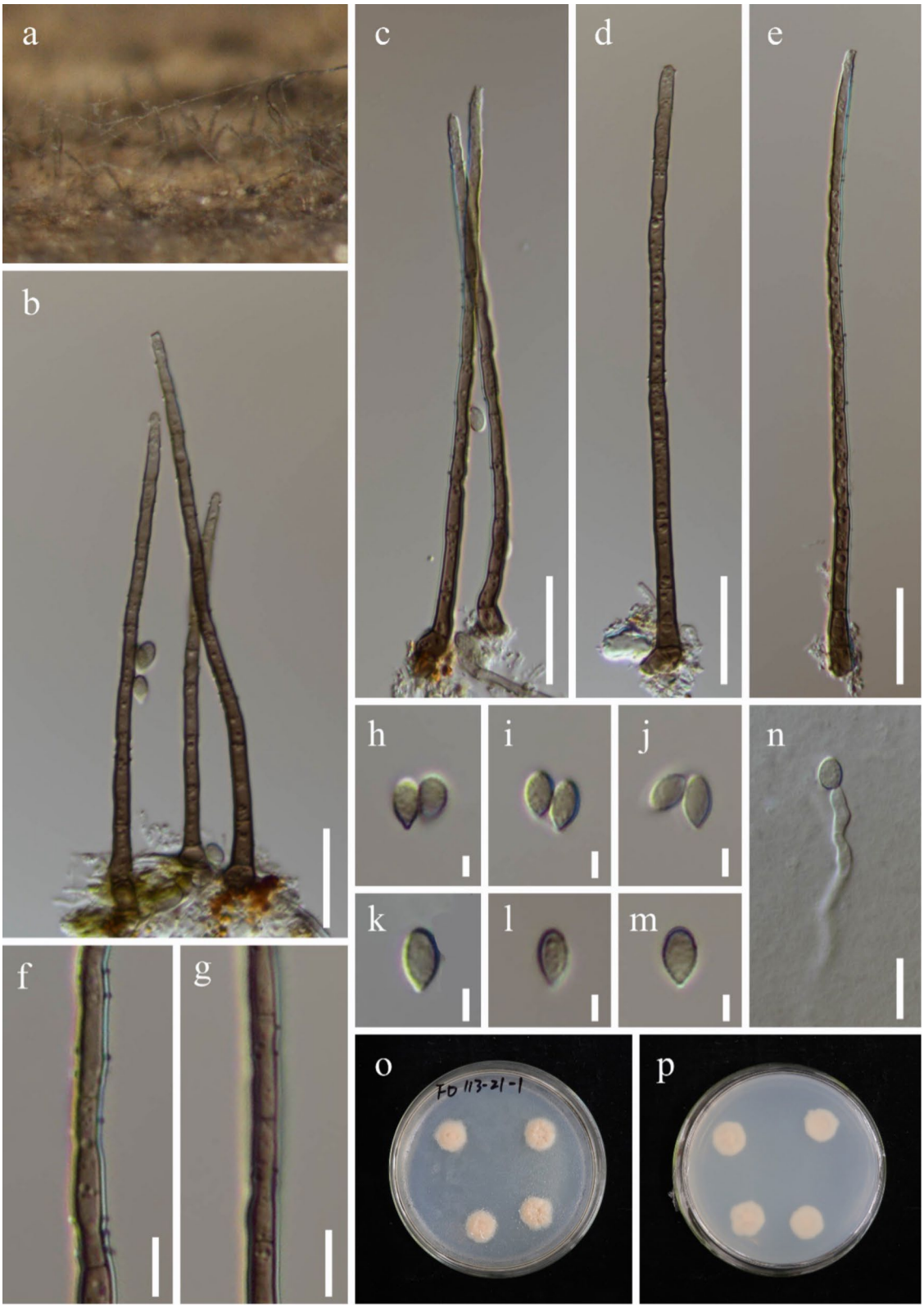


Fig. 54 ***Myrmecridium pulvericola*** (HKAS 136941) **a** Colonies on the substratum. **b–e** Conidiophores. **f, g** Denticulate conidiogenous loci. **h–m** Conidia. **n** Germinating conidium. **o, p** Colonies on PDA from surface and reverse. Scale bars: **b–e** = 20 µm, **f, n** = 10 µm, **g** = 5 µm, **h–m** = 2 µm

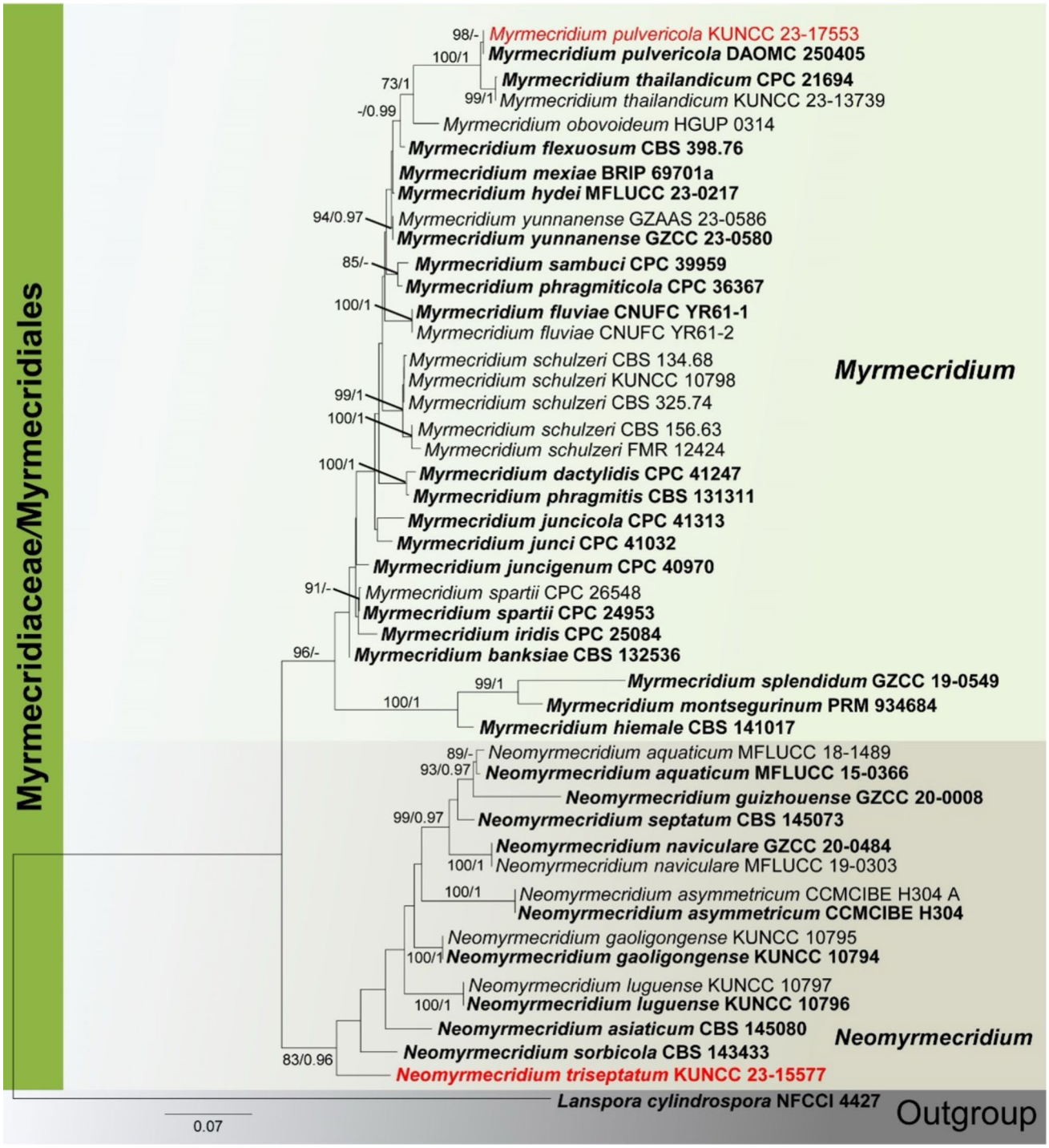


Fig. 55 Maximum Likelihood tree based on ITS and LSU sequences date. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities (PP) greater than 0.95 are given as ML/PP above the nodes. Newly obtained sequences are indicated in red and ex-type strains are in bold

98% ML support (Fig. 55). The new collection is similar to *M. pulvericola* in having unbranched, septate, cylindrical conidiophores sometimes inflated at the basal cells, pimple-like denticles conidiogenous cells, and ellipsoidal to obovoid, aseptate conidia with finely verrucose walled. Comparisons the ITS and LSU sequence data of the new collection and the ex-type strain of *M. pulvericola* showed 99.76% (420/421 bp) and 100.00% (813/813 bp, three gaps)

sequence similarity, respectively. Thus, we identify the new collection as *M. pulvericola*, a species was introduced by Crous et al. (2016a) from house dust in Uruguay, therefore, it is the first introduced this species from freshwater habitat in China.

Neomyrmecridium Crous.

Notes: Crous et al. (2018) introduced *Neomyrmecridium* to accommodate two new species (*N. septatum* and *N. asiaticum*) and a new combination (*N. sorbicola*), with *N. septatum* as the type species. Based on morphological and phylogenetic analysis, six species were successively accepted into *Neomyrmecridium* (Hyde et al. 2020a; Serrano et al. 2020; Xu et al. 2023; Yang et al. 2023a). Therefore, a total of nine asexual species are accepted in *Neomyrmecridium*, and all these species were isolated from plant tissues from freshwater and terrestrial habitats (Hyde et al. 2020a; Serrano et al. 2020; Xu et al. 2023; Yang et al. 2023a). *Neomyrmecridium* is characterized by erect, unbranched conidiophores, polyblastic conidiogenous cells bearing multiple denticles at upper part, and fusoid-ellipsoidal conidia most with 3-septate when mature (Crous et al. 2018; Xu et al. 2023). In this study, we introduce a new species *Neomyrmecridium triseptatum* with branched conidiophores, and this is the first report this character in *Neomyrmecridium*.

Neomyrmecridium triseptatum W.P. Wang & Z.L. Luo, **sp. nov.**

Fungal Names: FN 572040; *Facesoffungi*: FoF 16386; Figs. 55, 56

Etymology: Referring to the conidia with three septate.

Holotype: HKAS 136944.

Saprobic on submerged decaying wood. Asexual morph: **Colonies** on natural substrate superficial, scattered, solitary or gathered, brown to brownish-yellow, hairy. **Mycelium** mostly immersed, composed of septate, smooth-walled, hyaline to brown hyphae. **Conidiophores** (144–)204–332 × 3.4–4.8 µm ($\bar{x}$ = 253.7 × 4.2 µm, n = 20), macronematous, mononematous, erect, unbranched or branched, slightly flexuous to curved, cylindrical, with irregular contraction and then curved, septate, brown, paler towards the apex, subhyaline to pale brown at the apex, with multiple denticulate conidiogenous loci at the upper part. **Conidiogenous cells** polyblastic, integrated, terminal, becoming intercalary, sympodial, short, pimple-like denticles. **Conidia** 16–23 × 3.7–5.6 µm ($\bar{x}$ = 18.7 × 4.7 µm, n = 40), solitary, clavate to fusiform, truncate at the base, subhyaline to pale brown, 3-septate when mature without septum, verrucose, tapering to the base with a hilum, with a thin mucilaginous sheath at the middle part (Fig. 56j, l). Sexual morph: Undetermined.

Culture characteristics: Conidia germinating on PDA within 12 h, and germ tubes produced from both ends. Colonies growing on PDA, and after 3 weeks of incubation at room temperature, the diameter reaches about 2 cm. Mycelia damp, dense, colonies on the surface of PDA, thin, with a punctate protrusion in central, surface flat, with regular edges, yellow. Reverse circular, brownish-yellow to yellow with pale yellow edges, smooth.

Material examined: CHINA, Yunnan Province, Qujing City, Luoping County, Jiulonghe River (24°92′51.39″N 104°28′78.54″E), on submerged decaying stem of unknow species of Bambusoideae, 15 July 2023, *Wen-Peng Wang*, *S-5133* and *S-5134* (HKAS 136944, **holotype**; KUNCC 23–15,577, ex-type).

GenBank: KUNCC 23–15577: PQ143313 (ITS), PQ143315 (LSU).

Notes: *Neomyrmecridium triseptatum* matches the concept of *Neomyrmecridium* in having erect, cylindrical conidiophores paler towards the apex, polyblastic conidiogenous cells bearing multiple denticles at upper part, and clavate to fusiform conidia with 3-septate when mature (Crous et al. 2018; Hyde et al. 2020a; Serrano et al. 2020; Xu et al. 2023; Yang et al. 2023a). However, *N. triseptatum* has unbranched or branched conidiophores with irregular contraction and then curved, this feature can be easily distinguished from other species of *Neomyrmecridium*. In the phylogenetic analysis, *N. triseptatum* constitutes an independent lineage that are basal to other *Neomyrmecridium* species (Fig. 55). We therefore identify *Neomyrmecridium triseptatum* as a new species based on morphological and phylogenetic analysis.

Xylariales Nannf.

Notes: Xylariales was introduced by Nannfeldt (1932), and originally assigned to the class Hymenoascomycetes by Barr (1990). Subsequently, Eriksson and Winka (1997) established a new subclass Xylariomycetidae to accommodate it. Xylariales is a larger order in the subclass Xylariomycetidae, comprising 22 families 130 genera, and more than 3,300 species, with another 144 genera *incertae sedis* in Xylariales (Maharachchikumbura et al. 2015, 2016; Sugita et al. 2022, 2024; Wijayawardene et al. 2022; Peng et al. 2024).

Pallidoperidiaceae R. Sugita & Kaz. Tanaka.

Notes: Pallidoperidiaceae was established by Sugita et al. (2024) to accommodate bambusicolous Anthostomella-like fungi, viz. *Amphigermslita*, *Crassipseudostroma*, *Minuticlypeus*, *Pallidoperidium* and *Nigropunctata*, of which *Pallidoperidium* as type genus and *P. exasperatum* as the type species. It is worth mentioning that all members of Pallidoperidiaceae were collected from bamboo, while most of the species were reported as the sexual morph, and only a few species of asexual morph have been formed on rice straw agar (RSA) in culture, viz. *Amphigermslita fusiformis*, *Crassipseudostroma phyllostachydis*, *Minuticlypeus discosporus* and *Pallidoperidium paraexasperatum* (Samarakoon et al. 2022, 2023; Li et al. 2024c; Sugita et al. 2024).

Fig. 56 ***Neomyrmecridium triseptatum*** (HKAS 136944, holotype) **a, b** Colonies on the substratum. **c** Conidiophore. **d, e** Conidiophores and conidia. **f** Denticulate conidiogenous loci. **g, h** Conidiogenous cells with conidia. **i–l** Conidia. **m** Germinating conidium. **n, o** Colonies on PDA from surface and reverse. Scale bars: **c–e** = 40 μm, **f–h, m** = 10 μm, **i–l** = 5 μm

Nigropunctata Samarak. & K.D. Hyde.

Notes: The genus *Nigropunctata*, typified by *Ni. bambusicola*, was established by Samarakoon et al. (2022) to accommodate three Anthostomella-like species, *Ni. bambusicola*, *Ni. Nigrocircularis* and *Ni. thailandica*. This genus was initially placed under Xylariales genera incertae sedis (Samarakoon et al. 2022). Subsequently, Sugita et al. (2024) established Pallidoperidiaceae and accepted another four genera *Amphigermslita*, *Crassipseudostroma*, *Minuticlypeus* and *Pallidoperidium* in this family based on morphology and molecular analyses. There are seven *Nigropunctata* epithets listed in Index Fungorum (accessed in March 2024), and all of which are associated with bamboo. This genus is characterized by deeply immersed ascomata throughout the host tissue, globose to subglobose, a thick peridium composed of cells of *textura angularis*, 8-spored, unitunicate, cylindrical short-pedicellate asci, usually with a J + apical ring, and brown to dark brown, oblong to broadly ellipsoidal ascospores with thick, mucilaginous sheath (Samarakoon et al. 2022, 2023; Li et al. 2024c; Sugita et al. 2024). In this study we introduce *Ni. conspicosa* as a new species based on both morphology and phylogeny. We provide an updated tree for the genus (Fig. 57).

Nigropunctata conspicosa N. Wu & Jian K. Liu, **sp. nov.**

Index Fungorum: IF 902260; *Facesoffungi*: FoF 15930; Figs. 57, 58

Etymology: The specific epithet reflects the conspicuous sheath of ascospores.

Holotype: MFLU 24–0128.

Saprobic on dead branches of bamboo. Sexual morph: **Ascomata** deeply immersed throughout the host tissue, solitary, visible as black domes on the substrate, vertical sections subglobose or conical, ostioles centric. **Peridium** easily detached from substratum when dry, composed of two strata, outer stratum thick, consisting dark brown to hyaline cells of *textura angularius*, inner stratum thin. *Paraphyses* 2–5 µm ($\bar{x}$ = 3 µm, n = 10), wide, hyaline, branched, longer than the asci, septate, slightly constricted, guttulate, embedded in a gelatinous matrix, smooth-walled. **Asci** 126–145 × 10–11 µm ($\bar{x}$ = 136 × 10 µm, n = 20), 8-spored, unitunicate, cylindrical, short-pedicellate or sometimes apedicellate, apically rounded. **Ascospores** 14–19 × 7–8 µm ($\bar{x}$ = 17 × 7 µm, n = 30), oblong to broadly ellipsoidal, hyaline, mostly aseptate, sometimes 1-septate, slightly constricted at the septum when young, becoming dark brown at maturity, aseptate, guttulate, with or without a slightly curved germ slit running along with the entire ascospore-length, surrounded by a 5–12 µm ($\bar{x}$ = 8 µm, n = 30) thick mucilaginous sheath, slightly constricted at center. Asexual morph: Undetermined.

Culture characteristics: Ascospores germinated on PDA within 12 h at 25 °C. Colonies on PDA reached 5 cm diam. after 2 weeks at 20–25 °C, mycelium white, medium sparse, circular, flat, white to yellowish at the center.

Material examined: THAILAND, Chiang Rai Province, Amphoe Mae Sai, Tambon Wiang Phang Kham, Paholyothin Road, 20°24′16.6"N 99°52′42.4"E, on dead branches of bamboo (Poaceae), 4 July 2019, *Na Wu*, *YW87* (MFLU 24–0128, **holotype**; MFLUCC 24–0092, ex-type) and *YW88*.

GenBank: MFLU 24–0128: PP868305 (ITS), PP868306 (nucLSU), PP869337 (*rpb2*), PP869336 (*tef1*).

Notes: Multi-gene phylogenetic analyses showed that *Ni. conspicosa* (MFLUCC 24–0092) constitute a distinct lineage in *Nigropunctata* but claded closer to *Ni. khalidii* and *Ni. thailandica* (Fig. 57). *Nigropunctata conspicosa* can be distinguished from the above closely related species based on ITS, LSU and *tef* loci for *Ni. khalidii* (18/434 bp in ITS) and *Ni. thailandica* (30/582 bp in ITS, 23/947 bp in LSU, 31/935 bp in *tef1*). Morphologically, *Ni. conspicosa* is similar to *Ni. khalidii* and *Ni. thailandica*, which in having deeply immersed ascomata with two-layered peridium comprising cells of *textura angularis*, wide paraphyses and unitunicate, cylindrical asci with a short pedicel and hyaline to dark brown ascospores, covered with a mucilaginous sheath. However, *Ni. Conspicosa* differs from *Ni. khalidii* and *Ni. thailandica* by its shorter asci and ascospores with thicker mucilaginous sheath, and no germ slit was observed in *Ni. khalidii*.

Basidiomycota R.T. Moore.

Agaricomycetes Doweld.

Agaricales Underw.

Notes: Agaricales encompasses most of the so-called mushrooms and toadstools, and is one of the best studied and conspicuous morphologically varied assemblage of Agaricomycetes (Singer 1986; Hibbett et al. 2014; Kalichman et al. 2020). According to He et al. (2019), Agaricales contains 17,291 species grouped into 508 genera and 38 families. Kalichman et al. (2020), in their compilation of names of the Agaricales, considered 46 family names. Recently, some new taxa Agaricales with poroid hymenophore were described (Zhang et al. 2022a, 2023a, 2024). The first study to use genomic data for the Agaricales was conducted in Dentinger et al. (2016), providing a fully supported phylogeny of the order, enabling the recognition of seven suborders. Subsequently, the order is divided into 11 suborders: Agaricineae, Clavariineae, Hygrophorineae, Marasmiineae, Mycenineae, Pleurotineae, Pluteineae, Phyllotopsidineae, Sarcomyxineae, Schizophyllineae, and Tricholomatineae (He et al. 2024a). Some species of Agaricales are the important forest pathogens and edible mushrooms (Wu et al. 2019b; Qin et al. 2025).

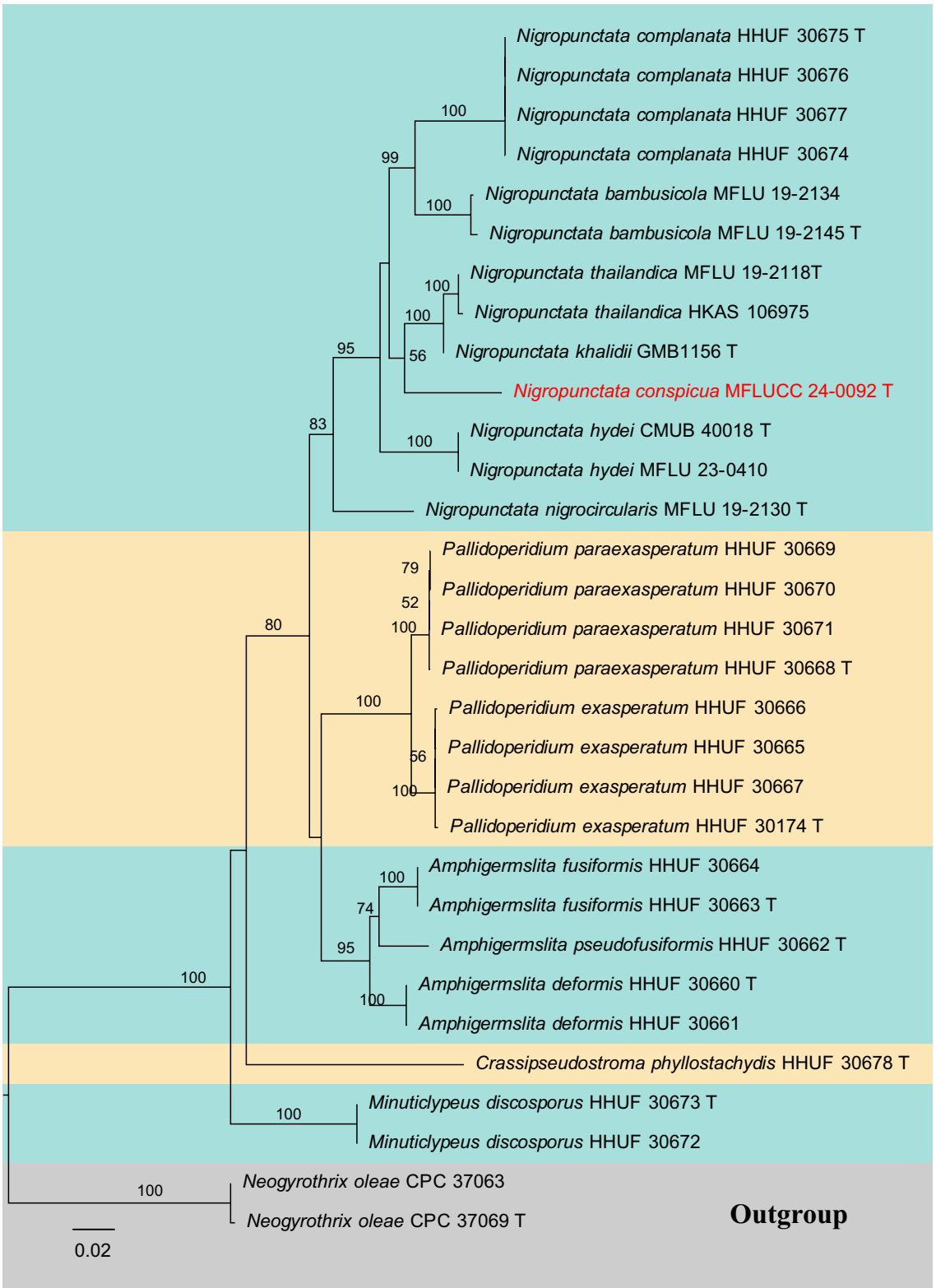


Fig. 57 Phylogenetic tree generated from the Maximum Likelihood analysis based on the combined ITS, LSU, *rpb2* and *tef* sequence data of Pallidoperidiaceae. The ML (≥50%) and BI (≥95%) bootstrap supports are given near the nodes, respectively. New species are shown in red. "T" refers to a type specimen. The tree is rooted with *Neogyrothrix oleae* (CPC 37063, CPC 37069)

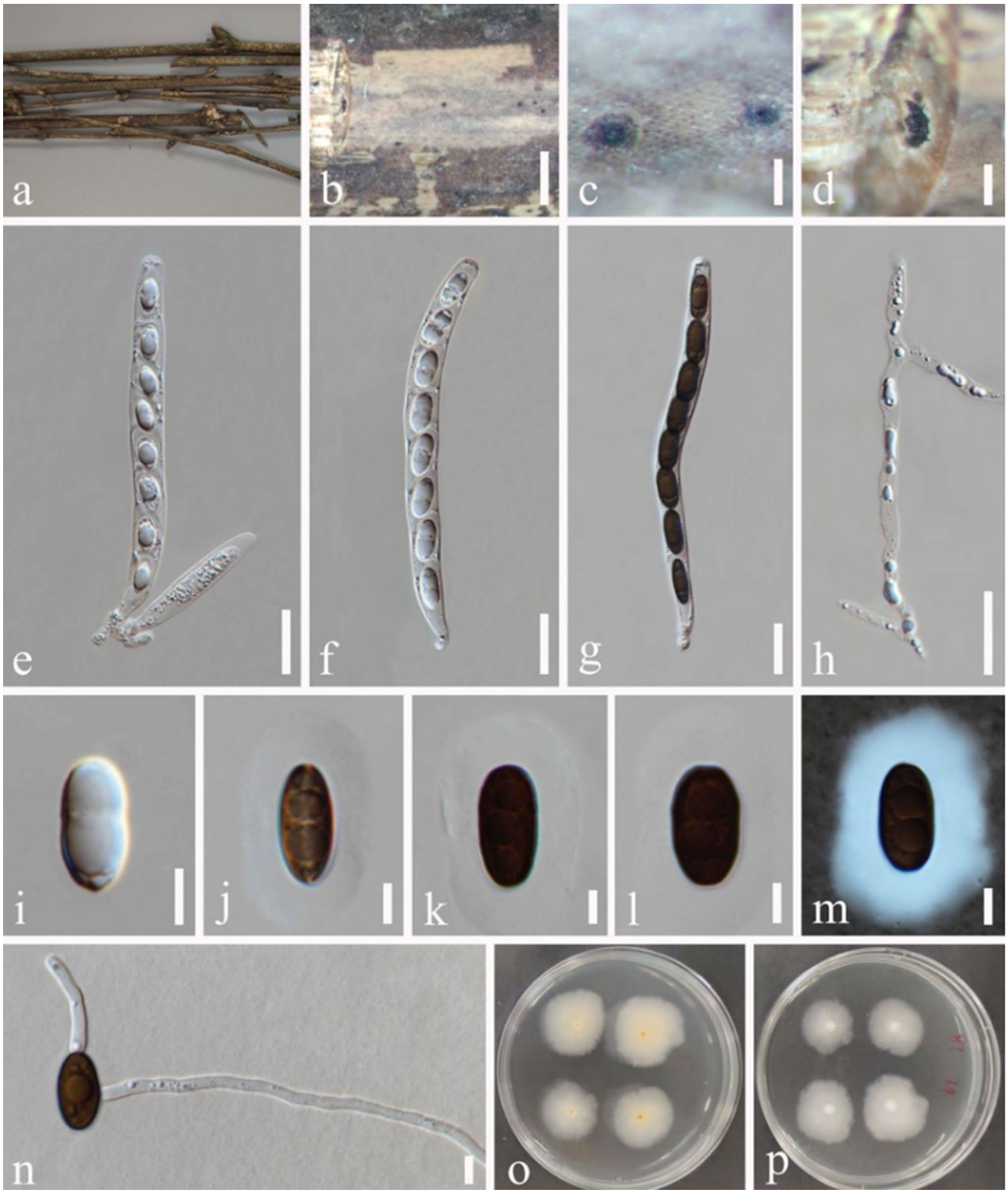


Fig. 58 ***Nigropunctata conspicosa*** (MFLU 24–0128, **holotype**). **a** Substrate. **b**, **d** Sections through ascomata. **c** ascomata in dead substrate. **e**–**g** Asci. **h** Paraphyses. **i**–**m** Ascospores (m in Indian ink showing the sheath). **n** Germinated ascospore. **o–p** Colonies on PDA, **o** from above, **p** from below. Scale bars: **b** = 100 µm, **c** = 10 µm, **d**–**h** = 20 µm, **i**–**n** = 5 µm

Agaricaceae Chevall.

Notes: Agaricaceae is a well-known family of Agaricales with a global distribution. Agaricaceae s.l. includes five families – Agaricaceae s.str., Coprinaceae, Lepiotaceae (nom. inval.), Lycoperdaceae and Tulostomataceae – as well as five genera with unknown phylogenetic position and no existing sequence data (*Endolepiotula, Hiatulopsis, Janauaria, Phyllogaster, Rugosospora*) (Kalichman et al. 2020). Genera in this group are agaricoid, gasteroid or secotioid, and the agaricoid species generally have a pluteoid, lepiotoid or tricholomatoid, rarely collybioid or mycenoid basidiomata. Typical are also free or rarely adnexed lamellae, a veil commonly forming an annulus and/or characteristic squamules on the pileal and stipe surfaces, hyaline to pigmented basidiospores seen as white, very pale pink or dark/black spore prints, and a regular to subregular and non-gelatinized trama (Pegler 1986; Vellinga 2004). The family is of great scientific interest comprising important decomposers but also symbionts as well as edible, poisonous and medicinal species (Singer 1986; Alexopoulos et al. 1996; Didukh et al. 2003).

Agaricus L.

Notes: *Agaricus* L. is among the large monophyletic genera belonging to the Agaricaceae family. The genus includes more than 500 known species from temperate and tropical regions of the world (Zhao et al. 2016). Characteristically, it has a wide range of fruiting bodies in different colors and sizes, membranous annuli (either simple or double), free gills in shades of brown, and brown basidiospores. According to recent phylogenetic studies, the genus is subdivided into six subgenera, viz., *Agaricus* subg. *Agaricus*, *A.* subg. *Flavoagaricus*, *A.* subg. *Minores*, *Agaricus* subg. *Minoriosis, A.* subg. *Pseudochitonia*, and *A.* subg. *Spissicaules* (Chen et al. 2017a; Parra et al. 2018). These subgenera consist of 25 sections (Chen et al. 2017a; Parra et al. 2018; He et al. 2018; Hussain et al. 2022).

Agaricus longistipitatus R.L. Zhao & B. Cao, **sp. nov.**

Fungal Names: FN 572241; *Facesoffungi*: FoF 17101; Figs. 59, 60

Etymology: refers to the species having a long stipe.

Holotype: HMAS 255764.

Pileus initially globose, then hemispherical, brown to dark brown, uplifted or appressed, squamose scales, more appressed and smaller at the center. Pileal surface dull, dry. **Lamellae** free, crowded, up to 0.6 cm broad, at first whitish, then reddish-brown, edge whitish. **Stipe** generally solitary, 14–26 × 2–4 cm, central, narrowly fistulose, cylindrical, progressively tapered towards the base, annulate in its upper part. **Annulus** superous, membranous, thick, smooth upper surface, fibrillose from the universal veil along the margin. **Context** first white, then reddish, slowly becoming reddish-brown everywhere on exposure.

Basidiospores (5.8–)6.3–7.2–7.6 × (4.2–)4.7–5.8–6.4(–6.9) µm, Q = 1.16–1.25–1.35, ellipsoid to broadly ellipsoid, brown, thick-walled, without germ pore. **Basidia** 29.2–44.3 × 9.9–13.1 µm, clavate. **Pleurocystidia** absent. **Cheilocystidia** hyaline, often with a basal septum, the terminal element being clavate to cylindrical 19.7–36.4 × 7.7–10.5 µm. **Pileipellis** constituted by cylindrical, radially arranged hyphae, 3.9–10.8 µm wide, not or slightly constricted at septa.

Chemical reactions: Schäffer's reaction positive.

Material examined: CHINA, Gansu Province, Wuwei City, Tibetan Autonomous County of Tianzhu, 22 August 2018, collected by *An-Qi Liu*, *ZRL20181453* (HMAS 281410); 24 August 2018, *Bin Cao, ZRL20181408* (HMAS 255764, **holotype**).

GenBank: HMAS 255764: PQ628228 (ITS); HMAS 281410: PQ628227 (ITS).

Notes: Neither of the two specimens of *Agaricus longistipitatus* had fully unfolded caps, preventing the observation of mature fruiting body morphology. The most notable characteristic of this species is its exceptionally long stipe, approximately 3/4 of which remains underground.

Agaricus pallidobrunneus R.L. Zhao, **new geographical record from India.**

Fungal Names: FN 570225; *Facesoffungi*: FoF 01182; Figs. 61, 62

Pileus 80–97 mm in diam., 6 mm thick at disc, convex to applanate; surface dry, white (1A1) fibrillous cap along with light brown (6D8) to grayish brown (7D3) appressed squamules denser at the center and in a scattered manner throughout the pileus; margins were decurved. **Lamellae** free, reddish gray to rose gray (12B2–12B4) in the young stage and chocolate brown (9E8–9F8) at maturity, 8.5 to 10 mm broad with 1 to 2 series of lamellulae being present. **Stipe** 98–105 × 15–19 mm, somewhat cylindrical but minutely wide towards the base, hollow, surface yellowish white (1A2) basal region is surrounded by minute grayish brown (7D3) squamules, no bruising was observed, and on cutting no significant color change was observed. **Annulus** membranous, pendant upper layer, smooth, white (1A1) and floccose lower layer, white (1A1). **Context** white (1A1) to both in pileus and stipe, no color observed on air exposure. **Odor** pleasant.

Basidiospores (6.4–)7.3–7.7–7.9(–8.2) × (3.8–)4.2–4.6–5.0(– 5.2) µm, Q = 1.6–1.7–1.8, ellipsoid to oblong, smooth, brown when viewed with water, inamyloid, thick-walled, 1–2 guttule present. **Basidia** 20–27 × 6.4–8.96 µm, clavate to broadly clavate hyaline, smooth, 4 spored. **Basidioles** 19–21 × 5.0–5.5 µm, clavate,

Fig. 59 *Agaricus longistipitatus*. **a, b** Basidiomata (HMAS 255764, **holotype**). **c** Basidiomata (HMAS 281410). **d** Basidiospores. **e** Basidia. **f** Cheilocystidia. **g** Pileipellis hyphae. Scale bars: **a–c** = 2 cm, **d–g** = 10 µm

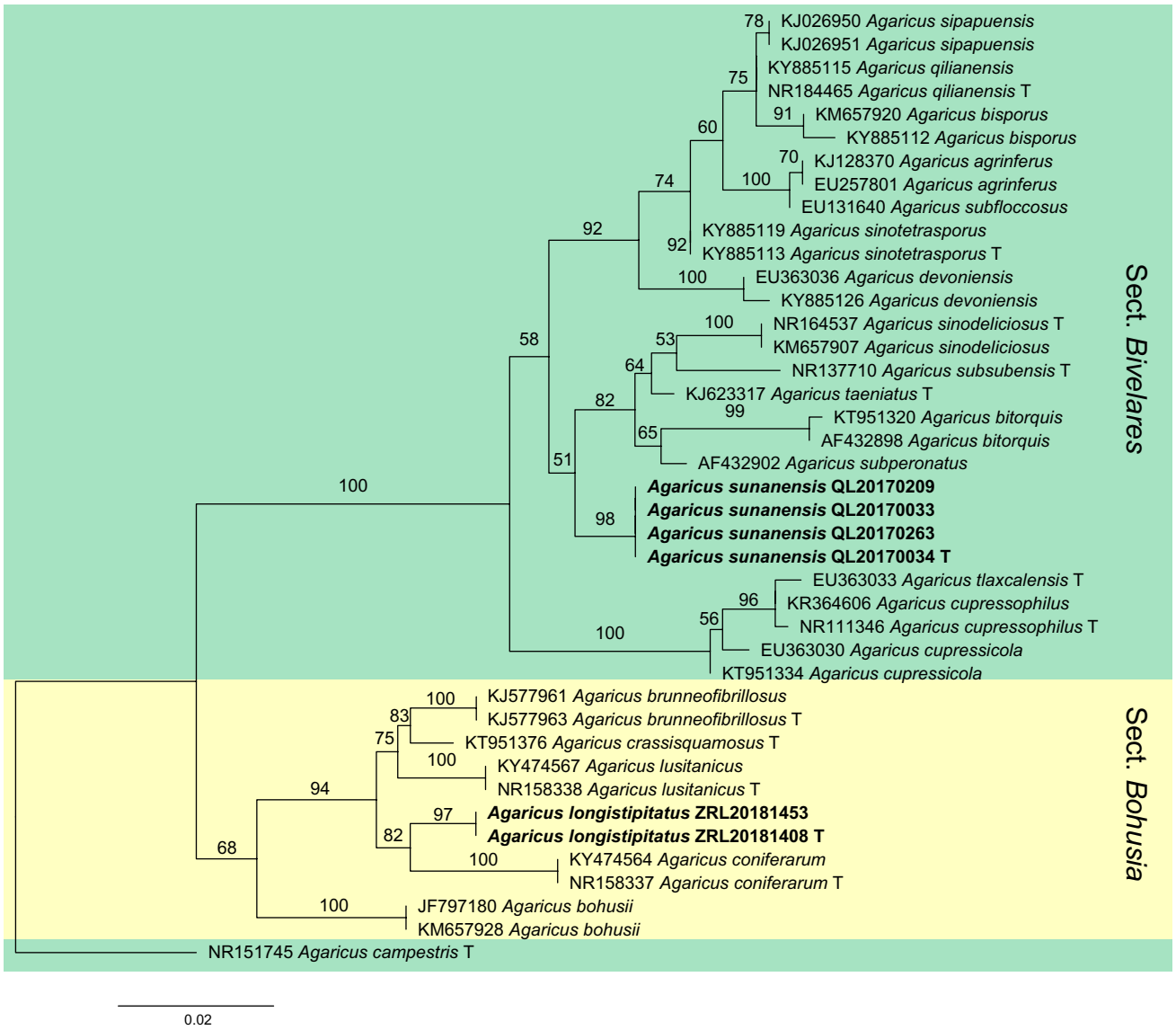


Fig. 60 Maximum Likelihood tree of Sect. *Bivelares* and *Bohusia* based on ITS sequences, bootstrap values greater than 50% are shown around nodes. New species are shown in blod. "T" refers to a type specimen

hyaline, thin-walled. **Pleurocystidia** absent. **Cheilocystidia** 18–24 × 11.5–15.5 µm, abundant, simple, clavate to ellipsoid or pyriform, hyaline, smooth. **Annulus** composed of hyaline hyphae of 23.5–24.5 × 8.0–9.0 µm. **Pileipellis** a cutis, composed of septate hyphae 23–39 × 7.5–13.0 µm, slightly ellipsoid to cylindrical, with brownish pigmentations. **Stipitipellis** composed of cutis hyphae of 6.0–9.0 µm width, cylindrical and hyaline. **Clamp connection** absent.

Macro-chemical reactions: Yellow on addition of KOH in all tissues; Schäffer's reaction negative.

Ecology and Distribution: Growing in gregarious form on decomposed humus of leaf litter mixed soil. Earlier known to occur from China and Thailand.

Material examined: INDIA, Assam, Kamrup metro district, Jalukbari, 26°09′07.7"N 91°39′36.2"E, 79.0 m asl., 11 Oct 2022, *A.K. Dutta & P. Chattopadhyay*, *PC22/GU/AG22* (GUBH 20457); Assam, Kamrup metro district, Jalukbari, 26°09′07.6"N 91°39′35.9"E, 79.0 m asl., 24 Aug 2023, *A.K. Dutta & P. Chattopadhyay*, *PC23/GU/AG38* (GUBH 20459).

GenBank: GUBH 20457: OR875413 (ITS); GUBH 20459: OR875414 (ITS).

Notes: The taxon *Agaricus pallidobrunneus* was first discovered in Yunnan Province, China (Zhao et al. 2016). Later, it was also reported from Thailand (Jaichaliaw et al. 2021). The characteristic features of the taxon include a

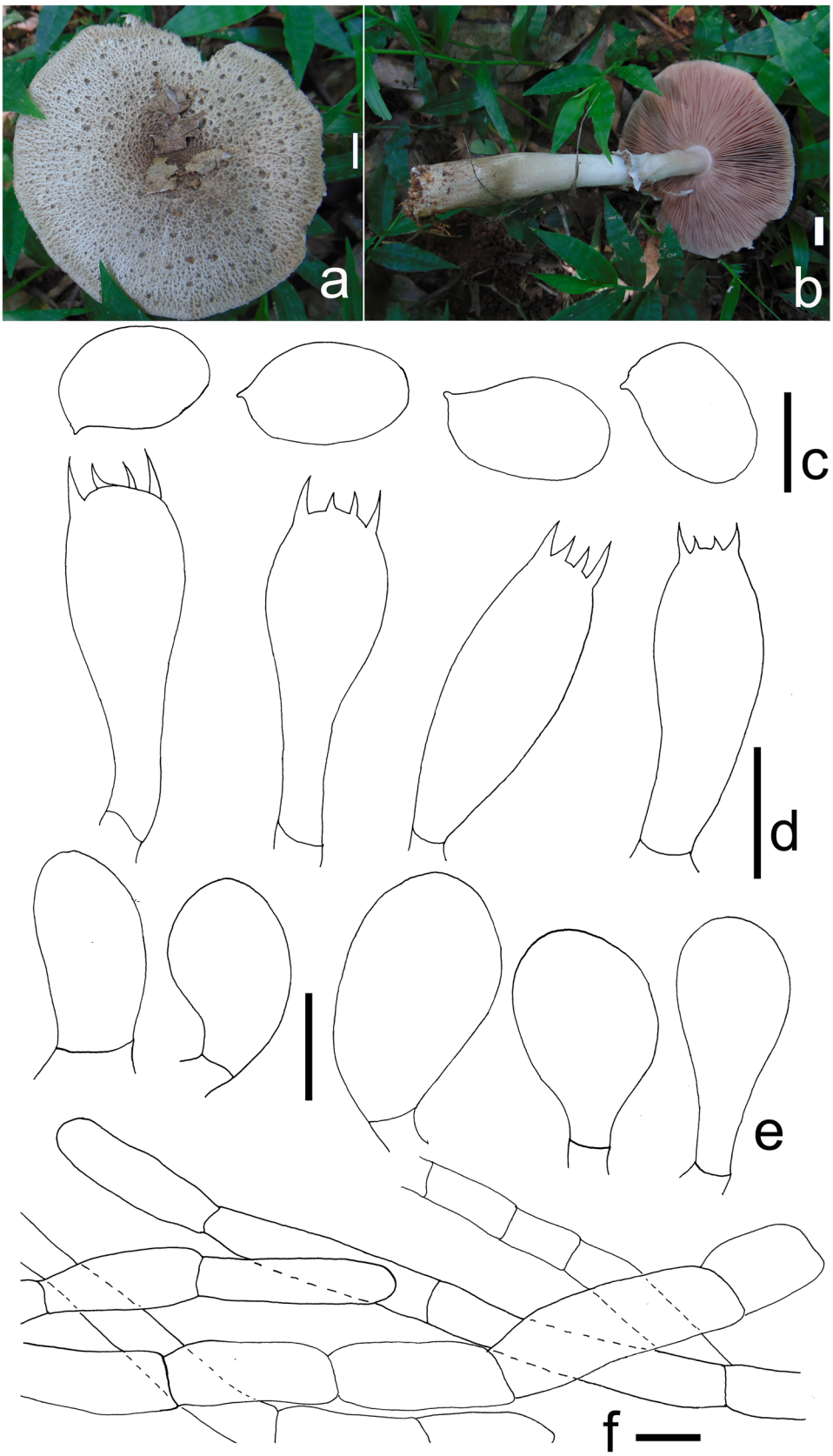


Fig. 61 *Agaricus pallidobrunneus* (GUBH 20457). **a** Fibrillose squamules over the pileus surface. **b** Lamellae and stipe view. **c** Basidiospores. **d** Basidia. **e** Cheilocystidia. **f** Pileipellis hyphae. Scale bars: **a, b** = 10 mm, **c** = 5 µm, **d–f** = 10 µm

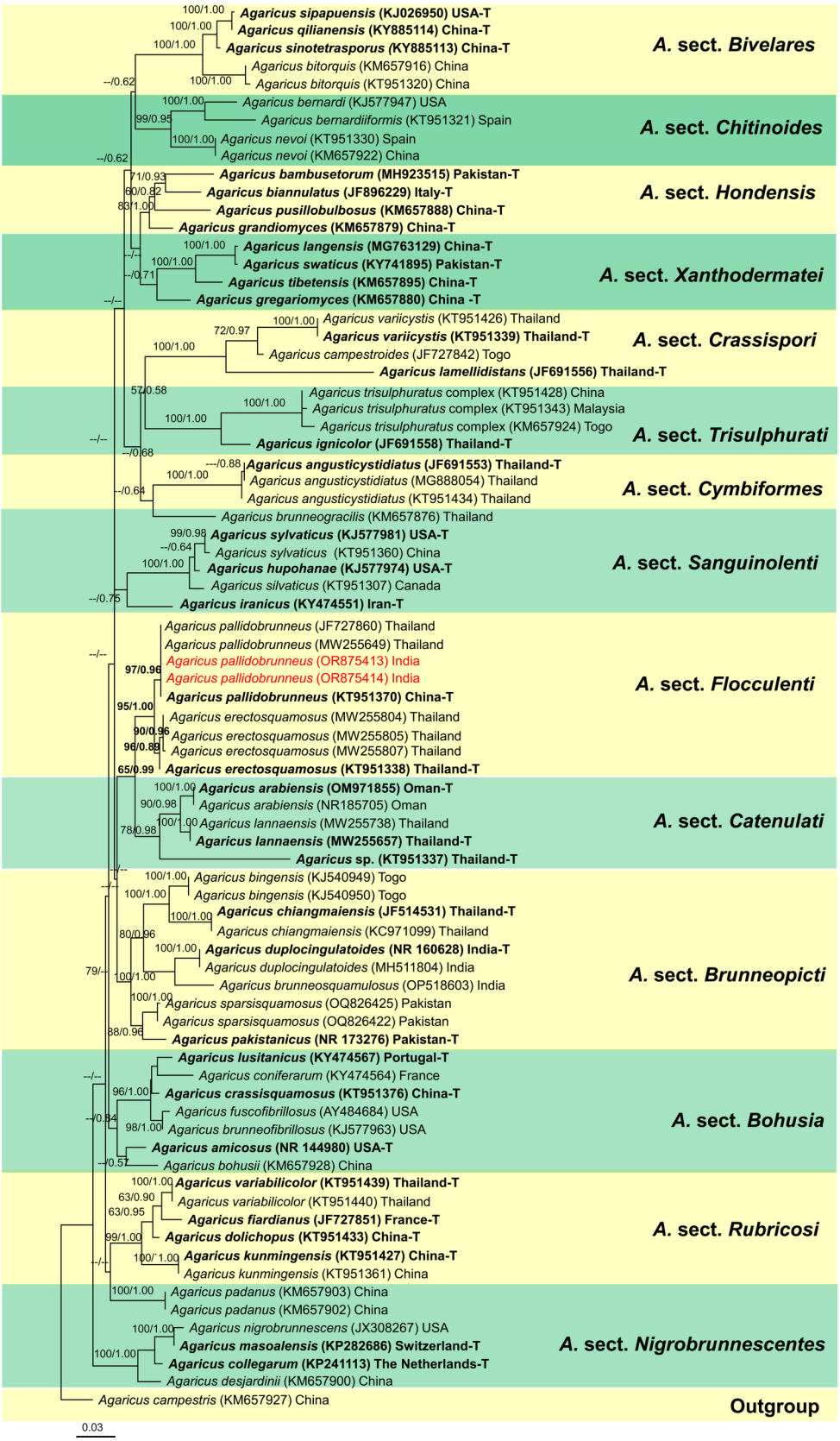


Fig. 62 Maximum Likelihood phylogram (*-InL* = 5828.769149) generated using GTR + I + G model of nucleotide evolution for nrITS sequences. The MLBS support values ≥ 50% is shown on the left of "/" and Bayesian posterior probabilities (PP) support of greater than ≥ 0.50 on the right side. Type sequences are shown in black bold and tagged "T" at the end. All the taxa are represented along with their GenBank accession numbers and respective country of origin. The sequences of *Agaricus pallidobrunneus* generated for this study are marked in red front

comparatively well-developed universal veil, no discoloration on bruising or exposure of context to air, larger basidiospores, and fibrillose squamules over pileus and stipe (Zhao et al. 2016).

In the phylogenetic analysis (Fig. 62), the newly generated two Indian sequences cluster together with the type specimen sequence of *Agaricus pallidobrunneus* (GenBank accession No. KT951370) and two sequences of *A. pallidobrunneus*, earlier deposited from Thailand (GenBank accession No. JF727860, MW255649), with strong support values (MLBS = 97%, PP = 0.96) suggesting all the sequences to be conspecific. Morphologically, the Indian collection nicely matches the type specimen description along with the morphology of the specimens reported from Thailand. In the tree, *Agaricus erectosqumulosus* appears to be sister to *A. pallidobrunneus* (MLBS = 95%, PP = 1.00), and this cluster together represents *A.* sect. *Flocculenti*. Morphologically, *A. erectosqumulosus* differs from *A. pallidobrunneus* by having erect squamules all over the pileus surface colored brown, an annulus that is often cogwheel-like colored white with a light brown margin, orange coloration with KOH, and somewhat smaller basidiospores (mean of 7.2 × 4.4 µm vs. 7.7 × 4.6 µm in *A. pallidobrunneus*; Zhao et al. 2016).

Agaricus sunanensis R.L. Zhao & B. Cao, **sp. nov.**

Fungal Names: FN 572242; *Facesoffungi*: FoF 17102; Figs. 60, 63

Etymology: refers to Yugur Autonomous County of Sunan, Gansu Province, China, the locality of the type specimen.

Holotype: HMAS 290957.

Pileus 5–13.5 cm in diameter, at first globose, then planoconvex, later truncate and finally applanate with a shallow depression in the middle, white towards the margin, with ochre colors more or less tinged yellowish, irregularly distributed over the pileus. Margin involute, exceeding the lamellae up to 0.5 cm in mature specimens. **Lamellae** free, crowded, up to 1 cm broad, at first whitish, then reddish-brown, finally blackish. **Stipe** usually 4–7.5 × 1.5–3 cm, central, cylindrical, base at times slightly bulbous, with one or two annuli, smooth in above the upper annulus, and furfuraceous scales below the lower annulus. **Annulus** inferous, one or double, membranous, thick, fibrillose upper surface, striate towards the margin on the underside. **Context** firm, on cutting first white, then grayish-brown in the stipe.

Basidiospores (6.1–)6.8–7.4–8.4(–9) × (5.2–)5.9–6.3–7(–7.9) µm, Q = 1.11–1.19–1.24, broadly ellipsoid to subglobose, brown, thick-walled, without germ pore. **Basidia** 27.1–38.5 × 8.9–13.2 µm, clavate. **Pleurocystidia** absent. **Cheilocystidia** hyaline, cespitose, simple or with 1 to 3 septa at the base, terminal element clavate or Pyriform, 18.8–31.2 × 7.6–12.7 µm. **Pileipellis** a cutis of cylindrical hyphae, slightly constricted at septa, 3.3–9.3 µm wide.

Chemical reactions: Schäffer's reaction negative.

Material examined: CHINA, Gansu Province, Zhangye City, Yugur Autonomous County of Sunan, 21 August 2017, collected by *Ming-Zhe Zhang*, *QL20170033* (HMAS 290956), *QL20170034* (HMAS 290957, **holotype**), and *QL20170208* (HMAS 290983); 22 August 2017, *Xin-Yu Zhu, QL20170263* (HMAS 290997).

GenBank: HMAS 290956: PQ628229 (ITS); HMAS 290957: PQ628230 (ITS); HMAS 290983: PQ628231 (ITS); HMAS 290997: PQ628232 (ITS).

Notes: Agaricus sunanensis belongs to *Agaricus* sect. *Bivelares*, a group that includes several well-known edible species, such as the cultivated *A. bisporus* (J.E. Lange) Imbach and *A. bitorquis* (Quél.) Sacc. *Agaricus sunanensis* is characterized by its large, robust fruiting bodies and is considered a palatable wild edible mushroom.

Coprinus Pers.

Notes: Type species *Coprinus comatus* (O.F. Mu¨ll.) Pers., ink caps, saprotrophic, worldwide (Vellinga et al. 2011), nineteen species described to date. The genus is characterized by having whitish pileus except for the center, and usually oblong, height-width ratio, annulus present on lower half of stipe, with a reflected veil, basidiospores ellipsoid to almond-shaped, with a truncated germ pore, dark brown, inamyloid. Polygenic phylogeny indicated members of *Coprinus* formed a unique lineage with excellent support, and closely related to the unusual genus *Montagnea* (Vellinga et al. 2011).

Coprinus variicolor R.L. Zhao, B. Cao & J.X. Li, **sp. nov.**

Fungal Names: FN 571924; *Facesoffungi*: FoF 17103; Figs. 64, 65

Etymology: in reference to its central veil, which changes color from grayish to orange-brown.

Holotype: HMAS 287619.

Diagnosis: this species is characterized by its veil first whitish to grayish, discolor orange-brown when mature. Basidiospores brown, thick-walled, up to 1 µm.

Pileus ovoid to ellipsoid when still closed, measuring 1.7–5 cm, up to 10.5 cm in diameter. As it matures, the margin becomes heavily revolute, and the cap surface changes from whitish to pinkish before splitting into several pieces and deliquescing, except for the center, which remains covered with a veil that transforms from grayish to orange-brown. **Veil** is thick and persistent, eventually breaking up into 3–5 pieces and deliquescing. **Lamellae** are free, crowded, and initially whitish, turning pinkish and eventually black as they deliquesce. **Stipe** 9–17 × 0.7–1.5 cm, whitish, cylindrical, hollow, and tapers upward, featuring a central strand and a sub-bulbous base. **Annulus** on lower part, up to 2 cm, fragile and fade away. **Context** white, later black.

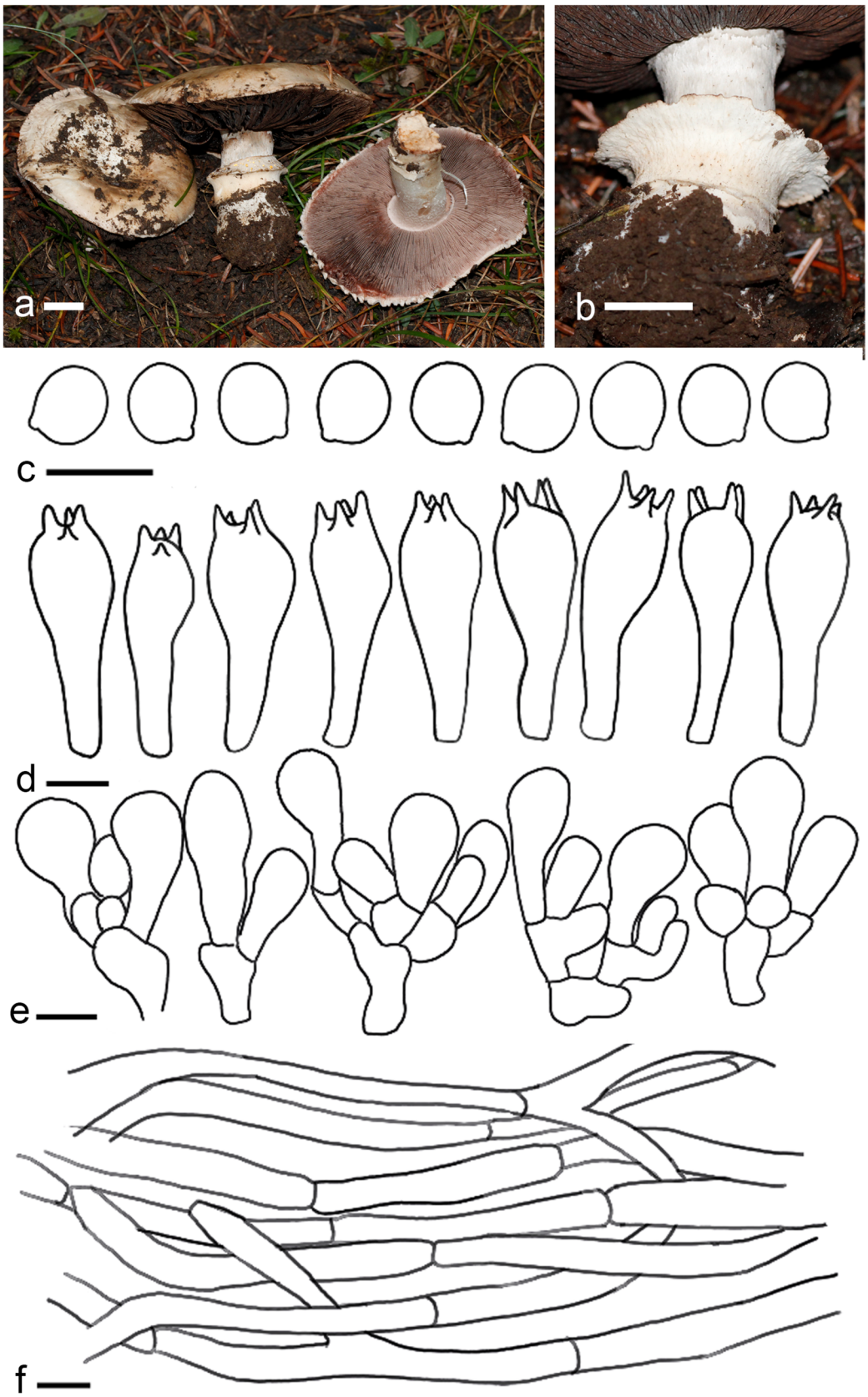


Fig. 63 *Agaricus sunanensis* (HMAS 290957, **holotype**). **a**, **b** Basidiomata. **c** Basidiospores. **d** Basidia. **e** Cheilocystidia. **f** Pileipellis hyphae. Scale bars: **a, b** = 2 cm, **c–f** = 10 µm

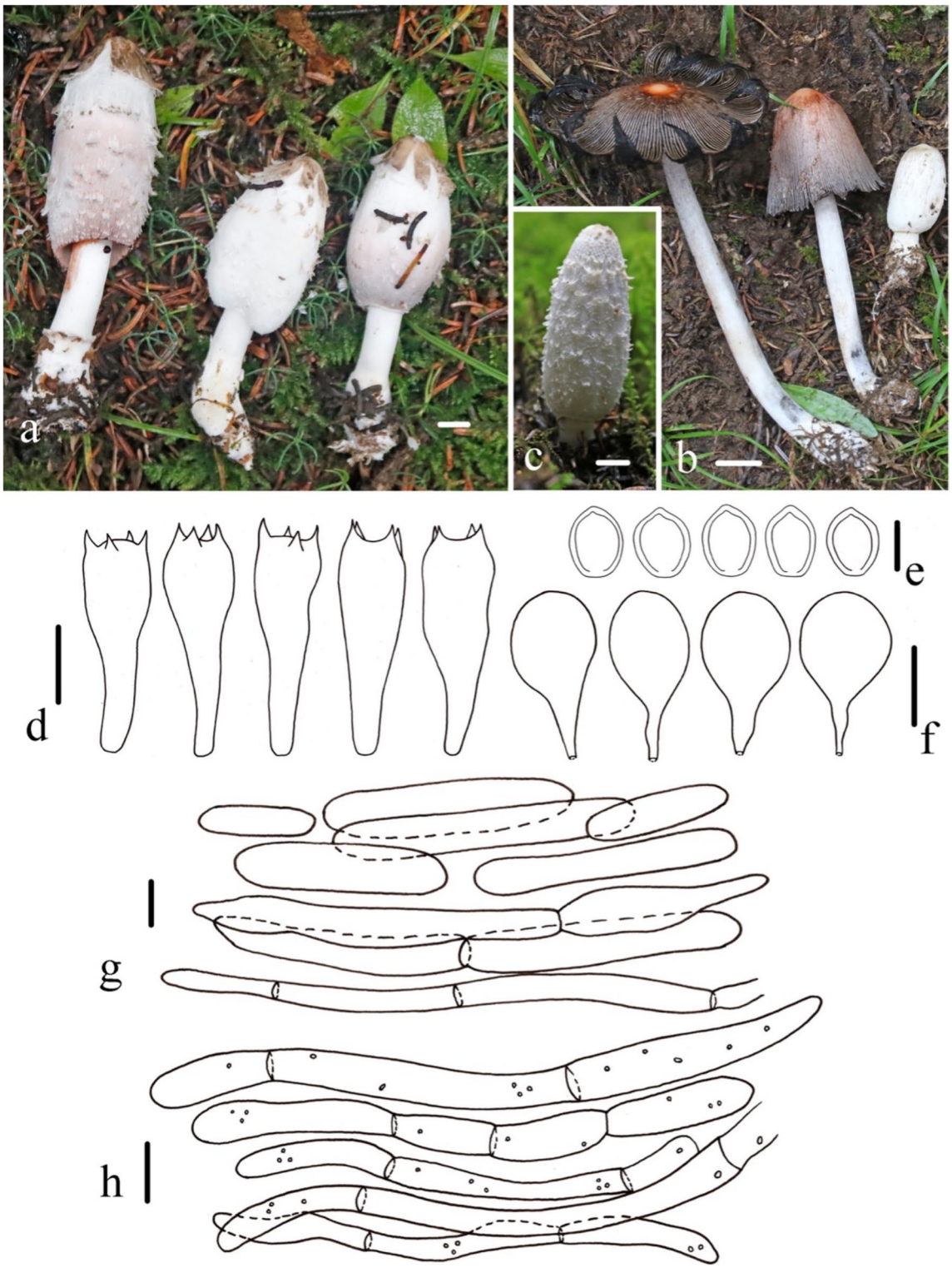


Fig. 64 ***Coprinus variicolor*** (HMAS 287619, **holotype**). **a–c** Basidiomata in field. **d** Basidia. **e** Basidiospore. **f** Cheilocystidia. **g** Veil on the pileus. **h** Element on the pileus. Scale bars: **a**, **c** = 1 cm, **b** = 2 cm, **d**, **g**, **h** = 10 µm, **e** = 5 µm, **f** = 20 µm

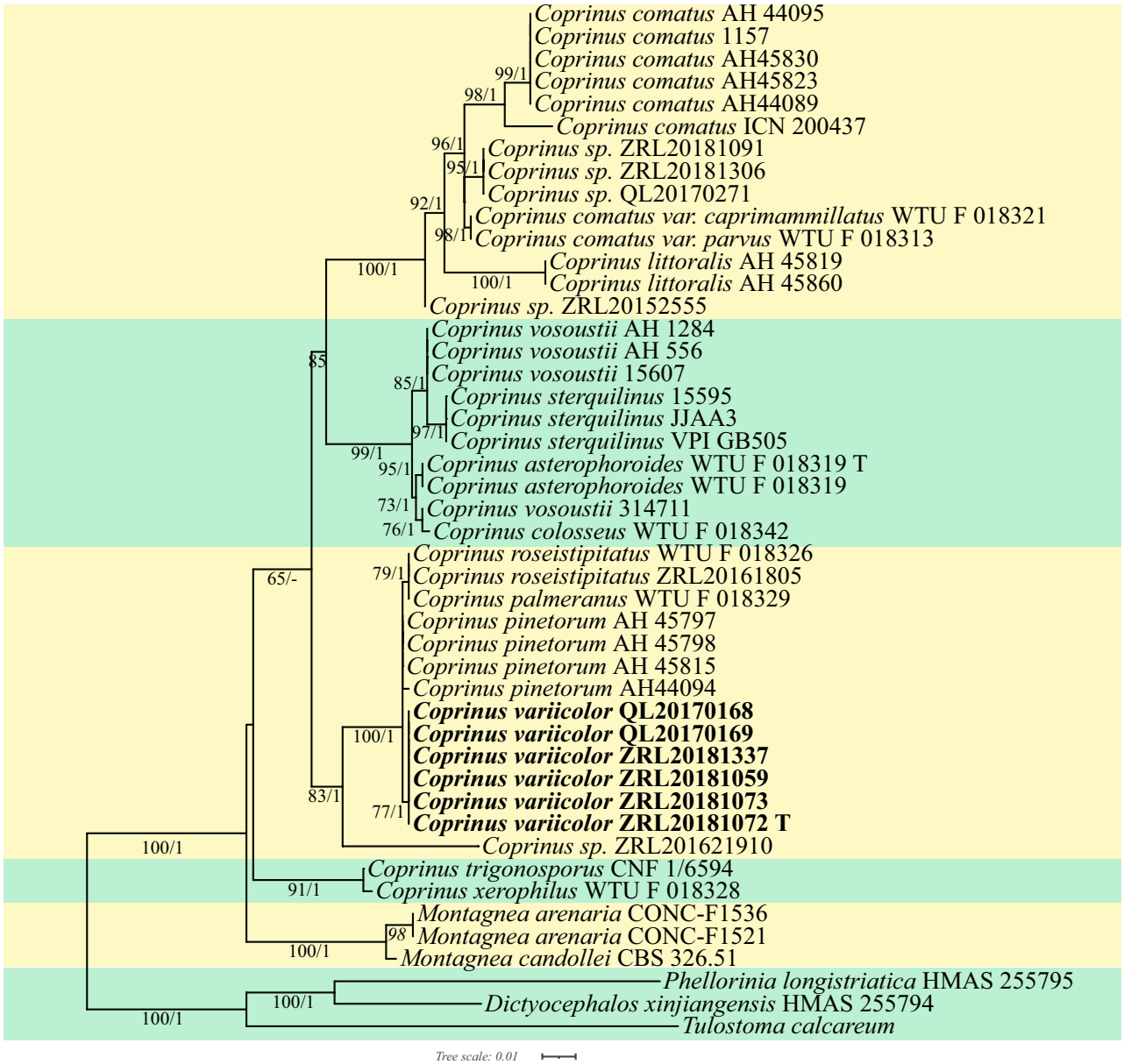


Fig. 65 Maximum Likelihood tree of *Coprinus* and *Montagnea* inferred from ITS sequences data, rooted with *Phellorinia longistriatica*, *Dictyocephalos xinjiangensis* and *Tulostoma calcareum*. Branches supported by both BS ≥ 70% and PP ≥ 0.90 were labeled. The examined specimens in this study are bolded

Basidiospores 7.6–9.8 × 5.5–7.5 µm (Q = 1.3–1.5, n = 30), amygdaliform, ellipsoid, smooth, brownish, germ-pore central, up to 1–1.5 µm, thick-walled. **Basidia** 30.2–45.2 × 9.3–12.6 µm, narrow clavate, hyaline, 4-spored. **Pleurocystidia** not observed. **Cheilocystidia** 42.6–64.4 × 22.8–37.5 µm, broadly to narrowly clavate, thick-walled. hyaline. **Pileipellis** a cutis, 7.5–21.8 µm, composed of thin-walled, subhyaline to brown hyphae, sometimes inflate in the middle. **Annulus hyphae** cylindrical to inflated, chains, abundant pores present, often constricted at the septa.

Habitat: Solitary or scattered on grasslands under spruce forests.

Known distribution: China, Gansu Province.

Material examined: CHINA, Gansu Province, Zhangye City, Yanzhishan, 20 August 2017, collected by *Ming-Zhe Zhang*, *QL20170168* (HMAS 282432), *QL20170169* (HMAS 282433); Gansu Province, Zhangye City, Matisi, 17 August 2018, collected by *Bin Cao*, *ZRL20181059* (HMAS 282434); Gansu Province, Wuwei City, Wushaoling Protection Station, Chashugou, 20 August 2018, collected by *Zhi-Lin Ling*, *ZRL20181072* (HMAS 287619, **holotype**) and

ZRL20181073 (HMAS 282435); Gansu Province, Wuwei City, Sharma Protection Station, shimenxia, 21 August 2018, collected by *Bin Cao*, *ZRL20181337* (HMAS 282436).

GenBank: HMAS 287619: PP718938 (ITS); HMAS 282432: PP718935(ITS); HMAS 282433: PP718934 (ITS); HMAS 282434: PP718936 (ITS); HMAS 282435: PP718937 (ITS); HMAS 282436: PP718935 (ITS).

Notes: Coprinus variicolor is characterized by its color-changing veil, which transitions from grayish to orange-brown as it matures, as well as its dark brown, thick-walled basidiospores with a central germ pore. Phylogenetic analysis reveals that *C. variicolor*, *C. roseistipitatus*, *C. palmeranus*, and *C. pinetorum* form a well-supported clade at the base of the tree (Fig. 65). However, these species exhibit distinct variations in the ITS region. Specifically, *C. variicolor* differs by 2 base pairs (bp) in ITS sequences from *C. pinetorum* and *C. roseistipitatus*, and by 4 bp from *C. palmeranus*. These species can be distinguished by other characteristics. *Coprinus roseistipitatus*, originally described from Washington State by Van De Bogart (1976), fruits on dung. In contrast, *C. pinetorum* closely resembles *C. variicolor* but has a thick, persistent veil that remains grayish to orange-brown. Additionally, *C. pinetorum* has narrower basidiospores (Q = 1.38–1.62) and smaller basidia (14–35 × 10–13 µm) (Crous et al. 2016b). *Coprinus palmeranus* is distinguished by its globose to subglobose, ellipsoid, ovoid, oblong, or utriform cheilocystidia (25–50 × 14–26 µm) (Uljé and Noordeloos 2001).

Hymenagaricus Heinem.

Notes: Hymenagaricus is a small genus of Agaricaceae with 16 validly described species (Index Fungorum Partnership 2024). The saprotrophic genus has a paleotropical distribution and is characterized by small- to medium-sized basidiomata with a squamulose pileus, yellowish-brown to brown basidiospores, and absence of pleurocystidia and clamp connections (Heinemann 1981; Heinemann and Little Flower 1984; Reid and Eicker 1998; Kirk et al. 2008; He et al. 2019).

Hymenagaricus ruber Ralaiv., Liimat. & Niskanen, **sp. nov.**

Index Fungorum: IF 903129; *Facesoffungi*: FoF 17104; Figs. 66, 67

Etymology: ruber (Latin) = red, refers to the colors of the basidiomata.

Holotype: K-M 251793.

Pileus 1 cm in diam., at first convex, then low convex and slightly depressed in the center; deep red in the center, followed by a white zone, especially when older, then pale pink towards the margin; surface dry, with appressed plate-like scale(s) in the center, with minute squamules towards the margin. **Lamellae** free, close, edge even, with lamellulae, white. **Stipe** up to 3 cm long, up to 4 mm wide, central, white at the very top of the stipe, pink lower down, surface at the top of the stipe with small squamules, woolly-squamulose lower down, cylindrical. **Context** not recorded. **Odor** and **Taste** not recorded.

Basidiospores 5–6.5 × 3.5–4.5(–5) µm, ellipsoid, smooth, brown in KOH, yellow brown in Melzer's reagent. **Basidia** (in KOH) 12–14 × 6–6.5 µm, sterigmata 1–3 µm long, subcylindrical to pyriform, usually 2-, 4-spored, rarely 1-spored, not clamped, hyaline. **Cheilocystidia** variable in size and form, 8.5–17 × 5–7.5 µm, subutriform (Fig. 66d); 16–26 × 3.5–5 low clavate to elongate (Fig. 66e). **Pileipellis** cutis made of parallel, non-septate hyphae up to 3.5 µm wide, with a pale olive color in Melzer's reagent.

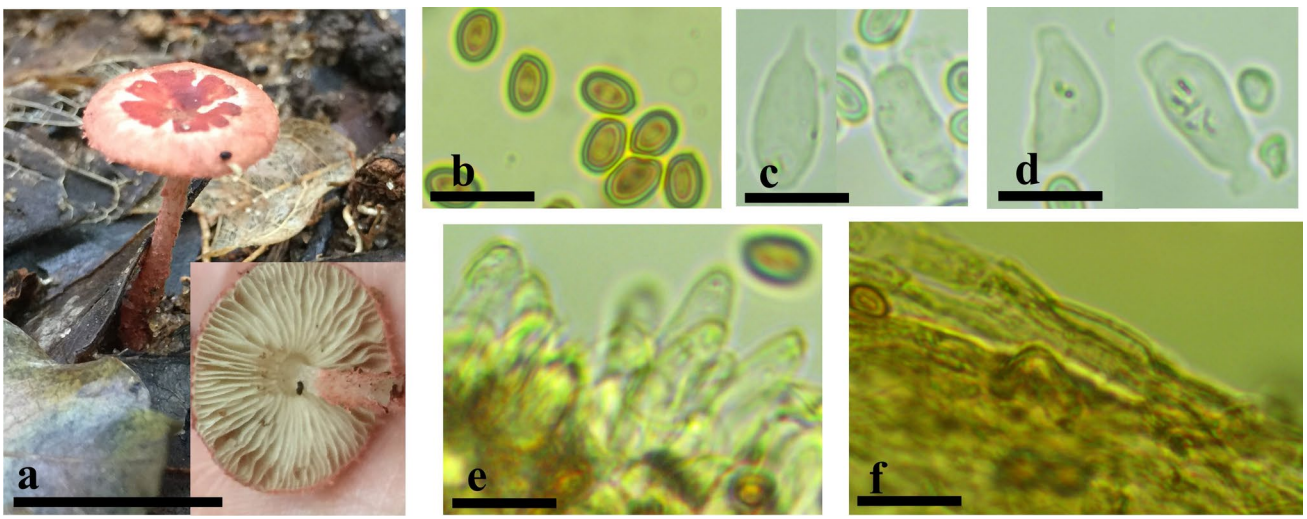


Fig. 66 ***Hymenagaricus ruber*** (K-M251793, **holotype**). **a** Basidiomata. **b** Basidiospores. **c** Basidia. **d, e** Cheilocystidia**. f** Pileipellis. Scale bars: **a** = 1 cm, **b**–**f** = 10 µm. Credit: S. Morris (**a**), Anna Ralaiveloarisoa (**b**–**f**)

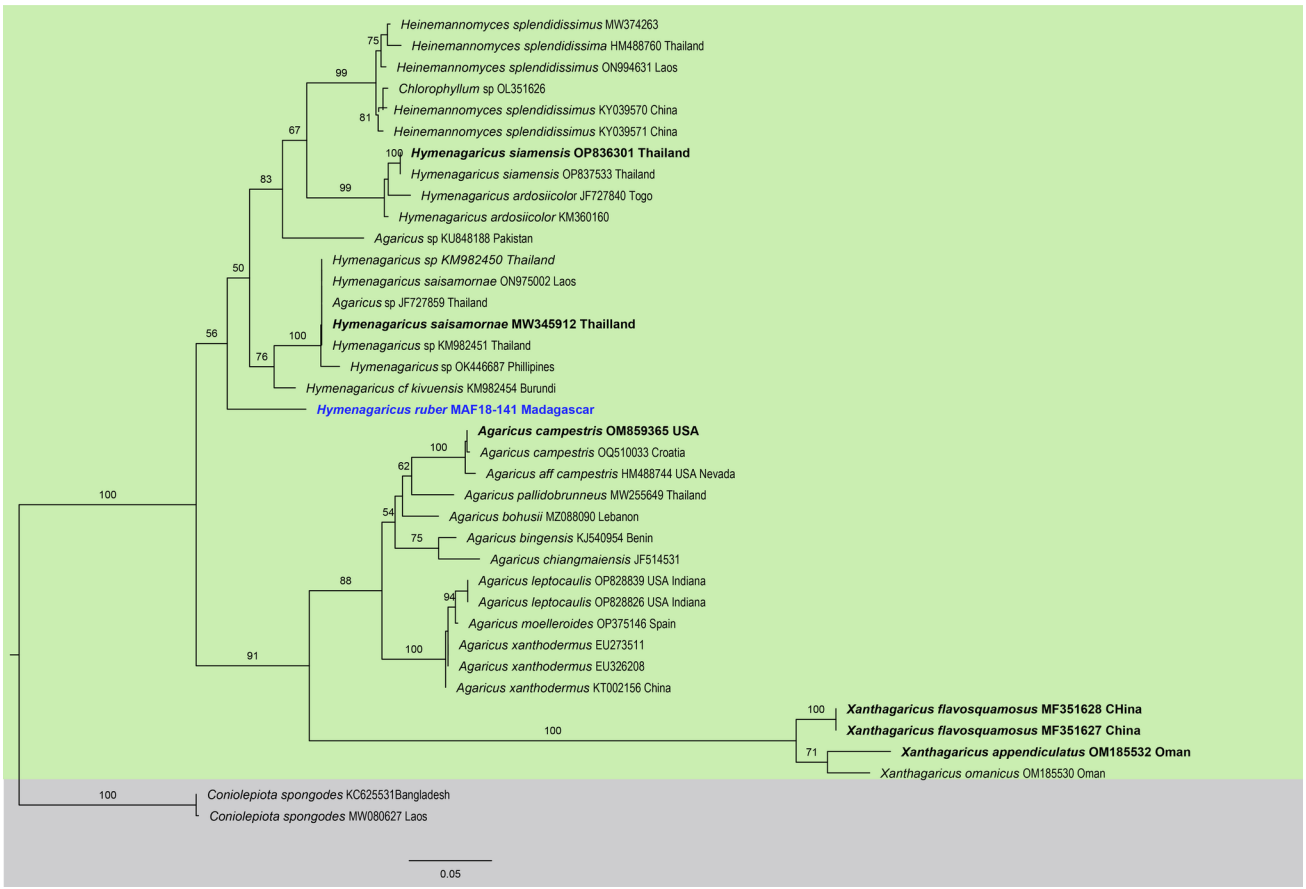


Fig. 67 The best scoring RAxML tree with a final likelihood value of -4096.148654 of the genus *Hymenagaricus* and *Agaricus* based on the ITS region. Related sequences were retrieved from GenBank. Thirty-eight specimens were included in the analysis of the ITS region which comprises 782 characters after alignment. The tree is rooted with *Coniolepiota spongodes* (KC625531) and *Coniolepiota spongodes* (MW080627). The matrix had 334 distinct alignment patterns, with 10,61% of undetermined characters or gaps. Estimated base frequencies were: A = 0.227093, C = 0.213184, G = 0.241131, T = 0.318593; substitution rates AC = 1.046018, AG = 3.987882, AT = 1.146073, CG = 0.203864, CT = 5.408419, GT = 1.000000. Maximum Likelihood bootstrap values greater than 50% are given near to each branch. The type specimens are in bold. The new species are in blue. Names, other than those originating from the type specimens, are only indicative and not confirmed via comparison with sequences from type specimens

Habitat: Dry, deciduous, tropical forest, on white sandy soil.

Distribution: So far only known from Madagascar.

Material examined: MADAGASCAR, Mahajanga, Boeny Region, Ankarafantsika National Park, north side of Lake Ravelobe, dominated by Euphorbiaceae, Rubiaceae, Malvaceae, Celastraceae, Ebenaceae, 19 Feb. 2018, coll. *S. Morris*, *MAF18-141* (K-M 251793, **holotype**; TAN, isotype).

GenBank: K-M 251793: PQ636523 (ITS).

Notes: *Hymenagaricus ruber* has basidiomata with whitish red, pink and pale pink colors, two types of cheilocystidia and ellipsoid, small spores 5–6.5 × 3.5–4.5(–5) µm. ITS sequence (GenBank PQ636523, holotype) is distinct from the other members of the genus *Hymenagaricus* and deviating from them by more than 5% (> 40 substitutions and indels). In our phylogenetic analysis, the new species forms a group with other species of *Hymenagaricus*, but with a very low support (BS 56%) and *Heinemannomyces splendidissimus* (a monotypic genus described from Asia in 1998). At the moment, we place the Malagasy species in this group and use the genus name *Hymenagaricus* that being the older name, has priority over *Heinemannomyces*.

Leucoagaricus Locq. ex Singer.

Notes: Leucoagaricus belongs to Agaricaceae s.str. (Kalichman et al. 2020). The traditional circumscription of the genus includes small- to medium-sized species with thin to fleshy basidiomata, a fibrillose or ± squamulose to scaly pileus, free lamellae, simple annulus, dextrinoid and metachromatic basidiospores, and cheilocystidia and hyphae without clamp connections (Singer 1986; Vellinga 2001a). The species with plicate pilei, spores with or without apical germ pore, and a hymenium with pseudoparaphyses have been placed in the genus *Leucocoprinus* (Singer 1986). The

phylogenetic studies have, however, shown that *Leucoagaricus* (type species *L. rubrotinctus* (Peck) Singer) is polyphyletic and intermixes with *Leucocoprinus* Pat. (type species *L. cepistipes* (Sowerby) Pat.) and the relationships of both genera are still unresolved (Vellinga 2003, 2004; Vellinga et al. 2011; Justo et al. 2021; Li et al. 2025). The morphologically delimited *Leucoagaricus* is widely distributed and contains approximately 150 species (Hussain et al. 2018). The species are saprotrophic occurring on soil, wood chips, and sawdust in a wide range of habitats.

Leucoagaricus ankarafantsikaensis Ralaiv., Liimat. & Niskanen, **sp. nov.**

Index Fungorum: IF 903130; *Facesoffungi*: FoF 17105; Figs. 68, 69

Etymology: The species epithet is derived from the type locality.

Holotype: K-M 251953.

Pileus 3 cm in diam., at first convex, then plane, brownish-red, background creamy-white, surface felty to felty-fibrillose. **Lamellae** free, crowded, edge even, with lamellulae, white, color unchanging. **Stipe** 4.5 cm long, up to 4 mm wide at the top, 7 mm wide at the base, white at the top of the stipe and very light brownish yellow at the base, cylindrical, somewhat clavate at the base, with a distinct pastel orange annulus. **Context** not recorded. **Odor** indistinct. **Taste** not recorded.

Basidiospores (6–)7–9 × (3.5–)4–5.5 µm, amygdaloid to somewhat citriform, without germ pore, smooth, hyaline in KOH, strongly dextrinoid in Melzer's reagent. **Basidia** 17–30 × 8–10 µm, sterigmata 1.5–5 µm long, clavate, usually 4-spored, rarely 2-spored, not clamped. **Cheilocystidia** 21–31 × 10–13 µm, cylindrical to ovoid to somewhat utriform. **Pileipellis** cutis made of smooth, parallel, non-septate hyphae, with an olive-green color, the hyphae vary in width up to 7.5–10 µm.

Habitat: Dry, deciduous, tropical forest, on sandy soil.

Distribution: So far only known from Madagascar.

Material examined: MADAGASCAR, Mahajanga, Boeny Region, Ankarafantsika National Park, dominated by Euphorbiaceae, Rubiaceae, Malvaceae, Celastraceae, Ebenaceae, 12 Feb. 2017, coll. *J. Gallan*, *MAF17-039* (K-M 251953, **holotype**).

GenBank: K-M 251953: PQ636524 (ITS).

Notes: *Leucoagaricus ankarafantsikaensis* is the second species of the genus described from Madagascar. The two species are not closely related although they both belong into the same clade with the type species of the genus. *Leucogaricus madagascarensis* differs from *L. ankarafantsikaensis* by having amygdaloid to ellipsoid basidiospores (6.5–9.5 × 3.5–5) µm and larger (22–50.5 × 10–20 µm), cylindrical to clavate cheilocystidia.

Leucoagaricus rutilus G.J. Li, **sp. nov.**

Fungal Names: FN 572273; *Facesoffungi*: FoF 17668; Figs. 70, 71, 72

Etymology: refers to reddish tinges at center of pileus.

Holotype: HBAU 16141.

Pileus small sized, 8–12 mm diam., initially ovoid, bell-shaped, hemispherical to campaniform, umbonate to convex when mature. Surface Coral (#FF7F50) to Light Salmon (#FFA07A), fibrillose squamules radially arranged at center, sometimes silky, Papaya Whip (#FFEFD5), Moccasin (#FFE4B5) to Peach Buff (#FFDAB9) towards the edge, often cracked. **Lamellae** 2–3 mm deep, free, dense, 20–25 pieces at pileus edge, white (#FFFFFF), unchanging, not forked; edge even to finely scalloped; lamellulae abundant at edge. **Stipe** 37–63 × 3–6 mm, cylindrical to clavate, often ventricose towards the base, white (#FFFFFF), often

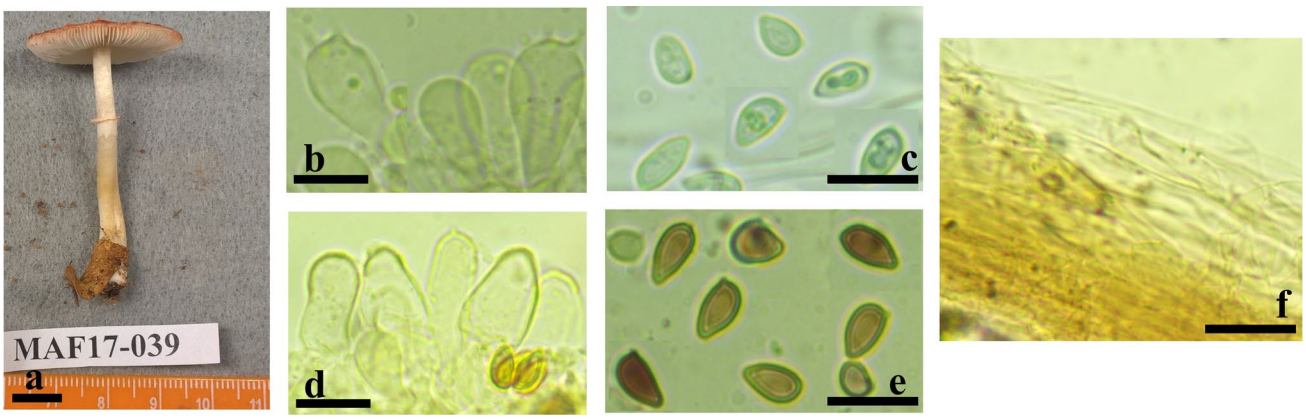


Fig. 68 *Leucoagaricus ankarafantsikaensis* (K-M251953, **holotype**). **a** Basidiomata. **b** Basidia in Melzer's reagent. **c** Basidiospores in KOH. **d** Cheilocystidia in Melzer's reagent. **e** Basidiospores in Melzer's reagent. **f** Pileipellis in Melzer's reagent. Scale bars: **a** = 1 cm, **b**–**f** = 10 µm. Credit: J. Gallan (**a**), Anna Ralaiveloarisoa (**b**–**f**)

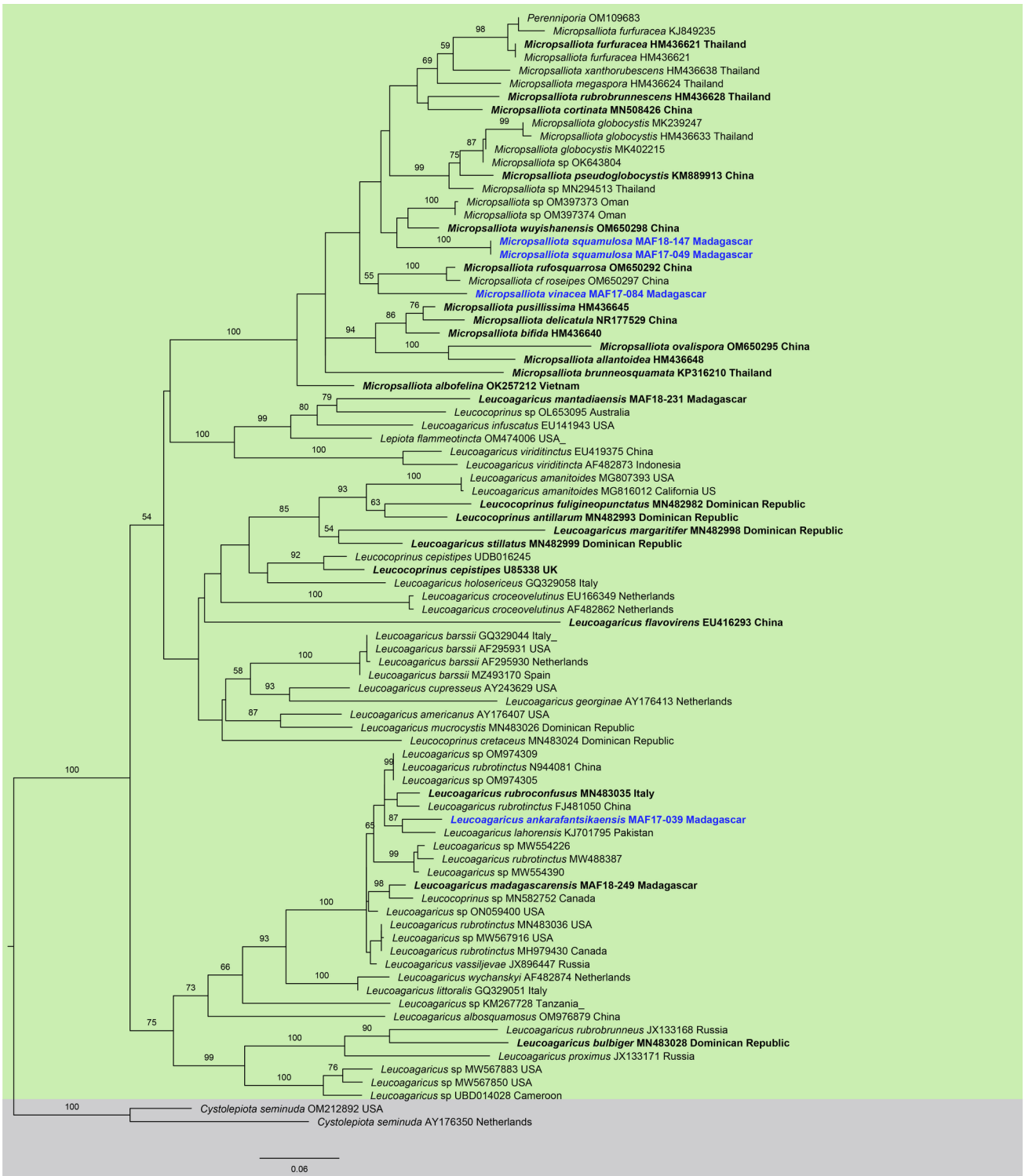


Fig. 69 The best scoring RAxML tree with a final likelihood value of -13,795.155676 of the genus *Leucoagaricus* and *Micropsalliota* based on the ITS region. Related sequences were retrieved from GenBank. Eighty-five specimens were included in the analysis of the ITS region which comprises 1111 characters after alignment. The tree is rooted with *Cystolepiota seminuda* (OM212892) and *Cystolepiota seminuda* (AY176350). The matrix had 722 distinct alignment patterns, with 45,12% of undetermined characters or gaps. Estimated base frequencies were: A = 0.236916, C = 0.218014, G = 0.236969, T = 0.308101; substitution rates AC = 1.217603, AG = 3.599005, AT = 1.611527, CG = 0.537104, CT = 3.659128, GT = 1.000000. Maximum Likelihood bootstrap values greater than 50% are given near to each branch. The type specimens are in bold. The new species are in blue. Names, other than those originating from the type specimens, are only indicative and not confirmed via comparison with sequences from type specimens

Fig. 70 *Leucoagaricus rutilus*. **a, b** HBAU16141 (**holotype**). **c** HBAU16142. Scale bars = 1 cm

slightly turning water soaked tinge of Ivory (#FFFFF0) when bruised. **Annulus** white, simple, unilaminar, located at upper position of stipe. **Context** 1–2 mm thick at pileus center, white (#FFFFFF), unchanging when bruised, no distinct color, taste mild. **Spore print** white (#FFFFFF).

Spores (4.3–)4.6–5.3–5.8(–6.1) × 3.5–4.2–4.8(–5.1) µm, Q = (1.05–)1.08–1.25–1.45(–1.52), amygdaliform to ovoid, rarely subglobose, hyaline, smooth, more or less thick-walled. **Basidia** (26–)28–29–31(–32) × (6–)7–7–8(–9) µm, clavate to subclavate, two or four spored; basidioles first cylindrical, then clavate, (15–)18–22–25(–28) × (4–)5–7(–8) µm. **Cheilocystidia** (28–)31–32–32(–35) × (7–)7–8–8(–8) µm, mainly clavate to subclavate, occasionally fusiform, apically obtuse, originating in subhymenium, thin-walled; gelatinous covering at apex, often intermixed with crystal contents. Pleurocystidia absent. **Pileipellis** a cutis, partial a trichoderm, composed of mostly repent, rarely suberect to oblique, septate, non-gelatinized, hyaline hyphae (5)6–7–8(9) µm in diam; pigments rare, yellowish brown, sparsely distributed on hyphal surface. **Clamp connections** absent.

Habitat and Habit: Solitary on ground of broad-leaved forest edge. Only known in Yanshan Mountains of North China.

Material examined: CHINA, Hebei Province, Tangshan City, Qianxi County, Tiemenguan Township, Shitizi Village, Xifengxiongguandadaoyuan Scenic Area, 40°25′N 118°22′E, 472 m asl, 4 Aug 2023, *Xia Kang*, *Jing Ren*, *Guo-Jie Li*, *20,230,024* (HBAU 16142); Hebei Province, Chengde City, Luanping County, Baicaowa National Forest Park, 40°49′N 117°35′E, 9 Aug 2023, 695 m asl, *Xia Kang*, *Jing Ren*, *Guo-Jie Li*, *20,230,240* (HBAU 16141, **holotype**).

GenBank: HBAU 16141: OR921716 (ITS); HBAU 16142: OR921717 (ITS).

Notes: This new species is characterized for a combination of leptosomatic basidiomata, erythrinus fibrillose squamules on pileus surface, clavate cheilocystidia with gelatinous covering at apex. The new species is a member of *L. rubrotinctus* clade in genus *Leucoagaricus*. It

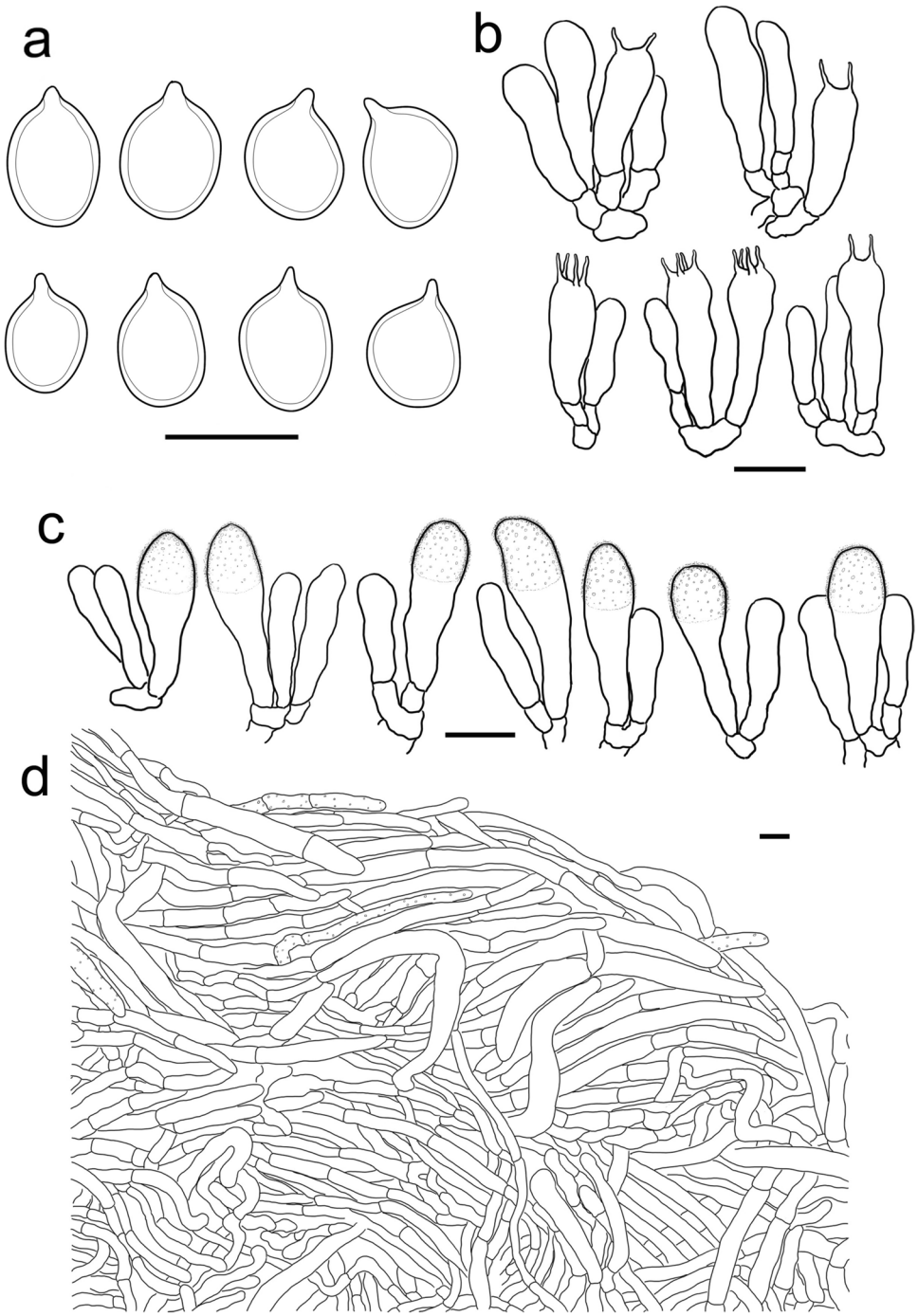


Fig. 71 *Leucoagaricus rutilus* (HBAU 16141, **holotype**). **a** Basidiospores. **b** Basidia and basidioles. **c** Cheilocystidia and basidioles. **d** Pileipellis. Scale bars: **a** = 5 µm, **b**–**d** = 10 µm

formed a well-supported clade with *Leucoagaricus centricastaneus* Y.R. Ma, Z.W. Ge & T.Z. Liu, *Leucoagaricus lahorensiformis* S. Hussain, H. Ahmad, Afshan & Khalid, *Leucoagaricus lahorensis* Qasim, T. Amir & Nawaz, *Leucoagaricus rubroconfusus* Migl. & Coccia, *Leucoagaricus rubrotinctus* (Peck) Singer, *Leucoagaricus subpurpureolilacinus* Z.W. Ge & Zhu L. Yang, *Leucoagaricus thallensis* Z. Khan, A. Izhar & Khalid, as well as three unknown taxa *Leucoagaricus* spp. 1, 2, 7 (Fig. 72). All of these above species in *L. rubrotinctus* have more or less orange, reddish or brownish tinges, ellipsoid to amygdaliform basidiospores, and subclavate to clavate cheilocystidia (Singer 1986; Candusso and Lanzoni 1990; Migliozzi and Coccia 1994; Vellinga 2001b; Ge et al. 2015; Qasim et al. 2015; Hussain et al. 2018; Ma et al. 2022; Khan et al. 2023). These closely related species can be differentiated from *L. rutilus* as following: *L. centricastaneus* has larger pileus 43–62 mm in diam., wider basdia

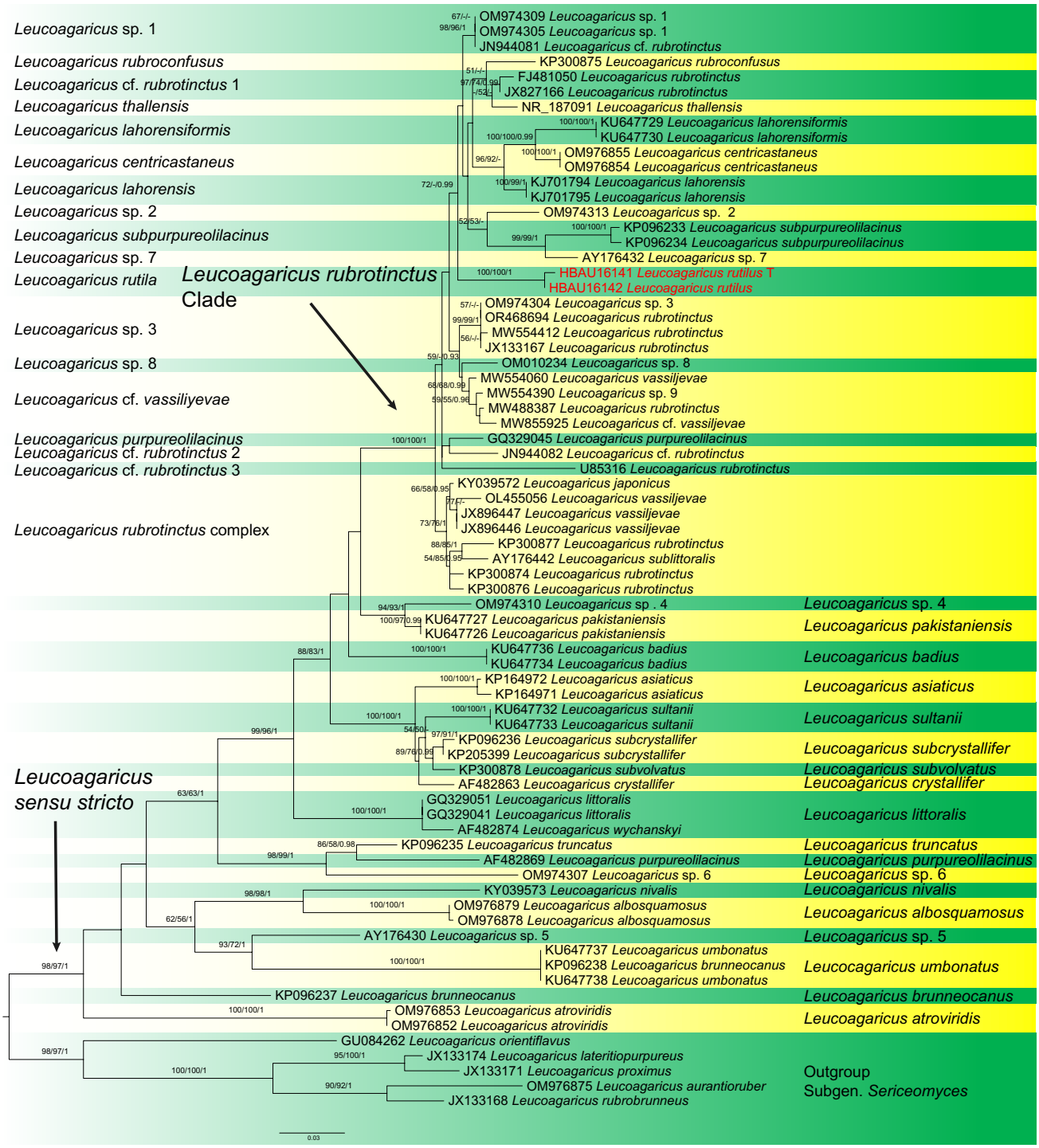


Fig. 72 Maximum Likelihood tree based on ITS sequences, bootstrap values of Maximum Likelihood and maximum parsimony analyses (MLBS and MPBS) higher than 50%, as well as Bayesian posterior probabilities higher than 0.90 (BIPP) are shown above nodes. New species are shown in red. "T" refers to a type specimen

8.5–10.5 µm, longer and wider cheilocystidia (Ma et al. 2022); *L. lahorensiformis* has larger basidiospores (6–) 6.5–7.5(–8) × (3–)3.5–4(–4.5) µm and shorter basidia/cheilocystidia 18–22 × 6–9 µm/20–26 × 8–11 µm (Hussain et al. 2018); *L. lahorensis* has larger basidiospores (7.3)8–10.6(10.9) × (6.1)6.4–7.6(7.8) µm, shorter basidia (17.2) 17.5–18.9(19.1) × (10.1)10.6–11.6(11.8) µm, and longer cheilocystidia (33.7)34.1–38.7(40) × (8)9.1–10.5(11.3)

µm without gelatinous/crystal covering at apex (Qasim et al. 2015); *L. rubroconfusus* has wider cheilocystidia (3–)3.5–4(–4.5) µm (Migliozzi and Coccia 1994); *L. rubrotinctus* has larger basidiospores 6–9 × 4–5 µm and longer cheilocystidia 30–50 × 5–10 µm (Candusso and Lanzoni 1990); *L. subpurpureolilacinus* has brown, gray and purplish hues on pileus surface, larger basidiospores (7.5)8–9(11.5) × 4.5–6 (7) µm and longer cheilocystidia 30–53 × 10–16 µm (Ge et al. 2015); *L. thallensis* has oblong ovoid to oblong amygdaliform basidiospores with Q values of 1.51–1.63, and shorter basidia/cheilocystidia (14.1–)14.6–19(–20) × (5.6–)5.8–8.6(–9.1) µm/(10.8–)11.5–18.6(–19) × (5)–8(–8.8) µm (Khan et al. 2023).

Micropsalliota Höhn.

Notes: *Micropsalliota* is a large genus with more than 70 species (Index Fungorum Partnership 2024). The genus belongs to the family Agaricaceae and is mainly distributed in tropical and subtropical area: Africa, America and Asia. The species of the genus can be distinguished by the presence of usually small, gracile basidiomata with a membranous partial veil, dark spore print, frequently capitate or subcapitate cheilocystidia, incrusted pileipellis hyphae that turn green in ammonia solution, and, in most species, basidiospores with an apically thickened endosporium and lack of a germ pore (Heinemann 1976; Zhao et al. 2010).

Micropsalliota squamulosa Ralaiv., Liimat. & Niskanen, **sp. nov.**

Index Fungorum: IF 903131; *Facesoffungi*: FoF 17106; Figs. 69, 73

Etymology: The species epithet is derived from the scaly pileus.

Holotype: K-M 251781.

Pileus up to 1 cm in diam., at first convex, then planoconvex with a small umbo in the center, whitish brown, center dark brown, surface dry, covered with fibrillose scales, more densely at the center. **Lamellae** free, crowded, edge even, with lamellulae, white, turning brownish vinaceous when damaged. **Stipe** 2.5 cm long, up to 3 mm wide, white to brownish whitish, cylindrical, with a brown, membraneous annulus and brown, somewhat woolly, incomplete girdles below the annulus. **Context** not recorded. **Odor** mild. **Taste** not recorded.

Basidiospores (5–)6–7.5 × 4–5.5 µm, amygdaloid to somewhat citriform, some ellipsoid, smooth, brownish gray in KOH, grayish brown in Melzer's reagent. **Basidia** 14–17.5 × (5–)5.5–8 µm, sterigmata 1.5–3 µm long, clavate to cylindrical, 4-spored, rarely 2-spored, not clamped, hyaline in KOH. **Cheilocystidia** variable in size 43.5–54 × 12–18 µm, fusiform, thick-walled. **Pleurocystidia** 34.5–44.5 × 13–18 µm fusiform, thick-walled. **Pileipellis** Cutis with short hyphae measuring 6–16.5 µm in width, and constituting of a smooth, parallel, and unclamped hyphae, mustard to pale chartreuse in color.

Habitat: Dry, deciduous, tropical forest, on white sandy-loamy soil.

Distribution: So far only known from Madagascar.

Material examined: MADAGASCAR, Mahajanga, Boeny Region, Ankarafantsika National Park, north side of Lake Ravelobe, dominated by Euphorbiaceae, Malvaceae and Fabaceae, 29 Feb 2018, coll. *Y. Lu*, *MAF18-147* (K-M 251781, **holotype**). Boeny Region, Ankarafantsika National Park, Euphorbiaceae, Rubiaceae, Malvaceae, Celastraceae, Ebenaceae, 12 Feb 2017, coll. *J. Elsey*, MAF17-049 (K-M 251981).

GenBank: K-M 251781: PQ636525 (ITS); K-M 251981: PQ636526 (ITS).

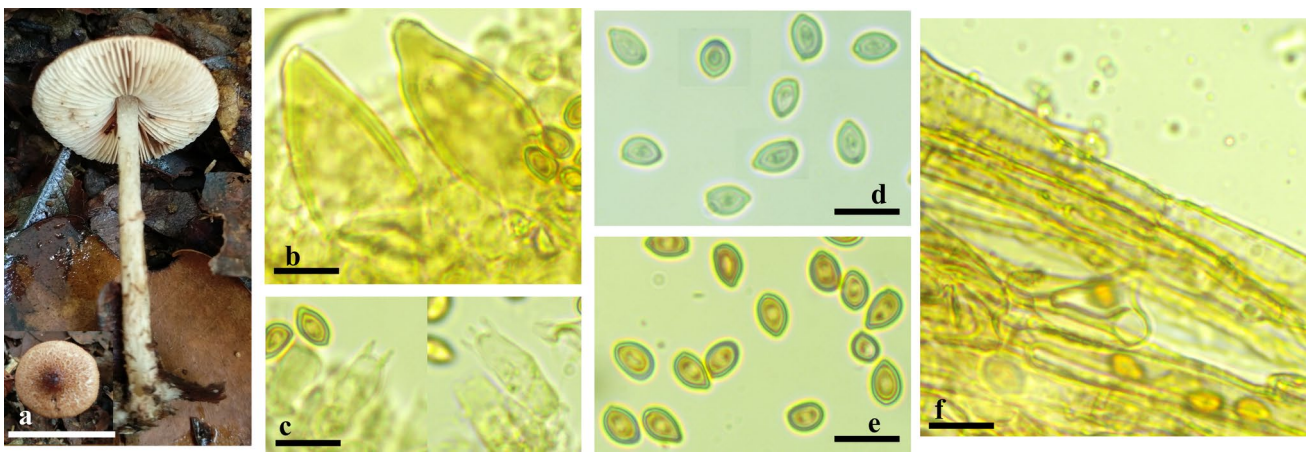


Fig. 73 ***Micropsalliota squamulosa*** (K-M 251781, **holotype**). **a** Basidiomata. **b** Cystidia. **c** Basidia. **d** Basidiospores in KOH. **e** Basidiospores in Melzer's reagent. **f** Pileipellis. Scale bars: **a** = 1 cm, **b**–**f** = 10 µm. Credit: Y. Lu (**a**), Anna Ralaiveloarisoa (**b**–**f**)

Notes: *Micropsalliota squamulosa* is the first species of the genus described from Madagascar and forms an independent clade. The new species is characterized by brown scaly pileus, amygdaloid to citriform basidiospores (6–7.5 × 4–5.5 µm), fusiform cheilocystidia (43.5–54 × 12–18 µm) and pleurocystidia (34.5–44.5 × 13–18 µm), and pileipellis with hyphae up to 16.5 wide. ITS sequences (GenBank PQ636525, holotype; GenBank PQ636526): the two sequences are identical. In our phylogenetic analysis they group, but without support, with *Micropsalliota* sp OM397374 and OM397373 from Oman, and *Micropsalliota wuyishanensis* OM650298 from China and differ from them by 5% (30 indels and substitutions).

Micropsalliota vinacea Ralaiv., Liimat. & Niskanen, **sp. nov.**

Index Fungorum: IF 903132; *Facesoffungi*: FoF 17107; Figs. 69, 74

Etymology: The species epithet refers to the color of the basidiomata.

Holotype: K-M 252043.

Pileus up to 2 cm in diam., at first convex, then low convex to almost plane, with a small umbo in the center, pinkish brown to vinaceous brown, dark vinaceous brown in the center, surface dry, squamulose, more densely so at the center. **Lamellae** free, crowded, edge even, with lamellulae, at first white, later dark brown. **Stipe** 4 cm long, up to 4 mm wide, white at the very top of the stipe, pale vinaceous

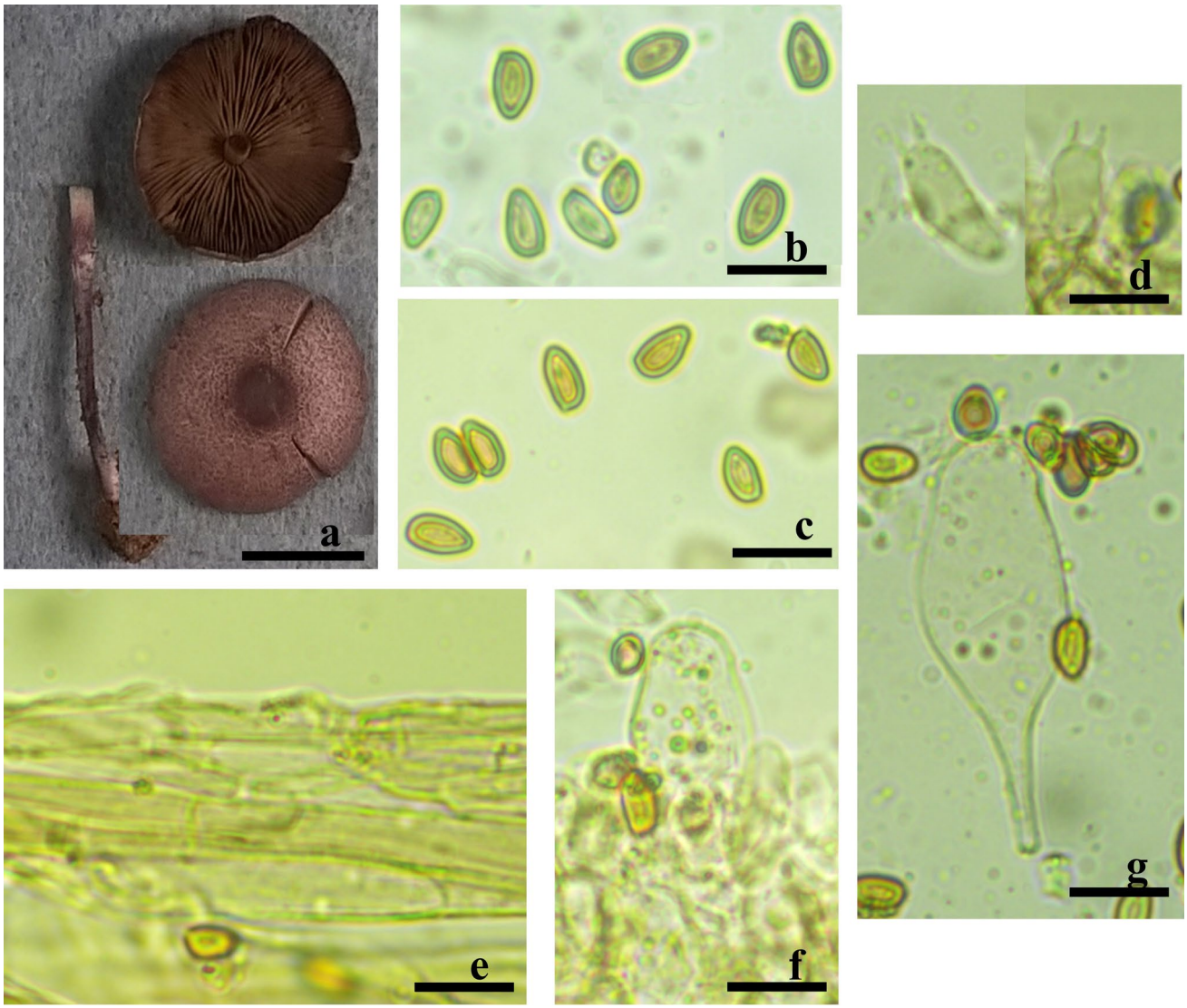


Fig. 74 ***Micropsalliota vinacea*** (K-M 252043, **holotype**). **a** Basidiomata. **b** Basidiospores in KOH. **c** Basidiospores in Melzer's reagent. **d** Basidia in Melzer's reagent. **e** Pileipellis. **f** Cheilocystidia. **g** Pleurocystidia. Scale bars: **a** = 1 cm, **b**–**g** = 10 µm. Credit: S. Skarha (**a**), Anna Ralaiveloarisoa (**b**–**g**)

towards the base, with a vinaceous, small, membraneous annulus and vinaceous, somewhat woolly, incomplete girdles below the annulus. **Context** not recorded. **Odor** and **Taste** not recorded.

Basidiospores 5.5–8 × (3–)3.5–4.5(–5) µm, amygdaloid, rarely ellipsoid, smooth, brown in KOH and Melzer's reagent. **Basidia** 12.5–14.5 × 5–6.5 µm, sterigmata 1–2 µm long, clavate to cylindrical, 4-spored, rarely 2-spored, not clamped, hyaline in KOH. **Cheilocystidia** 28–35 × 10–13 µm, clavate to somewhat broadly utriform. **Pleurocystidia** 28.5–47 × 10.5–15 µm, clavate to somewhat broadly utriform. **Pileipellis** cutis with parallel, unclamped hyphae, up to 3–7.5 µm in diameter and with a light olive or light olive-green color.

Habitat: Dry, deciduous, tropical forest, on sandy soil among leaves.

Distribution: So far only known from Madagascar.

Material examined: MADAGASCAR, Mahajanga, Boeny Region, Ankarafantsika National Park, dominated by Euphorbiaceae-*Cephalocroton*, Rubiaceae, *Grevia*, *Salacia madagascariensis*, *Diospyros*, 13 Feb 2017, coll. *S. Skarha*, *MAF17-084* (K-M 252043, holotype).

GenBank: K-M 252043: PQ636527 (ITS).

Notes: *Micropsalliota vinacea* is a second species of the genus described from Madagascar. It is not closely related to the other Malagasy species, *M. squamulosa,* that lacks vinaceous colors and has broader spores 6–7.5 × 4–5.5 µm. ITS sequence (GenBank PQ636527, holotype) distinct from other species of *Micropsalliota.* In our phylogenetic analysis groups together, but with a very low support (BS 55%), with a species from China, *Micropsalliota rufosquarrosa* (OM650292) and *Micropsalliota* cf. *roseipes* (OM650297) and deviating from them > 9% (64 indels and substitutions).

Asproinocybaceae T. Bau & G.F. Mou.

Notes: Asproinocybaceae is a small, recently delimited family with a wide distribution containing two genera: *Asproinocybe* and *Tricholosporum* (Mou and Bau 2021). To date less than 30 species have been described (Index Fungorum Partnership 2024). The species are tricholomatoid with distinctive purplish, violaceous, or lilac-vinaceous colors in their basidiomata and white spore-print. They are characterized by a broadly convex, subumbonate to flat-hemispherical pileus that becomes plane to depressed with age; close to crowded, adnate, adnexed, sinuate or emarginate to free lamellae that sometimes are with a small decurrent tooth; cylindrical to slightly clavate, violet to bluish violet stipe with a base that is usually with white rhizomorphs; colorless, inamyloid, thin-walled, subglobose to tuberculate to stellate (*Asproinocybe*), or cruciform to stauriform (*Tricholosporum*) spores; presence of cheilo-, pleurocystidia and laticifers (Mou and Bau 2021).

Tricholosporum Guzmán.

Notes: Tricholosporum is a small, widely distributed genus with 16 species (Index Fungorum Partnership 2024). The species of the genus are characterized by purplish or violaceous lamellae, cruciform to stauriform basidiospores, presence of cheilo- and pleurocystidia in lamellae, with the exception of *T. atroviolaceum* (Murrill) T.J. Baroni that lacks hymenial cystidia (Angelini et al. 2017; Xu et al. 2018; Mou and Bau 2021).

Tricholosporum madagascariense Ralaiv., Liimat. & Niskanen, **sp. nov.**

Index Fungorum: IF 903128; *Facesoffungi*: FoF 17108; Figs. 75, 76

Etymology: This is the first *Tricholosporum* described from Madagascar.

Holotype: K-M 252063.

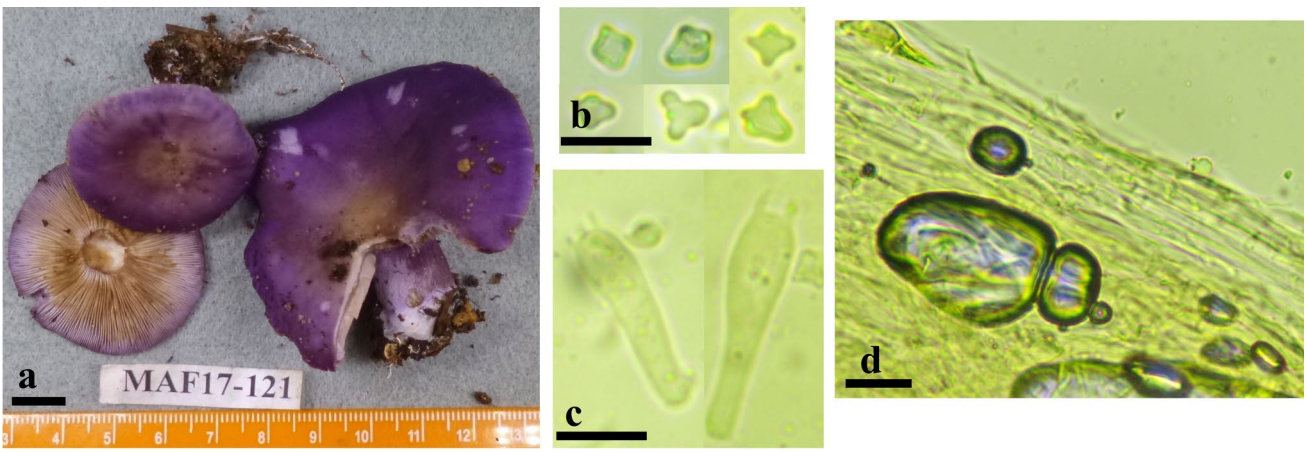


Fig. 75 ***Tricholosporum madagascariense*** (K-M252063, **holotype**). **a** Basidiomata. **b** Basidiospores. **c** Basidia. **d** Pileipellis. Scale bars: **a** = 1 cm, **b–d** = 10 µm. Credit: Shannon Skarha (**a**), Anna Ralaiveloarisoa (**b–d**)

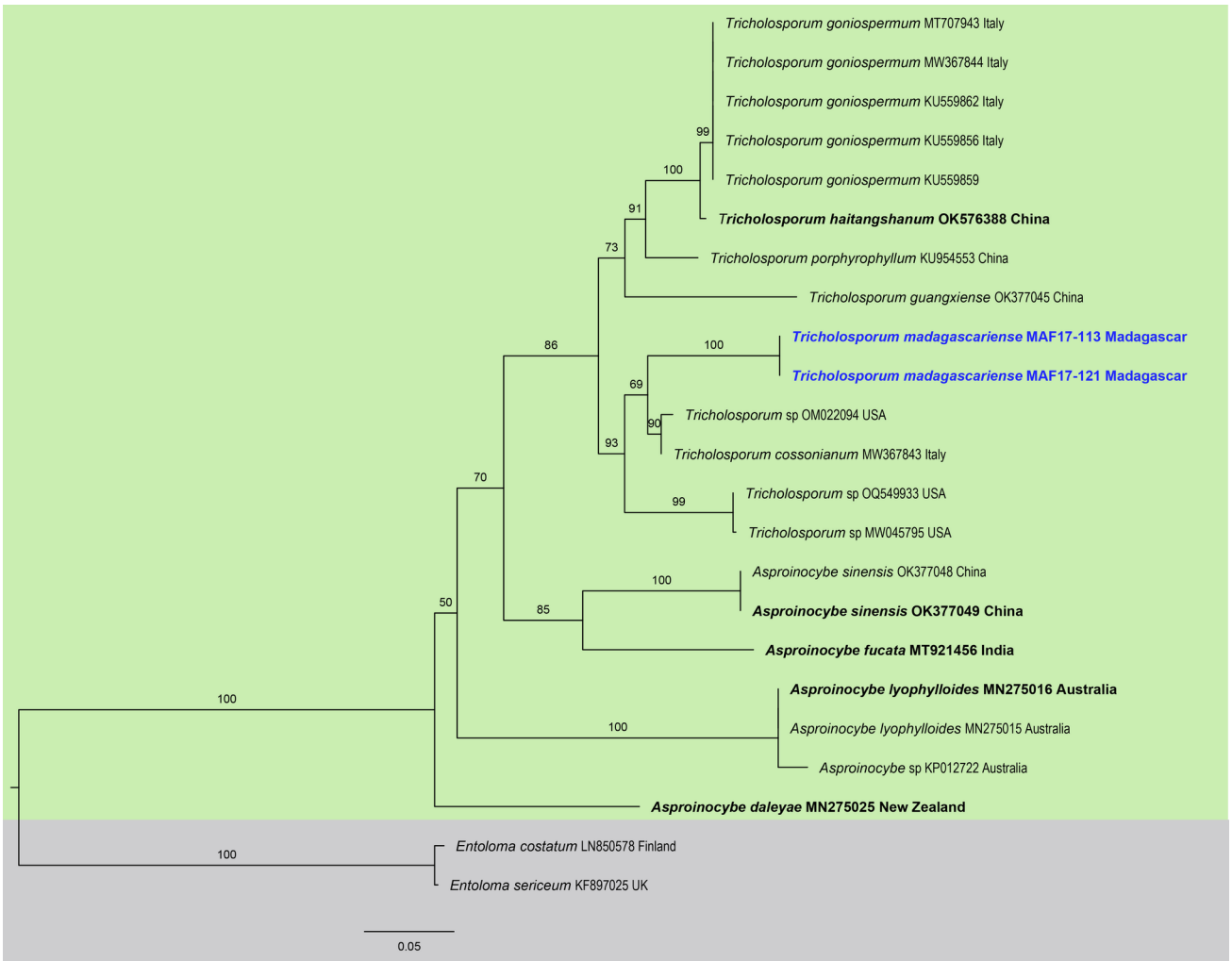


Fig. 76 The best scoring RAxML tree with a final likelihood value of -3861.641074 of the genus *Tricholosporum* and *Asproinocybe* based on the ITS region. Related sequences were retrieved from GenBank. Twenty-three specimens were included in the analysis of the ITS region which comprises 811 characters after alignment. The tree is rooted with *Entoloma costatum* (LN850578) and *Entoloma sericeum* (KF897025). The matrix had 418 distinct alignment patterns, with 20,26% of undetermined characters or gaps. Estimated base frequencies were: A = 0.267154, C = 0.184148, G = 0.191398, T = 0.357300; substitution rates AC = 0.961632, AG = 2.682519, AT = 1.405174, CG = 0.340012, CT = 2.939152, GT = 1.000000. Maximum Likelihood bootstrap values greater than 50% are given near to each branch. The type specimens are in bold. The new species are in blue. Names, other than those originating from the type specimens, are only indicative and not confirmed via comparison with sequences from type specimens

Pileus 3–5.5 cm in diam., at first convex, then very low convex, later almost plane and slightly depressed in the center, at first purple then becoming pale brown in the center, surface smooth, dry, waxy, not hygrophanous. **Lamellae** adnate, edge even, crowded with lamellulae, at first very pale to pale purple, turning pale brown when bruised. **Stipe** 2.5–3.5 cm long, up to 1.5 cm wide, whitish purple, swollen at base, mycelium white. **Context** not recorded. **Odor** and **Taste** not recorded.

Basidiospores 3.5–5.5 × 2.5–5 µm, cruciform to stauriform, thin-walled, hyaline in Melzer's reagent. **Basidia** 19–27 × 5–6.5 µm, sterigmata 1–2 µm long, clavate, (2-)4-spored, clamped or not. **Cheilocystidia** and **Pleurocystidia** similar, 16–25.5 × 9.5–12.5 µm, clavate, thin-walled, with gray-violet to brownish green pigment, sometimes with an acute apex. **Pileipellis** cutis with parallel, irregular, non-septate hyphae, 4 µm wide, pale lime-green to yellow-olive in color.

Habitat: Dry, deciduous, tropical forest, on sandy soil.

Distribution: So far only known from Madagascar.

Material examined: MADAGASCAR, Mahajanga, Ankarafantsika National Park, tropical dry forest, dominated by Euphorbiaceae, Rubiaceae, Malvaceae, Celastraceae, Ebenaceae, 14 Feb 2017, coll. *Shannon Skarha*,

MAF17-121 (K-M 252063, **holotype**). Mahajanga, Ankarafantsika National Park, tropical dry forest, 14 Feb 2017, coll. *Melinda*, *MAF17-113* (K-M 1434141).

GenBank: K-M 252063: PQ636521 (ITS); K-M 1434141: PQ636522 (ITS).

Notes: The generic limits of *Tricholosporum* and *Asproinocybe* have not been fully resolved. The phylogenetic analysis of Mou and Bau (2021) showed that the genus *Tricholosporum* forms a well-supported clade whereas *Asproinocybe* is non-monophyletic. Our species belongs to a group (BS 86%) with other species of *Tricholosporum*. In addition, it has the typical basidiospores of the genus, whereas the spores of *Asproinocybe* are tuberculate to stellate. Therefore, we place our species in the genus *Tricholosporum*. ITS sequences (GenBank PQ636521, holotype; GenBank PQ636522): the two sequences are identical and group with low support (69% BS) with species *Tricholosporum cossonianum* (MW367843) from Italy and *Tricholosporum* sp (OM022094) from USA and deviate from them by more than 5% (> 40 substitutions and indels). The Malagasy species belongs to the group of species with small spores, usually under 6 µm in length, subgroup of species with pigmented hymenial cystidia, which are gray-violet or brownish but differs from the other members of the group, which occur in the other continents, by having smallest cystidia.

Clavariaceae Chevall.

Notes: The family Clavariaceae is basidiomata morphology diverse family, comprising clavarioid, coralloid, agaricoid and resupinate genera (Birkebak et al. 2016). Traditionally, the agaricoid genus *Camarophyllopsis* was placed within the family Hygrophoraceae; however, phylogenetic studies in recent years have indicated that *Camarophyllopsis* belongs to the family Clavariaceae. To date, there are three agaricoid genera in Clavariaceae, including *Camarophyllopsis*, *Hodophilus*, and *Lamelloclavaria* (Birkebak et al. 2016).

Camarophyllopsis Herink.

Notes: The genus *Camarophyllopsis* Herink was described by Herink (1958) and *Camarophyllopsis schulzeri* (Bres.) Herink was selected as the type species. As one of the agaricoid genera within Clavariaceae, *Camarophyllopsis* is characterized by the usually small agaricoid basidiomata, hygrophanous pileus and basidia, subglobose to broadly ellipsoid basidiospores, and cutis pileipellis composed of chains of ellipsoid or cylindrical cells with numerous repent hyphal terminations (Birkebak et al. 2016; Zhang et al. 2019c). Recent phylogenetic studies support the genus as a monophyletic group (Birkebak et al. 2016; Zhang et al. 2019c).

Camarophyllopsis brunnea C.Q. Wang & W.X. Xia, **sp. nov.**

Fungal Names: FN 572240; *Facesoffungi*: FoF17109; Figs. 77, 78

Etymology: *brunnea* = brown, refers to the brown pileus surface.

Holotype: GDGM 91597.

Pileus small sized, 5–12 mm diam., hemispherical to convex at first, expanding to plano-convex to depressed, dry but strongly hygrophanous, brown (6E4–8, 7E4–8); margin crenulate and slightly striate, usually paler. **Lamellae** arcuate, subdecurrent to decurrent, distant with 1–3 lamellulae of different lengths, thick, fragile, white (1A1) to brownish orange (6C3) or pinkish white (9A2, 10A2) to light brown (6D4–8); margins even, concolorous or slightly paler. **Stipe** 10–25 × 1–3 mm, cylindrical but usually tapering downwards, usually hollow when mature, smooth, light brown to brown (6D–E4–8), concolorous to the lamellae to darker near the lamellae, sometimes finely hirsute at the base. **Context** thin.

Basidiospores (3.0–)3.5–3.7–4.0(–4.5) × 3.0–3.2–3.5(–4.0) µm, Q = 1.0–1.15–1.33, subglobose to globose, hyaline,

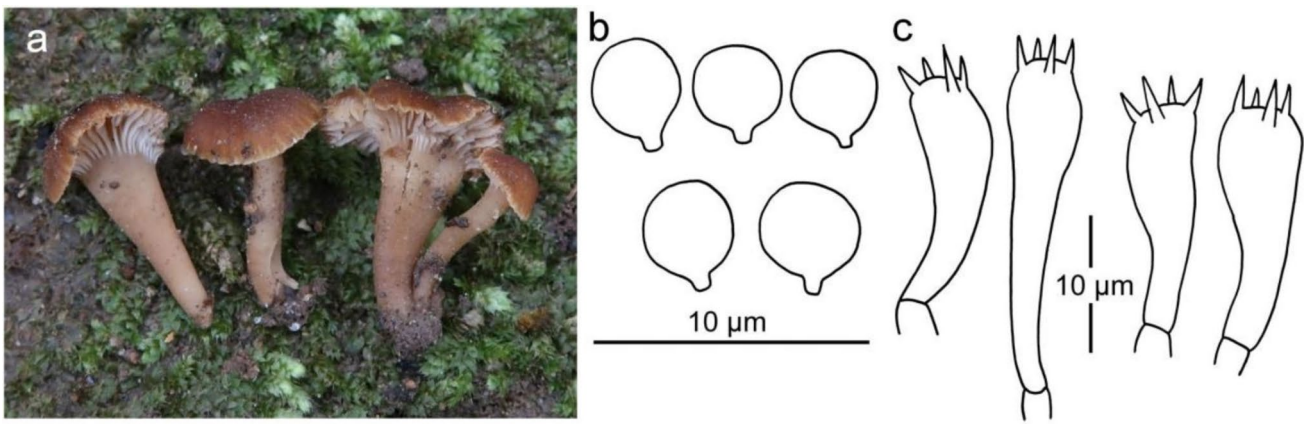


Fig. 77 ***Camarophyllopsis brunnea*** (GDGM 91597, **holotype**). **a** Basidiomata. **b** Basidiospores. **c** Basidia. Credit: Guo-Rui Zhong (**a**), Chao-Qun Wang (**b–c**)

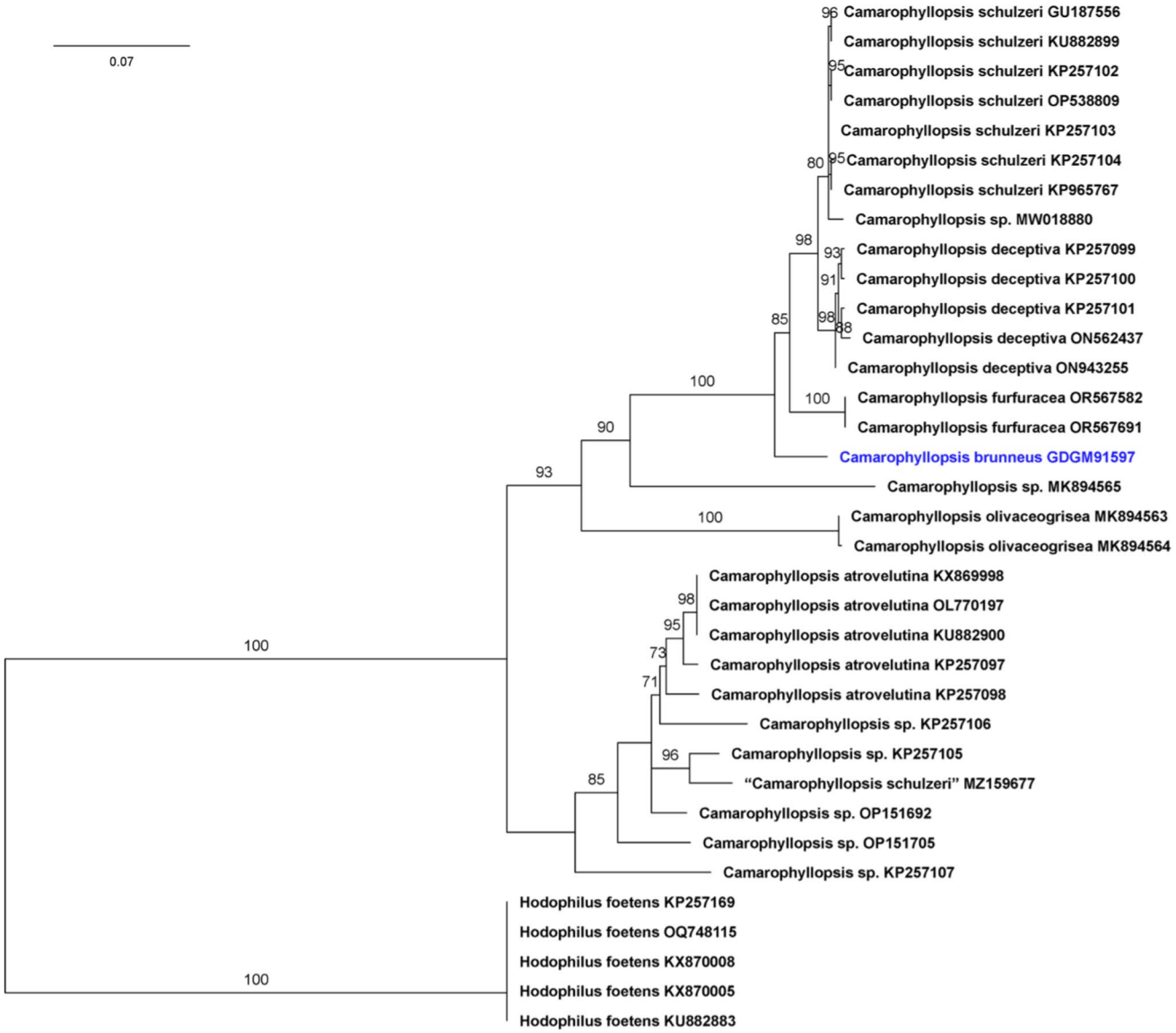


Fig. 78 Maximum Likelihood tree based on ITS sequences, bootstrap values greater than 70% are shown around nodes. The new species is shown in blue

smooth, thin-walled. **Basidia** (14–)16–19.6–24(–26) × 3–4.2–6.5 µm, clavate, 4-spored; sterigmata up to 4.5 µm long. **Lamellar trama** regular, composed of cylindrical or inflated hyphae 6–15 µm. **Stipitipellis** a cutis of cylindrical, thin-walled and hyaline hyphae, usually less than 200 um long, 5–10.5 µm broad.

Material examined: CHINA, Guangdong Province, Shenzhen City, Luohu District, Wutongshan Mountain, 30°11′N 120°18′E, 305 m asl, 30 Jun 2023, *Guo-Rui Zhong*, *Wei-Xin Zhang* (GDGM 91597, **holotype**).

GenBank: GDGM 91597: PQ638426 (ITS), PQ637230 (nrLSU).

Notes: *Camarophyllopsis brunnea* represented by GDGM 91597 from Shenzhen City is phylogenetically close to *C. deceptiva*, *C. furfuracea* and *C. schulzeri* (Fig. 78). However, *C. deceptiva*, firstly published as *Hygrophorus deceptivus* A.H. Sm. & Hesler, has bigger pileus (10–40 mm), longer and broader stipe measuring (2–)4–10 × 3–10 mm (Hesler and Smith 1963); *C. furfuracea*, originally described from New Zealand, has gray-beige, brownish to dark beige, squamulose pileus and bigger basidia measuring 25–36 × 5 µm (Horak 1973); *C. schulzeri*, originally described from Italy, has shorter lamellae and bigger basidiospores measuring 4.5–5 × 3.5–5 µm (Læssøe and Petersen 2019).

Entolomataceae Kotl. & Pouzar.

Notes: According to updated MycoBank data, the family Entolomataceae consists of 39 genera, which are globally

distributed. *Entoloma* P. Kumm is the type genus of the family. The other members of the family could be recognized by their similarity in characters such as pink or grayish pink to brownish spore prints, angular spores, thick-walled angular spores, and ornamented spores (Clémençon et al. 2004). In the order Agaricales, the feature of pink angular spores is only found in this family, therefore making it a prominent character of identification (Kühner 1980; Singer 1986).

Clitopilus (Fr. ex Rabenh.) P. Kumm.

Notes: The genus *Clitopilus* (Fr. ex Rabenh.) P. Kumm. is a globally distributed saprophytic genus proposed by Kummer (Jian et al. 2020a). To date, there are 39 accepted species of *Clitopilus* (Kirk et al. 2008; Kumla et al. 2019; Baroni et al. 2020; Jian et al. 2020a, b; Fatima et al. 2022). The genus belongs to the family Entolomataceae and is often characterized by the clitocyboid to omphalinoid or pleurotoid basidiomata with a decurrent pattern of attachment of gills and pink spore prints. The genus occupies a distinct position based on the molecular sequence data and is easily separated from that of *Rhodocybe* Maire (Vizzini et al. 2011). A recent study shows that *Clitopilus* spp. promoted triterpenoid accumulation of *Ganoderma lingzhi* (Zhang et al. 2023b).

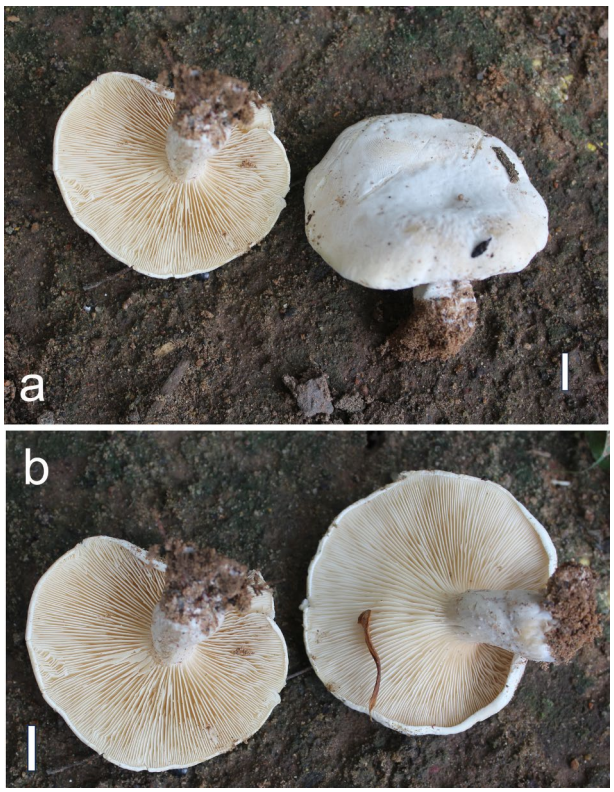


Fig. 79 Basidiomata of ***Clitopilus chichawatniensis*** (GUBH 20327). **a** Pileus surface morphology. **b** Lamellae attachment to the stipe. Scale bar = 10 mm

Clitopilus chichawatniensis N. Fatima, Usman & Khalid, **new geographical record from India.**

Fungal Names: FN 844802; *Facesoffungi*: FoF 15273; Figs. 79, 80, 81

Basidiomata clitocyboid to pleurotoid. **Pileus** 52–68 mm diam., surface white (1A1) to yellowish white (1A2), glabrous, margin non striate; context 1–2 mm thick at center, gradually thinner towards margin, white (1A1). **Lamellae** ca. 2 mm broad, decurrent, ventricose, yellowish white (1A2), concolorous, crowded with 2–3 series of lamellulae. **Stipe** 25–32 × 12–17 mm, gradually broader towards base, white (1A1) to yellowish white (1A2), unchanging on bruising; context white; base with well-developed mycelia. **Taste** not recorded. **Odor** unpleasant. **Spore-print** pinkish.

Basidiospores (6.4–)6.6–7.3–7.9(–8.4) × (4.8–)5.2–5.7–6.3(–6.4) µm, Q = 1.1–1.3–1.4, ovoid to broadly ellipsoid, apically angular, almost 3 to 5 ridges present, hyaline, thin-walled. **Basidia** 26–31 × 7.5–10.5 µm, broadly clavate, hyaline, thin-walled; 4-spored. **Basidioles** 23–33.5 × 5.5–9.0 µm, clavate, hyaline, thin-walled. **Pleurocystidia** and **Cheilocystidia** absent. **Pileipellis** a cutis, composed of irregular, agglutinated, smooth, cylindrical, branched, thin-walled hyphae measuring 23–26 × 2.5–5.5 µm. **Stipitipellis** hyphae 2.5–4.1 µm broad, regular, hyaline, thin-walled. **Clamp-connections** absent in all tissues.

Material examined: INDIA, West Bengal, Paschim Bardhaman district, Durgapur, Malandighi, 23°33′51.2"N 87°24′11.2"E, 92.9 m asl., 11 Sept 2022, *A.K. Dutta & P. Chattopadhyay*, GUBH 20327.

GenBank: GUBH 20327: OR880555 (ITS).

Notes: The species *Clitopilus chichawatniensis* was first discovered in Pakistan and herein reported for the first time from India. Morphologically, the Indian collection nicely match with the type specimen description (Fatima et al. 2022). In the phylogenetic tree (Fig. 81), the newly generated sequence of the Indian collection cluster together with the type specimen sequence (GenBank ON980767) with full support values (MLBS = 100%, PP = 1.00), suggesting them to be conspecific. However, morphologically, the present collection consists of well-developed, clavate pleurocystidia measuring 23–33.5 × 8.0–9.0 µm, which was reported to be absent in the type specimen. Otherwise, all the remaining morphological features of the Indian collection nicely match with the type specimen description (Fatima et al. 2022). Phylogenetically, *C. albidus* appears to be related to *C. chichawatniensis* but differs in having smaller pileus (7–34 mm) colored white and much smaller (mean of 4.5 × 3.6 µm vs. 7.3 × 5.7 µm in *C. chichawatniensis*), subglobose to ellipsoid basidiospores (Raj and Manimohan 2018).

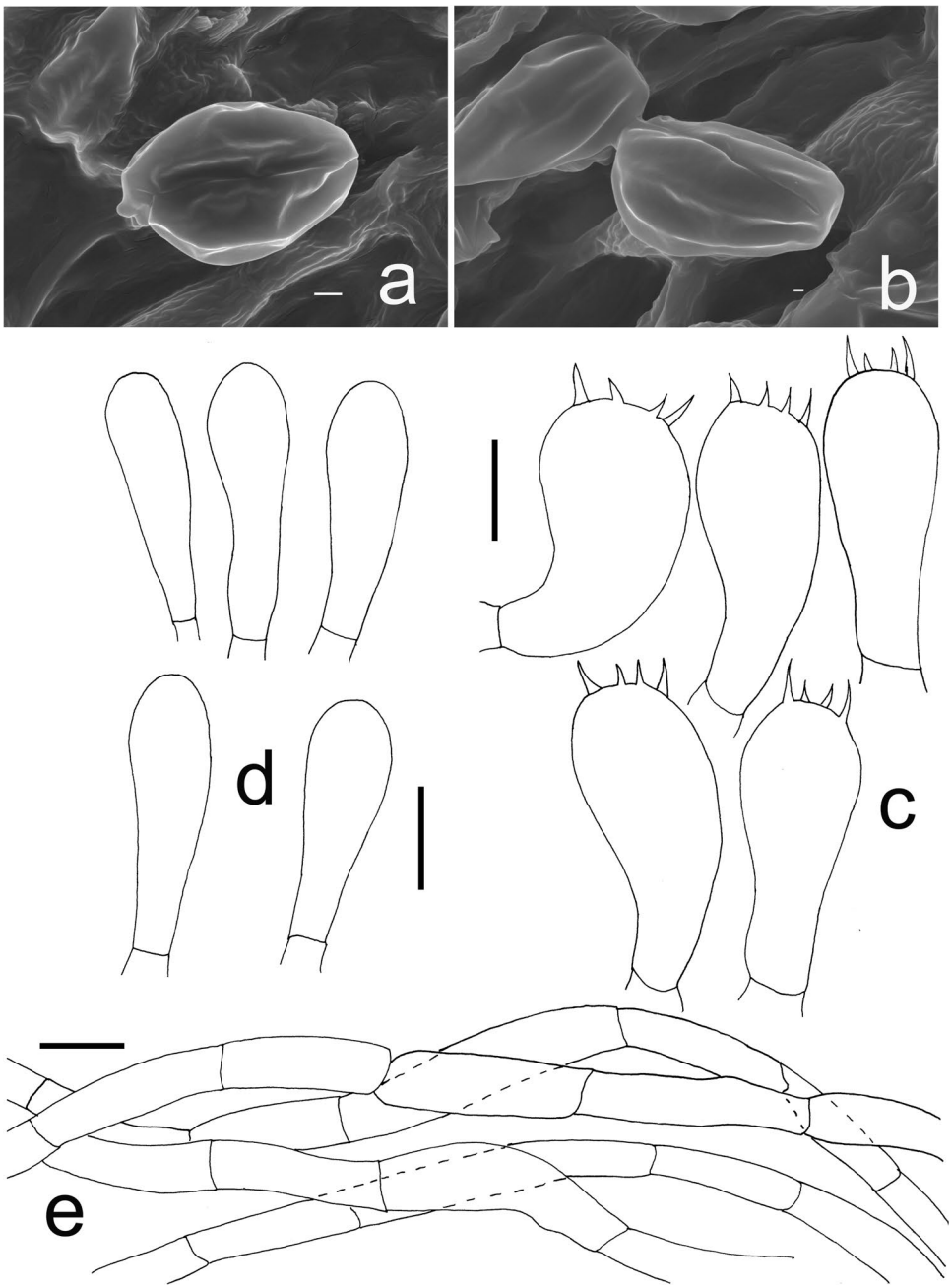


Fig. 80 Microscopic features of ***Clitopilus chichawatniensis*** (GUBH 20327). **a–b** SEM microphotographs of basidiospores. **c** Basidia. **d** Basidioles. **e** Stipitipellis hyphae. Scale bars: **a** = 1 µm, **b** = 300 nm, **c–d** = 10 µm, **e** = 5 µm

Galeropsidaceae Singer.

Notes: Galeropsidaceae is proposed for the secotioid taxa with *Galeropsis* Velen. as the type genus (Singer 1962). Molecular phylogenetic analyses showed that the type species of *Galeropsis*, *G. desertorum* Velen. & Dvořák, is a member of the *Panaeolus sensu* lato (Malysheva et al. 2019). Based on phylogenomic, multigene phylogenetic and molecular clock analyses, He et al. (2024b) proposed *Panaeolus* s.l. as family Galeropsidaceae in Agaricales. There are five genera included in Galeropsidaceae, viz. *Anellaria*, *Bresadoliomyces*, *Panaeolus*, *Panaeolina*, and *Sinopanaeolus*. Species of this family are characterized by small- to medium-sized basidiomata, dark spore print, variegated lamellae, and dark brown basidiospores with a germ pore.

Panaeolus (Fr.) Quél.

Notes: *Panaeolus* is a group of small mushrooms commonly found on dung, in pasturing areas, grasslands, and forests. Species of this genus are characterized by small- to medium-sized basidiomata, dark spore print, pileus always being hygrophanous, variegated lamellae, and dark brown basidiospores with a germ pore. Species identification

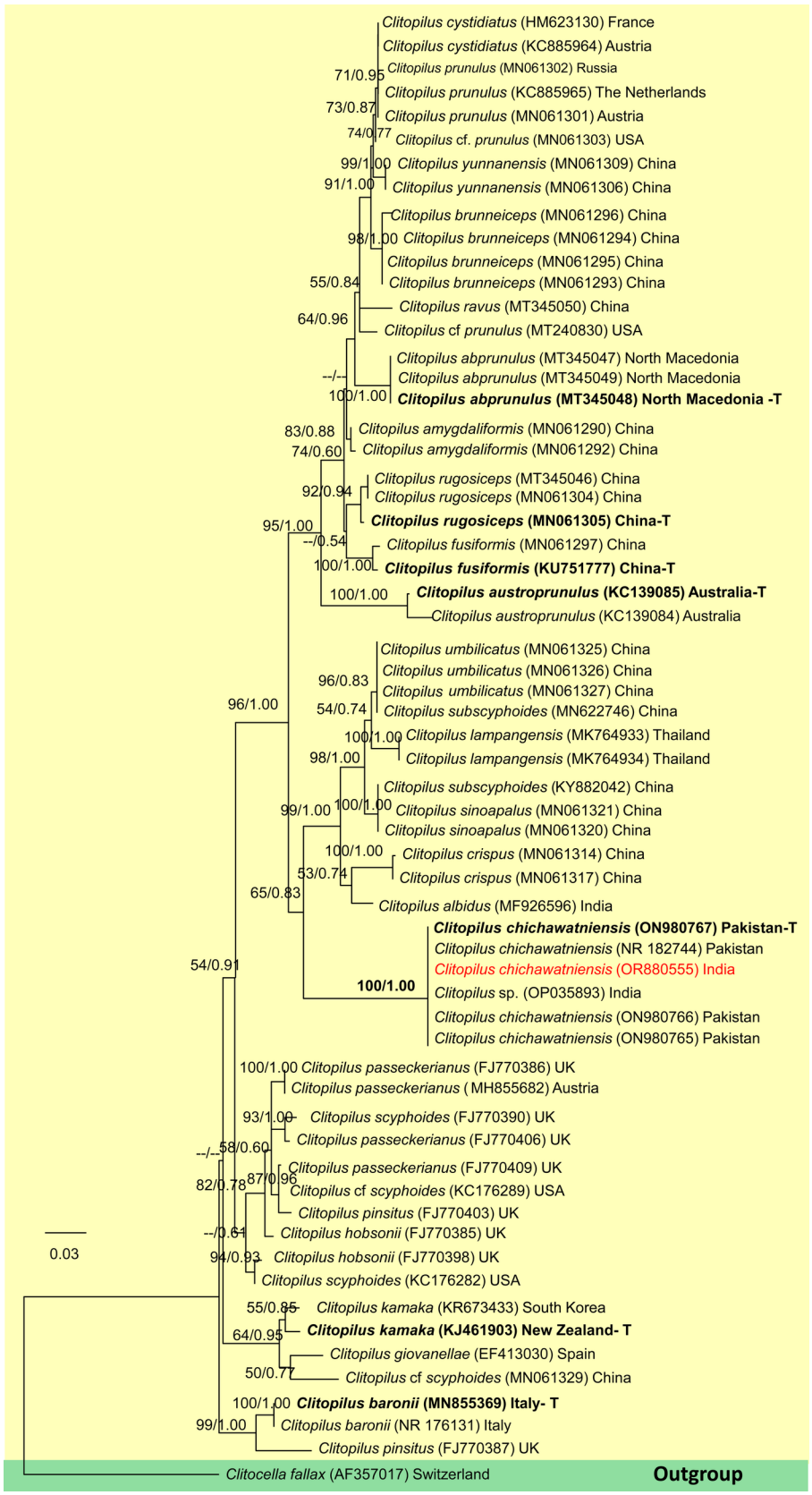


Fig. 81 The Maximum Likelihood tree (-*lnL* = 3663.063549) was generated using a GTR + I + G model of nucleotide evolution based on the nrDNA ITS sequence data. ML bootstrap support (MLBS) ≥ 50% (on the left of '/') and Bayesian posterior probability support values (PP) ≥ 0.50 (on the right of '/') are indicated above or below the nodes. The scale bar represents the expected changes per site. The newly generated sequences for the present study are placed in red font. The GenBank accession number along with the country of origin are indicated after each taxon name in the tree

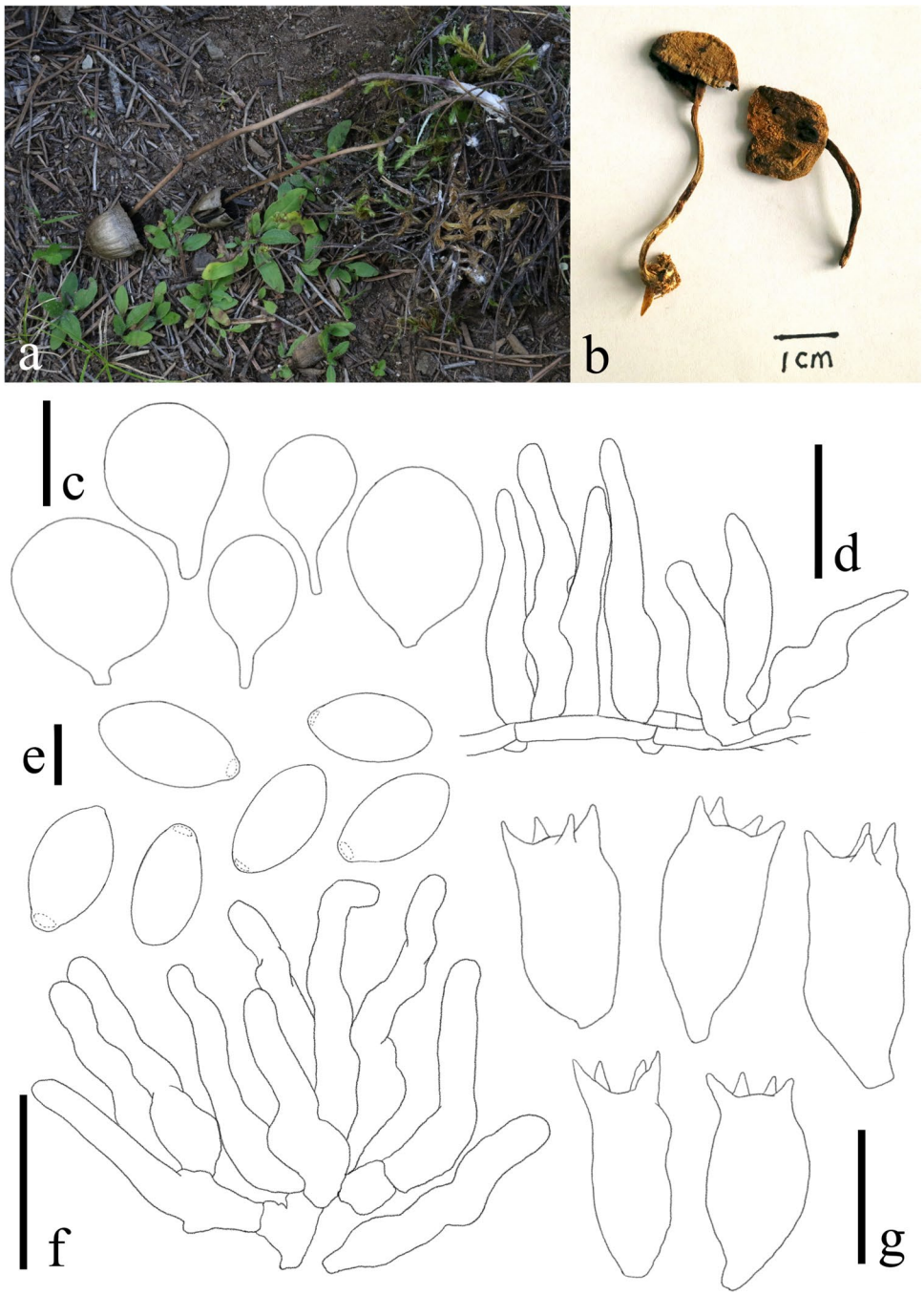


Fig. 82 ***Panaeolus ranwuensis***. **a** Basidiomata in the field (HMAS 287965, **holotype**). **b** Old specimen deposited in HMAS (HMAS 69910). **c** Pileocystidia. **d** Caulocystidia. **e** Basidiospores. **f** Cheilocystidia. **g** Basidia. Scale bars: **e** = 10 µm, **c**, **d**, **f**, **g** = 20 µm

only based on morphological characteristics is difficult in *Panaeolus*. The morphological characteristics of a species could be different due to their different habitat. Thus, molecular data is necessary in the species identification of *Panaeolus*, especially the protein coding genes (*rpb2*, *tef1*) (He et al. 2024b). There are two species described from China in recent years, *P. axfordii* Y. Hu, S.C. Karunarathna, P.E. Mortimer & J.C. Xu [current name *Bresadoliomyces axfordii* (Y. Hu, S.C. Karunarathna, P.E. Mortimer & J.C. Xu) M.Q. He & R.L. Zhao] and *P. xiaolanii* M.Q. He & R.L. Zhao (Hu et al. 2020; He et al. 2024b).

Panaeolus ranwuensis M.Q. He, R.L. Zhao & B. Cao, **sp. nov.**

Fungal Names: FN 572243; *Facesoffungi*: FoF 17110; Figs. 82, 83

Etymology: "ranwu" refers to Ranwu town, the locality of the type specimen.

Holotype: HMAS 287965.

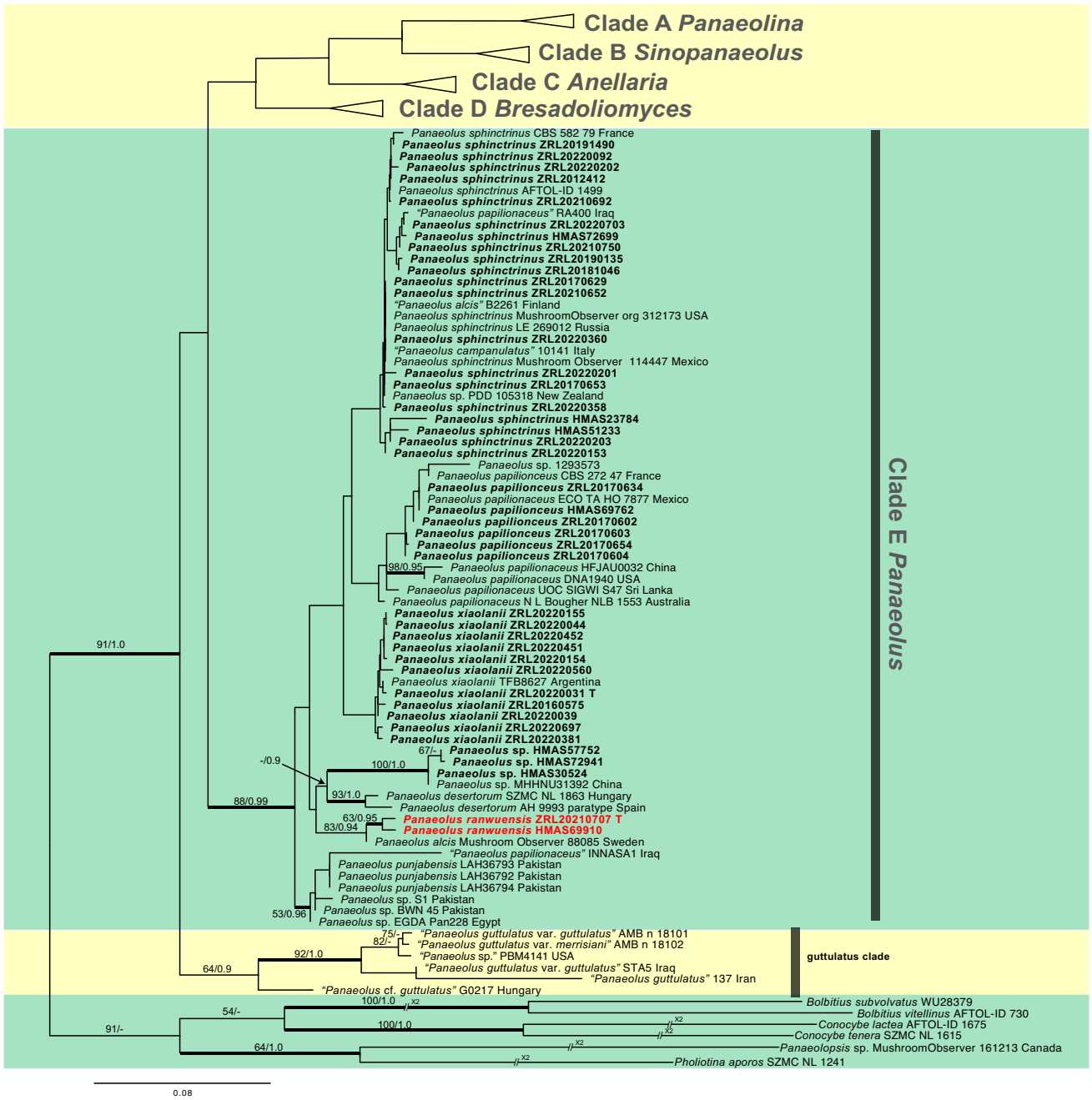


Fig. 83 Maximum Likelihood tree of Galeropsidacea based on six-genes (ITS, LSU, *tef1*, *rpb1*, *rpb2*, and SSU) with outgroup species from Bolbitiaceae

Pileus 9.3–14.1 mm in diam., obtusely conic, campanulate, darkish olive (pantone 5747 c), sometimes paler at margin, surface dry, silk-like, smooth, margin uplifted when basidiomata is dry. **Lamellae** adnate, subdistant, broad, mottled grayish to blackish, entire, edge white. **Stipe** equal, hollow, 78.7–109.9 mm long, 2.0 mm thick, darkish olive, the same color as pileus (pantone 5747 c), lower surface paler, smooth, base with whitish mycelium.

Basidiospores 19.3–24.2 × 10.2–12.9 µm ($\bar{x}$ = 21.2 ± 1.3 × 11.7 ± 0.9, Q = 1.7–1.8, Q_m = 2.0 ± 0.1, n = 20), oblong, smooth, brown, blackish brown, protruding germ pore. **Basidia** 26.6–34.6 × 11.4–14.7 µm, 4-spored, smooth, hyaline. **Cheilocystidia** 14.5–37.0 × 4–14.2 µm, ventricose-rostrate, cylindrical, flexuous, hyaline, smooth. **Pleurocystidia** absent. **Cuticle** composed of large vesicles, **pileocystidia** 24.1–42.2 × 12.1–30.6 µm, pyriform,

hyaline, some with brown pigment. **Caulocystidia** 17.0–33.9 × 3.5–6.9 µm, cylindrical, flexuose. **Clamp connections** present in all hyphae.

Material examined: CHINA, Inner Mongolia Autonomous Region, Aug 1994, *Xiao-Lan Mao*, *You-Zhi Wang*, HMAS 69910; Xizang Autonomous Region, Qamdo Municipality, Baxoi County, 29°47′37″N 95°53′20″E, 2870 m alt, 23 July 2021, *Mao-Qiang He*, *Zhi-lin Ling*, *ZRL20210707* (HMAS 287965, **holotype**).

GenBank: HMAS 287965: PP475220 (ITS), PP472785 (LSU), PP556788 (*tef1*), PP850966 (*rpb1*), PP852735 (*rpb2*), PP472894 (SSU); HMAS 69910: PP475221 (ITS), PP472781 (LSU), PP556789 (*tef1*), PP852734 (*rpb2*).

Notes: *Panaeolus ranwuensis*, represented by HMAS 69910 and HMAS 287965, is clustered in *Panaeolus* with statistical supports as BS/PP = 63/0.95. The sister species is *P. alcis*, represented by a sample collected from Sweden (Mushroom Observer 88,085). Compared with *P. alcis*, *P. ranwuensis* has olive pileus, while *P. alcis* is pale gray. In addition, the pleurocystidia is absent in *P. alcis* (Moser 1984).

Hydnangiaceae Gäum. & C.W. Dodge.

Notes: Hydnangiaceae, with *Hydnangium* Wallr. as the type, was established by Gäum. & C.W. Dodge. The latest classification system shows that the family comprises four genera, *Hydnangium*, *Laccaria* Berk. & Broome, *Maccagnia* Mattir., and *Podohydnangium* G.W. Beaton, Pegler & T.W.K. Young. Hydnangiaceae species exhibit a diverse range of fruit body morphologies, including those with stipes and caps (termed pileate-stipiate) or gasteroid forms that internally produce spores. These species are widely distributed across both temperate and tropical regions.

Laccaria Berk. & Broome.

Notes: *Laccaria* Berkeley and Broome (1883), a cosmopolitan gilled-mushroom genus (Hydnangiaceae, Agaricales, Basidiomycota), is one of the most readily identifiable mushroom genera and is characterized by thick, widely spaced lamellae, purple or orange to brown or flesh-colored fruiting bodies with adnate to slightly decurrent gills and hyaline and ornamented basidiospores, Cheilocystidia normally present in most species.

Laccaria guizhouensis J. Wang & Y.H. Yang, **sp. nov.**

Mycobank: MB 853733; *Facesoffungi*: 17,112; Figs. 84, 85

Etymology: referring to the type locality.

Holotype: HGASMF01-10872.

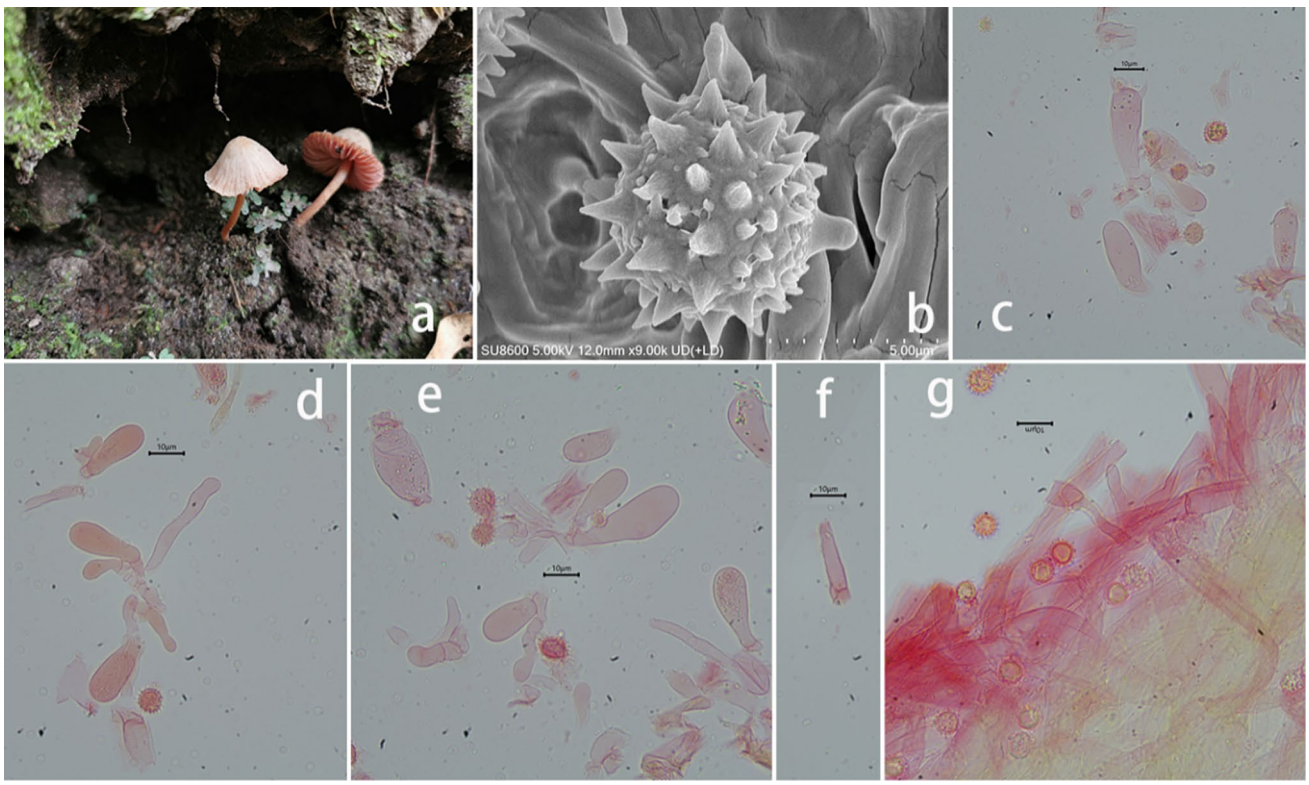


Fig. 84 ***Laccaria guizhouensis***. **a** Basidiomata. **b** basidiospores. **c** Basidia. **d** Pleurocystidia. **e** Cheilocystidia. **f** Clamp connection. **g** Pileipellis. Scale bars: **c**–**g** = 10 µm

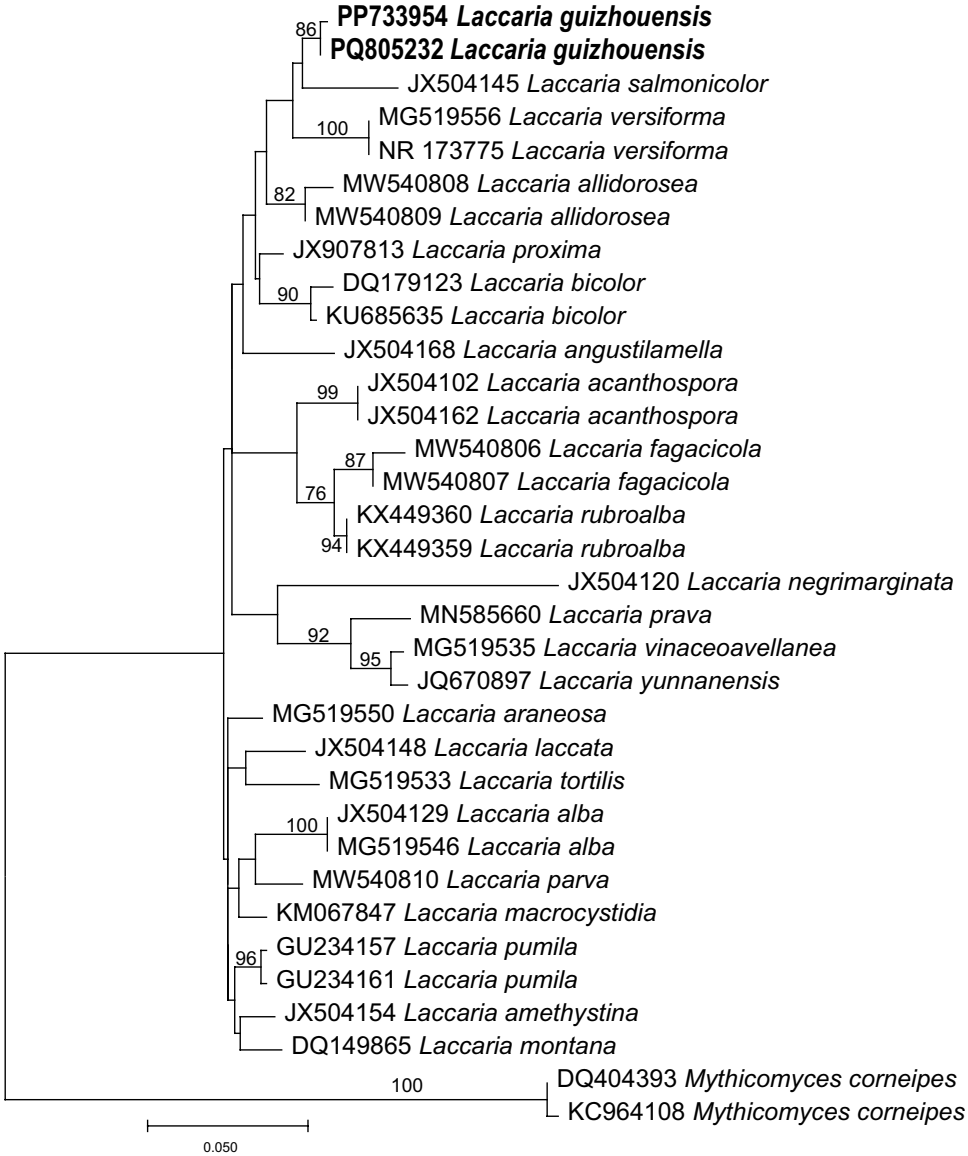


Fig. 85 Maximum Likelihood tree based on ITS sequences, bootstrap values greater than 50% are shown around nodes. New species are shown in bold

Pileus medium-sized, 25–35 mm diam., hemispherical to campanulate, orange white (5A2-6A2) to pinkish white or reddish white (7A2), concolorous finely hairy-scaly, roughened or scaly at the center; margin thin, wavy and slightly striate. **Lamellae** 3–5 mm deep, adnate to free, arcuate, distant, pastel red (8A4-8A5); lamellulae attenuate. **Stipe** 34–45 × 2–3 mm, central, cylindrical, basal mycelium absent; surface grayish red (8B4-8B5), subglabrous, with inconspicuous longitudinal stripes. **Spore print** not obtained.

Basidiospores (6.0–)6.5–7.6–8.7(–9.5) × (5.0–)5.5–6.4–7.0(–7.5) µm, Q = 1.0–1.18–1.38(–1.45), Qm = 1.18 ± 0.09, subglobose to broadly ellipsoid, rare globose and ellipsoid, echinulate, spines up to 2.0 µm in length, echinulae up to 3.0 µm high; **Basidia** (21–)25–31–35(–41) × 8–10(–11) µm, clavate, hyaline, thin-walled, 2- to 4-spored; sterigmata 3–7 µm long. **Pleurocystidia and Cheilocystidia** (12–)18–38(–42) × 3–11 µm, similar, hyaline, smooth, flexuous, subcylindrical to narrowly-cylindrical. **Pileus trama** interwoven, hyphae 2–6 µm wide, with a pale yellow wall pigment. **Pileipellis** a cutis, 5–22(–28) µm diam thickness, thin-walled, hyaline, hyphae 3–8 µm diam. **Clamp connections** present in all hyphae.

Material examined: CHINA, Guizhou Province, Qiannan Prefecture, Duyun City, hahe Factory, 26.37N 107.37E, 1077 m asl, 21 nov. 2020, *Chun-Ying Deng*, *dcy2973* (HGASMF01-10872, **holotype**); Qiannan Prefecture, Duyun City, near Qingshan Factory, 26.37N 107.36E, 1154.4 m asl, 21 nov. 2020, *Chun-Ying Deng*, *dcy2991* (HGASMF01-10854).

GenBank: HGASMF01-10872: PP733954 (ITS); HGASMF01-10854: PQ805232 (ITS).

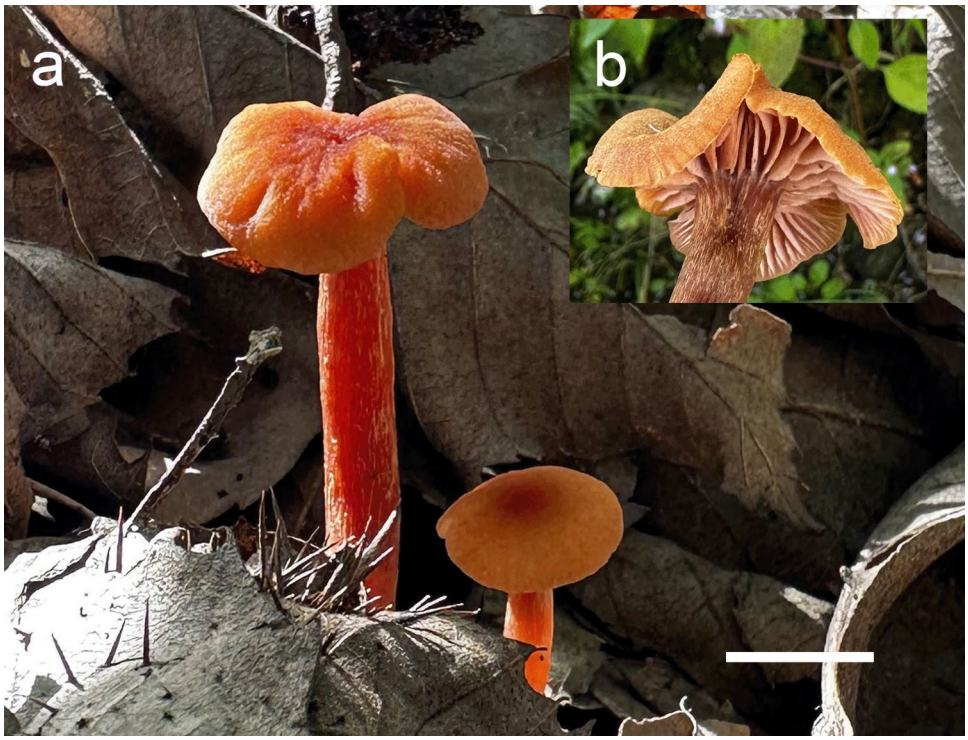


Fig. 86 ***Laccaria macrobasidia***. **a, b** Basidiomata. Scale bars = 2 cm

Notes: *Laccaria guizhouensis* is phylogenetically related to *L. salmonicolor* A.W. Wilson & G.M. Muell. and *L. versiforma* H.J. Cho & Y.W. Lim (Fig. 85). However, there are clear morphological differences, with *L. guizhouensis* having smaller pleurocystidia and cheilocystidia [(12–)18–38(–42) × 3–11 µm], and a pinkish white pileus color. In addition, *L. versiforma* has globose basidiospores with smaller echinulae which are 1 µm long and 0.8–1 µm wide at base, bigger basidia 41–55 × 10–14 µm and hyaline lamellar trama hyphae (Cho et al. 2018); *L. salmonicolor* has copious basal mycelium on the stipe, bigger basidia 39–52 × 12–14 µm (Wilson et al. 2013).

Laccaria macrobasidia H.J. Cho & Y.W. Lim, **new geographical record from China.**

MycoBank: MB 835319; *Facesoffungi*: FoF 17111; Fig. 86

Pileus small, 20–35 mm diam., hemispherical to plane, orange brown to light brown, margin involute to decurved, entire, finely crenate or wavy. **Lamellae** adnate to sub-decurrent, thick, distant, light brown. **Stipe** 20–45 × 1–2 mm, tapering toward the apex, solid, becoming hollow with age, minutely fibrillose the entire length; concolorous with pileus, sometimes darker. **Spore print** not obtained.

Basidiospores 8.5–11.2 × 7.3–10.8 µm, Q = 1.0–1.3, subglobose to broadly ellipsoid, hyaline. **Basidia** 45–69 × 8–13 µm, clavate, hyaline, 4-spored; sterigmata 7–10 µm long. **Pleurocystidia** 18–42 × 3–9 µm, filamentous, hyaline, smooth. **Stipitipellis** composed of parallel, cylindrical, repent, hyaline hyphae. **Pileipellis** composed of interwoven, cylindrical, mostly repent, hyaline hyphae. **Lamellar trama** composed of subparallel to interwoven, cylindrical, repent, hyaline hyphae; subhymenium undifferentiated. **Clamp connections** present in all hyphae.

Material examined: CHINA, Beijing, Yanqing District, 20 Sep 2023, *Kai-Lin Liu*, *ZRL20236173* (HMAS 287968).

GenBank: HMAS 287968: PQ620227 (ITS).

Notes: The morphological and molecular data from the Chinese specimen is consistent with the holotype (Cho et al. 2020). New geographical record from Beijing, China.

Hymenogastraceae Vittad., **s.l.**

Notes: Currently, according to the proposal of Kalichman et al. (2020), *Deconica* belongs to Hymenogastraceae s.l. along with 27 genera. This family is composed by the following: 1) Hymenogastraceae s.str. (four genera), 2) Strophariaceae (nine genera), and 3) 15 genera not assigned to any group. Formerly, *Deconica* was a member of Strophariaceae (Singer 1986). According to Matheny et al. (2006), Strophariaceae s.str. includes: *Agrocybe* Fayod, *Deconica*, *Hypholoma* (Fr.) P. Kumm., *Kuehneromyces* Singer & A.H. Sm., *Pholiota* (Fr.) P. Kumm., and *Stropharia* (Fr.) Quél. Later, Tian and Matheny (2020) also recovered *Bogbodia* Redhead and *Pyrrhulomyces* E.J. Tian & Matheny in this family. In Varga et al. (2019), the following genera were recovered in Strophariacae: *Bogbodia*, *Clavogaster* Henn., *Leratiomyces* Bresinsky & Manfr. Binder ex Bridge, Spooner, Beever & D.C. Park, *Phaeonematoloma* (Singer) Bon, *Pholiota*,

Protostropharia Redhead, Moncalvo & Vilgalys, *Hypholoma*, and *Stropharia*, but *Deconica* and *Kuehneromyces* were placed outside this family. For this reason, Kalichman et al. (2020) do not considered *Deconica* to be within Strophariacae. However, according to Index Fungorum (http://www.indexfungorum.org), it is considered a member of Strophariaceae. The placement of *Gymnopilus* and *Psilocybe* has also always been problematic. Based on Varga et al. (2019), Kalichman et al. (2020) considered *Gymnopilus* and *Psilocybe* to be part of Hymenogastraceae s.l.

Deconica (W.G. Sm.) P. Karst.

Notes: The genus was first proposed by Karsten (1879). For over a century, *Deconica* was synonymous with the genus *Psilocybe* (e.g., Guzmán 1983; Singer 1986), until the works of Moncalvo (2000, 2002) and Matheny et al. (2006) provided molecular evidence of their evolutionary divergence, showing that both genera were distinct and do not share a most recent common ancestor. Subsequently, a nomenclatural proposal was performed by Redhead et al. (2007) to conserve the name *Psilocybe* for species known to produce hallucinogenic effects and revive the name *Deconica* for species that lack psychoactivity. Pertinent combinations were made by Noordeloos (2009) for European species and by Cooper (2012), Ramírez-Cruz et al. (2012, 2013a), and Silva et al. (2013, 2014) for other species collected around the world. Estimates on the number of species in the genus are between 45 (Kalichman et al. 2020) and 133 (Ramírez-Cruz et al. 2020). The broadest sampling work was made by Ramírez-Cruz et al. (2020), in which 60 species of *Deconica* (including seven type specimens) were used to determine their phylogenetic relationships based on ITS sequences. In this work, 18 specimens representing distinct lineages were not associated with any previously described species, showing that *Deconica* may be much more diverse than previously thought. Recently, progress has been made in phylogenomic and chemical aspects of *Psilocybe* (Bradshaw et al. 2022, 2024), including molecular characterization of many type specimens. These advances synergistically affect the genus *Deconica*, allowing a clear separation between both genera and, consequently, requiring new combinations and synonyms. Here, nine new combinations and one synonymy in *Deconica* are proposed based on phylogenetic analysis employing the barcoding region rDNA ITS (Fig. 87), incorporating sequences derived from Ramírez Cruz et al. (2019, 2020), species hypothesis (SH) sequences from the curated fungal ITS database UNITE (Abarenkov et al. 2010), and eight previously unpublished sequences (Supplementary data, Online Resource 2).

Deconica caespitosa (Murrill) Bradshaw, Ram.-Cruz & Dentinger, **comb. nov.**

Basionym: *Psilocybe caespitosa* Murrill, Mycologia 15(1):5 (1923).

Mycobank: MB 853498; *Facesoffungi*: FoF 17113; Fig. 87

Holotype: USA, New York City, New York Botanical Garden, 9 Jun 1910, *W.A. Murrill s.n.* (NY–7616594).

Description and illustration: see Murrill (1923), Smith (1948), and Noordeloos (2001).

Additional material examined: USA, New York City, New York Botanical Garden, 1 Jul 1915, *W.A. Murrill s.n.* (NY–761596, **paratype**).

GenBank: NY–7616594: PP599671 (ITS); NY–761596: PP599670 (ITS).

Notes: This species was collected and described in the USA by Murrill (Murrill 1923). Smith (1948) was the first to note similarities of this species with *Psilocybe subviscida* (Peck) Kauffman, currently *Deconica subviscida* Peck as Noordeloos (2001) proposed. Guzmán (1983) considered it synonymous with the non-hallucinogenic *P. physaloides* (Bull.) Quél. The results of this study (Fig. 87) show its unresolved position within clade D with the following taxa: *D. bullacea* (Bull.) Sacc., *D. californica* comb. nov. (holotype), *D. castanella* (Peck) Noordel., a UNITE species hypothesis SH1171616.09FU as *D. crobula*, *D. graminicola* P.D. Orton, *D. josecastilloi* comb. nov. (holotype), *D. novozoncuantlensis* comb. nov. (holotype), *D. oregonensis* comb. nov. (holotype), and *D. subviscida*. It is difficult to elucidate species limits among all these species based on the ITS region, alone. Multigene or phylogenomic analyses will be necessary to understand the phylogenetic relationships in this clade to confirm previous synonymies or propose novel ones.

Deconica californica (Earle) Bradshaw, Ram.-Cruz & Dentinger, **comb. nov.**

Basionym: *Psilocybe californica* Earle, Bull. New York Bot. Gard. 3(no. 11):301 (1905).

Mycobank: MB 853499; *Facesoffungi*: FoF 17114; Fig. 87

Holotype: USA, California, Stanford University, 30 Nov 1901, *C.F. Baker 152* (NY–761602).

Description and illustration: see Earle (1905) and Guzmán (1983).

GenBank: NY–761602: PP599674 (ITS).

Notes: This species was described by Earle (1905) providing a macromorphological description including the size of basidiospores. Smith (1948) and Guzmán (1983) studied the type and considered it synonymous with *Psilocybe castanella* Peck var. *castanella* [= *Deconica castanella* (Peck) Noordel.] based on micromorphology, particularly basidiospores and cheilocystidia. The holotype of *D. californica* was recovered unresolved in the clade D, as well a sample vouchered as *D. castanella* from the

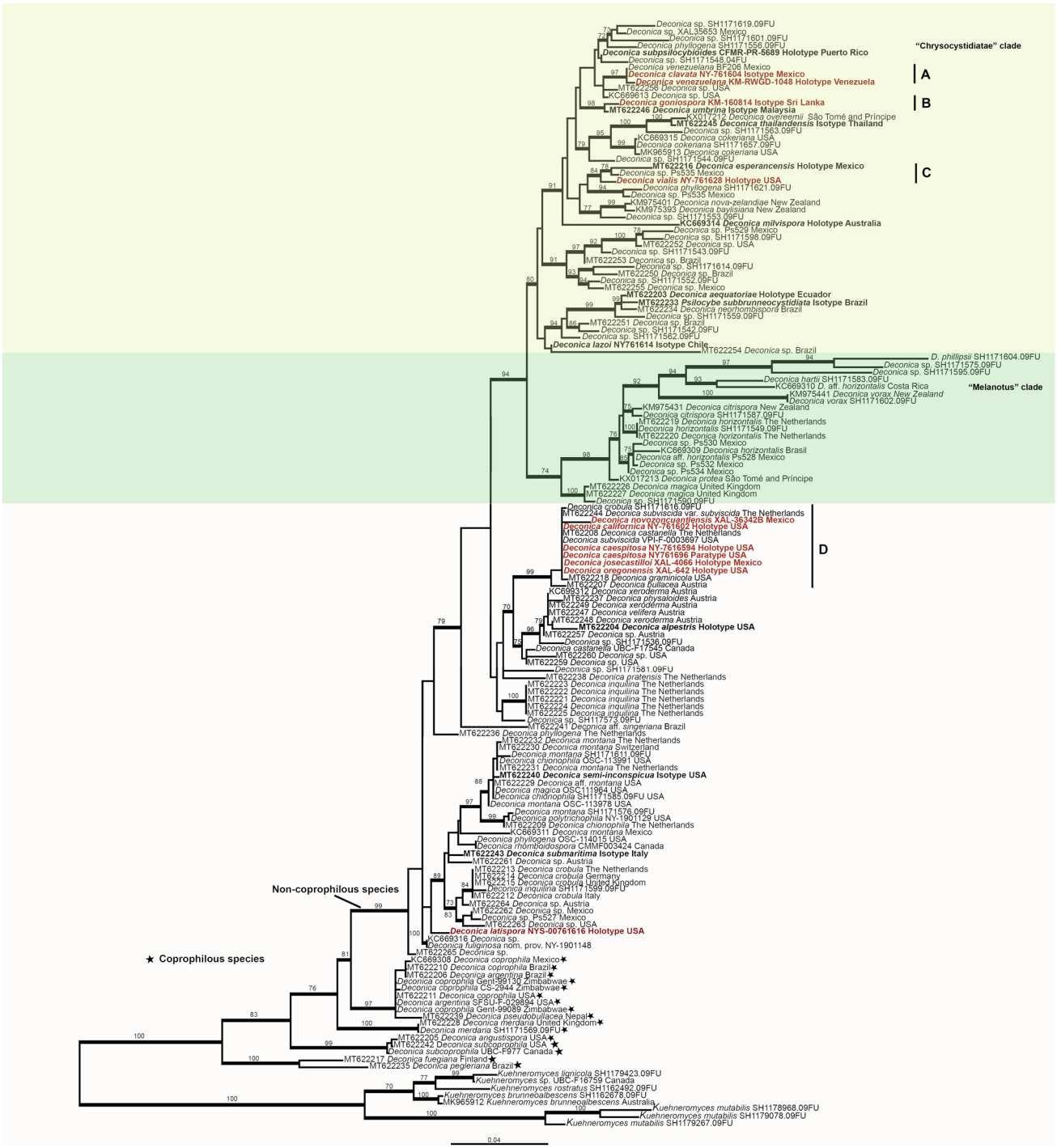


Fig. 87 Phylogram generated from Maximum Likelihood obtained through IQtree analysis based on rDNA ITS sequences of *Deconica*. Branch lengths are scaled to the expected number of nucleotide substitutions per site. Sequences obtained from the type specimens are indicated in bold and those of the types involved in the new combinations proposed here are indicated in bold and red. Highly supported clades (bootstrap support above 70%) appear with thickened branches. Yellow shading indicates the "Chrysocystidiatae" clade and green shading the "Melanotus" clade. For subclades indicated as A, B, C, and D see text

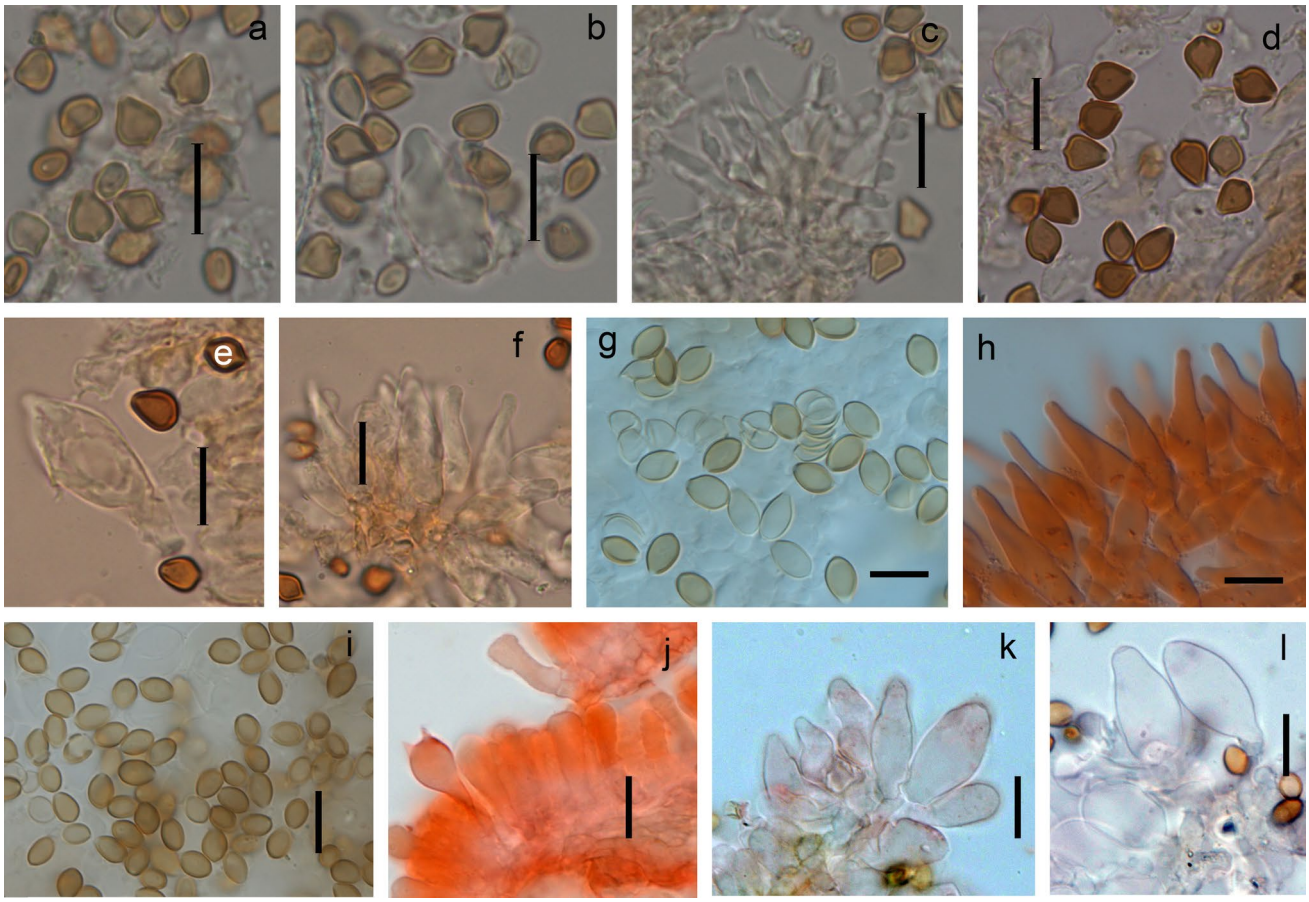


Fig. 88 Micromorphology features of the type specimens of *Deconica*. **a–c** *Deconica goniospora* (isotype Gardner 835). **a** Basidiospores. **b** Basidiospores and pleurochrysocystidium. **c** Cheilocystidia. **d–f D. josecastilloi** (isotype Valenzuela 4066). **d** Basidiospores. **e** Pleurochrysocystidium. **f** Cheilocystidia. **g–h** *D. oregonensis* (holotype Morgan 642). **g** Basidiospores. **h** cheilocystidia. **i–l** *D. novozoncuantlensis* (holotype Guzmán 36,342–B). **i** Basidiospores. **j** Basidium and basidioles. **k–l** Cheilocystidia. Scale bar = 10 µm. **a–g**, **i**, and **l** in KOH, **h**, **j**, and **k** in Congo red

Netherlands. With the information available, it is best to consider *D. californica* separately from *D. castanella* until further evidence suggests otherwise.

Deconica goniospora (Berk. & Broome) Bradshaw, Ram.-Cruz & Dentinger, **comb. nov.**

Basionym: *Agaricus gonisporus* Berk. & Broome, J. Linn. Soc., Bot. 11(no. 56):541 (1871).

≡ *Flammula goniospora* (Berk. & Broome) Sacc., Syll. fung. (Abellini) 5:827 (1887).

≡ *Naucoria goniospora* (Berk. & Broome) Henn., in Engler & Prantl, Nat. Pflanzenfam., Tail. I (Leipzig) 1(1**):251 (1898) [1900].

≡ *Deconica goniospora* (Berk. & Broome) Singer, Sydowia 9(1–6):404 (1955), nom. inval.

≡ *Psilocybe goniospora* (Berk. & Broome) Singer, Sydowia 15(1–6):70 (1962) [1961].

Mycobank: MB 853514; *Facesoffungi*: FoF 17115; Figs. 87, 88a–c

Isotype: SRI LANKA, Peradeniya, Nov 1868, *Thwaites 835* [K(M) 160814].

Description and illustration: see Ramírez-Cruz et al. (2013a).

GenBank: K(M) 160,814: PP599660 (ITS).

Notes: This species was recovered in subclade B of the "Chrysocystidiatae" clade. The synapomorphies of this clade are pleurochrysocystidia —pleurocystidia having a refractive content— and growing on wood (Ramírez-Cruz et al. 2013b, 2020). Based on the refractive content of the pleurocystidia (Fig. 88b), Ramírez-Cruz et al. (2013a) had already indicated that the isotype belonged to *Deconica* and that it was morphologically similar to *D. neocaledonica* (Guzmán & E. Horak) Ram.-Cruz & Guzmán, *D. thailandensis* (E. Horak, Guzmán & Desjardin) Ram.-Cruz & Guzmán, and *D. umbrina* (E. Horak, Guzmán & Desjardin) Ram.-Cruz & Guzmán. The sister taxon of *D. goniospora* is *D. umbrina* from Malaysia (clade B, Fig. 87). Both species are similar in macro- and micromorphology and may

be synonymous; however, multigene phylogenetic evidence is needed to confirm this.

Deconica josecastilloi (Guzmán) Bradshaw, Ram.-Cruz & Dentinger, **comb. nov.**

Basionym: *Psilocybe josecastilloi* Guzmán [as '*josecastilloa*'], Revta. Mex. Micol. 20:29 (2005).

Mycobank: MB 538394; *Facesoffungi*: FoF 17116; Figs. 87, 88d–f

Isotype: MEXICO, Estado de México, Valle de Bravo region, Los Sauces, 16 Sep 1984, *Valenzuela 4066* (XAL).

Description and illustration: see Guzmán (2005).

GenBank: *Valenzuela 4066*: PP599672 (ITS).

Notes: This species was described by Guzmán (2005) from Mexico. In the ITS tree (Fig. 87), it was recovered in clade D, but is unresolved. It is distinguished from other members of the clade by the rhomboid basidiospores and its pleurochrysocystidia (Fig. 88e).

Deconica latispora (Earle) Bradshaw, Ram.-Cruz & Dentinger, **comb. nov.**

Basionym: *Psilocybe latispora* Murrill, Mycologia 15(1):10 (1923).

Mycobank: MB 853519; *Facesoffungi*: FoF 17117; Fig. 87

Holotype: USA, New York City, New York Botanical Garden, 25 Jun 1903, *F.S. Earle 1462* (NYS–00761616).

Description and illustration: see Murrill (1923), Smith (1948), and Guzmán (1983).

GenBank: NYS–00761616: PP599679 (ITS).

Notes: This species was described by Murrill (1923), then the type was studied by Smith (1948) and Guzmán (1983), who considered it similar to *Deconica phyllogena* (Sacc.) Noordel., differing in smaller basidiospores and the presence of cheilocystidia. The sequence of the type specimen was recovered as unresolved in the non-coprophilous *Deconica* clade (Fig. 87).

Deconica novozoncuantlensis (Guzmán, Ram.-Cruz, Ram.-Guill. & E. Gándara) Bradshaw & Dentinger, **comb. nov.**

Basionym: *Psilocybe novozoncuantlensis* Guzmán, Ram.-Cruz, Ram.-Guill. & E. Gándara, Revta. Mex. Micol. 23:5 (2006).

Mycobank: MB 853520; *Facesoffungi*: FoF 17118; Figs. 87, 88i–l

Holotype: MEXICO, Veracruz, Coatepec, Zoncuantla, old road Xalapa to Coatepec, Mariano Escobedo street, 17 Sep 2006, *Guzmán 36,342–B* (XAL).

Description and illustration: see Guzmán et al. (2006).

GenBank: *Guzmán 36,342–B*: PP599673 (ITS).

Notes: This species was described from Mexico by Guzmán et al. (2006). Micromorphologically, it is very similar to *D. xeroderma* (Huijsman) Noordel.; however, the three included samples of *D. xeroderma* are in a sister clade to clade D, where *D. novozoncuantlensis* was placed (Fig. 87).

Deconica oregonensis (Guzmán) Bradshaw, Ram.-Cruz & Dentinger, **comb. nov.**

Basionym: *Psilocybe oregonensis* Guzmán, Docums Mycol. 29(no. 116):43 (2000).

Mycobank: MB 853521; *Facesoffungi*: FoF 17119; Figs. 87, 88g–h

Holotype: USA, Oregon, Linn Co, without specific locality, 15 Mar 1984, *Morgan 642* (XAL).

Description and illustration: see Guzmán (2000).

GenBank: *Morgan 642*: PP599669 (ITS).

Notes: This species was described by Guzmán (2000) from the USA. According to Guzmán (2000), this taxon is similar to three non-hallucinogenic species: *Psilocybe bulbosa* (Peck) A.H. Sm., *P. tuxtlensis* Guzmán, and *Deconica castanella* var. *castanella* (=*P. californica* sensu Guzmán 1983); all these species share similar macro- and micromorphology, such as the shape of basidiospores and cheilocystidia. In the ITS tree (Fig. 87), *D. oregonensis* was unresolved in clade D.

Deconica venezuelana (Dennis) Bradshaw, Ram.-Cruz & Dentinger, **comb. nov.**

Basionym: *Psilocybe venezuelana* Dennis, Kew Bull. 15(1):137 (1961).

Synonym: *Psilocybe clavata* Guzmán [as '*clavatum*'], Beih. Nova Hedwigia 74:307 (1983).

Mycobank: MB 853522; *Facesoffungi*: FoF 17120; Figs. 87, 89, 90

Holotype: VENEZUELA, Dept. Federal, El Avila, 13 Jun 1958, *Dennis 1048* (holotype of *Psilocybe venezuelana*, KM–RWGD–1048).

Isotype: MEXICO, Oaxaca, near Totontepec, 7 Jul 1978, *Jacobs 63* (isotype of *Psilocybe clavata* NY–761604).

Description and illustration: see Dennis (1961), Guzmán (1983).

Additional material examined: MEXICO, Jalisco, Mpio. San Sebastián del Oeste, Jardín Botánico Haráveri, camino a Las Guacas, 21 Oct 2023, O. Castro-Jauregui 2997A (IBUG).

GenBank: KM–RWGD–1048: PP599666 (ITS); O. Castro-Jauregui 2997A: PP599667 (ITS); *Jacobs 63*: PP599668 (ITS).

Notes: *Deconica venezuelana* was described by Dennis (1961) and studied by Guzmán (1983). Our results show that it is conspecific with *D. clavata* described from Mexico. A recent collection of *D. venezuelana* from Mexico is illustrated in color for the first time (Fig. 89a) and enable new observations not described in the protologue: clamp connections present, caulocystidia present, 16–36 × 8–20 µm, subglobose, claviform,

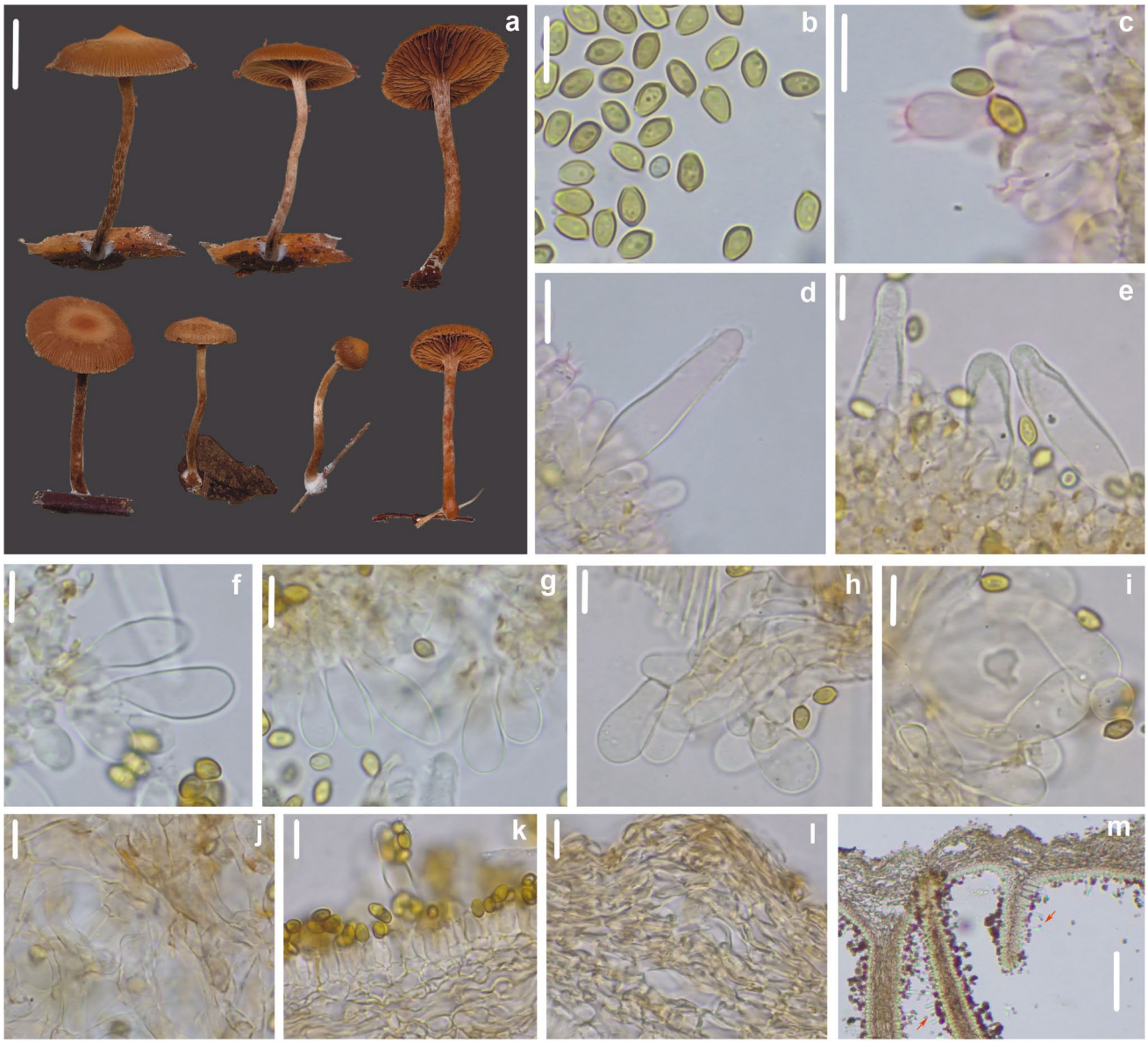


Fig. 89 Macro- and micro-morphology of ***Deconica venezuelana*** (O. Castro-Jauregui 2997A). **a** Basidiomata. **b** Basidiospores. **c** Basidium and basidiospores. **d**–**e**, **k** pleurocystidia. **f**–**g** cheilocystidia. **h**–**i** Caulocystidia. **j** Hyphae of the pileus trama. **l** Pileipellis. **m** Section of the pileus showing pleurocystidia projecting from the lamellae (red arrows). Scale bar: **a** = 1 mm, **b**–**l** = 10 µm, **m** = 100 µm. **a**, **b**, **e**–**m** in KOH; **c**, **d** in Congo red

sphaeropedunculate, or fusiform, hyaline with yellowish brown pigment encrusted in the wall, and thin-walled. There are records of this species from Brazil, Guadeloupe, Martinique, Mexico, and Venezuela (Dennis 1961; Bononi et al. 2008). Considering that *D. clavata* is conspecific, this is the second record of the species for Mexico. In the ITS tree (Fig. 87), the three samples (two types and a recent collection) form a monophyletic group, subclade A, in the "Chrysocystidiatae" clade, which shares a most recent common ancestor with two unidentified *Deconica* spp. from the USA, although this relationship is not supported. Furthermore, two other species, *Psilocybe largicystidiata* E. Horak & Desjardin from Indonesia (Horak and Desjardin 2006), and *P. megacystis* Horak from Papua New Guinea (Horak 2006), could be conspecific with this species due to their distinctive large pleurocystidia with mucilaginous cover at the apices (Fig. 89d). It is necessary to reinvestigate the morphology and to sequence the

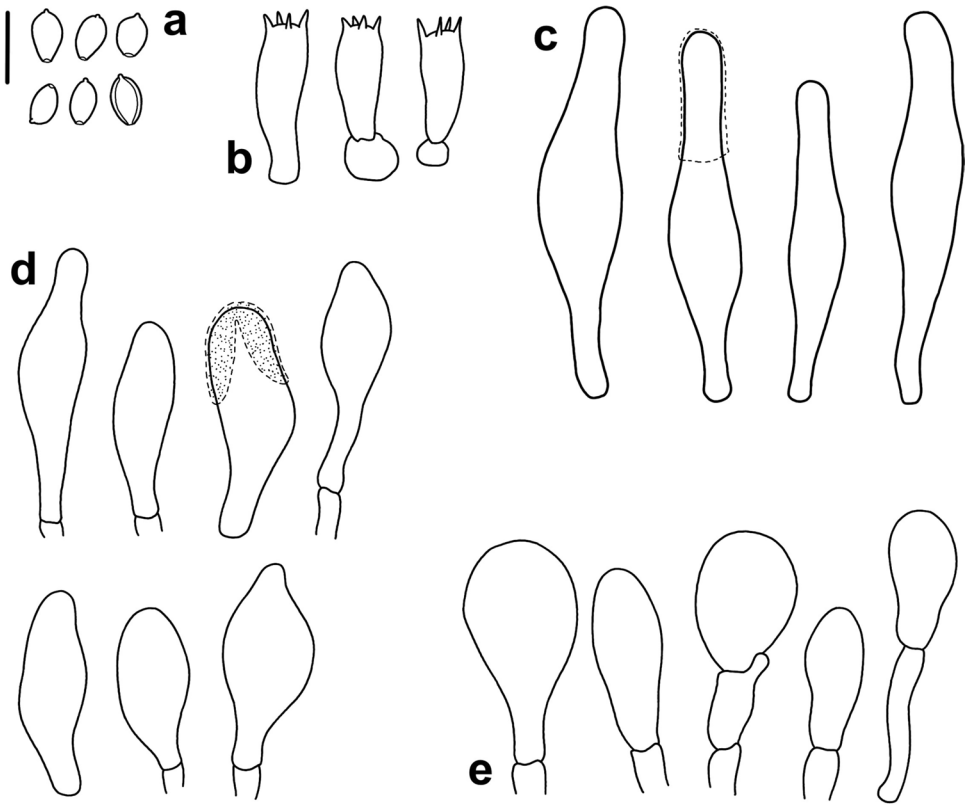


Fig. 90 ***Deconica venezuelana*** (O. Castro-Jauregui 2997A). **a** Basidiospores. **b** Basidia. **c** Pleurocystidia. **d** Cheilocystidia. **e** Caulocysitida. Scale bar = 10 µm

DNA of the types of these species to confirm if they are synonyms.

Deconica vialis (Murrill) Bradshaw, Ram.-Cruz & Dentinger, **comb. nov.**

Basionym: *Psilocybe vialis* Murrill, Mycologia 15(1):11 (1923).

≡ *Naematoloma vialis* (Murrill) Guzmán, in Guzmán & Vergeer, Mycotaxon 6(3):476 (1978).

Mycobank: MB 853523; *Facesoffungi*: FoF 17121; Fig. 87

Holotype: USA, New York City, Bronx County, New York Botanical Garden, 27 Jul 1902, *F.S. Earle 725* (NY–761602).

Description and illustration: see Murrill (1923) and Smith (1948).

GenBank: NY–761602: PP599661 (ITS).

Notes: Based on the ITS tree (Fig. 87), this taxon belongs to the subclade C of the "Chrysocystidiatae" clade and has a sister relationship with a clade composed of *Deconica esperancensis* Ram.-Cruz & Glez.-Adame and an unnamed species of *Deconica* from Mexico (Ps535). *Deconica vialis* is similar to *D. esperancensis* in shape of basidiospores and pleurochrysocystidia, but they can be distinguished by smaller basidiospores, smaller cheilocystidia, and solitary basidioma in *D. esperacensis*. Ramírez-Cruz et al. (2020) noted that *D. esperancensis* is similar in morphology to *D. alnetorum* nom. prov. and *D. chrysocystidiatae* nom. prov. The species in clade C shares the following features: subrhomboid in frontal view (not mitriform) basidiospores, presence of pleurochrysocystidia, and to grow on wood or wood chips.

Gymnopilus P. Karst.

Notes: *Gymnopilus* is a large genus, with more than 200 names published worldwide, and is an important component of fungal biodiversity on wood (Kirk et al. 2008; Khan et al. 2017; He et al. 2019). The genus is characterized by yellowish brown, greenish, reddish to rusty brown, or purple colored basidiomata, usually a bitter taste, yellow to rusty brown basidiospores with verrucose to rugulose warts, generally capitate to subcapitate lageniform to narrowly utriform cheilocystidia, and presence of clamp connections on all hyphal elements (Singer 1986; Guzmán-Dávalos 1996, 2003; Campi et al. 2021; Khurshid et al. 2023). The majority of *Gymnopilus* species are saprobes, and some species generate psilocybin, a psychedelic compound which can lead to nervous poisoning (Gartz 1989; Bau et al. 2014).

Gymnopilus rimopileus R.L. Zhao, B. Cao & W.Q. Yang, **sp. nov.**

Fungal Names: FN 571925; *Facesoffungi*: FoF 17122; Figs. 91, 92

Etymology: '*rimopileus*' refers to the cracks that develop along the margin of the mature pileus.

Holotype: HMAS 287453.

Fig. 91 *Gymnopilus rimopileus* (HMAS 287453, **holotype**). **a** Basidiomata. **b**, **c** Basidiospores. **d** Basidia. **e** Cheilocystidia. **f** Pleurocystidia. **g** Pileipellis. **h** Stipitipellis. Scale bars: **a** = 1 cm, **b**, **c** = 3 μm, **d** = 6 μm, **e** = 8 μm, **f** = 6 μm, **g** = 4 μm, **h** = 5 μm

Pileus 4–19 mm diam, hemispherical, later shallowly convex, yellowish brown to brown (5B8–6C8), surface smooth and glabrous, with undulating and rimose margin, not scaly. **Context** thin, yellowish brown (1A4), unchanging upon cutting. **Lamellae** adnate to slightly adnexed, pale yellow to yellowish brown (2A3–2B3), crowded, finally ferruginous, edges even or entire. **Stipe** 0.9–1.1 × 0.1–0.2 cm, cylindrical, pale white to pale yellow at young (1A1–2A3), yellowish brown to brown when mature, hollow, terete, soft to solid, fragile, with or without cortinate veil. **Odor** indistinct.

Basidiospores (5.6–)6.2–7.3(–7.7) × (3.6–)4.4–5.4(–5.8) μm, Q = 1.35–1.41, ellipsoid, some amygdaliform, rarely ovoid, yellow–brown (2A7–5B7), verrucose with small warts, thick-walled, small suprahilar depression present. **Basidia** (16–)18–22(–24.6) × 5–6.7(–7) μm, clavate, two to four sterigmata, up to 2–4 μm in length, colorless, oil droplets present. **Cheilocystidia** (15–)16–34(–36) × (4–)5–6.3(–7) μm, narrowly lageniform with inflated basal part, utriform to narrowly lageniform, some cylindrical to narrowly clavate, with obtuse or subcapitate apex, base pedunculate or pedicellate. **Pleurocystidia** 12.6–24.8(26) × (2)3.5–6.9(7.4) μm, narrowly clavate, lecythiform to narrowly utriform, capitate to sub-capitate, with obtuse or subcapitate apex, hyaline, oil droplets present, thin-walled, with well-defined basal clamp. **Stipitipellis** a cutis, hyphae 4–10 μm in diameter, septate, branched, thin-walled, clamp connections present. **Pileipellis** a cutis of filamentous hyphae with some inflated cells,

7–14 µm in diameter, with very light rusty brown plasmatic pigment, septate, crowded, branched, clamp connections present, thin-walled, some inflated hyphae observed with constrictions at septa. **Smell** and **taste** not recorded.

Material examined: CHINA, Sichuan Province, Tibetan Autonomous Prefecture of Garzê, Derong county, Xiayong Nature Reserve, 28°22′38.07″N 99°21′4.34″E, 3451.27 m asl, 22 August 2020, collected by *Mao-Qiang He* and *Mei-Qi Wang*, *ZRL20201778* (HMAS 287453, **holotype**) and *ZRL20201838* (HMAS 287997).

GenBank: HMAS 287453: OR913460 (ITS), OR915150 (LSU), OR915213 (SSU), PP058967 (*rpb2*).

Habitat: Summer to autumn scattered or in clusters on rotten hardwood in later stages of decay.

Notes: *Gymnopilus rimopileus* is easily distinguished by its brownish, rimose pileus. Phylogenetic analyses in this study revealed that *G. rimopileus* forms a distinct lineage with well support, positioned as a sister species to *G. picreus* (Fig. 92). In the field, *G. rimopileus* closely resembles *G. picreus* in macromorphology; both species exhibit similarly colored pilei and grow on dead coniferous trees. However, *G. rimopileus* can be differentiated by its dehiscent pileus and slightly sparser lamellae. Additionally, *G. picreus* has larger spores (8.7–9.2 × 5.1–5.5 µm) and basidia (26.7–30.3 × 6.6–7.9 µm) (Cho et al. 2016).

Psilocybe (Fr.) P. Kumm.

Notes: Members of the genus *Psilocybe* (Fr.) P. Kumm. are undoubtedly among the most renowned and extensively studied psychoactive mushrooms globally. The genus is widely distributed across temperate and particularly tropical regions, where species thrive as saprotrophs, decomposing herbaceous or woody plant debris as well as herbivore dung (Guzmán 1983). Comprising approximately 165 species (Bradshaw et al. 2024), the genus designates *P. semilanceata* (Fr.) P. Kumm. as its type species (Redhead et al. 2007).

Psilocybe zhushanensis R.L. Zhao & B. Cao, **sp. nov.**

Fungal Names: FN 572498; *Facesoffungi*: FoF 17669; Figs. 93, 94

Etymology: refers to Zhushan County, Hubei Province, China, the locality of the type specimen.

Holotype: HMAS 282438.

Pileus 8–20 mm broad, convex to more-or-less hemispherical when young, becoming convex to pulvinate with a slight umbo or plane at center when mature, yellowish brown to orange brown, margin sometimes with a thin band of whitish veil remnants when young, often disappearing in age. **Lamellae** adnate to sinuate, relatively broad, buff to drab when young, become medium brown at maturity. **Lamellulae** present, 1–3 between each lamellum. **Stipe** up to 50 mm in length, central, smooth, fibrillose-striate, cylindric, equal, whitish to sorrel brown, solid or hollow, with white radiating rhizomorphs at the base. **Context** off-white.

Basidiospores (7.9–)8.3–8.8–9.2(–9.6) × (4.5–)4.8–5.1–5.3(–5.4) µm, Q = 1.6–1.7–1.9 (holotype, n = 30), ellipsoid to oblong, brown, thick-walled, with germ pore. **Basidia** 21.2–29.3 × 6.1–9.5 µm (holotype, n = 30), clavate. **Pleurocystidia** absent. **Cheilocystidia** 24.5–36.1 × 4.4–7.6 µm (holotype, n = 30), hyaline, thin-walled but sometimes with a gradually thickening wall toward apices, variable in shape, typically narrowly lageniform. **Pileipellis** constituted by cylindrical, radially arranged hyphae, 2.2–6.1 µm wide. **Clamp connections** present in all tissues.

Ecology: Gregarious, growing on decomposed wood.

Material examined: CHINA, Hubei Province, Shiyan City, Zhushan County, Duheyuan National Nature Reserve, 31°31′32.19″N 110°0′32.10″E, 1824 m asl, 28 August 2023, collected by *Xin-Yu Zhu*, *ZRL20237000* (HMAS 282437) and *ZRL20237017* (HMAS 282438, **holotype**).

GenBank: HMAS 282437: PV389794 (ITS); HMAS 282438: PV389795 (ITS).

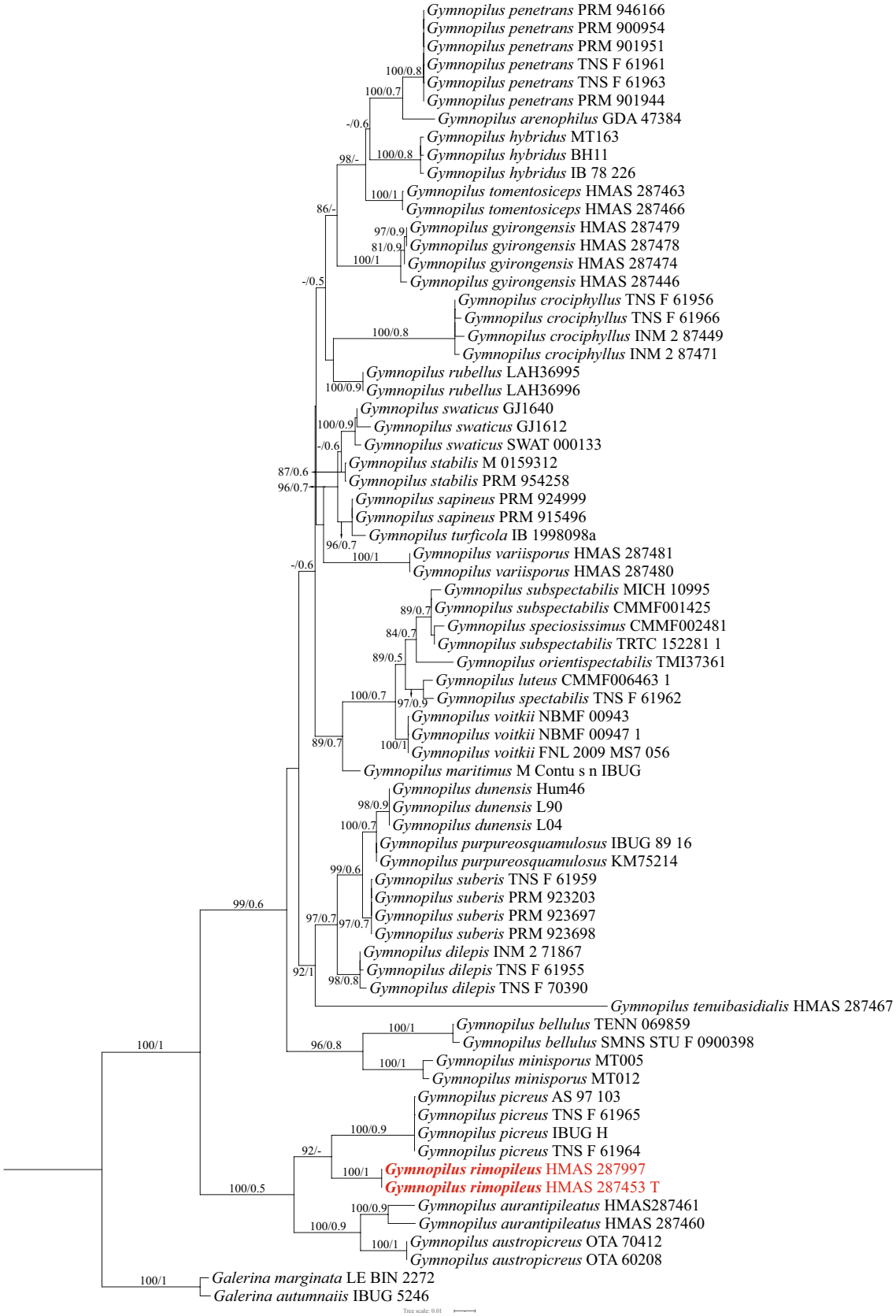
Notes: In the BLAST analysis conducted on NCBI, the sequence most similar to *Psilocybe zhushanensis* was *Psilocybe medullosa* (Bres.) Borov. (GenBank HF912357), with a percent identity of 97.7%. We incorporated these similar sequences into the phylogenetic tree, and the results demonstrated that *P. zhushanensis* could be clearly distinguished from *P. medullosa*, forming an independent clade.

Lycoperdaceae F. Bercht. & J. Presl.

Notes: Members of the family Lycoperdaceae, commonly known as puffballs, are widely distributed saprotrophic fungi. Based on morphological and phylogenetic analyses, a revised taxonomic system for the Lycoperdaceae family comprising 26 genera has been proposed (Li et al. 2024b). Nineteen of these genera are supported by molecular data, while seven genera (*Acutocapillitium*, *Calvatiopsis*, *Calbovista*, *Gastropila*, *Glyptoderma*, *Japonogaster*, *Lycoperdopsis*) currently lack available molecular data.

Bovista Pers.

Notes: A multigene phylogeny of the Lycoperdaceae family revealed that the previous genus *Bovista* was not monophyletic; instead, *Bovista* subgenus *Bovista* and subgenus *Globaria* formed distinct, well-supported clades. Consequently, these subgenera have been elevated to the rank of genera. *Bovista* is now redefined with *Bovista plumbea* Pers. as its type species. The main morphological features distinguishing *Bovista* from *Globaria* include the absence or reduction of the subgleba, Bovista-type capillitium, and pedicellate spores (Li et al. 2024b).


Gymnopilus penetrans PRM 946166
Gymnopilus penetrans PRM 900954
Gymnopilus penetrans PRM 901951
Gymnopilus penetrans TNS F 61961
Gymnopilus penetrans TNS F 61963
Gymnopilus penetrans PRM 901944
Gymnopilus arenophilus GDA 47384
Gymnopilus hybridus MT163
Gymnopilus hybridus BH11
Gymnopilus hybridus IB 78 226
Gymnopilus tomentosiceps HMAS 287463
Gymnopilus tomentosiceps HMAS 287466
Gymnopilus gyirongensis HMAS 287479
Gymnopilus gyirongensis HMAS 287478
Gymnopilus gyirongensis HMAS 287474
Gymnopilus gyirongensis HMAS 287446
Gymnopilus crociphyllus TNS F 61956
Gymnopilus crociphyllus TNS F 61966
Gymnopilus crociphyllus INM 2 87449
Gymnopilus crociphyllus INM 2 87471
Gymnopilus rubellus LAH36995
Gymnopilus rubellus LAH36996
Gymnopilus swaticus GJ1640
Gymnopilus swaticus GJ1612
Gymnopilus swaticus SWAT 000133
Gymnopilus stabilis M 0159312
Gymnopilus stabilis PRM 954258
Gymnopilus sapineus PRM 924999
Gymnopilus sapineus PRM 915496
Gymnopilus turficola IB 1998098a
Gymnopilus variisporus HMAS 287481
Gymnopilus variisporus HMAS 287480
Gymnopilus subspectabilis MICH 10995
Gymnopilus subspectabilis CMMF001425
Gymnopilus speciosissimus CMMF002481
Gymnopilus subspectabilis TRTC 152281 1
Gymnopilus orientispectabilis TMI37361
Gymnopilus luteus CMMF006463 1
Gymnopilus spectabilis TNS F 61962
Gymnopilus voitkii NBMF 00943
Gymnopilus voitkii NBMF 00947 1
Gymnopilus voitkii FNL 2009 MS7 056
Gymnopilus maritimus M Contu s n IBUG
Gymnopilus dunensis Hum46
Gymnopilus dunensis L90
Gymnopilus dunensis L04
Gymnopilus purpureosquamulosus IBUG 89 16
Gymnopilus purpureosquamulosus KM75214
Gymnopilus suberis TNS F 61959
Gymnopilus suberis PRM 923203
Gymnopilus suberis PRM 923697
Gymnopilus suberis PRM 923698
Gymnopilus dilepis INM 2 71867
Gymnopilus dilepis TNS F 61955
Gymnopilus dilepis TNS F 70390
Gymnopilus tenuibasidialis HMAS 287467
Gymnopilus bellulus TENN 069859
Gymnopilus bellulus SMNS STU F 0900398
Gymnopilus minisporus MT005
Gymnopilus minisporus MT012
Gymnopilus picreus AS 97 103
Gymnopilus picreus TNS F 61965
Gymnopilus picreus IBUG H
Gymnopilus picreus TNS F 61964
Gymnopilus rimopileus HMAS 287997
Gymnopilus rimopileus HMAS 287453 T
Gymnopilus aurantipileatus HMAS287461
Gymnopilus aurantipileatus HMAS 287460
Gymnopilus austropicreus OTA 70412
Gymnopilus austropicreus OTA 60208
Galerina marginata LE BIN 2272
Galerina autumnaiis IBUG 5246
Tree scale: 0.01

◂**Fig. 92** Maximum Likelihood phylogram of *Gymnopilus* inferred from ITS, nrLSU, nrSSU and *rpb2* sequences. The tree is rooted by *Galerina marginata*. Maximum Likelihood support values (> 70) and posterior probabilities (> 0.90) are shown on the branch (ML/PP). The new species is in red

Bovista cretacea T.C.E. Fr., **new geographical record from China.**

MycoBank: MB 101538; *Facesoffungi*: FoF 17123; Figs. 95, 96

Basidiomata globose, subglobose, depressed globose, 16–22 mm in diameter. **Pseudostipe** abscent or not indistinct, the base encrusted with soil. **Peridium** layered. **Exoperidium** whitish overall when young, the upperpart possesses irregular cracking, whitish, cream white, and scattered grayish brown flaky squamulose, gradually fall off with age. **Endoperidium** papery, smooth, cream white, grayish white. **Gleba** powdery, at first whitish then yellowish brown, slightly yellowish green at maturity.

Basidiospores globose to subglobose, 3.8–4.8 µm, ($\bar{x} = 4.4 \pm 0.2$, n = 30), smooth to asperulate, slightly thick-walled (about 0.5 µm), with an oil drop central, often with a pedicel (8–12 µm), under SEM ornamented with cylindrical to sub-cylindrical verrucae. **Capillitium** of *Bovista*-type, 2–10 µm width, smooth to asperulate, slightly thick-walled (1.2–1.7 µm in width), tapering to the end. **Paracapillitium** absent. **Exoperidium** was made up of inflated cells, globose to subglobose, thick-walled, smooth, hyaline in 5% KOH. **Endoperidium** was made up of straight hyphae rare branched, septa abundant.

Material examined: CHINA, Xizang Autonomous Region, Ngari Prefecture, Burang County, 30°29′N 81°10′W, ca. 4437 m asl, 1 Aug 2024, *Xi-Xi Han* and *Lin-Hui Liu*, *ZRL20240263* (HMAS 287969), *ZRL20240264* (HMAS 287970) and *ZRL20240265* (HMAS 287971).

GenBank: HMAS 287969: PQ620228 (ITS); HMAS 287970: PQ620229 (ITS); HMAS 287971: PQ620230 (ITS).

Notes: This species is very rare and has been documented in only a few European countries, including Sweden (Fries et al. 1914), Iceland, Norway (Larsson and Jeppson 2008), and Russia (Rebriev et al. 2020). Molecular data from the Chinese specimen aligns with data from European specimens (Fig. 96), establishing a new geographic record from the Xizang Autonomous Region, China.

Omphalotaceae Bresinsky.

Notes: Omphalotaceae is a family of widely distributed and morphologically diverse marasmioid and gymnopoid agaric genera. Phylogenetic studies have placed this family within the Agaricales, encompassing many traditionally and recently described genera of saprotrophic or parasitic mushroom-producing fungi. However, some genera within Omphalotaceae have not yet achieved a stable classification that reflects monophyletic groups with clearly identifiable morphological characteristics (Oliveira et al. 2019).

Collybiopsis (J. Schröt.) Earle.

Notes: Petersen and Hughes (2021) accepted *Collybiopsis* as the correct generic name for *Marasmiellus* Murrill. The classification system of *Collybiopsis* has recently undergone large changes through molecular approaches (Kim et al. 2022). All species of *Collybiopsis* and some species of *Gymnopus* sect. *Vestipedes*, as well as some species of *Marasmiellus*, are included in the genus *Collybiopsis* (Petersen and Hughes 2021). However, this classification likely requires a multi-gene analysis to determine if this large group truly represents a monophyletic lineage.

Collybiopsis gibbosa (Corner) R.H. Petersen, **new geographical record from India.**

Fungal Names: FN 556187; *Facesoffungi*: FoF 16480; Figs. 97, 98, 99

Pileus 36–78 mm diam., convex to hemispheric when young, becoming broadly convex to plano-convex when old, with a small umbo at the center, slightly rugulose, translucent striate, mostly glabrous to sometimes radially fibrillose, disc light brown (7D6) to brown (7D7-8), extending grayish orange (5B3) to brownish orange (5C4, 6C4-5) with white to cream margin, hygrophanous. **Context** cream, ca. 1 mm broad. **Lamellae** ca. 3 mm broad, adnexed to sinuate, some lamellae extend ¼th of the stipe like a thin vein, close to moderately crowded with up to 3 series of lamellulae, entire, ventricose, white, turns light yellow (4A5) with moisture loss, concolorous. **Stipe** 51–74 × 3–7 mm, central, cylindrical, equal, fibrous, pliant, glabrous, longitudinally striate, pastel red (7A5) to brownish orange (6C4-5, 7C5), non-insititious, basal tomentum white to cream. **Odor** and **taste** not distinctive.

Basidiospores (7–)8–9–9.5(–11) × (3.5–)4–4.5–5(–6) µm, ellipsoid to amygdaliform, hyaline, acyanophilic, inamyloid, smooth, thin-walled. **Basidia** not observed. **Basidioles** cylindrical to clavate, hyaline, thin-walled. **Lamellae edge** sterile, with well-developed crowded cystidia. **Cheilocystidia** 25–55 × 5–8 µm, crowded, cylindrical to clavate or ventricose, sometimes lobed, hyaline, thin-walled. **Pleurocystidia** absent. **Pileipellis** a cutis, hyphae 3–5 µm broad, radially arranged, cylindrical, slightly gelatinous, incrusted, incrustation brownish. **Pileocystidia** present, 25–35 × 5.5–6.5 µm, clavate to nodulose, hyaline, thin-walled. **Pileus trama** hyphae 3–6 µm broad, interwoven, cylindrical, hyaline, smooth, inamyloid. **Lamellae trama** hyphae 4–6 µm broad, parallel to subparallel, cylindrical, smooth, hyaline, inamyloid, thin-walled. **Stipitipellis** hyphae 3.5–6.5 µm broad, cylindrical, hyaline, thin-walled. **Caulocystidia** present, 30–45 × 5–7 µm, clavate, occur in chains,

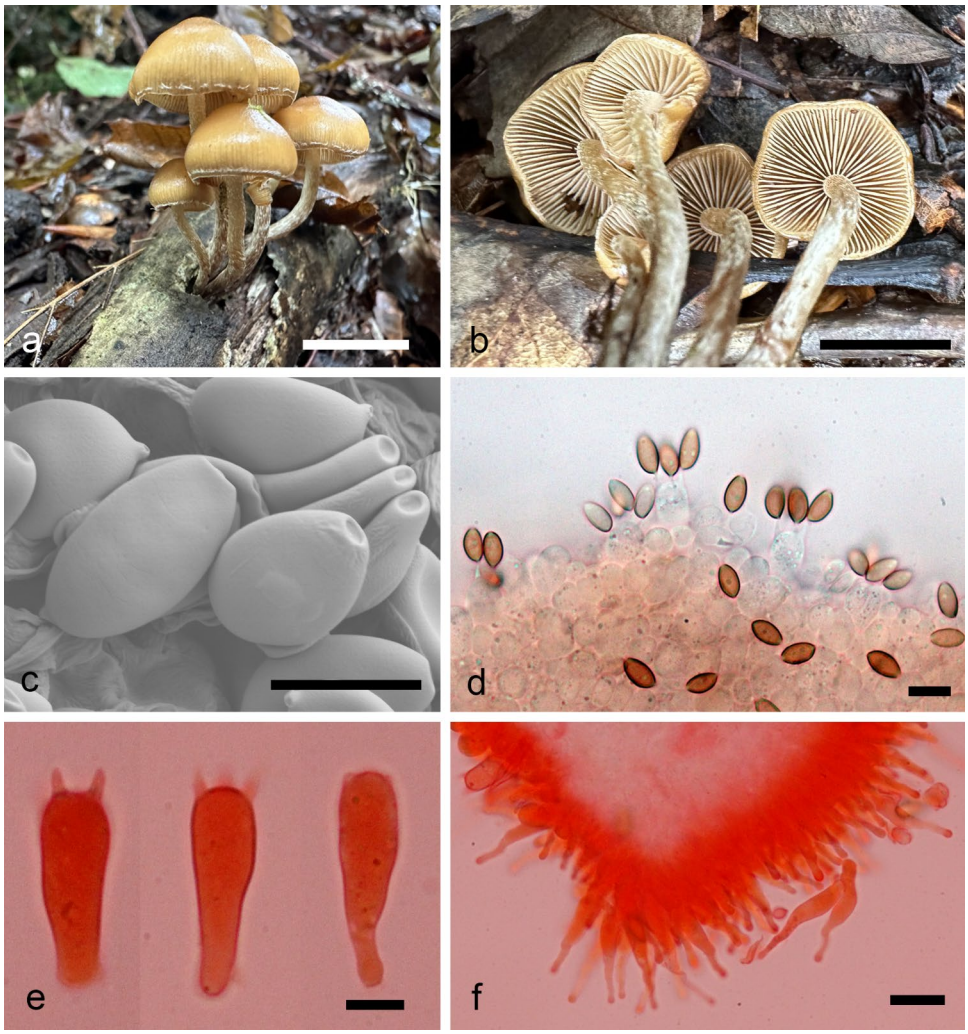


Fig. 93 *Psilocybe zhushanensis* (HMAS 282438, **holotype**). **a, b** Basidiomata. **c, d** Basidiospores. **e** Basidia. **f** Cheilocystidia. Scale bars: **a–b** = 1 cm, **c, e** = 5 µm, **d, f** = 10 µm

smooth, hyaline, thin-walled. **Clamp connections** present in all the tissues.

Material examined: INDIA, West Bengal, North-24-Parganas district, Barasat, 22°43′27.5"N 88°30′19.8"E, elev. 13 m, 16 July 2015, *A.K. Dutta & S. Paloi*, *AKD 316/2015* (CUH AM294).

GenBank: CUH AM294: MF189076 (ITS).

Notes: Characteristic features of *Collybiopsis gibbosa* include a striate, medium to large pileus colored grayish orange to brownish orange with light brown to brown disc and white to cream margin, close to moderately crowded lamellae, and a broad, longitudinally striate stipe colored pastel red to brownish orange, and basidiospores measuring 7–11 × 3.5–6 µm. The morphological details of our Indian collection nicely match those of Corner (1996), who described the present taxon as *Marasmius gibbosus* Corner based on his collection made from Singapore. The present collection shows slightly larger pileus (36–78 × 12–52 mm) and stipe (51–74 × 16–62 mm) as compared to the Indonesian collection (Wilson et al. 2004), which otherwise fits well based on other morphological features.

Within the molecular phylogenetic tree (Fig. 99), all included species of *Collybiopsis* appear in a single clade. The previously deposited sequences of *Collybiopsis gibbosa* from Brazil, the USA, and West Africa, identified by GenBank KY061202, AY263436, DQ450020, and MF100978, grouped together with the newly generated sequence (GenBank MF189076) with full statistical supports (100% BS, 1.00 PP). However, among closely related taxa, *Collybiopsis luxurians* (Peck) R.H. Petersen differs from *C. gibbosa* by a slightly smaller radially striate pileus (25–65 mm in diam.) colored reddish brown to reddish gray, pale brown lamellae, pale brown stipe, a slightly smaller basidiospore with a mean of 8.8 × 4.5 µm, and smaller cheilocystidia measuring 15.5–24 × 4–7 µm (Jang et al. 2015). *Collybiopsis polygramma* (Mont.) R.H. Petersen has a medium-sized pileus (50–140 mm in diam.) colored brown to grayish brown at disc and light grayish brown to yellowish brown towards the margin, presence of a central depression encircling the

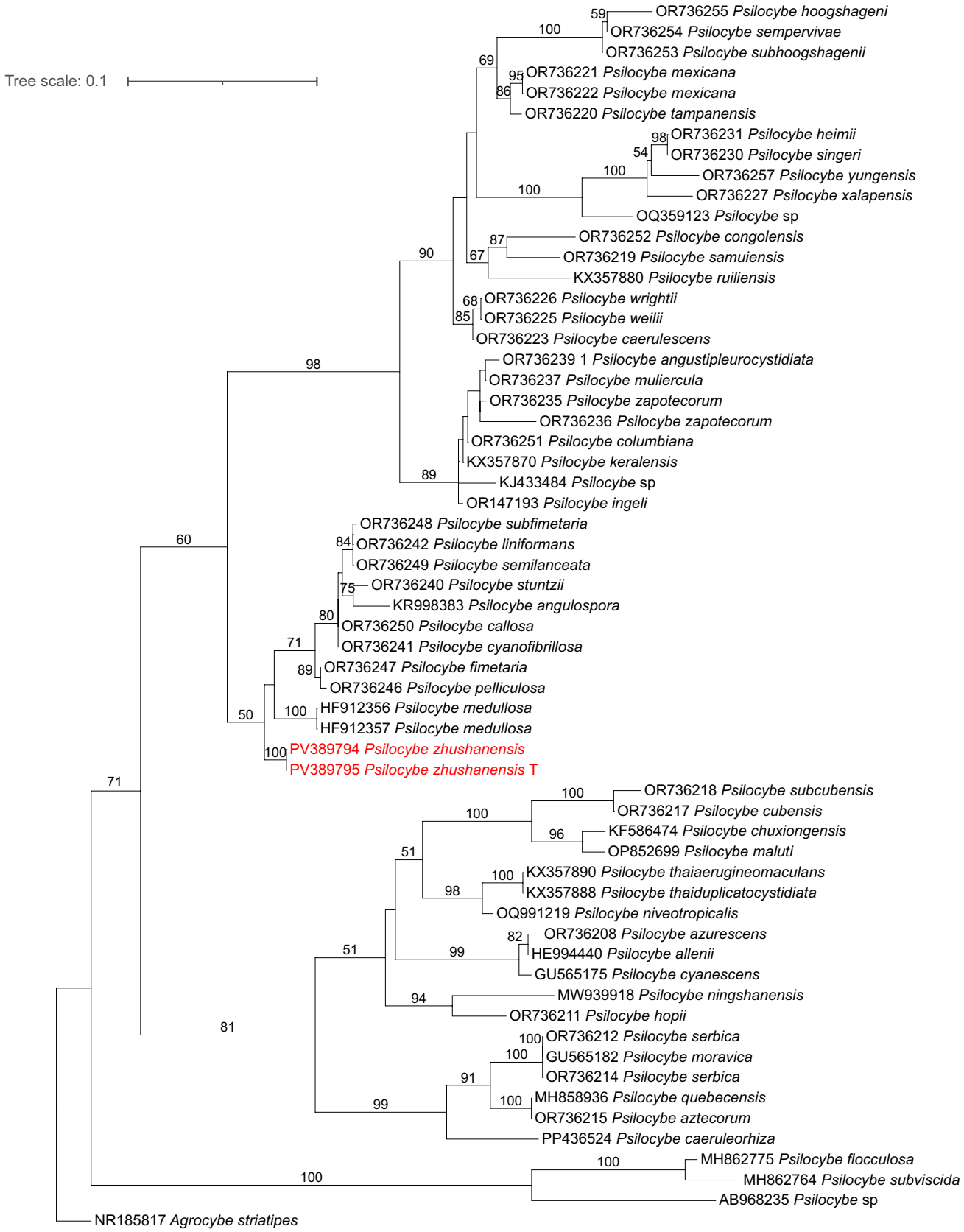


Fig. 94 Maximum Likelihood tree of *Psilocybe* based on ITS sequences, bootstrap values greater than 50% are shown around nodes. New species are shown in red

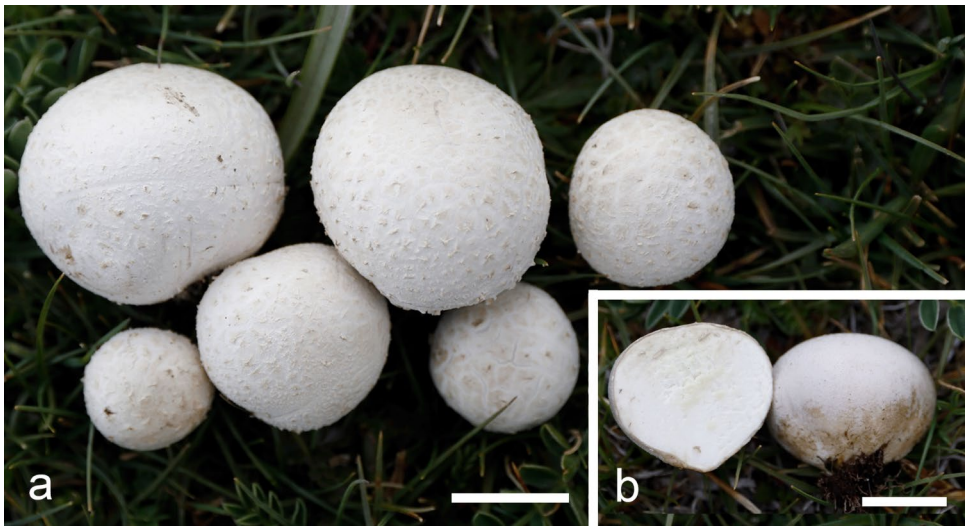


Fig. 95 ***Bovista cretacea.*** **a** Basidiomata (HMAS 287971). **b** Basidiomata (HMAS 287969). Scale bars = 1 cm

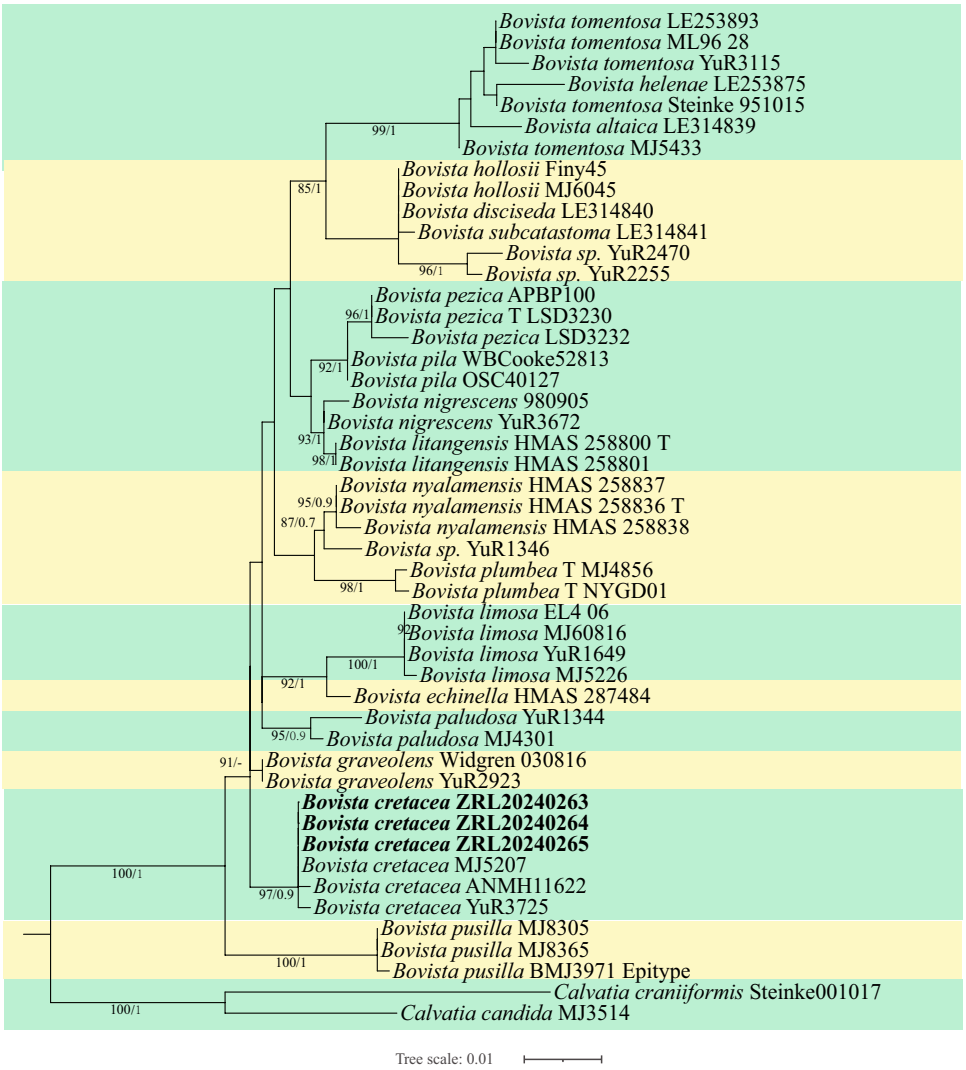


Fig. 96 Phylogenetic tree of *Bovista* inferred from ITS sequences data, rooted with *Calvatia craniiformis* and *C. candida*. Branches supported by both BS ≥ 70% and PP ≥ 0.90 were labeled. The examined specimens in this study are in bold

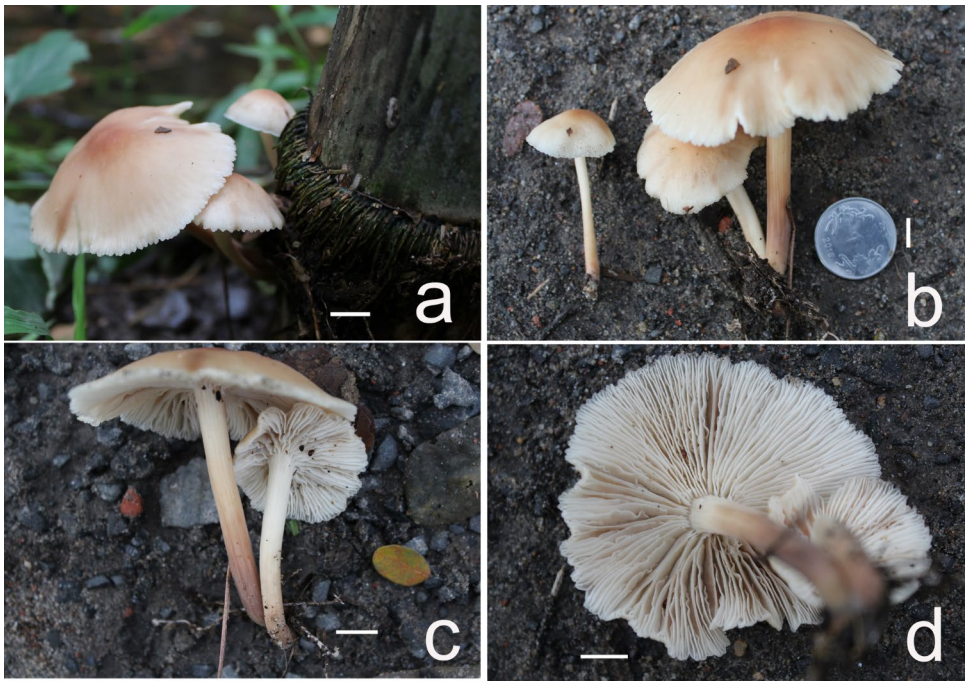


Fig. 97 *Collybiopsis gibbosa* (CUH AM294). **a–d** Basidiomata. Scale bars: **a–d** = 10 mm

umbo, creamy white lamellae with light brown to vinaceous brown patches, slightly longer stipe (40–68 × 3–5 mm) colored creamy white to light brownish cream with creamy brown to creamy vinaceous brown base, slightly smaller basidiospore with a mean of 7.9 × 4.3 µm, and a longer cheilocystidia measuring 35–72 × 5–7.5 µm (Dutta et al. 2015). *Collybiopsis menehune* (Desjardin, Halling & Hemmes) R.H. Petersen differs by its small-sized pileus (21–38 mm diam.) colored buff brown to brownish yellow at disc that turn paler at maturity, creamy white-colored lamellae with adnate attachment, smaller stipe (25–55 × 2–4 mm) colored dingy buff at the base with brownish gray elsewhere, presence of rhizomorphs, smaller basidiospore with a mean of 8.7 × 4.0 µm, and presence of cylindrical pleurocystidia (Desjardin et al. 1999; Dutta et al. 2015).

Collybiopsis subumbilicata J.S. Kim & Y.W. Lim, **new geographical record from China.**

MycoBank: MB 842057; *Facesoffungi*: FoF 17124; Fig. 100

Pileus 10–40 mm diam., plano-convex to plano-concave, subumbili-cate, becoming undulate and uplifted in age, grayish orange to brown. **Context** cream, ca. 1 mm broad. **Lamellae** subdistant, free to adnexed, white. **Stipe** 40–65 × 2−4 mm, cylindrical, tomentose, hollow, light brown to dark brown, becoming paler to the apex, covered with pubescence.

Basidiospores 5.5−7.5 × 2.5−3.5 µm, Q = 1.8–2.3, oblong to subcylindrical, smooth, hyaline, non-dextrinoid, with drops. **Basidia** 18–25.5 × 3.5–5.5 µm, 4-spored, narrowly clavate, cylindrical. **Cheilocystidia** and **Pleurocystidia** not observed. **Trama hyphae** cylindrical, subinflated, branched, smooth, non-dextrinoid, 2−8 µm wide. **Pileipellis** a cutis made up of cylindrical, often incrusted, with heavy annular ornamentation, 5−15 µm wide hyphae. **Stipitipellis** a cutis of cylindrical, smooth, thin-walled, 2−6 µm wide hyphae. **Clamp connections** present in all the tissues.

Material examined: CHINA, Hubei Province, Shennongjia National Park, 31°29′N 110°17′W, ca. 2283 m asl, 23 Jun 2023, *Jia-Xin Li* and *Wen-Qiang Yang*, *ZRL20230148* (HMAS 287967).

GenBank: HMAS 287967: PQ620225 (ITS).

Notes: The morphological and molecular data from the Chinese specimen is consistent with the holotype (Kim et al. 2022). New geographical record from the Shennongjia National Park, China.

Pleurotaceae Kühner.

Notes: The family Pleurotaceae is a monophyletic lineage characterized by pileate, conchate, or spathulate basidiomata, dry or viscid pileus, without or with lateral to eccentric stipe, and white to cream spore-print. In addition, the spores are colorless, smooth, thin-walled, inamyloid, non-dextrinoid and acyanophilous; basidia are 2- or 4-spored; and pileipellis is a cutis or a trichoderm of smooth hyphae. Genera in this group are lignicolous, herbicolous, saprotrophic, or parasitic on angiosperms and gymnosperms (Moncalvo et al. 2000, 2002; Thorn et al. 2005; Matheny et al. 2006; Vizzini et al. 2024).

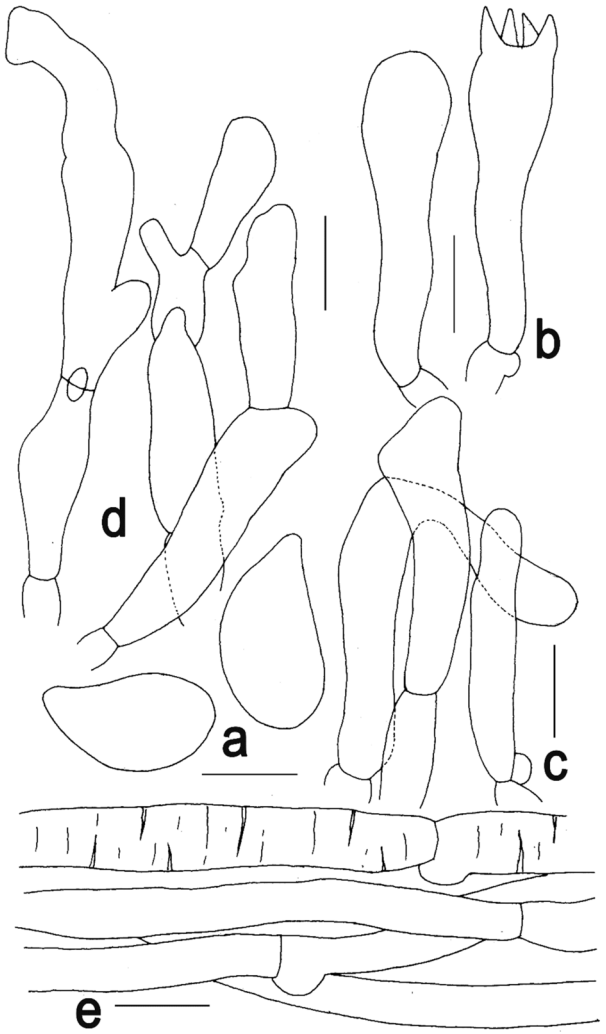


Fig. 98 Microscopic features of ***Collybiopsis gibbosa*** (CUH AM294). **a** Basidiospores. **b** Basidium and basidiole. **c** Cheilocystidia. **d** Pileocystidia. **e** Pileipellis hyphae. Scale bars: **a** = 5 µm, **b**–**e** = 10 µm

Hohenbuehelia Schulzer.

Notes: *Hohenbuehelia* is a large genus with around 120 validly described species (Index Fungorum Partnership 2024) and has a worldwide distribution. Anamorphic species of the genus were previously placed in the genus *Nematoctonus* Drechsler but following the One Name nomenclatural rule, both the asexual and sexual stages are now placed under *Hohenbuehelia*. Species of *Hohenbuehelia* have pleurotoid and gelatinous basidiomata, white basidiospores with a germ spore, lecythiform cheilocystidia (if present) and thick-walled, fusiform, metuloid pleurocystidia (Drechsler 1941; Thorn and Barron 1986; Taylor 2011; McNeill et al. 2012; Thorn 2013; Silva-Filho and Cortez 2017; Holec and Zehnálek 2020).

Hohenbuehelia triloba Ralaiv., Liimat. & Niskanen, **sp. nov.**

Index Fungorum: IF 903133; *Facesoffungi*: FoF 17125; Figs. 101, 102

Etymology: The species epithet is derived from the shape of the basidiomata.

Holotype: K-M 252108.

Pileus 3 cm in diam., very low convex, trilobed, margin incurved, very pale (grayish) brown, margin white, surface velvety, with white pruinose coating. **Lamellae** crowded, edge even, with lamellulae, white. **Stipe** rudimentary. **Context** not recorded. **Odor** and **Taste** not recorded.

Basidiospores 7–10 × 4–6 µm, ellipsoid to somewhat phaseoliform, smooth. **Basidia** 14–16 × 4–5 µm, sterigmata 1.5–2 µm long, clavate, 4-spored, clamped. **Cheilocystidia** 19–22 × 5.5–9.5 µm, lecythiform with capitate (usually 2 rostra) apex, numerous, thin-walled. **Pleurocystidia** 40.5–56 × 15.5–19 µm, metuloid, acute to acuminate-lageniform. **Pileipellis** a trichoderm, consisting of irregularly arranged, parallel, long hyphae with a width of 4 µm, clamped, yellow-olive in color, oriented perpendicular to the cap surface.

Habitat: Lowland, humid, evergreen, tropical forest, Myristicaceae-Uapaca forest; on compact lateritic soil.

Distribution: So far only known from Madagascar.

Material examined: MADAGASCAR, Toamasina, Antsinanana Region, Analalava Forest Reserve, dominated by *Uapaca* (Myristicaceae), 18 Feb 2017, coll. *L. Choo*, *MAF17-164* (K-M 252108, **holotype**).

GenBank: K-M 252108: PQ636528 (ITS).

Notes: ITS sequence (GenBank PQ636528, holotype) distinct from the other species of *Hohenbuehelia*. Forming a sister clade, but with low support (67% BS), in our phylogenetic analysis with the type species *Hohenbuehelia petaloides* (KY488678) from China and *Nematoctonus geogenius* from Canada (EF409726). Differs from them by > 3.5% (> 20 indels and substitutions). *Hohenbuehelia triloba* is the first species of the genus described from Madagascar and is characterized by a very pale brown trilobed pileus, rudimentary stipe, 7–10 × 4–6 µm spores, 19–22 × 5.5–9.5 µm cheilocystidia and 40.5–56 × 15.5–19 µm pleurocystidia.

Psathyrellaceae Vilgalys, Moncalvo & Redhead.

Notes: Psathyrellaceae has a worldwide distribution. The family includes species with soft, fragile basidiomata and black, dark brown, rarely reddish or pastel-colored spore print. About 50% of species produce fruiting bodies that dissolve into ink-like ooze via autodigestion when the spores are mature (Redhead et al 2001; Örstadius et al. 2015). On the basis of molecular phylogenetic analyses, Psathyrellaceae were divided from other coprinoid taxa

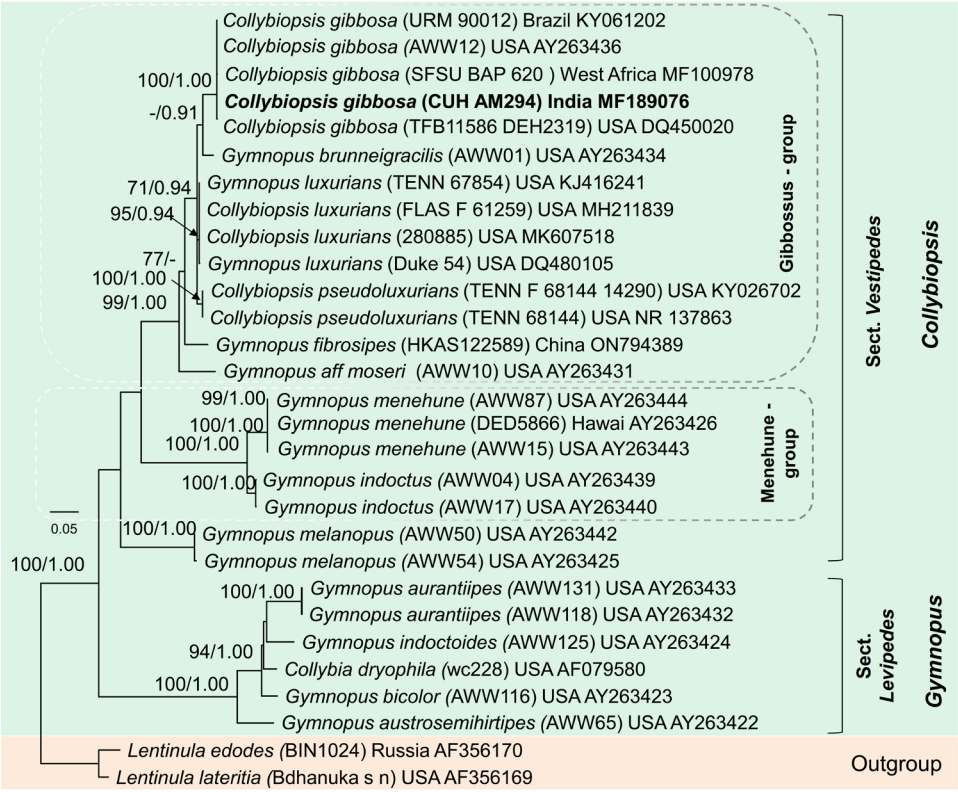


Fig. 99 Maximum Likelihood phylogram ($-\ln L = -3482.518768$) made from the GTR + I + G nucleotide evolution model. In the phylogenetic tree, the given support values indicate MLBS ≥ 50% on the left of "/" and PP ≥ 0.50 on the right side of "/", respectively. The study highlights the newly generated sequence in bold font. Each species in the phylogenetic tree has its voucher number, geographic origin, and GenBank accession number mentioned

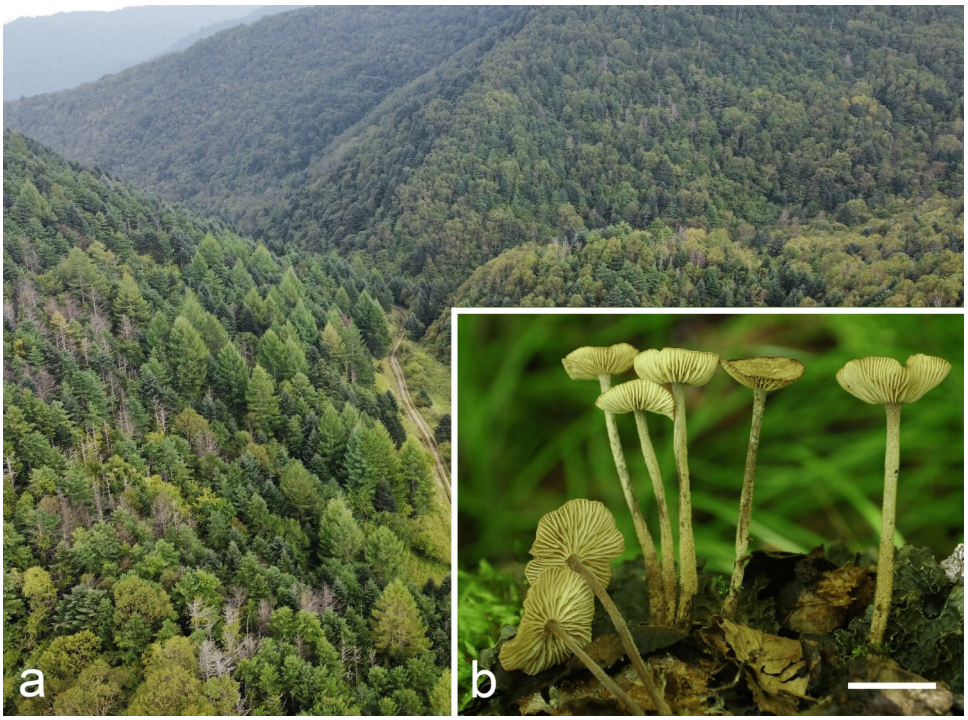


Fig. 100 *Collybiopsis subumbilicata* (HMAS 287967). **a** Habitat. **b** Basidiomata. Scale bar: **b** = 2 cm

(Redhead et al. 2001). Thereafter, six new monophyletic genera were introduced into Psathyrellaceae (Wächter and Melzer 2020), which now accepts a total of 21 genera (Wijayawardena et al. 2022). Recently some new taxa of Psathyrellaceae were described from China (Zhu and Bau 2024).

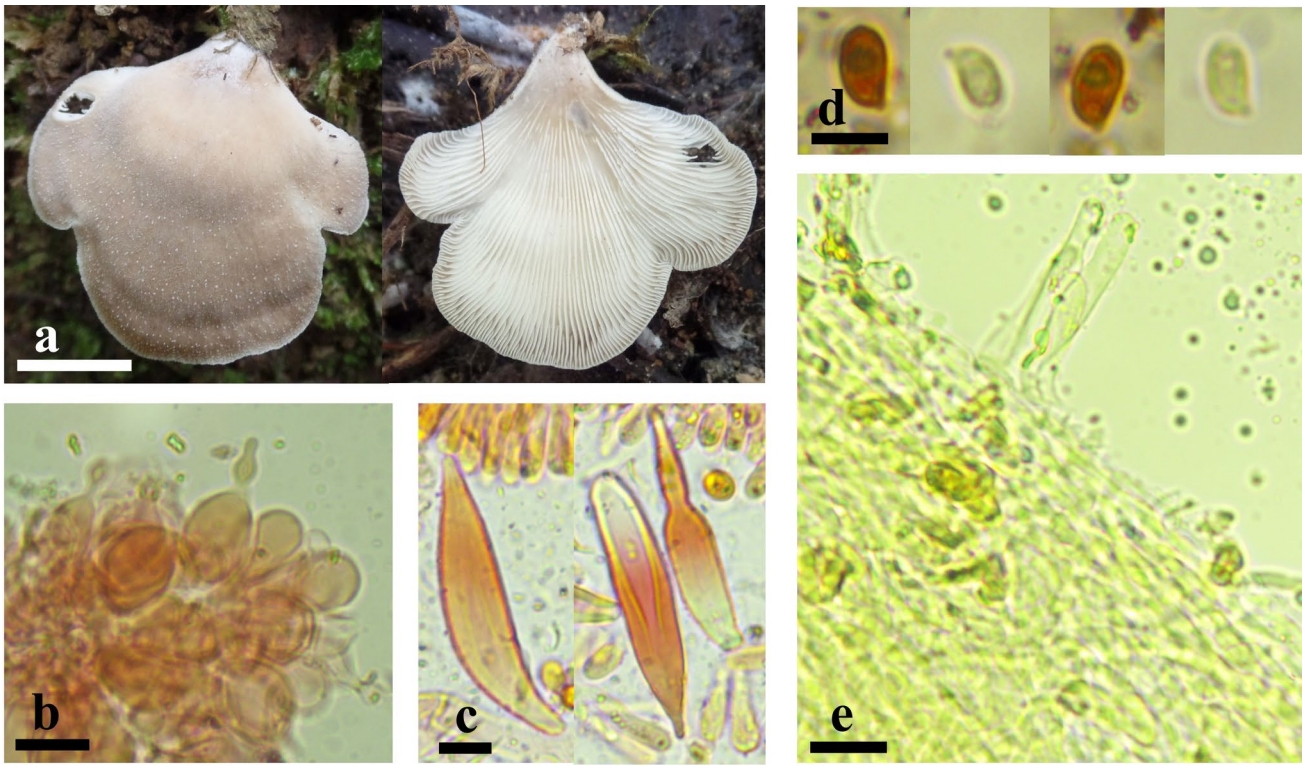


Fig. 101 ***Hohenbuehelia triloba*** (K-M252108, **holotype**). **a** Basidiomata. **b** Cheilocystidia in Congo Red. **c** Pleurocystidia in Congo Red. **d** Basidiospores in Congo Red and KOH. **e** Pileipellis. Scale bars: **a** = 1 cm, **b–e** = 10 µm. Credit: L. Choo (**a**), Anna Ralaiveloarisoa (**b–g**)

Candolleomyces D. Wächt. & A. Melzer.

Notes: Candolleomyces contains around 30 species that are lignicolous, rarely fimicolous (Index Fungorum Partnership 2024). The genus has been recently split from *Psathyrella* (Wächter and Melzer 2020) and thus part of the sequences in the public repositories and part of the species have not yet been transferred into *Candolleomyces* but appear as *Psathyrella* (Fig. 103). Morphological differences separating the genus from *Psathyrella* were suggested to be the absence of pleurocystidia and presence of sphaerocysts with slightly thickened walls in the veil. *Candolleomyces* is further characterized by small to large basidiomata and medium-sized often phaseoliform, pale to medium dark spores with a central germ pore central that is often invisible. Typical are also utriform, subutriform, to subcylindrical cheilocystidia. In recent years, advances in molecular biology techniques, particularly the analyses of nrITS, nrLSU, and *tef-1α* gene sequences, have greatly enhanced the systematic taxonomic studies of this genus (Bau and Yan 2021; Yang et al. 2023b; Han et al. 2024).

Candolleomyces analalavaensis Ralaiv., Liimat. & Niskanen, **sp. nov.**

Index Fungorum: IF 903134; *Facesoffungi*: FoF 17126; Figs. 103, 104

Etymology: The species epithet is derived from the type locality.

Holotype: K-M 252139.

Pileus 0.8 cm in diam., convex, brown. **Lamellae** adnate, crowded, white when young. **Stipe** 3.5 cm, white, cylindrical. **Odor** not recorded. **Pileus** 0.8 cm in diam., convex to hemispherical, warm reddish brown from the center, paler towards the margin, margin pale brown, with a translucent striate margin, surface smooth, hygrophanous. **Lamellae** adnate, crowded with lamellulae, white when young. **Stipe** 3.5 cm long, up to 4 mm wide, white, cylindrical with a bulbous base, surface minutely pubescent. **Context** not recorded. **Odor** and **Taste** not recorded.

Basidiospores (6–)6.5–8(–9) × (4–)5–6 µm, ovoid, smooth. **Basidia** 13.5–17.5 × 7.5–10 µm, sterigmata 1.5–5 µm long, clavate, 4-spored, not clamped, hyaline in KOH. **Cheilocystidia** (16.5–)21–34.5 × (7.5–)9–16.5 µm, utriform to subutriform. **Pileipellis** hymeniderm, upper most layer consisting of 2–3 cells deep layer, cells short and broad, 18–24.5 × 12–14 µm, smooth and hyaline.

Habitat: Lowland, humid, evergreen, tropical forest, Myristicaceae-*Uapaca* forest; on soil and decaying wood.

Distribution: So far only known from Madagascar.

Material examined: MADAGASCAR, Toamasina, Antsinanana Region, Analalava Forest Reserve, dominated by

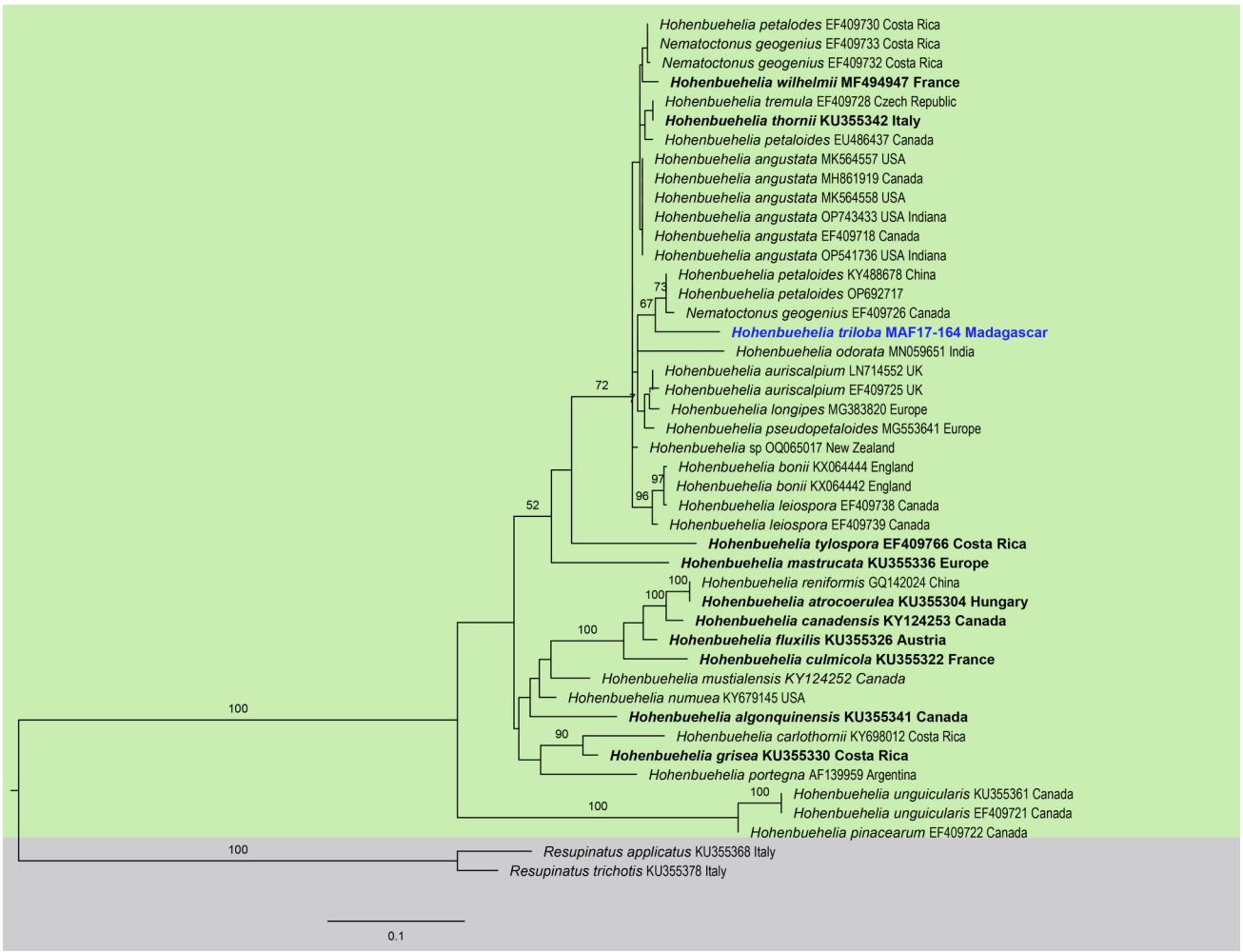


Fig. 102 The best scoring RAxML tree with a final likelihood value of -4259.273758 of the genus *Hohenbuehelia* based on the ITS region. Related sequences were retrieved from GenBank. Forty-five specimens were included in the analysis of the ITS region which comprises 693 characters after alignment. The tree is rooted with *Resupinatus applicatus* (KU355368) and *Resupinatus trichotis* (KU355378). The matrix had 323 distinct alignment patterns, with 9,64% of undetermined characters or gaps. Estimated base frequencies were: A = 0.238485, C = 0.216781, G = 0.228926, T = 0.315807; substitution rates AC = 1.373547, AG = 3.404199, AT = 1.990271, CG = 0.627864, CT = 5.583460, GT = 1.000000. Maximum Likelihood bootstrap values greater than 50% are given near to each branch. The type specimens are in bold. The new species are in blue. Names, other than those originating from the type specimens, are only indicative and not confirmed via comparison with sequences from type specimens

Uapaca forest, 19 Feb 2017, coll. *B. Fabian*, MAF17-265 (K-M 252139, **holotype**). Toamasina, Antsinanana Region, Analalava Forest Reserve, 18 Feb 2017, coll. *L. Choo*, *MAF17-190* (K-M 252109).

GenBank: K-M 252139: PQ636530 (ITS); K-M 252109: PQ636529 (ITS).

Notes: ITS sequences (GenBank PQ636530, holotype; GenBank PQ636529): the two sequences are identical and distinct from other species of *Candolleomyces*. In our phylogenetic analysis they group together (63% BS) with *Candolleomyces* sp from India (as *Psathyrella* sp KR155029, KR154989, KR155112) and deviates from them by > 3% (22, 23, 27 substitutions and indels respectively). *Candolleomyces analalavaensis* is characterized by brown pileus, ovoid, smooth, basidiospores (6.5–8 × 5–6 µm) and more or less utriform cheilocystidia (21–34.5 × 9–16.5 µm).

Candolleomyces kely Ralaiv., Liimat. & Niskanen, **sp. nov.**

Index Fungorum: IF 903135; *Facesoffungi*: FoF 17127; Figs. 103, 105

Etymology: The species epithet is derived from the Malagasy word kely (= tiny, small) and refers to the small size of the basidiomata.

Holotype: K-M 252085.

Pileus up to 1 cm in diam., convex to hemispherical, dark brown at the very center, warm medium brown with orange undertones towards the margin, white at the very margin, surface smooth, hygrophanous. **Lamellae** adnate, crowded,

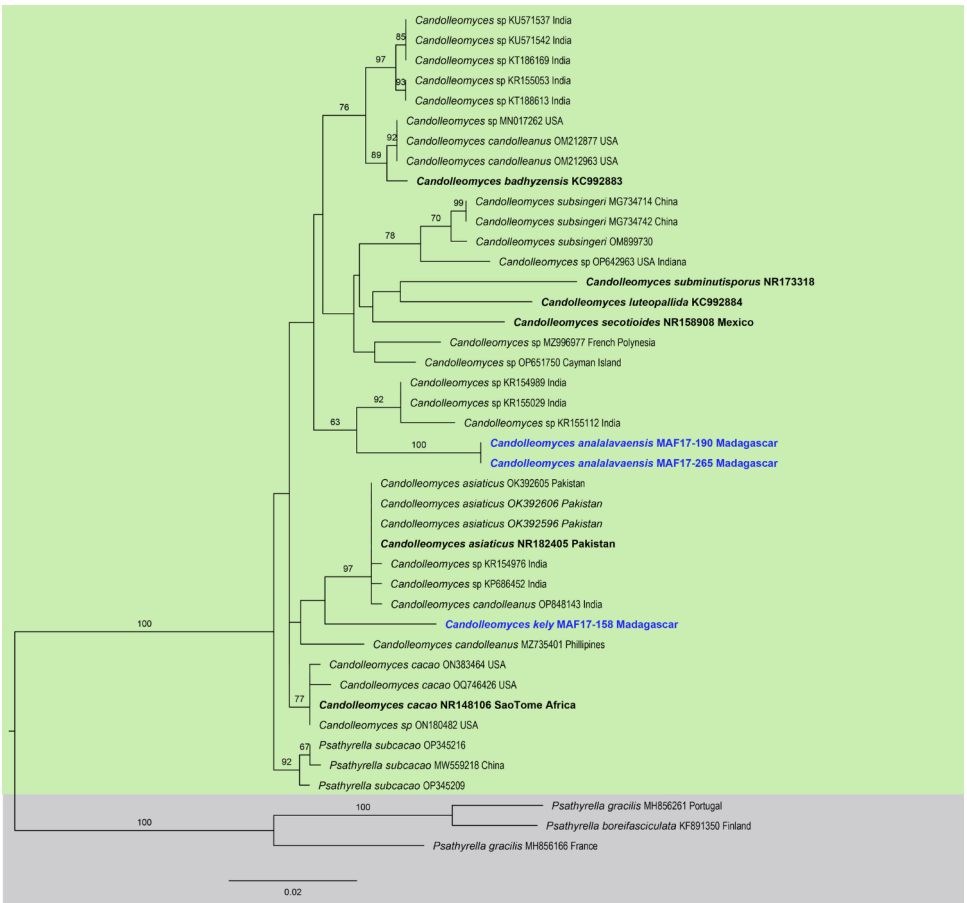


Fig. 103 The best scoring RAxML tree with a final likelihood value of -2261.591396of the genus *Candolleomyces* based on the ITS region. Related sequences were retrieved from GenBank. Forty-two specimens were included in the analysis of the ITS region which comprises 675 characters after alignment. The tree is rooted with *Psathyrella gracilis* (MH856261), *Psathyrella boreifasciculata* (KF891350) and *Psathyrella gracilis* (MH856166). The matrix had 182 distinct alignment patterns, with 3,37% of undetermined characters or gaps. Estimated base frequencies were: A = 0.239322, C = 0.232353, G = 0.230630, T = 0.297695; substitution rates AC = 2.679995, AG = 3.428282, AT = 1.148355, CG = 0.141615, CT = 7.976893, GT = 1.000000. Maximum Likelihood bootstrap values greater than 50% are given near to each branch. The type specimens are in bold. The new species are in blue. Names, other than those originating from the type specimens, are only indicative and not confirmed via comparison with sequences from type specimens

edge even, with lamellulae, at first white. **Stipe** 1.5 cm long, up to 4 mm wide, white, cylindrical. **Context** not recorded. **Odor** and **Taste** not recorded.

Basidiospores (5–)6–7.5 × (3–)3.5–5 µm, ellipsoid, smooth. **Basidia** 16–22.5 × 7–7.5 µm, sterigmata 1–1.5 µm long, clavate, 4-spored, not clamped, hyaline in KOH. **Cheilocystidia** 16–24.5 × 9.5–12 µm, utriform. **Pileipellis** hymeniderm, upper most layer consisting of 1–2 cells deep layer, cells short and broad, up to 24 µm wide, smooth and hyaline.

Habitat: Dry, deciduous, tropical forest, on sandy soil among leaves.

Distribution: So far only known from Madagascar.

Material examined: MADAGASCAR, Mahajanga, Boeny Region, Ankarafantsika National Park, dominated by Euphorbiaceae, Rubiaceae, Malvaceae, Celastraceae, Ebenaceae, 14 Feb 2017, coll. *G. Porteous* and *P. Peteo*, *MAF17-158* (K-M 252085, **holotype**).

GenBank: K-M 252085: PQ636531 (ITS).

Notes: ITS sequence (GenBank PQ636531, holotype) distinct from other sequenced members of *Candolleomyces*. Forming a group, but with no support, in our phylogenetic analysis with specimens of *Candolleomyces asiaticus* from Pakistan and *Candolleomyces* sp from India. *Candolleomyces kely* is characterized by its small and tiny basidiomata. The distantly related *C. analalavensis*, that also occurs in Madagascar, has ovoid, smooth and larger basidiospores (6.5–8 × 5–6), and larger cheilocystidia (21–34.5 × 9–16.5 µm).

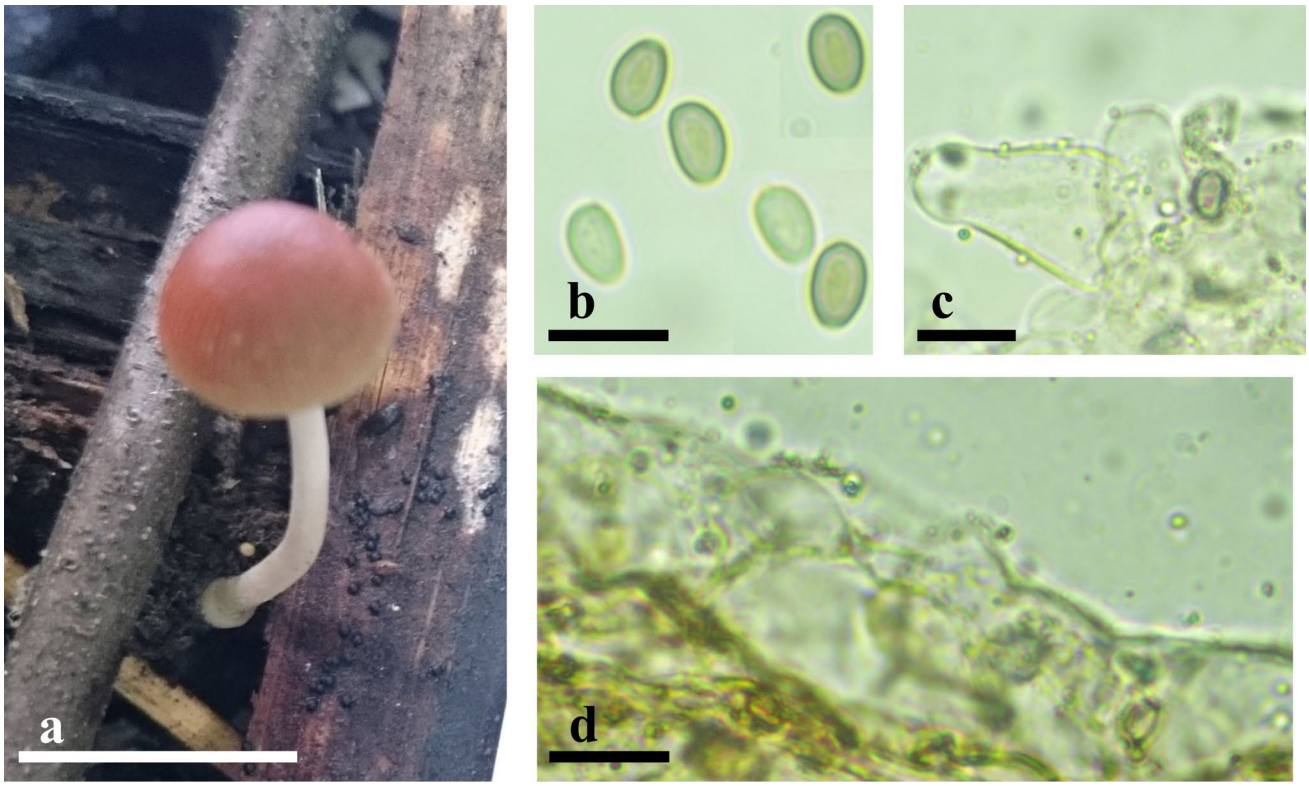


Fig. 104 ***Candolleomyces analalavaensis*** (K-M 252139, **holotype**). **a** Basidiomata. **b** Basidiospores. **c** Cheilocystidia. **d** Pileipellis. Scale bars: **a** = 1 cm, **b**–**d** = 10 µm. Credit: B. Fabian (**a**), Anna Ralaiveloarisoa (**b**–**d**)

Candolleomyces macrosporus R.L. Zhao, B. Cao & X.X. Han, **sp. nov.**

Fungal Names: FN 572050; *Facesoffungi*: FoF 16396; Figs. 106, 107

Etymology: refers to the large basidiospores compared to other species in genus *Candolleomyces*.

Holotype: HMAS 259472.

Pileus 20–35 mm diam, fragile, hemispherical to convex when young, becoming plano-convex to nearly plane when mature, hygrophanous, presence of veil elements, with pellucid striate margin, orange white (6A2) to brown (6E7) at the center, brownish orange (6C4) to dark brown (6F7) at the margin. **Veil** is white (6A1), fibrillose, evanescent. **Context** thin and very fragile, the same color as the pileus. **Lamellae** moderately close, broad, narrowly adnate to adnexed, light brown (6D5) to dark brown (6F7). **Stipes** 21–35 × 1–3 mm, smooth, cylindrical, hollow, slightly thicker near the base, with a surface covered with slight white fibrils, and is evanescent, orange white (5A2) to brownish orange (5C4), light brown (6D4) to dark brown (6F7) at the base. **Odor** not distinctive. **Taste** indistinct.

Basidiospores (8.5)8.8–9.7(9.9) × (5.1)5.4–6.1(6.3) µm, Q = 1.53–1.69, narrowly ellipsoid to oblong-ellipsoid, brownish orange to brown in water, smooth, often with small germ pore. **Basidia** 19.8–21.6 × 9.6–10.4 µm, clavate, hyaline, 2 or 4-spored. **Pileipellis** a 2–3 layered irregular epithelium composed of subglobose cells, oval, (13.5)16.0–22.7(26.9) µm broad. **Cheilocystidia** (32.6)36 .9–40.3(43.0) × (10.5)11.3–13.0(13.8) µm, narrowly utriform to utriform. **Trama of gills** subregularly. **Pleurocystidia** absent. **Clamp connections** absent.

Habit and habitat: Solitary, scattered in meadows. So far found only in the Xizang Autonomous Region, China.

Material examined: CHINA, Xizang Autonomous Region, Baxoi County, Baxoi County, Ranwi Town, 29°23′6″N 96°52′15″E, 4226 m asl, 11 Aug 2023, *Ming-Zhe Zhang*, *Xi-Xi Han*, *Xi-Hao Yu*, *Lin-Hui Liu*, *Yan-Yan Zheng*, *ZRL20231785* (HMAS 259472, **holotype**), *ZRL20231789* (HMAS 259473) and *ZRL20231794* (HMAS 259474).

GenBank: HMAS 259472: PQ218995 (ITS), PQ218998 (nucLSU), PQ219530 (*tef1*); HMAS 259473: PQ218996 (ITS), PQ218999 (nucLSU), PQ219531 (*tef1*); HMAS 259474: PQ218997 (ITS), PQ219000 (nucLSU), PQ219532 (*tef1*). Supplementary data, Online Resource 2.

Notes: *Candolleomyces macrosporus* is sister to *C. leucotephrus* according to phylogenetic analyses. However, *C. leucotephrus* can be distinguished from C. *macrosporus* by its longer and thicker stipes (70–160 × 5–8–12 mm), slightly smaller basidiospores (8.4–9.2 × 5.2–5.4 µm) that lack a germ pore, and longer basidia (21–29 × 9.5–11 µm)

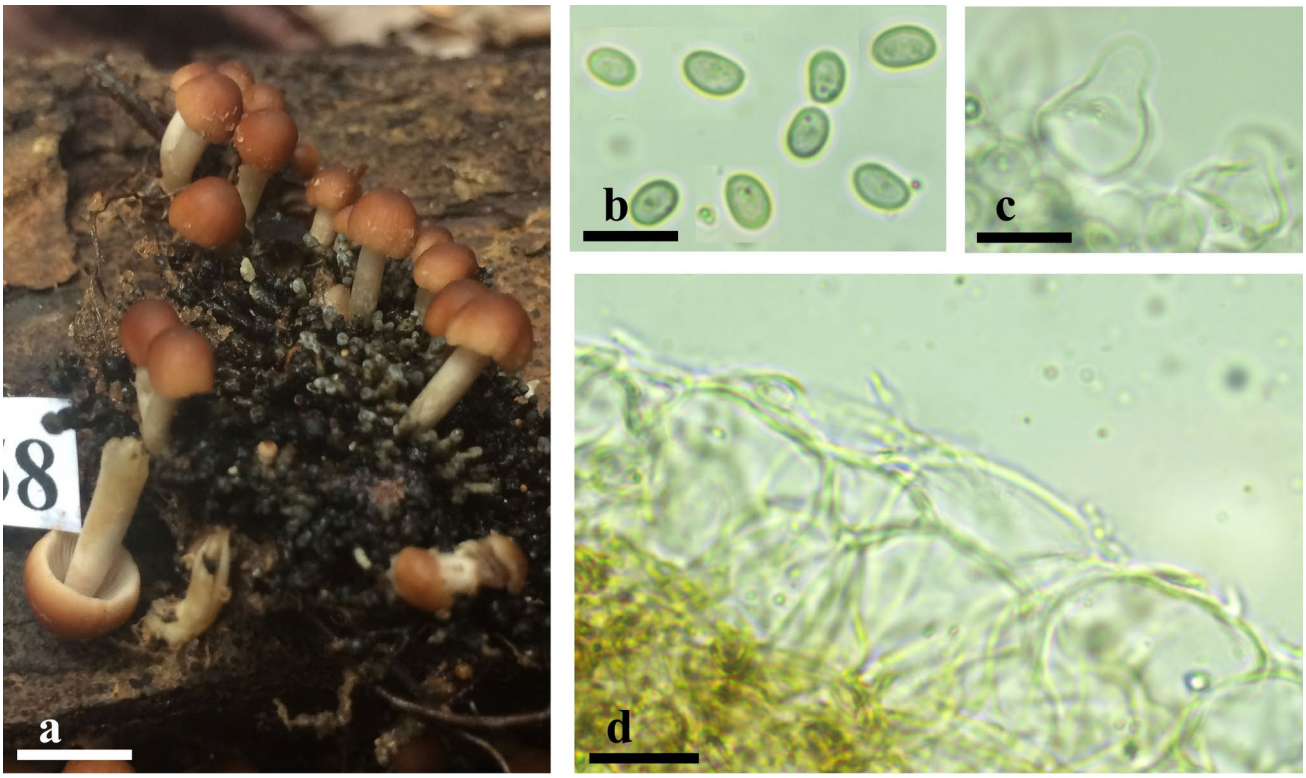


Fig. 105 ***Candolleomyces kely*** (K-M 252085, **holotype**). **a** Basidiomata. **b** Basidiospores. **c** Cheilocystidia. **d** Pileipellis. Scale bars: **a** = 1 cm, **b–d** = 10 µm. Credit: G. Porteous and P. Peteo (**a**), Anna Ralaiveloarisoa (**b–d**)

(Kits van Waveren 1985). Additionally, the nrITS sequence difference between the two species is approximately 4.8%.

Candolleomyces subsingeri (T. Bau & J.Q. Yan) D. Wächt. & A. Melzer, **new geographical record from India.**

Fungal Names: FN 832282; *Facesoffungi*: FoF 16383; Figs. 108, 109, 110

Pileus 15–35 mm, paraboloid to campanulate, with obtuse umbo at the disc, hygrophanous, grayish orange to orange gray (5B3–5B2) becoming brown-orange (6C4–6C3) with maturity, surface fibrillose, with minute velar squamules scattered throughout, prominent at the young stage, dense at the center, striate indistinct, margin irregular, appendiculate when young. **Lamellae** adnate, grayish orange (6B4), 3–4 mm broad, close with lamellulae of 2–3 tiers, edges serrated, white (6A1). **Stipe** 30–48 × 2–3 mm, cylindrical, hollow, equal, slightly tapering towards apex, fragile, slightly covered with white fibrils. **Odor** and taste indistinctive.

Basidiospores 5.98–7.2–7.98(–8.6) × 4.8–5.1–5.4(–5.7) µm, Q = 1.2–1.4–1.52, ellipsoid, very pale, slightly yellowish in 5% KOH, smooth, germ pore absent. **Basidia** 16.24–20 × 7.1–9.2 µm, 4- or 2-spored, clavate, hyaline, thin-walled. **Pleurocystidia** absent. **Cheilocystidia** 34.2–39.9 × 10.83–14.3 µm, crowded, abundant, utriform to broadly utriform, rarely clavate with an obtuse apex. **Paracystidia** 13.7–27.9 × 11.4–14.2 µm, subglobose to clavate, hyaline. **Caulocystidia** 31.1–46.2 × 8.55–12 µm, rarely, various, clavate, utriform, rarely bifurcate. Hymenophoral trama irregular, hyphae inflated up to 18 µm broad. **Pileipellis** 2–3 layered epithelium, composed of globose to subglobose cells, 20–34.2 µm broad, thin-walled, hyaline. **Velar squamules** consist of thin-walled, hyaline, branched, 8.5–16.5 µm broad hyphae**. Clamps** present.

Habit and habitat: Solitary to scattered on dead logs or on decomposed humus of leaf litter in mixed forests.

Distribution: Previously reported from China (Yan and Bau 2018) and Korea (Yoo et al. 2022) as *Psathyrella subsingeri* T. Bau & J.Q. Yan. This is the first report of *C. subsingeri* from India.

Material examined: INDIA, West Bengal, Kalimpong District, Lava, Kuwapani, 27°05′00"N 88°37′58"E, elevation 1993 m, 30 May 2023, *J. Tamang F-2/2023* (CUH AM979).

GenBank: CUH AM979: PQ152960 (ITS).

Notes: Candolleomyces subsingeri is distinguished by paraboloid to conical pileus, basidiospore 5.98–8.6 × 4.8–5.7 µm, without germ pore, very pale, subhyaline to hyaline in 5% KOH and utriform to broadly utriform, rarely clavate with obtuse apex cheilocystidia. This taxon was first reported from Jilin Province, China (Yan and Bau

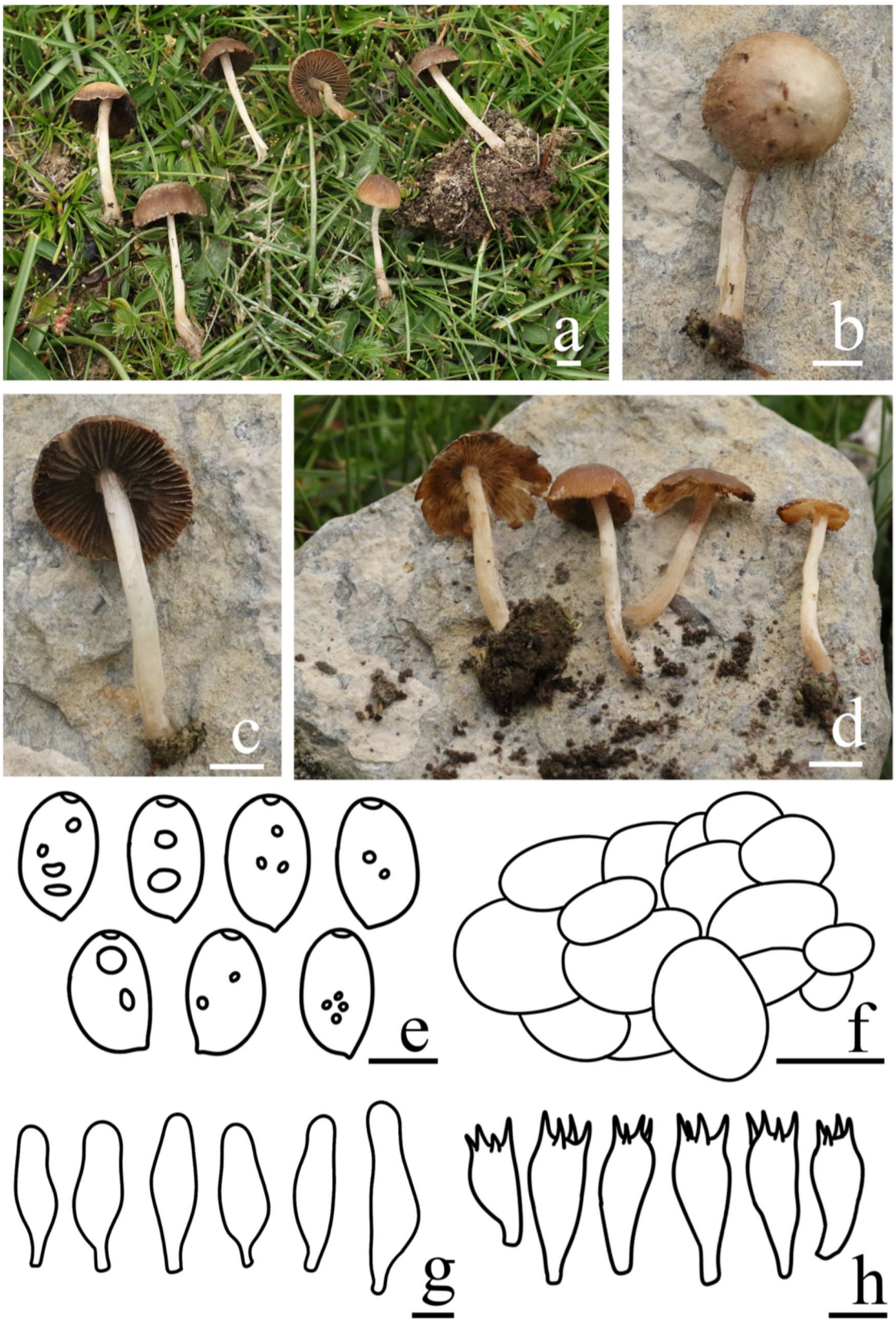


Fig. 106 ***Candolleomyces macrosporus***. **a**–**d** Basidiomata: **a** ZRL20231785. **b, c** ZRL20231789. **d** ZRL20231794. **e** Basidiospores. **f** Pileipellis. **g** Cheilocystidia. **h** Basidia. Scale bars: **a**–**d** = 10 mm, **e** = 5 µm, **f** = 20 µm, **g**–**h** 10 µm

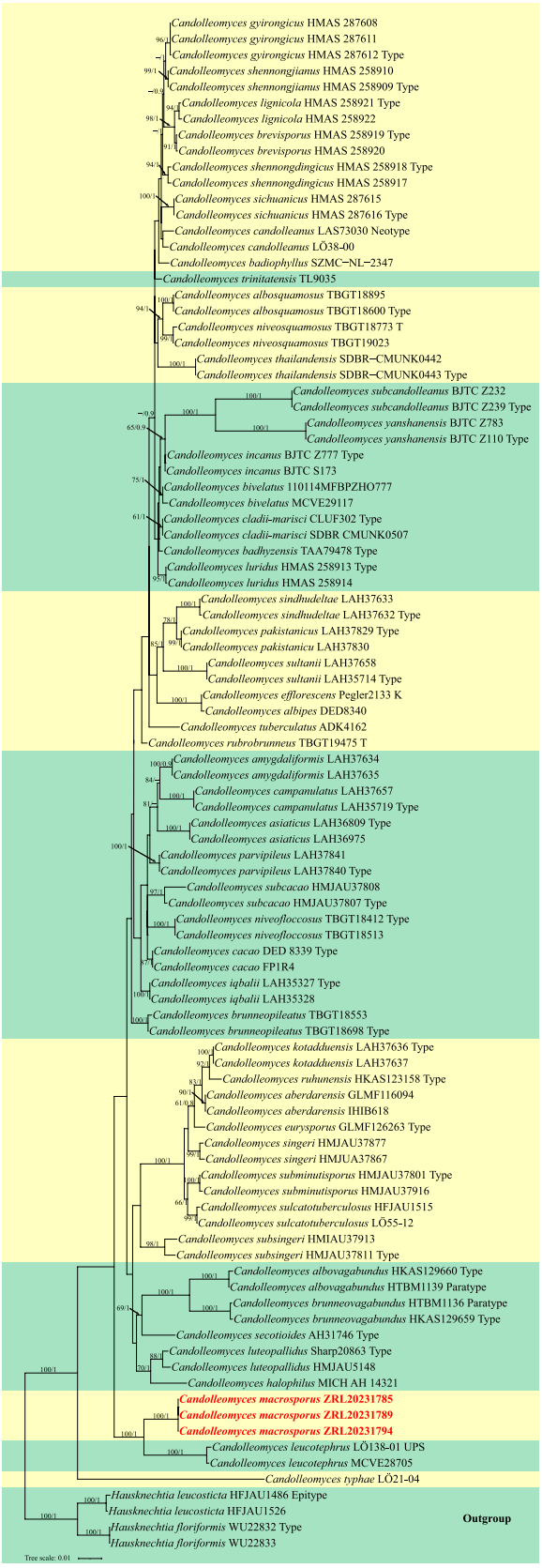


Fig. 107 Maximum Likelihood bootstrap support values greater than 60% and Bayesian posterior probabilities greater than 0.80 are shown around nodes as ML/PP. *Candolleomyces* species produced in this study are indicated in red

2018) and later, it was also reported from Korea (Yoo et al. 2022). This is the first record of *C. subsingeri* from India.

The morphological identification of *C. subsingeri* is well supported by the phylogenetic analyses (Fig. 110). Phylogenetic analyses reveal that our sequence cluster together with the type specimen (NR_160505) reported from China and other deposited sequences of *C. subsingeri* with well-supported bootstrap values (MLBS = 93%, PP = 0.99) suggests all the sequences to be conspecific. Our Indian collection *C. subsingeri* nicely matches with the description of the type specimen in morphology but slightly differs in size (26–37 µm) and shape of caulocystidia (Yan and Bau 2018). Morphologically, it is also similar to *C. luteopallidus* (A.H. Sm.) D. Wächt. & A. Melzer but differs in having basidiospore size longer than 8 µm (Yan and Bau 2018; Yoo et al. 2022).

Squamanitaceae Jülich.

Notes: The Squamanitaceae family, within the order Agaricales, is characterized by its small size and distribution in tropical and subtropical regions. This family is notable for its members having a scaly pileus surface and white to light-colored spores (Matheny et al. 2015; Griffith et al. 2019; Vizzini et al. 2019; Liu et al. 2021a; Saar et al. 2022). The key genera within the Squamanitaceae, such as *Squamanita* and *Dissoderma*, range from saprotrophic to parasitic and display a variety of morphologies and lifestyles (Liu et al. 2021a; Saar et al. 2022). The taxonomic placement of the Squamanitaceae family has been a subject of recent debate. While some studies have provided equivocal support for its circumscription (Vizzini et al. 2019), other researchers have placed the genus *Squamanita* together with *Cystoderma*, *Phaeolepiota*, *Floccularia*, and *Leucopholiota* within the Squamanitaceae, which is situated in the Agaricineae of the order Agaricales (Kalichman et al. 2020; Liu et al. 2021a).

Cystoderma Fayod.

Notes: The genus *Cystoderma* Fayod, typified by *C. amianthinum* (Scop.) Fayod, was established in 1889. It belongs to the family Squamanitaceae within the order Agaricales (Vizzini et al. 2019; Kalichman et al. 2020; Liu et al. 2021a). Members of the *Cystoderma* genus are commonly found in forest ecosystems, thriving in open areas on soil, among mosses and litter, and some species even grow on rotten wood (Saar 2012; Li et al. 2022a). Morphologically, *Cystoderma* species are distinguished by their basidiomata, which usually have heavy universal veil remnants. These basidiomata may have an evanescent floccose-scaly ring zone or a well-developed persistent membranous ring. Furthermore, the basidiospores of *Cystoderma* species are weakly to strongly amyloid (Saar 2012; Li et al. 2022a; Liu et al. 2023).

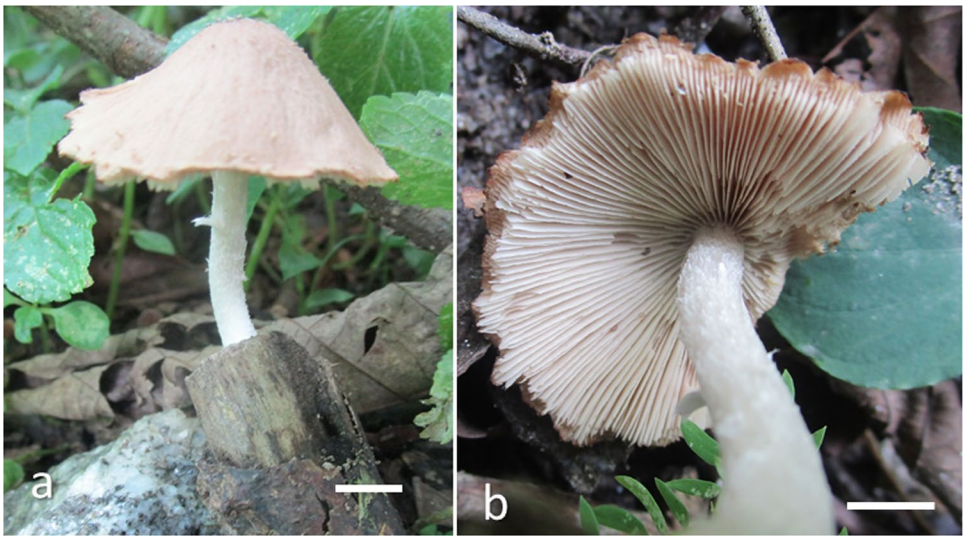


Fig. 108 Basidiomata of ***Candolleomyces subsingeri***. **a, b** Basidiomata in the field. Scale bars: **a**, **b** = 5 cm

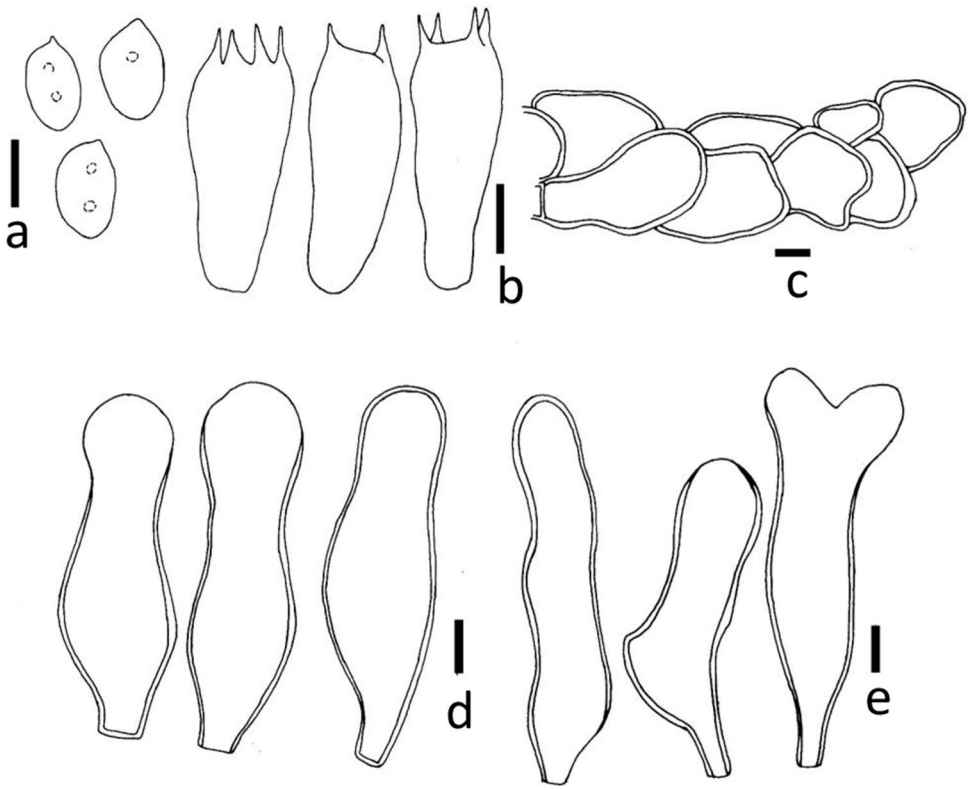


Fig. 109 Microscopic features of ***Candolleomyces subsingeri*** (CUH AM979). **a** Basidiospores. **b** Basidia. **c** Pileipellis. **d** Cheilocystidia. **e** Caulocystidia. Scale bars: **a**–**e** = 5 µm

Cystoderma alticola R.L. Zhao, B. Cao & J.X. Li, **sp. nov.**

Fungal Names: FN 572413; *Facesoffungi*: FoF 17670; Figs. 111, 112

Etymology: alticola (Latin), made up of "altus" (high) and "cola" (dweller, inhabitant), referring to the habitat of this species in high-altitude regions of Xizang Autonomous Region, China, where all specimens were collected at elevations above 3800 m.

Holotype: HMAS 288001.

Pileus 12–30 mm in diameter, initially hemispherical to paraboloid with obtuse umbo, gradually becoming convex to plano-convex with age, surface dry, yellowish-ochre to pale yellow, darker toward the disc, covered with granulose scales or fine powdery texture, slightly wrinkled, an incurved margin at first, then applanate with age, the margin often separates from the partial veil, yellowish-ochre and yellowish-white. **Lamellae** adnate, white to pale cream, crowded, with 2–3 lamellulae of different lengths, 1–3 mm

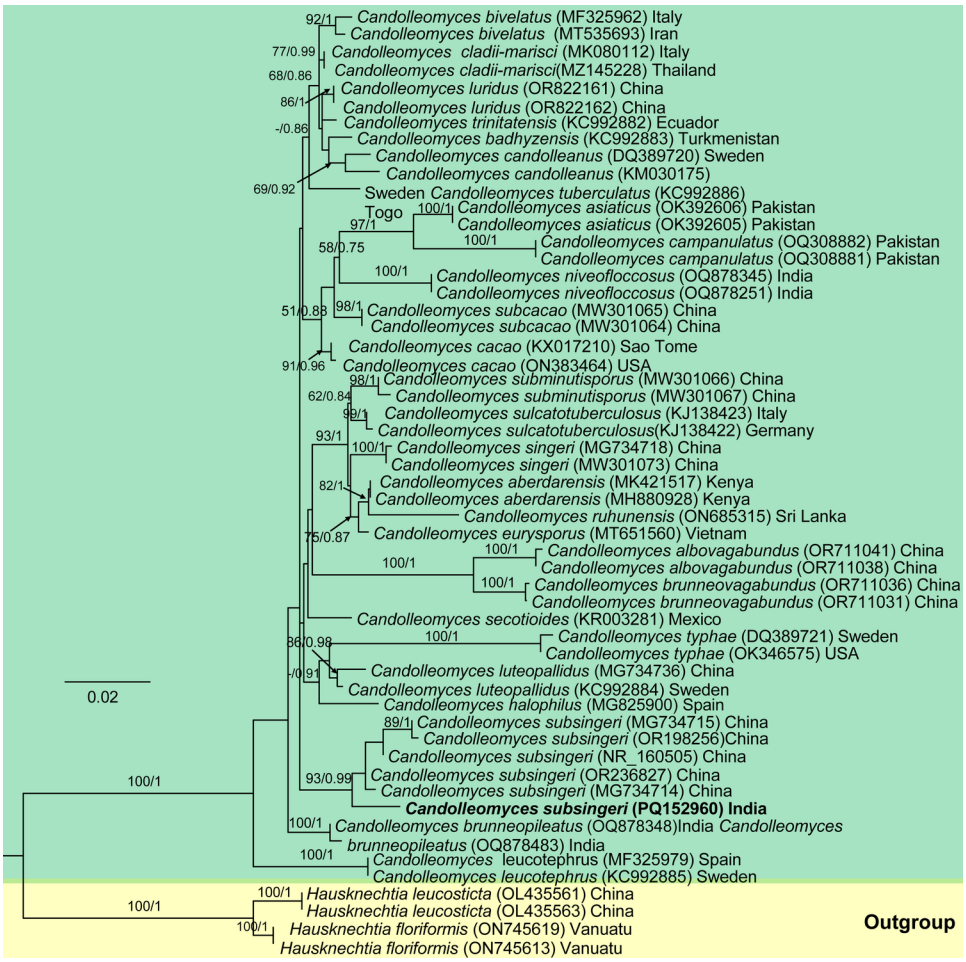


Fig. 110 Maximum Likelihood (ML) phylogram (-InL = 11,172.247881) of *Candolleomyces* inferred from nrITS sequences. Maximum Likelihood bootstrap support values (MLBS) ≥ 50% and Bayesian posterior probabilities values ≥ 0.70 are given above the nodes exclusively. All the taxa are represented along with their GenBank accession numbers and respective country of origin. The tree is rooted with *H. leucosticta* and *H. floriformis*. The newly generated sequences from India are kept in bold font

broad, ventricose. **Stipe** 25–60 × 2.5–5.5 mm, cylindrical, yellowish, yellowish-brown, or brownish, with an evanescent floccose-scaly ring zone, persistent, yellowish brown and silky striate above the ring zone, below the ring zone yellowish-ochre to pale yellow, attached with numerous small granular furfuraceous squamules. **Odor** and taste are undocumented.

Basidiospores (4.1–)5.1–6.0(–6.9) × (2.8–)3.1–3.7(–4.2) µm ($\bar{x}$ = 5.5 ± 0.5 × 3.4 ± 0.3, Q = 1.5–1.8, Qm = 1.6 ± 0.2, n = 60), ellipsoid both in side view and front view, smooth, hyaline, thin-walled, without a germ pore, inamyloid. **Basidia** 22.1–31.0 × 6.0–7.6 µm, clavate, smooth, hyaline and thin-walled, 4-spored. Pleurocystidia and cheilocystidia absent. **Pileipellis** on the upper layers composed of chains of numerous sphaerocytes, globose to subglobose, ellipsoid, thick-walled, the lower layers composed of tightly interwoven hyphae, with internal brown pigment. The composition of the evanescent floccose-scaly ring zone and pileipellis is identical. **Clamp connections** present in all tissues.

Habitat: Solitary, scattered, sometimes gregarious. Saprobic on mixed coniferous-broadleaf forest, found at elevations above 3,000 m, approaching 4,000 m in highland regions.

Materials examined: CHINA, Xizang Autonomous Region, Bomi to Motuo, 24 July 2021, *Mao-Qiang He & Zhi-Lin Ling*, *ZRL20210848* (HMAS 288001, **holotype**) and *ZRL20210866* (HMAS 288002); Linzhi City, Forest Ecology Monitoring Station, 27 July 2021, *Mao-Qiang He & Zhi-Lin Ling*, *ZRL20211049* (HMAS 288003); Shigatse City, Yadong County, Lower Sima Township, 14 September 2015, *Xu-Ming Bai*, *ZRL20152147* (HMAS 288005).

GenBank: HMAS 288005: PV389788 (ITS), PV389796 (LSU); HMAS 288001: PV389789 (ITS), PV389797 (LSU); HMAS 288002: PV389790 (ITS), PV389798 (LSU); HMAS 288003: PV389791 (ITS), PV389799 (LSU).

Notes: Phylogenetic analyses based on ITS and nrLSU sequences indicate that *Cystoderma alticola* clusters with *C. carcharias*, *C. granosum*, and *C. tuomikoskii*, forming a well-supported lineage within *Cystoderma* (Fig. 111). Morphologically, *C. carcharias* can be distinguished by its white pileus and stipe, which exhibit a grayish-pink or vinaceous tinge (Saar 2003, 2012). *Cystoderma granosum* features basidiospores measuring 4.5–5.2 × 2.9–3.5 µm, which are shorter and narrower than those of *C. alticola* (Li et al. 2022a). *Cystoderma tuomikoskii* closely resembles *C.*

alticola due to its brownish pileus and similar basidiospore dimensions. However, *C. tuomikoskii* has been reported from low-altitude regions (Saar 2003), whereas *C. alticola* occurs in the Xizang Autonomous Region at elevations above 3,000 m.

Cystoderma japonicum Thoen & Hongo, **new geographical record from China.**

MycoBank: MB 105232; *Facesoffungi*: FoF 17128; Figs. 111, 113

Pileus around 20 mm in diam. when young, plano-convex, convex, gradually flattening with age, with a distinct

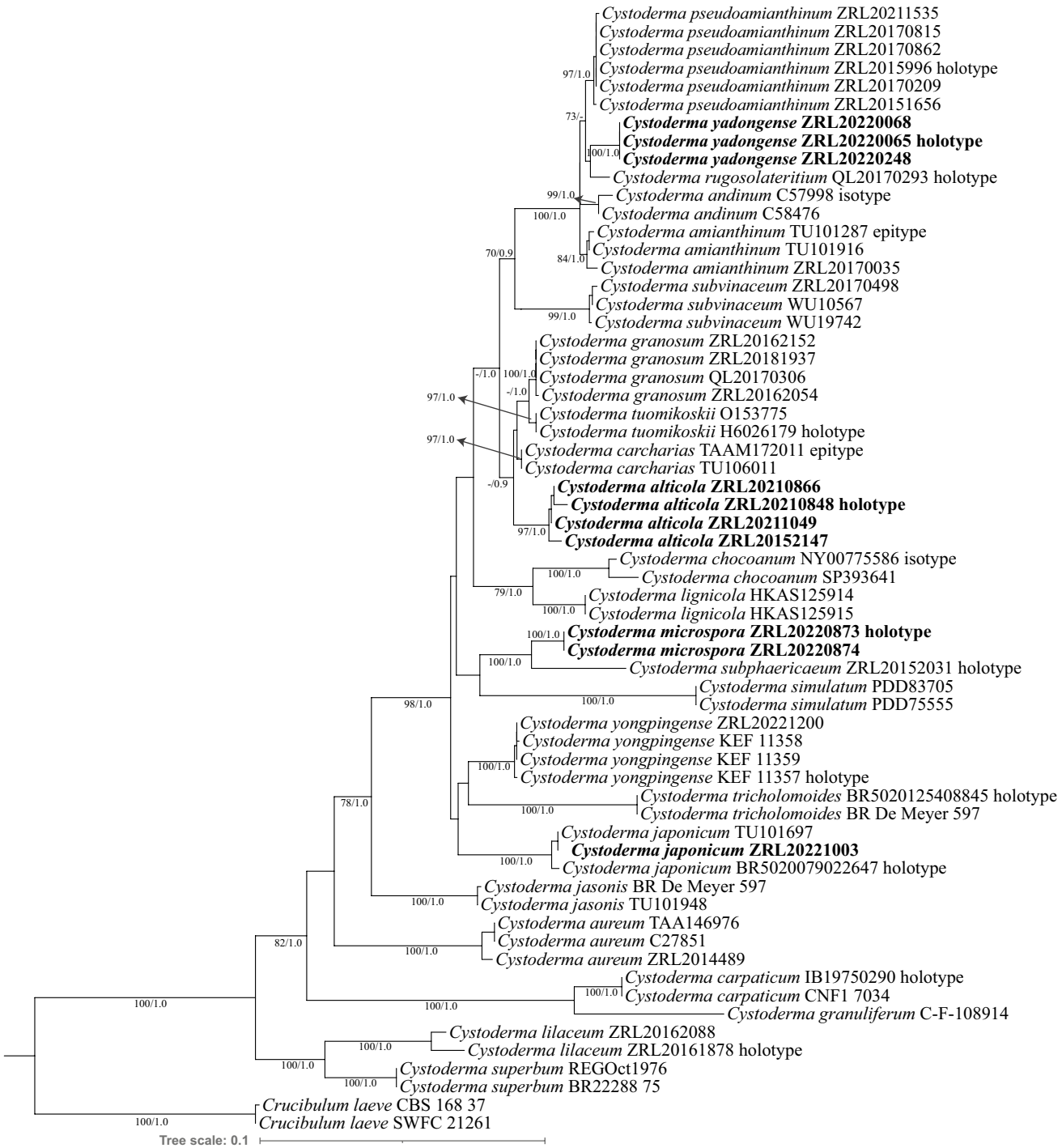


Fig. 111 Maximum Likelihood tree of *Cystoderma* inferred from ITS and nrLSU sequences data, rooted with *Crucibulum leave*. Branches supported by both BS ≥ 70% and PP ≥ 0.90 were labeled. The examined specimens in this study are bolded

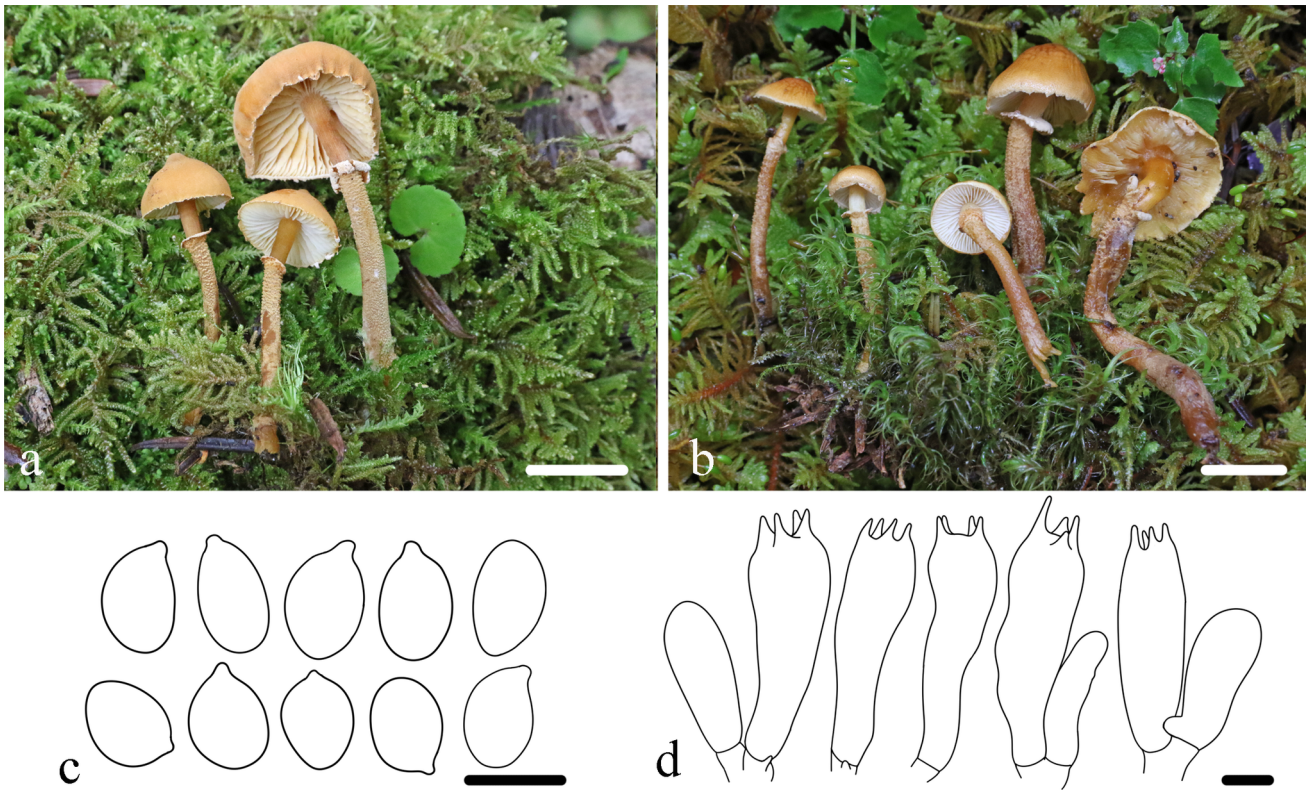


Fig. 112 ***Cystoderma alticola.*** **a** Basidiomata (HMAS 288001, **holotype**). **b** Basidiomata (HMAS 288002). **c** Basidiospores. **d** Basidia. Scale bars: **a**–**b** = 1 cm, **c**–**d** = 5 µm

umbo central, surface dry, yellowish-ochre, orange-yellow covered fine granular warts, or with a fine powder, an incurved margin at first, then applanate to plane with age, the margin usually appendiculate with remnants of partial veil, yellowish-ochre and yellowish-white. **Lamellae** whitish, adnate to adnexed, subdistant, with 1–2 lamellulae of different lengths, ventricose. **Stipe** 26 × 40 mm, cylindrical, with evanescent floccose-scaly ring zone, above the ring zone scattered silky striate, whitish to yellowish, below the ring densely covered with furfuraceous squamules, yellowish to light orange. **Odor** and taste are undocumented.

Basidiospores (4.8–)5.1–5.9(–6.1) × (2.4–)2.6–3.1(–3.4) µm ($\bar{x}$ = 5.5 ± 0.4 × 2.9 ± 0.2, Q = 1.7–2.1, Qm = 1.9 ± 0.2, n = 30), elongate-ellipsoid in side view and front view, smooth, thin-walled, hyaline, inamyloid. **Basidia** 15.6–20.4 × 5.4–7.0 µm, clavate, hyaline and thin-walled, with 4-spored. **Cystidia** absent. **Pileipellis** on the upper layers composed of chains of numerous sphaerocytes, globose to subglobose, ellipsoid, slightly thick-walled, the lower layers composed of tightly interwoven hyaline hyphae, branched. **Ring zone** composed of hyaline hyphae, with attached sphaerocytes. **Clamp connections** present.

Material examined: CHINA, Hubei Province, Shennongjia National Park, 31°27′N 110°16′W, ca. 2886 m asl, 26 Aug 2022, *Mao-Qiang He* and *Mei-Qi Wang*, *ZRL20221003* (HMAS 287966).

GenBank: HMAS 287966: PQ620226 (ITS).

Notes: This species is characterized by yellow-ochre to orange-yellow pileus, a persistent membranous ring on stipe and inamyloid ellipsoid basidiospores (Saar et al. 2009). The morphological and molecular data from the Chinese specimen is consistent with the holotype (Fig. 111). New geographical record from the Shennongjia National Park, China.

Cystoderma microspora R.L. Zhao, B. Cao & J.X. Li, **sp. nov.**

Fungal Names: FN 572414; *Facesoffungi*: FoF 17671; Figs. 111, 114

Etymology: "microspora"(Latin), made up of "micro-" meaning "small" and "spora" meaning "spore," referring to the relatively small basidiospores of this fungal species.

Holotype: HMAS 288006.

Pileus 20–40 mm in diameter at a young stage, hemispherical, then becoming convex to plano-convex at maturity, surface dry, yellowish-ochre, yellowish-brown, darker toward the disc, covered with granular warts and fine powdery texture, with radially acute rugose, less prominent when mature, the margin incurved at first, then applanate when mature, often separates from the partial veil, yellowish-ochre

Fig. 113 *Cystoderma japonicum*. **a, b** Basidiomata. **c** Basidiospore. **d** Basidia. Scale bars: **a**–**b** = 1 cm, **c**–**d** = 5 µm

to yellowish-white. **Lamellae** adnate, whitish, crowded, with 1–2 lamellulae of different lengths, less than 2 mm broad, straight. **Stipe** 40–70 × 6–10 mm, cylindrical, yellowish-ochre yellowish-brown, with an evanescent floccose-scaly ring zone, yellowish brown and silky striate above the ring zone, below the ring zone yellowish-ochre to pale yellow, attached with numerous small granular furfuraceous squamules. **Odor** and taste are undocumented.

Basidiospores (2.8–)3.3–4.1(–4.7) × (2.3–)2.6–3.3(–3.7) µm ($\bar{x}$ = 3.7 ± 0.4 × 2.9 ± 0.3, Q = 1.2–1.4, Qm = 1.3 ± 0.1, n = 30), globose to subglobose, smooth, hyaline, thin-walled, without a germ pore, inamyloid. **Basidia** 20.5–28.0 × 5.8–7.2 µm, clavate, smooth, hyaline and thin-walled, 4-spored. **Pleurocystidia** and cheilocystidia absent. **Pileipellis** on the upper layers composed of chains of numerous sphaerocytes, globose to subglobose, ellipsoid, thick-walled, with internal brown pigment, the lower layers composed of tightly interwoven hyphae, the composition of the evanescent floccose-scaly ring zone and pileipellis is identical. **Clamp connections** present in all tissues.

Habitat: Gregarious and saprobic on mixed coniferous-broadleaf forest, found among *Abies balsamea*, *Rosa* spp., and alpine Rhododendron spp. at elevations of approximately 2,500 m.

Materials examined: CHINA, Hubei Province, Shennongjia Forest District, Shennongding Area, Jinhouling, 25 August 2022, *Rui-Lin Zhao*, *ZRL20220873* (HMAS 288006, **holotype**) and *ZRL20220874* (HMAS 288007).

GenBank: HMAS 288006: PV389792 (ITS), PV389800 (LSU); HMAS 288007: PV389793 (ITS), PV389801 (LSU).

Notes: Phylogenetic analyses based on ITS and nrLSU sequences indicate that *Cystoderma microspora* and *C. subglobisporum* form a fully supported lineage distinct from other *Cystoderma* species. This lineage is phylogenetically closest to *C. simulatum* (Fig. 111). All three species have relatively small basidiospores compared to other *Cystoderma* species. For instance, basidiospores measure 3.6–4.3 × 3.2–3.7 µm in *C. subglobisporum* and 3.5–5 × 2.5–3.5 µm in *C. simulatum* (Saar 2012; Kibby and Harding 2016; Li et al. 2022a). However, *C. simulatum* can be distinguished by its dark brick-red to cinnamon-red coloration and its highly wrinkled, puckered cap surface. Additionally, it grows in woodchip mulch under hazel and birch and fruits strictly in winter (Saar 2012; Kibby and Harding

Fig. 114 ***Cystoderma microspora.*** **a** Basidiomata (HMAS 288006, **holotype**). **b** Basidiomata (HMAS 288007). **c** Basidiospore. **d** Basidia. Scale bars: **a**–**b** = 1 cm, **c**–**d** = 5 µm

2016). *Cystoderma subglobisporum*, recently described from the Xizang Autonomous Region in China, has a yellowish-buff to yellowish-ochre pileus. Morphologically, it is distinguished by a distinct central papilla, a strongly radially acute rugose surface, and an inflexed margin (Li et al. 2022a).

Cystoderma yadongense R.L. Zhao, B. Cao & J.X. Li, **sp. nov.**

Fungal Names: FN 571629; *Facesoffungi*: FoF 17129; Figs. 111, 115

Etymology: yadongense (Latin), refers to the distribution where the type specimen was collected, Yadong County, Shigatse City, Xizang Autonomous Region in China.

Holotype: HMAS 287489.

Diagnosis: Cystoderma yadongense is characterized by a yellowish-ochre, granulose pileus with radial wrinkles, whitish lamellae, yellowish-brown stipe with evanescent ring zone, ellipsoid, smooth, weakly amyloid, small basidiospores. Gregarious under coniferous trees, surrounded by herbs, at high altitudes over 3000 m.

Pileus 20–45 mm in diameter, initially convex to plano-convex, eventually expanding to applanate; surface dry, yellowish-ochre, slightly granulose when young but becoming less apparent with maturity; developing radial wrinkles from the center towards the margin, less prominent when mature. Sometimes appendiculate with remnants of a partial veil, but not conspicuous. **Lamellae** adnexed or adnate, often with 1–2 lamellulae, approximately 3 mm broad, whitish, subdistant, occasionally ventricose in the middle. **Stipe** 37–64 × 3–6 mm, cylindrical, yellowish, yellowish-brown, or brownish, with an evanescent floccose-scaly ring zone; yellowish above the ring zone, brown to dark brown below the ring zone towards the base, attached with numerous small squamules similar to the ring zone. **Context** 1–3 mm broad, concolorous with the stipe; odor not distinctive.

Basidiospores (3.9–)4.1–5.0(–5.4) × (2.5–)2.7–3.2(–3.8) µm ($\bar{x}$ = 4.6 ± 0.4 × 3.0 ± 0.2, Q = 1.4–1.7, Qm = 1.5 ± 0.1, n = 60), ellipsoid, smooth, hyaline, without a germ pore, weakly amyloid. **Basidia** 18.4–21.2 × 6.1–7.1 µm, clavate, smooth, hyaline, 4-spored. **Pleurocystidia** and **cheilocystidia** absent. **Pileipellis** composed of chains of numerous sphaerocytes, globose to subglobose, ellipsoid, slightly thick-walled, 12.9–25.4 µm, hyaline in KOH. **Clamp connections** present. Ring zone composed of hyaline hyphae, 3.2–10.8 µm in diameter, with attached sphaerocytes.

KOH reaction: strongly black on pileus of dry specimen.

Habitat: Gregarious on soil under coniferous trees, usually surrounded by herbaceous vegetation.

Known distribution: Southwest China.

Materials examined: CHINA, Xizang Autonomous Region, Shigatse City, Yadong County, Lower Yadong Town, 26 July 2022, *Mao-Qiang He & Bin Cao*, *ZRL20220065* (HMAS 287489, **holotype**) and *ZRL20220068* (HMAS 287490); 27 July 2022, *Rui-Lin Zhao*, *ZRL20220248* (HMAS 287491).

GenBank: HMAS 287489: PP505410 (ITS), PP505413 (LSU); HMAS 287490: PP505411 (ITS), PP505414 (LSU); HMAS 287491: PP505412 (ITS), PP505415 (LSU).

Notes: *Cystoderma yadongense* can be distinguished by its yellowish-brown basidiomata with a slightly granulose surface and the presence of a well-developed but evanescent floccose-scaly ring zone. It produces relatively small basidiospores (4.1–5.3 × 2.6–3.1 µm). Phylogenetic analyses using ITS and nrLSU sequences indicated that *C. yadongense* clustered with *C. amianthinum*, *C. pseudoamianthinum*, *C. rugosolateritium*, and *C. andinum*, forming a well-supported lineage in *Cystoderma* (BS = 95, PP = 1). Morphologically, *C. rugosolateritium* and *C. andinum* can be differentiated by producing brick-colored Basidiomata with strongly radially wrinkled pilei in the field (Saar and Laessoe 2006; Li et al. 2022a). While *C. yadongense*, *C. amianthinum*, and *C. pseudoamianthinum* are similar in having pale yellow

Fig. 115 ***Cystoderma yadongense*** (HMAS 287489, **holotype**). **a** Basidiomata in field. **b** Basidiospore. **c** Basidia. Scale bars: **a** = 1 cm, **b**, **c** = 5 µm

to yellowish-brown pilei and evanescent floccose-scaly ring zones (Li et al. 2022a), *C. yadongense* produces smaller basidiospores (4.1–5.3 × 2.6–3.1 µm) compared to the larger ones in *C. amianthinum* (4.0–)5.0–6.0(–7.0) × (2.5–)3.0–3.5(–4.0) µm and *C. pseudoamianthinum* (5–6.6 × 3–3.9 µm) (Li et al. 2022a). Morphologically, *C. subglobisporum* and *C. granosum* also form yellowish buff to pale-yellow pilei; however, both species develop a persistent membranous ring. Additionally, the basidiospores of *C. subglobisporum* are smaller (3.6–4.3 × 3.2–3.7 µm) (Li et al. 2022a).

Strophariaceae Singer & A.H. Sm.

Notes: The agaric family Strophariaceae was proposed by mycologists Rolf Singer and Alexander H. Smith in 1946. The type genus of this family is *Stropharia* (Fr.) Quel. (Singer and Smith 1946). Current systematic studies have changed the generic composition and included some genera that were previously added to other agaric families (Silva et al. 2012). With the advancement of molecular investigations, generic limits are under revision and discussion. Recent phylogenetic classification placed 12 genera of macrofungi within this family (Wijayawardene et al. 2022).

Hypholoma (Fr.) P. Kumm.

Notes: *Hypholoma* was proposed at the rank of genus by P. Kummer in 1871 with *H. fasciculare* (Fr.) as the type species (Farr and Farr 1981). According to Hawksworth et al. (1995), the genus *Hypholoma* comprises about 30 species worldwide, but Index Fungorum records show many species of *Hypholoma*, but amongst them, 49 taxa have been fully recognized (www.indexfungorum.org). The genus *Hypholoma* is reported to be distributed from temperate to tropical areas, growing on decomposing wood, live trees, mosses, or soil, playing an important role as active wood and litter decomposers in forest ecosystems (Cortez and Silveira 2007).

Hypholoma darjeelingensis J. Tamang & K. Acharya, **sp. nov.**

Fungal Names: FN 571926; *Facesoffungi*: FoF 16382; Figs. 116, 117, 118

Etymology: The species epithet refers to the type locality.

Holotype: CUH AM904.

Pileus 5–15 mm in diameter, convex to broadly convex with age, surface smooth, dry, surface uniformly orange (6A6) in color; margin non-striate, incurved bearing dense white velar remnants. Pileus context thin < 1 mm. **Lamellae** adnexed to sinuate, close to sub-distant, regular, brownish orange (5C3) with lamellulae of 3–4 tier; lamellae edges slightly wavy. **Stipe** 25 × 2 mm, orange white (5A2) to pale orange (5A3) in color, hollow, cylindric, equal, slightly fibrillose with a white mycelial pad at the base. **Partial veil**, a fragile fringe of fibrils forming an

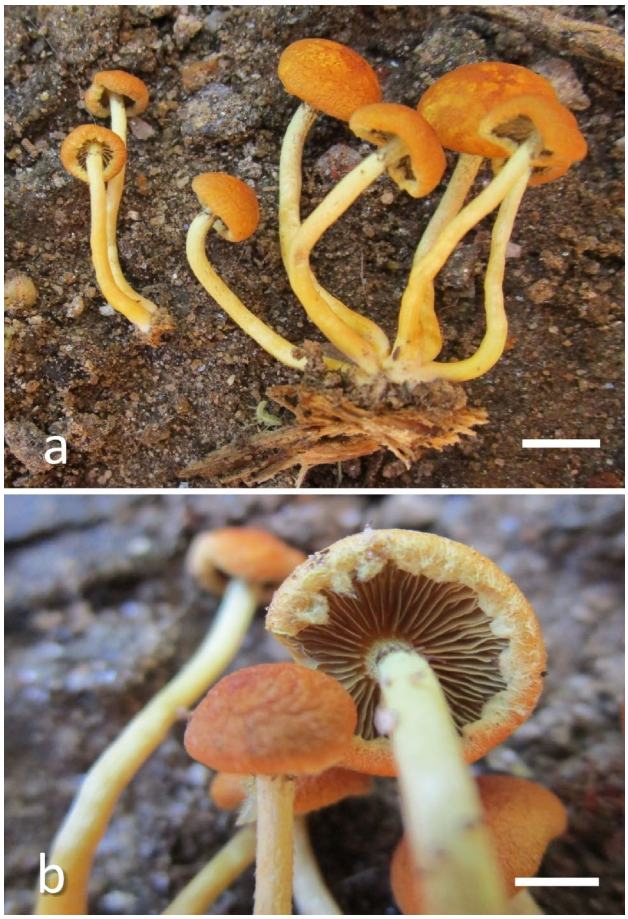


Fig. 116 ***Hypholoma darjeelingensis*** *(*CUH AM952**, holotype**). **a, b** Basidiomata. Scale bars: **a, b** = 10 mm

annular zone at the stipe upper region in both immature and mature stages.

Basidiospores 5.6–6.84–7.5(–8.2) × 3.9–4.7–5.1 3 µm, Q = 1.25–1.60–1.66, ellipsoid to elongate, yellowish brown, smooth and thick-walled, turn yellowish brown in KOH, apically truncated by a broad germ pore. **Basidia** 15.7–20.8 × 5.7–6.6 µm, clavate, hyaline, 4-spored. **Pleurocystidia** present as abundant chrysocystidia, 22.8–31.35 × 7.6–10.83 µm, smooth, thin-walled, with amorphous yellowish contents, fusoid to clavate with mucronate apex. Lamellae edge heteromorphous; **cheilocystidia** 21.37–25.65 × 5.98–8.5 µm, abundant in clusters, hyaline, subcylindrical to lageniform, subcapitate and thin-walled. **Pileipellis** cutis of parallel, hyaline, thin-walled hyphae, 2.2–5.7 µm wide. Hymenophoral trama regular, hyaline or yellow of thin-walled hyphae, 2–6 µm in diameter, inflated to 10.2 µm diameter. Clamp connections present in most hyphae.

Habit and habitat: Caespitose, growing in clusters on decaying stumps.

Material examined: INDIA, West Bengal, Darjeeling District, Love Road, 27°03′41″N 88°15′13″E, elevation 1999 m, 21 June 2019, *J. Tamang & A. Thapa, ALI-240/2019* (CUH AM952, **holotype**); West Bengal, Darjeeling District, Love Road, 27°03′41″N 88°15′13″E, elevation 1999 m, 17 July 2022, *J. Tamang, F–59/2022* (CUH AM951).

GenBank: CUH AM952: PP474310 (ITS); CUH AM951: PP474299(ITS).

Notes: *Hypholoma darjeelingensis* is characterized by its small-sized brightly colored basidiomata, non-striate margin covered with dense white velar remnants; the presence of a fibrillose partial veil forming an annular zone in stipe in both immature and mature basidiomata; and basidiospores ellipsoid to elongate with a broad germ pore.

Morphologically, *Hypholoma darjeelingensis* is similar to *H. australe* (Murrill) Murrill, but it differs in having a larger basidiomata (15–45 mm broad) along with the absence of partial veil remnants in the stipe at mature stages (Miller and Pearce 1996). The collected specimen also shows morphological similarity with *H. subviride* (Berk and M.A. Curtis) Dennis but differs in having a flattened pileus surface at a mature stage, slightly smaller stipe (6–16 mm) and the partial veil covering the gills in the early stage and absent in mature basidiomata (Cortez and Silveira 2007). Phylogenetic and blastn analyses reveal that *H. darjeelingensis* is closely related to *H. frowardii* (Speg.) Garrido, *H. australe, H. brunneum* (Massee) D.A. Reid and undescribed species of *Hypholoma* sp. reported from Vietnam (Fig. 118). *Hypholoma* sp. from Vietnam, which is forming a sister clade with our specimen *H. darjeelingensis*, has no published data, so morpho-anatomical comparison is not possible. However, *H. australe* differs in having a larger basidiomata (15–45 mm broad), larger size pleurocystidia (31–46 µm), along with the absence of partial veil remnants in the stipe at mature stages (Miller and Pearce 1996); *H. brunneum* from New Zealand differs in having a large size (40–50 mm broad) dark olive brown to nearly black basidiomata (Horak 1971).

Typhulaceae Jülich.

Notes: Typhulaceae was established by Jülich (1981) with *Typhula* as the type. Subsequently, the members of Typhulaceae have been reclassified as the molecular phylogeny (Olariaga et al. 2020). This family contains species producing typical typhuloid (Corner 1950, 1970; Berthier 1976). *Macrotyphula* R.H. Petersen was also accepted in *Typhulaceae* (Berthier 1976; Knudsen and Vesterholt 2012). This genus differs from *Typhula* in having large, yellow–brown basidiomata (30–300 mm) that never arise from sclerotia and non-amyloid spores (Berthier 1976). Phylogenetical analysis suggested that *Macrptyphula* was another family, Phyllotopsidaceae Locquin ex Olariaga, Huhtinen, Læssøe, J.H. Petersen & K. Hansen (Olariaga et al. 2020).

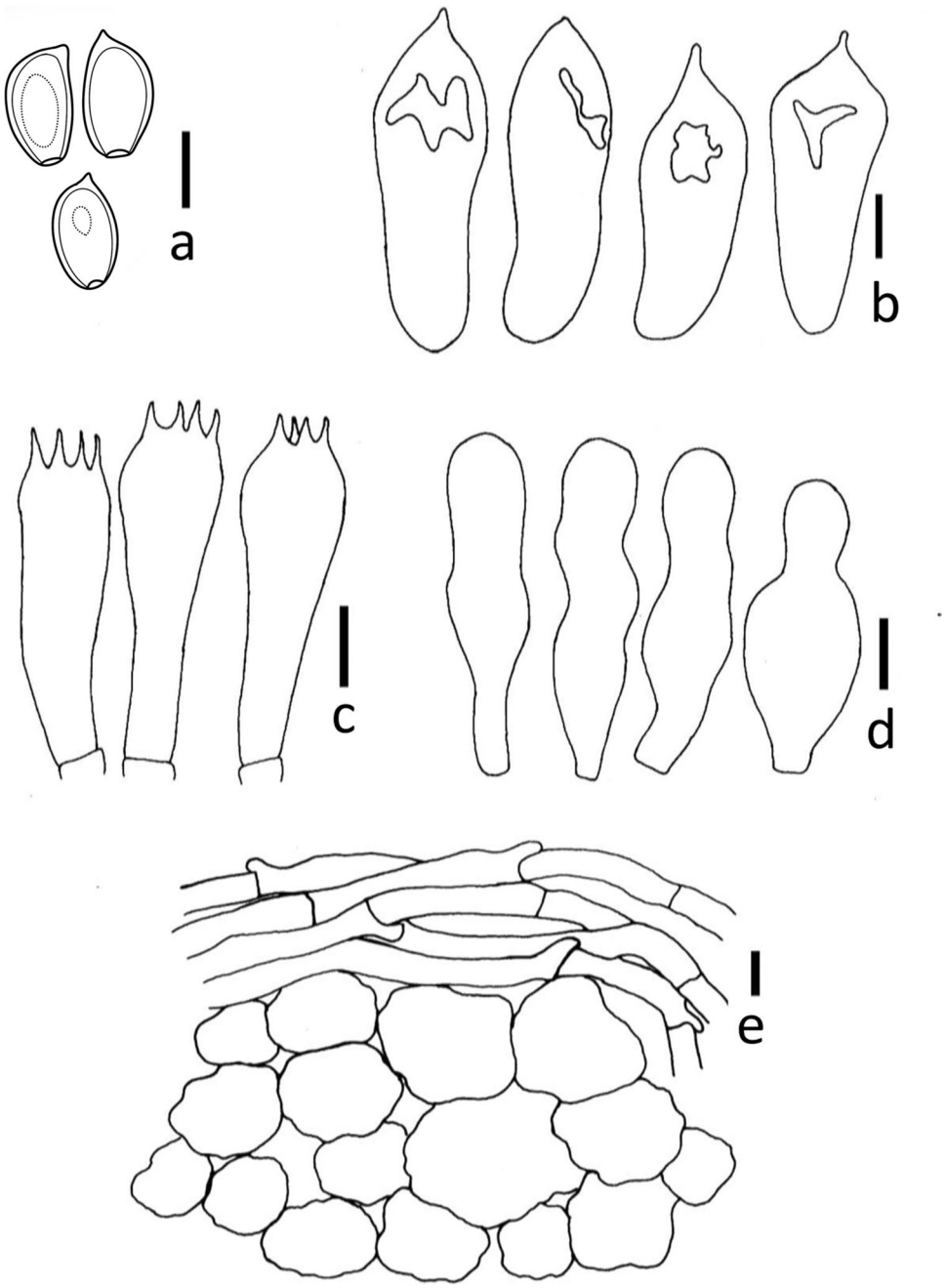


Fig. 117 ***Hypholoma darjeelingensis*** (CUH AM952, **holotype**). **a** Basidiospores. **b** Pleurocystidia. **c** Basidium. **d** Cheilocystidia. **e** Pileipellis. Scale bars: **a**–d = 5 µm, **e** = 10 µm

Typhula (Pers.) Fr.

Notes: The genus *Typhula* was described by Fries (1818) and is ca. 180 species of Agaricomycetes. *Typhula incarnata* is the current type species in this genus (Olariaga et al. 2020, 2022). *Typhula* includes species with smaller basidiomata (generally under 10 mm long) that often arise from sclerotia and usually have amyloid spores (Olariaga et al. 2020). Phylogenetic analysis suggested that this genus included the following genera as synonyms: *Cnazonaria* Corda, *Dacryopsella* Höhn., *Gliocoryne* Maire, *Phacorhiza* Pers., *Pistillaria* Fr., *Pistillina* Quel., *Scleromitra* Corda, *Sphaerula* Pat., *Sclerotium* Tode, and *Tygervalleyomyces* Crous (Olariaga et al. 2020, 2022).

Typhula incarnata Lasch, **new geographical record from USA.**

MycoBank: MB 155480; *Facesoffungi*: FoF 15230.

Material examined: USA, Alaska, Adak, Kuluk Dr., 51°52′N 176°38′W, ca. 25 m asl, 26 Jul 2003, *Tamotsu Hoshino*, TNS-F-86989.

Notes: This fungus is typical sclerotium-forming snow mold, widely distributed in continentals of the Northern Hemisphere and islands such as Iceland (Kristinsson and

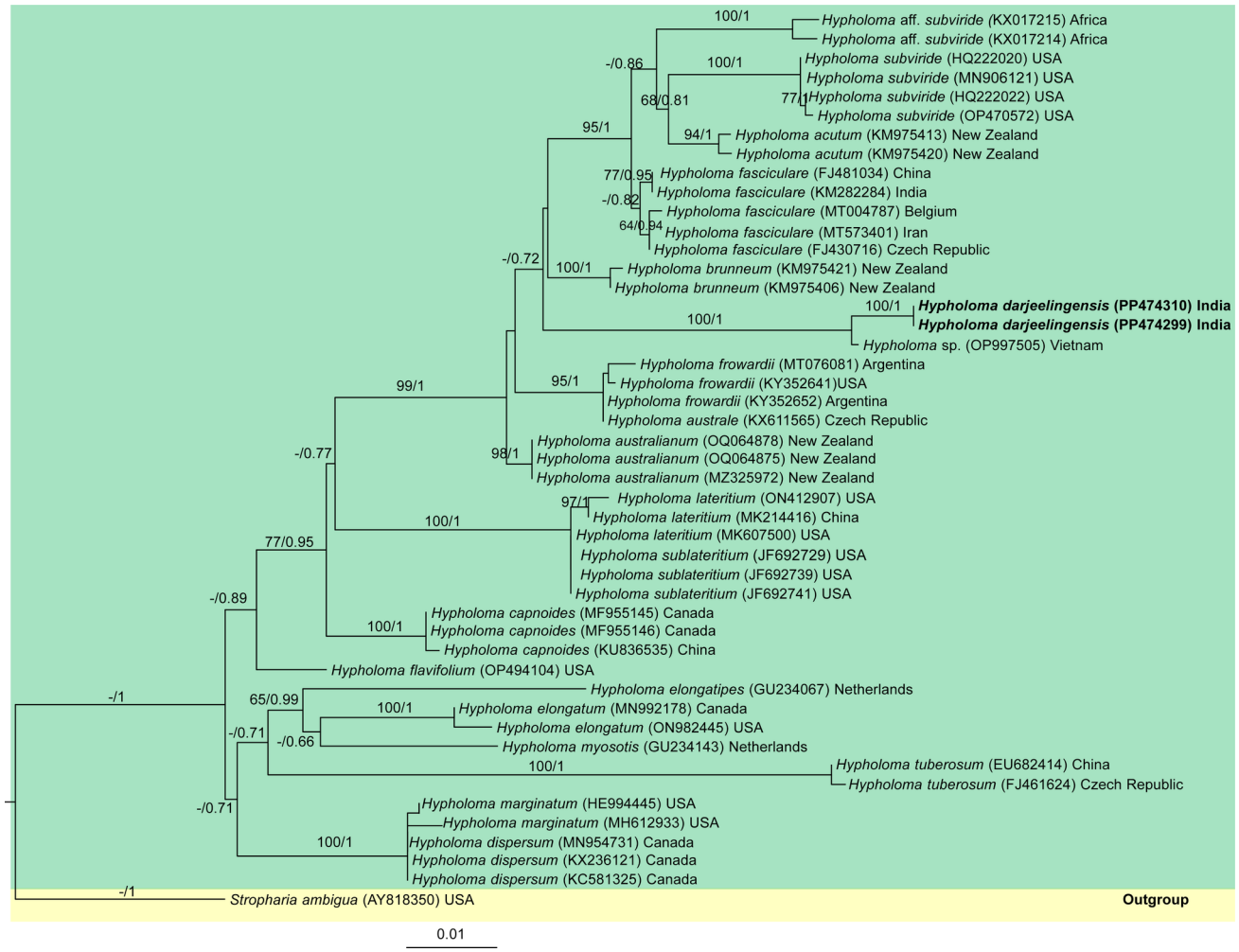


Fig. 118 Maximum Likelihood phylogram (−InL = 3660.029079) of *Hypholoma* inferred from nrITS sequences. Maximum Likelihood bootstrap support values (MLBS) ≥ 60% and Bayesian posterior probabilities values ≥ 0.7 are given above the nodes exclusively. All the taxa are represented along with their GenBank accession numbers and respective country of origin. The tree is rooted with *Stropharia ambigua*. The newly generated sequences are kept in bold font

Guðleifsson 1976), the Faroe Islands (Hoshino et al. 2004), Ireland (O'Rourke 1975), UK (Woodbridge and Coley-Smith 1991), Denmark (Welling and Jensen 1970), Svalbard (Shiryaev and Mukhin 2010), Novaya Zemlya (Shiryaev 2006), Japan (Matsumoto et al. 1995), Sakhalin (Hoshino et al. 2008) and Greenland (Hoshino et al. 2006). New geographical record from the Aleutian Islands, Alaska, USA.

Morphological characteristics of sclerotia from *T. incarnata* on Adak Is. did not differ from other localities, and the physiological characteristics of strains from Adak Is. were also as same as other strains (ex. Hoshino et al. 2004). However, strains of Adak Is and Khamar-Daban, East Siberia, separated from the major clade of *T. incarnata*. Røed (1969) carried out mon-mon mating experiment among *T. incarnata* collected from Nederland, Norway, Japan and Canada, and all of the tested monokaryons were mated with other monokaryons from different localities. Our result suggested that some strains in Pacific and East Asia were the possibility of intraspecies in *T. incarnata* (Fig. 119), we should elucidate the mating compatibility among *T. incarnata*, including Pacific and East Siberian strains.

Hymenochaetales Oberw.

Notes: The order Hymenochaetales within Agaricomycetes comprises 16 families, 88 genera, and 1,205 species, including wood-inhabiting and ectomycorrhizal fungi with diverse basidiomata types, such as polyporoid, stereoid, corticioid, hydnoid, coralloid, and agaricoid forms (Zhou et al. 2023; He et al. 2024a). Despite this diversity, the order forms a well-supported clade, though its internal structure remains largely unresolved (Hibbett et al. 2014). To improve resolution within Hymenochaetales, additional nuclear markers and comprehensive genome sequencing of more species are needed (Zhao et al. 2023c, 2024a).

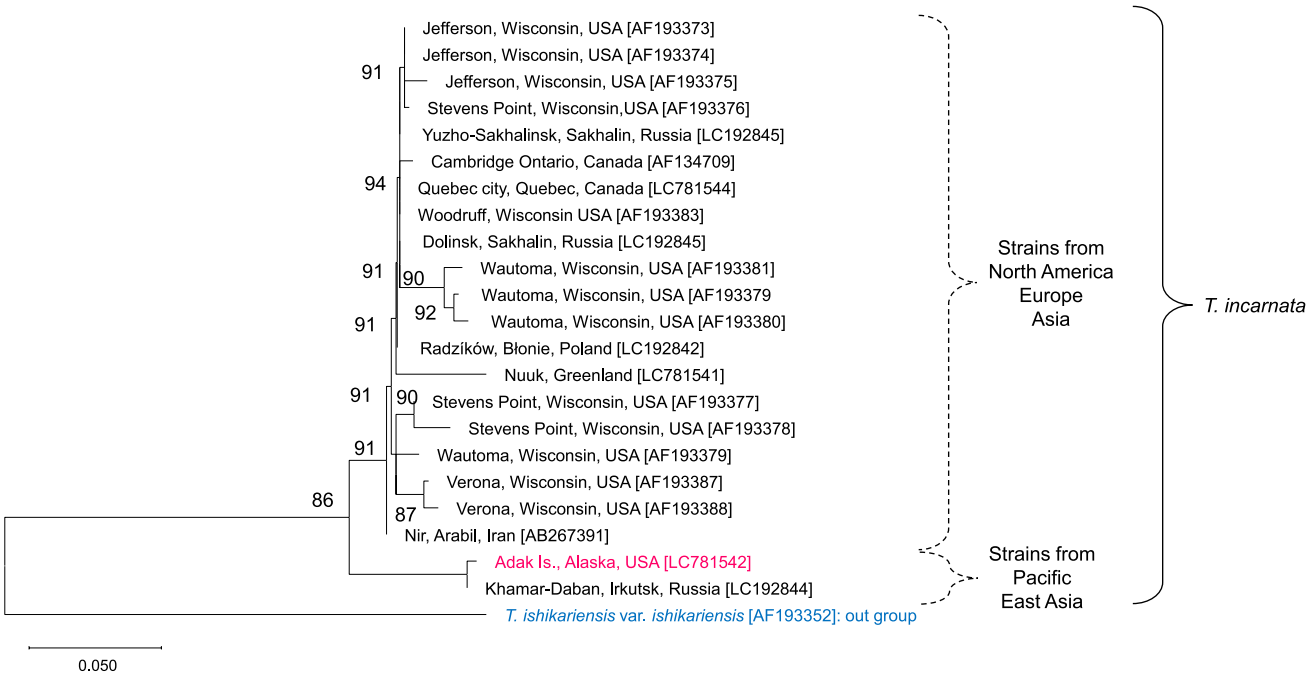


Fig. 119 Maximum Likelihood tree based on ITS sequences of *T. incarnata*, bootstrap values greater than 50% are shown around nodes. The new geographical record is shown in red

Hymenochaetaceae Donk.

Notes: The family Hymenochaetaceae Donk (1948) accommodates xanthochroid polypores and some corticioid species, which are causing wood decay in angiosperms and gymnosperms. Members of Hymenochaetaceae are distinguished by annual to perennial, resupinate, effused reflex, pileate and imbricate, substipitate or stipitate to spathulate, yellow to brownish basidiomata, with smooth, poroid, or corticioid hymenophore, a monomitic, mono-dimitic, or dimitic hyphal system, with simple generative hyphae lacking clamp connections, thin- to thick-walled basidiospores, color ranging from hyaline to golden yellow or yellow to brown, and shapes varying from globose to cylindrical, presence or absence of sterile elements (cystidia, cystidioles, hyphidia, and setae) are the distinguishing features of Hymenochaetaceae (Ryvarden 1991; Dai 2010). Fiasson and Niemela (1984) studied the morphological characteristics along with the chemical, cultural, and nuclear behaviour of *Inonotus* and *Phellinus* complex and revised the *Inonotus* s.l. and *Phellinus* s.l. complex. Zhou et al. (2015) studied the morphology and molecular phylogeny of the *Inonotus linteus* complex and introduced two new genera, *Tropicoporus* L.W. Zhou, Y.C. Dai & Shen. H. Wu and *Sanghuangporus* Sheng H. Wu, L.W. Zhou & Y.C. Dai. Recently, poroid Hymenochaetoid fungi were systematically studied and revised and classified under 34 genera, including 7 new genera, 37 new species, and 108 new combinations (Wu et al. 2022a).

Fulvifomes Murrill.

Notes: *Fulvifomes* is characterized by annual to perennial, pileate, effused-reflexed or substipitate basidiomata with a pilear surface ranging from tomentose, velutinate, smooth, glabrous to cracked, with or without a crust, context homogenous or duplex, microscopically a monomitic or dimitic hyphal system, presence or absence of cystidioles, absence of setal elements and thick-walled, colored, inamyloid, cyanophilic or acyanophilic, subglobose to ellipsoid basidiospores, and causing a white rot (Ji et al. 2017).

Fulvifomes aurantiacus Ma. Fatima, Usman & Khalid, **new geographical record from India.**

Index Fungorum: IF 845746; *Facesoffungi*: FoF 17130; Figs. 120, 121

Basidiomata perennial, solitary, pileate, applanate, meagerly ungulate to triquetrous, firmly attached to the surface. **Pileus** dimidiate projecting up to 9.2 cm length, 14.5 cm wide, 4.3 cm at the base near attachment 14.5 cm wide and 9.2 cm length. **Pileal** surface smooth or with unevenly tuberculate near margin, azonate, glabrous, irregularly cracked with age, brown (6F8) (Kornerup and Wanscher 1978) to dark brown (6F4). **Margin** smooth to velutinate, obtuse to round, brown (6E7), 3.8 cm, sterile. **Pore surface** yellowish orange (4A7, 4B7). **Pores** regular, round, 4–5 per mm. **Context** brown (6E7), homogenous, zonate, up to 7 cm thick. **Tube** layer brown (6E8), 4 mm, stratified, each stratum up to 2 mm.

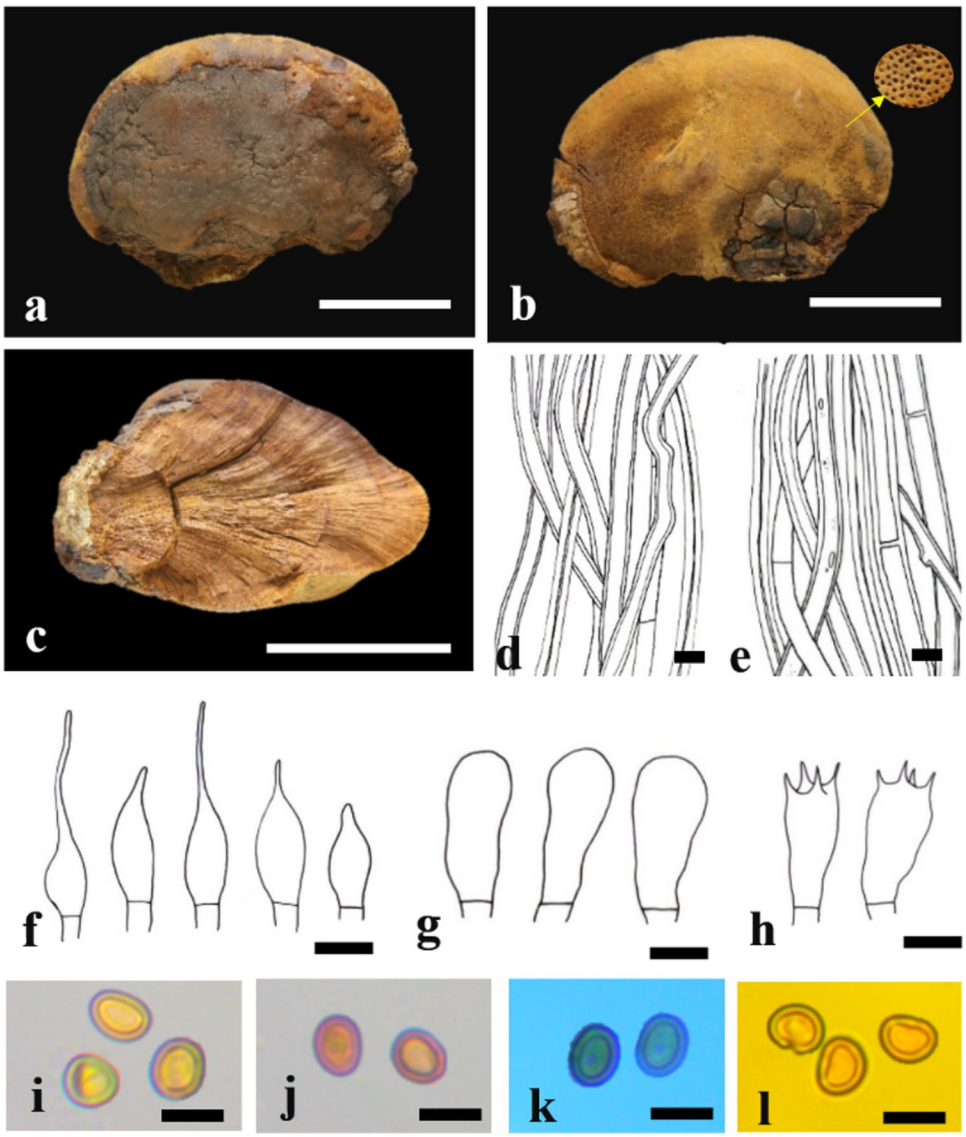


Fig. 120 ***Fulvifomes aurantiacus*** (MUBL1101). **a** Pilear surface. **b** Pore surface with enlarged pores. **c** Transverse section of basidiomata. **d** Contextual hyphae. **e** Tramal hyphae. **f** Cystidioles. **g** Basidioles. **h** Basidia. **i–l** Basidiospores: Basidiospores in water; Basidiospores in KOH; Basidiospores in cotton blue; Basidiospores in Melzer's reagent. Scale bars: **a–c** = 5 cm, **d–l** = 5 µm

Hyphal system dimitic, tissue darkening in KOH without hyphal swelling. **Context Generative hyphae** thin- to thick-walled, pale yellow to brown, simple septate, rarely branched, 3–4.5 µm diam. Skeletal hyphae thin- to thick-walled with a narrow lumen, yellow to yellowish brown, aseptate, unbranched, 3.3–4 µm diam. **Trama Generative hyphae** thin- to thick-walled, hyaline to dark brown, simple septate, rarely branched, 2.5–4.5 µm diam. Skeletal hyphae, thick-walled with a narrow to wide lumen, yellow to yellowish brown, aseptate, unbranched, 3.3–4 µm diam. **Cystidioles** thin walled, hyaline, ventricose to fusoid with elongated tapering apical portion, or abruptly narrow apices, 13.5–21 × 2.2–3.1 µm. **Basidia** clavate to subclavate, 4–10.3 × 3.1–4.1 µm, with four sterigmata. **Basidioles** clavate, 5–10 × 3–4.5 µm. **Basidiospores** smooth, subglobose to broadly ellipsoid, thick-walled pale yellow to golden yellow in water, turning golden yellow to brown in KOH, (5.2–)5.7–5.9(–6.5) × (4.4–)4.9–5.2(–5.4) µm (n = 30), Q = 1.14 (Q range 1.10–1.18), CB–, IKI–.

Material examined: INDIA, Karnataka, Mysore, 12°28′05″N 76°65′92″E on living angiosperm tree *Peltophorum pterocarpum* (*Fabaceae*), 04 September 2021, *Elangovan Arumugam* (MUBL1101). Karnataka, Mysore, 12°28′06″N 76°65′91″E on living angiosperm tree *Peltophorum pterocarpum* (*Fabaceae*), 04 September 2021, *Malarvizhi Kaliyaperumal* (MYS1a).

GenBank: MUBL1101: PP378351 (ITS), PP373823 (LSU).

Notes: Our isolate MUBL1101 exhibits similarities with *F. aurantiacus* (LAH 37530) in pores and dimitic hyphal system, but differs in other morpho-microtaxonomic characters (Fatima et al. 2023). However, molecular analysis based on ITS and LSU reveals a close phylogenetic relationship between our isolate and *F. aurantiacus*, suggesting a shared

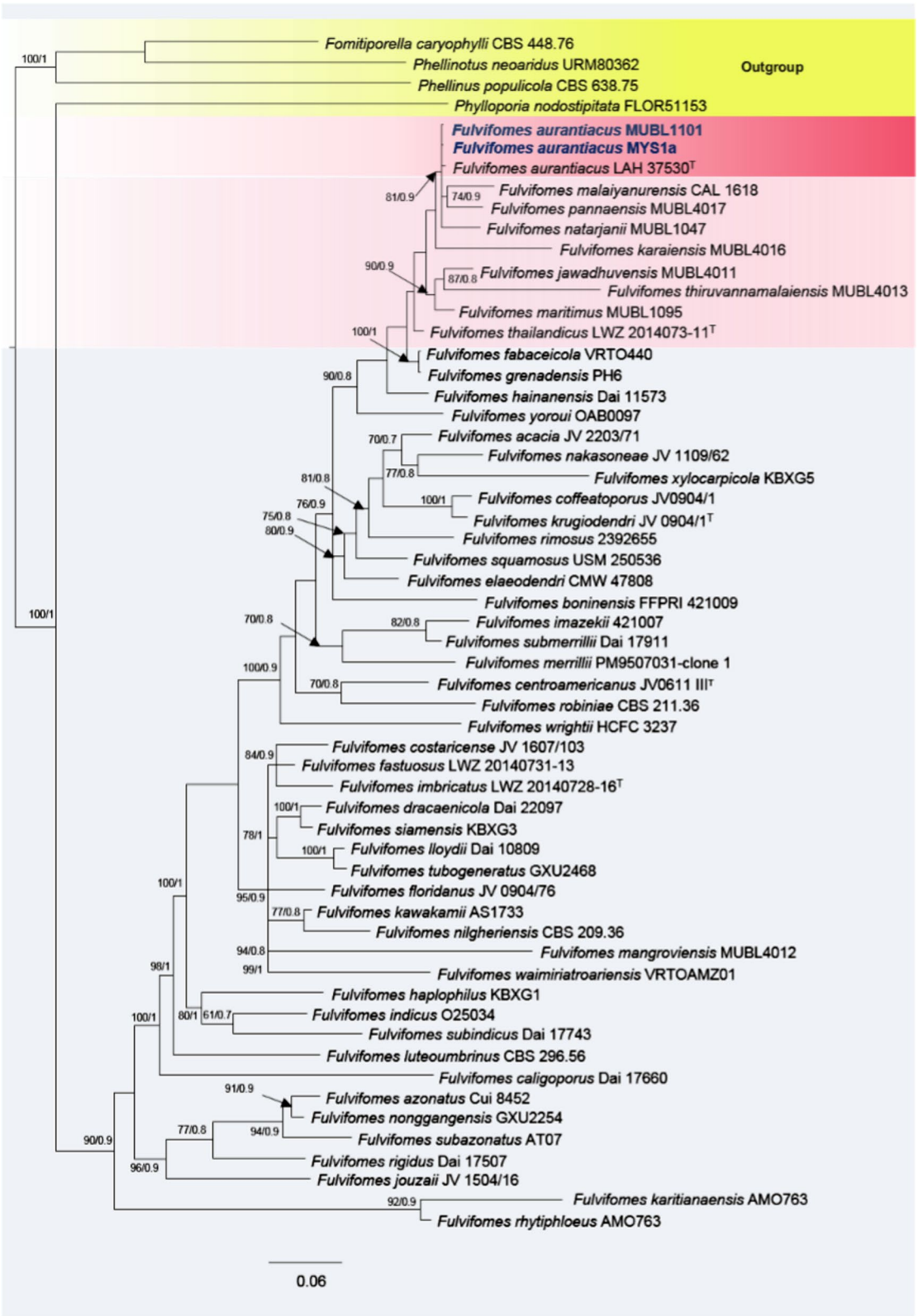


Fig. 121 Maximum Likelihood consensus tree inferred from the combined ITS and LSU. Bootstrap support values for Maximum Likelihood (ML, first value) equal to or greater than 80% and Bayesian posterior probabilities from MCMC analyses (BPP, second value) equal to or greater than 0.95 are given above the nodes. The tree is rooted to *Fomitiporella caryophylli* (CBS 448.76) and *Phellinotus neoaridus* (URM80362). Ex-type strains are indicated with "^{T}". The newly generated sequences are bold and indicated in blue

ancestry. The observed variations in morpho-micotaxonomic features may be attributed to environmental influences or adaptive responses, further has to be resolved with additional protein-coding genes. This study is the first report in India.

Fulvifomes shailashikhara S. Gunaseelan, E. Arumugam & M. Kaliyaperumal, **sp. nov.**

Mycobank: MB 856326; *Facesoffungi*: FoF 17133; Figs. 122, 123

Etymology: The species epithet "*shailashikhara*" is a Sanskrit word that refers to 'mountain top' of Jawadhu hills.

Holotype: MUBL1141.

Basidiomata perennial, solitary, sessile, applanate to meagrely ungulate, imbricate, broadly attached to the substrate, hard, woody, light in weight when dry. **Pileus** dimidiate, projecting up to 7.2 cm length, 13.3 cm wide and 5.5 cm thick near the attachment. **Pilear** surface brown (6E7) to dark brown (6F7) broadly zonate, smooth at young, distinctly cracked, concentrically sulcate with narrow zones. **Margin** brown (6E8), obtuse, velutinate to smooth. **Pore surface** brown (6E6). **Pores** round, 5–7 per mm. **Context** brown (6D7) to dark brown (6F8) homogeneous, 0.8 cm. **Tubes** light brown (6D6), up to 2.4 cm thick, tubes layers stratified, each stratum up to 2 mm.

Hyphal system strictly dimitic. **Context** Generative hyphae dominant, thin- to thick-walled, hyaline to brown, frequently septate and branched, 2–5.7 µm diam.; skeletal hyphae, thick-walled with a narrow to wide lumen, unbranched, brown, aseptate, 3–4.1 µm diam. **Trama generative hyphae**, thin- to thick-walled, hyaline to brown, septate, rarely branched, 2–4.8 µm diam.; skeletal hyphae, thick-walled with a narrow to wide lumen, brown,

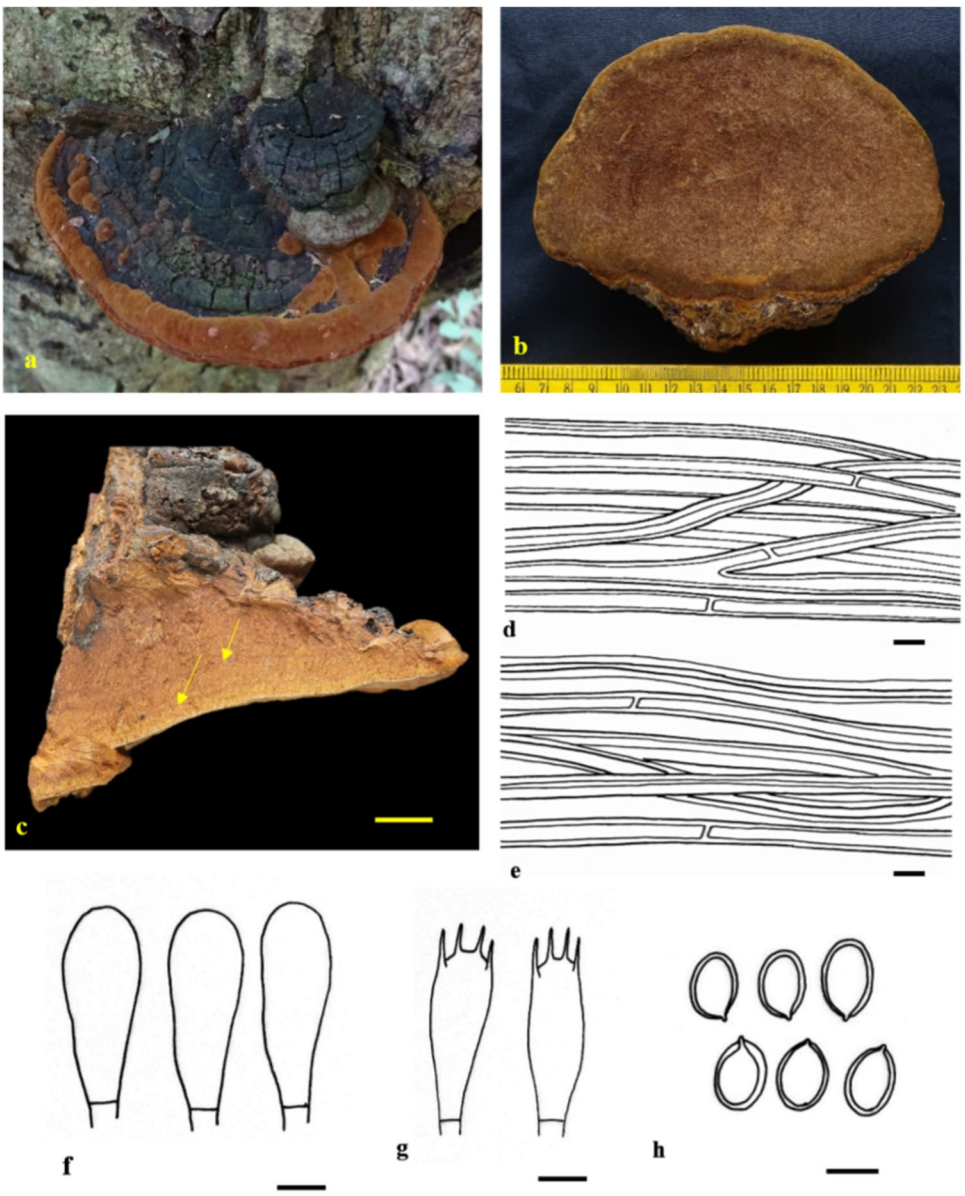


Fig. 122 ***Fulvifomes shailashikhara (MUBL1141) a*** Habitat. **b** Pore surface. **c** Transverse section of basidiomata (yellow arrow indicates the stratified tubes) **d** Contextual hyphae. **e** Tramal hyphae. **f** Basidioles. **g** Basidia. **h** Basidiospores. Scale bars: **c** = 2 cm, **d–h** = 5 µm

aseptate, unbranched, 3–4.3 µm diam. **Setae** absent. **Cystidioles** absent. **Basidioles** clavate to broadly clavate, 7.4–15.5 × 4.4–5.7 µm. **Basidia** clavate to broadly clavate, with four sterigmata, 9.4–15.5 × 4.6–6.2 µm. **Basidiospores** thick-walled, smooth, yellow in water, turning brown to rust brown in KOH, subglobose to broadly ellipsoid (5.2–)5.4–5.7(–6.1) × (4.6–)4.9–5.4(–5.7) µm (n = 30), Q = 1.10 (1.04–1.19), CB–, IKI–.

Specimen examined: INDIA, Tamil Nadu, Thiruvannamalai district, Jawadhu hills, Thenmalai, 12.47° 77′49″N 78°82′64″E, on living angiosperm tree (*Albizia amara*), 11 January 2020, *Malarvizhi Kaliyaperumal* (MUBL1141, **holotype**). Thenmalai, 12.47° 76′40″N 78°82′68″E, on dead wood, 14 January 2020, *Malarvizhi Kaliyaperumal* (TMII7 & TM41).

GenBank: MUBL1141: PQ513519 (ITS), PQ510487 (LSU); TMII7: PQ513520 (ITS), PQ510488 (LSU); TM41: PQ513521 (ITS), PQ510489 (LSU).

Notes: The Maximum Likelihood (ML) and Bayseian posterior probability (BPP) analyses inferred from combined ITS and nLSU sequence data revealed that *Fulvifomes shailashikhara* forms a distinct lineage with *F. maritimus* (60% ML, 1.00 BPP) (Crous et al. 2023).

Fulvifomes shailashikhara shares characteristics with *Fulvifomes maritimus* in having homogenous context, stratified tubes, number of pores and absence of cystidioles. However, the former varies by having applanate to meagrely ungulate basidiomata, distinctly cracked, broadly zonate, obtuse margin and larger basidiospores (5.2–6.1 × 4.6–5.7) µm whereas the latter is distinct by having crusted, azonate basidiomata, meagrely cracked and scrupose pilear surface, acute to obtuse margin and smaller basidiospores (4.9–5.7 × 4.6–5.7) µm (Crous et al. 2023). *Fulvifomes shailashikhara* resemblance with *F. thiruvannamalaiensis* by sharing a sharing meagrely ungulate, cracked basidiomata, concentrically sulcate, homogenous context and dimitic hyphal system, yet *F. shailashikhara* shows distinct features like imbricate basidiomata, broadly zonate, absence of cystidioles while *F. thiruvannmalaiensis* shows pileate, scrupose pilear surface and presence of cystidioles (Jayawardena et al. 2022). *Fulvifomes shailashikhara* shares similarities with *F. karaiensis* and *F. pannaensis* in having homogenous context and dimitic hyphal system but differs significantly in morphological characters such as imbricate, broadly zonate basidiomata and stratified tubes while the latter two spp. are pileate, weakly zonate basidiomata with non-stratified tubes (Senanayake et al. 2023). *Fulvifomes shailashikhara* and *F. jawadhuvensis* are identical in homogenous context, zonate basidiomata, dimitic hyphal system and absence of cystidioles but latter differs by having pileate basidiomata, round margin and presence of chlamydospores while our new species shows imbricate, obtuse margin and absence of chlamydospores (Jayawardena et al. 2022). *Fulvifomes shailashikhara* is similar to *F. malaiyanurensis* in zonate basidiomata, dimitic hyphal system, number of pores and absence of cystidioles but varies in imbricate, obtuse margin and larger basidiospores (5.2–6.1 × 4.6–5.7) µm but latter shows pileate, obtuse to round margin and smaller basidiospores (4.2–5.7 × 3.9–5.2) µm (Jayawardena et al. 2022). *Fulvifomes shailashikhara* distinctly differs with *F. aurantiacus* except sharing a few identical characters such as obtuse margin, dimitic hyphal system, and absence of cystidioles (Fatima et al. 2023). Our new Indian species having imbricate, distinctly cracked basidiomata with homogenous context, lacks stipe, while the latter species have pileate to substipitate basidiomata and duplex context.

Phellinus Quél.

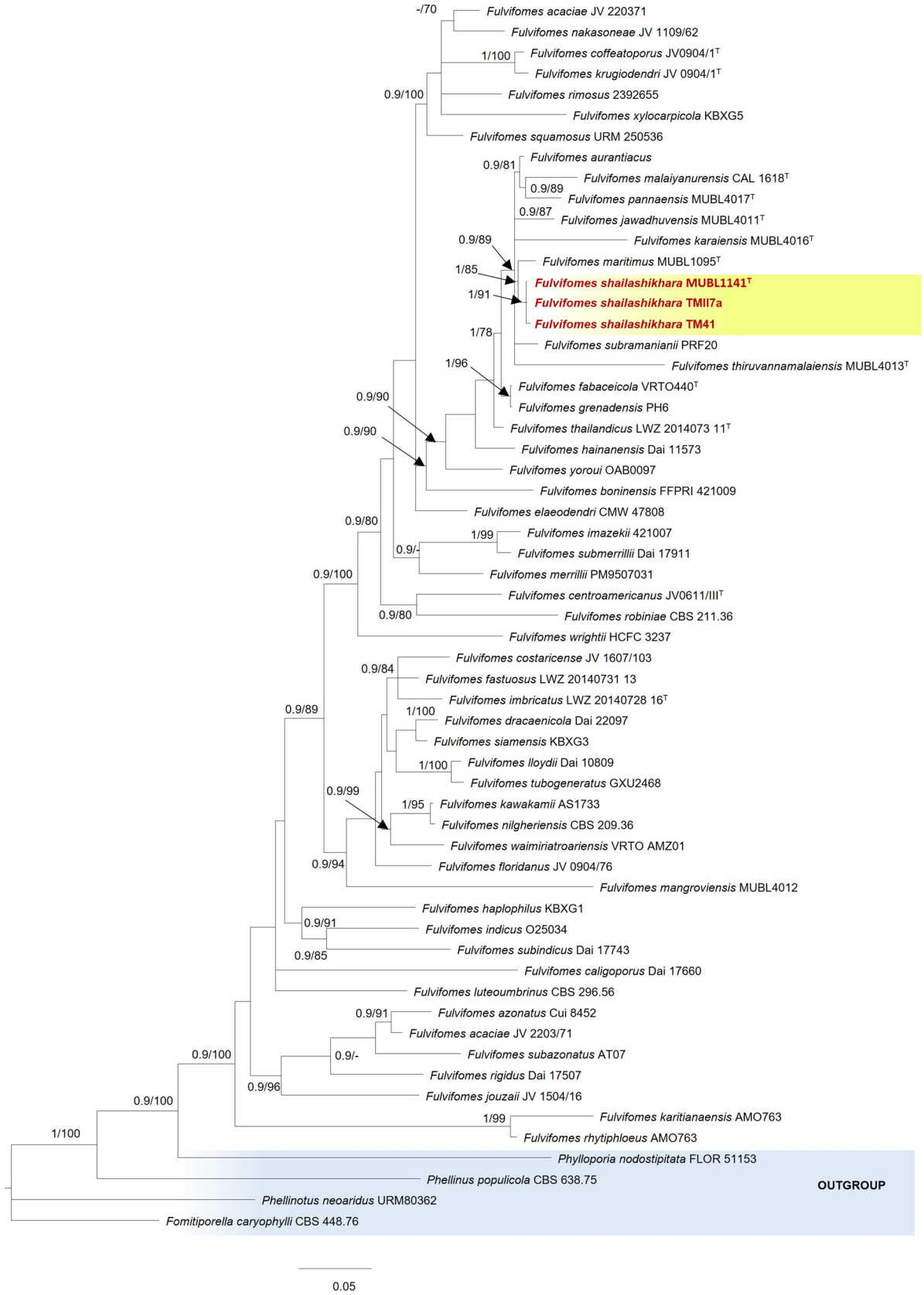
Notes: The genera *Phellinus* characterized by perennial, resupinate or effused-reflexed to pileate, solitary or imbricate, encrusted pileal surface usually, context homogeneous with a dimitic hyphal system, presence of hymenial setae arising from subhymenium, presence of absence of cystidioles and thick-walled smooth, inamyloid, cyanophilic to partially cyanophilic, subglobose to broadly ellipsoid basidiospores, and causing a white rot (Zhou et al. 2016). Many species of *Phellinus* are forest pathogens (Yuan et al. 2023).

Phellinus resupinatus M. Fisch., M. Cloete, L. Mostert & F. Halleen, **new geographical record from India.**

Mycobank: MB 810783; *Facesoffungi*: FoF 17135; Figs. 124, 125

Basidiomata resupinate, firmly attached to the substratum, perennial, yellowish brown (5E8) (Kornerup and Wanscher 1978), golden yellow (5B7), velutinate, up to 68 cm long, 10 cm wide and 6 mm thick, with distinct sterile yellowish margin. **Context** brownish yellow (5C7), up to 1 mm in thickness. **Pore surface** yellowish brown (5D7), cushion shaped near edges, cracked in maturity. **Pores** circular to angular, very small, 7–9 per mm; dissepiments thin, entire. **Tube** layer yellowish brown (5D7), up to 2– 4 mm thick, concolorous to pore surface.

Hyphal system strictly dimitic, Generative hyphae dominant; both skeletal and generative hyphae acyanophilous; tissue darkening with KOH without swelling. **Context** generative hyphae, thin- to thick-walled, hyaline to yellow, simple septate, branched, 2.4–6.5 µm diam.; skeletal hyphae, thick-walled with a narrow lumen, unbranched, yellowish brown, aseptate, 2–5.2 µm diam. **Trama generative hyphae**, thin- to thick-walled, yellow to brown, septate, rarely branched, 2.5–5.2 µm diam.; skeletal hyphae, thick-walled with a narrow to wide lumen, yellowish brown, aseptate, unbranched, 1.8–4.8 µm diam. **Hymenial setae** thick-walled, dark brown, ventricose to subulate with sharp


-/70
Fulvifomes acaciae JV 220371
Fulvifomes nakasoneae JV 1109/62
1/100
Fulvifomes coffeatoporus JV0904/1T
Fulvifomes krugiodendri JV 0904/1T
0.9/100
Fulvifomes rimosus 2392655
Fulvifomes xylocarpicola KBXG5
Fulvifomes squamosus URM 250536
0.9/81
Fulvifomes aurantiacus
Fulvifomes malaiyanurensis CAL 1618T
0.9/89
Fulvifomes pannaensis MUBL4017T
0.9/87
Fulvifomes jawadhuvensis MUBL4011T
Fulvifomes karaiensis MUBL4016T
0.9/89
Fulvifomes maritimus MUBL1095T
1/85
Fulvifomes shailashikhara MUBL1141T
1/91
Fulvifomes shailashikhara TMII7a
Fulvifomes shailashikhara TM41
1/78
Fulvifomes subramanianii PRF20
Fulvifomes thiruvannamalaiensis MUBL4013T
1/96
Fulvifomes fabaceicola VRTO440T
0.9/90
Fulvifomes grenadensis PH6
0.9/90
Fulvifomes thailandicus LWZ 2014073 11T
Fulvifomes hainanensis Dai 11573
Fulvifomes yoroui OAB0097
Fulvifomes boninensis FFPRI 421009
Fulvifomes elaeodendri CMW 47808
0.9/80
1/99
Fulvifomes imazekii 421007
0.9/-
Fulvifomes submerrillii Dai 17911
0.9/100
Fulvifomes merrillii PM9507031
Fulvifomes centroamericanus JV0611/III T
0.9/80
Fulvifomes robiniae CBS 211.36
Fulvifomes wrightii HCFC 3237
Fulvifomes costaricense JV 1607/103
0.9/84
Fulvifomes fastuosus LWZ 20140731 13
Fulvifomes imbricatus LWZ 20140728 16T
0.9/89
1/100
Fulvifomes dracaenicola Dai 22097
Fulvifomes siamensis KBXG3
1/100
Fulvifomes lloydii Dai 10809
Fulvifomes tubogeneratus GXU2468
0.9/99
1/95
Fulvifomes kawakamii AS1733
Fulvifomes nilgheriensis CBS 209.36
Fulvifomes waimiriatroariensis VRTO AMZ01
0.9/94
Fulvifomes floridanus JV 0904/76
Fulvifomes mangroviensis MUBL4012
Fulvifomes haplophilus KBXG1
0.9/91
Fulvifomes indicus O25034
Fulvifomes subindicus Dai 17743
0.9/85
Fulvifomes caligoporus Dai 17660
Fulvifomes luteoumbrinus CBS 296.56
0.9/91
Fulvifomes azonatus Cui 8452
Fulvifomes acaciae JV 2203/71
0.9/100
0.9/-
Fulvifomes subazonatus AT07
Fulvifomes rigidus Dai 17507
0.9/96
Fulvifomes jouzaii JV 1504/16
0.9/100
1/99
Fulvifomes karitianaensis AMO763
1/100
Fulvifomes rhytiphloeus AMO763
Phylloporia nodostipitata FLOR 51153
Phellinus populicola CBS 638.75
OUTGROUP
Phellinotus neoaridus URM80362
Fomitiporella caryophylli CBS 448.76
0.05

◂**Fig. 123** Molecular phylogeny of *Fulvifomes* inferred through a Bayesian analysis of the combined ITS and nLSU sequence data were aligned in MEGA X v10.02 and edited manually to increase the similarity of alignment (Kumar et al. 2018) the same was used for the Maximum Likelihood (ML) analysis and Bayseian Posterior Probabilities (BPP) analysis using raxmlGUI 2.0 (Edler et al. 2021) MrBayes 3.2.7a (Ronquist et al. 2012). Bayesian posterior probability (BPP, first value) equal to or greater than 0.9 and Bootstrap support values Maximum Likelihood (ML, second value) equal to or greater than 70% are given above the nodes. Ex-type strains are indicated with "[T]". The newly generated sequences are highlighted in color and bold

to blunt tips, 10–23 × 3.7–8 µm. **Cystidioles** hyaline, thin-walled, ventricose to fusoid with elongated tapering apical portion, 7.2–24 × 2.6–5.2 µm. **Basidioles** dominant, clavate, 7.7–14 × 3.8–7.2 µm. **Basidia** clavate to broadly clavate, with four sterigmata, 8.5–15 × 5–8.5 µm. **Basidiospores** broadly ellipsoid to subglobose, thin- to thick-walled, smooth, hyaline to pale yellow in water, turning rust brown in KOH, (4.6–)4.9–5.4(–5.7) × (4.1–)4.4–5.2(–5.4) µm (n = 50), Q = 1.08 (Q range 1–1.18), CB–, IKI–. **Chlamydospores** globose to subglobose, thick-walled rust brown to reddish brown, 5.2–8.5 × 4.1–7 µm, CB–, IKI–.

Specimen examined: INDIA, Puducherry, 12.18°20′25″N 79°92′18″E, on dead wood, 23 December 2022, *Sugantha Gunaseelan* (MUBL1126), *Elangovan Arumugam* (KAT16/22); Tamil Nadu, Chennai, 13°01′17″N 80°13′23″E, on living tree of *Peltophorum pterocarpum*, 27 Oct 2023, *Ramesh Murugadoss* (MUBL1127), *Ramesh Murugadoss* (SP03/23).

GenBank: MUBL1126: PQ168987 (ITS), PQ168992 (LSU); KAT16/23: PQ168988 (ITS), PQ168993 (LSU); MUBL1127: PQ168989 (ITS), PQ168994 (LSU); SP03/23: PQ168990 (ITS), PQ168995 (LSU).

Notes: Indian isolates MUBL1126 and MUBL1127 share similar morphological characters like resupinate basidiomata, distinct sterile margin, pores shape and size with *Phellinus resupinatus* reported from South Africa (Cloete et al. 2016). Phylogenetic analysis inferred from ITS and LSU revealed close clustering of our isolates with the reported *P. resupinatus* (STE-U7769, STE-U7771 and STE-U7775) (100% ML, 1.0 BPP). Hence, we identified our isolates as *P. resupinatus*, though our isolates have larger basidiospores size and the presence of cystidioles. The variation in size of basidiospore can possibly be caused by their climatic factors, modes of nutrition, and the effect of temperature on drying (Kauserud et al. 2005; Hu et al. 2022b). This study is the first report and first molecular evidence of genera *P. resupinatus* from India.

Phylloporia Murrill.

Notes: The genus is characterized by annual or perennial, effused-reflexed, pileate or stipitate, solitary or imbricate, soft corky to hard corky basidiomata, tomentose to velutinate pileal surface, a duplex context with monomitic hyphal system, presence or absence of cystidioles, cyanophilic to partially cyanophilic, broadly ellipsoid to ellipsoid basidiospores, and causing a white rot (Wu et al. 2019c).

Phylloporia afrospathulata Yombiy. & Decock, **new geographical record from India.**

Mycobank: MB 811591; *Facesoffungi*: FoF 17134; Figs. 126, 127

Basidiomata annual, solitary, stipitate, stipe up to 2.5 cm long, tapering at the apex. **Pilear** surface circular to semicircular, velutinate, olive yellow (3C6) when fresh, yellowish brown (5D6) brown while aging, concentrically sulcate, thinly applanate, projecting up to 2.6 cm long, 1.9 cm wide, up to less than 1.2 mm thick at the base and less than 0.5 mm thick at the margin. **Margin** acute, light yellow (3A5) when fresh, light brown when dried, incurved inwards while drying. **Pores** round, 9–11 per mm. **Context** (both pileus and stipe) duplex with a thin black line between the upper tomentum and lower context. **Stipe** light brown (6D6) to brown (6E5) cylindrical or more frequently flattened, lateral, up to 1.7 cm long and 0.1 cm in diam. **Tube** layer light brown (6D6) up to less than 0.4 mm.

Hyphal system strictly monomitic; tissue darkening but otherwise unchanged in KOH. **Context generative hyphae** turning golden brown to rusty brown in KOH, thin- to thick-walled with a wide lumen, rarely branched, frequently septate, 1.8–5.2 µm wide. **Tubes generative hyphae** hyaline to pale yellowish, thin- to slightly thick-walled, occasionally branched, frequently septate, 1.6–2.5 µm in wide. **Cystidia** and **Setae** absent. **Cystidioles** fucoid with tapering ends, 6–20.5 × 1.5–3 µm. **Basidioles** clavate to broadly clavate, 4.8–14 × 2.4–5.3 µm. **Basidia** clavate, with four sterigmata up to 3 µm long and a simple septum at the base, 3.8–11 × 3.2–6.4 µm. **Basidiospores** broadly ellipsoid to ellipsoid, hyaline to pale yellowish, thin- to thick-walled, smooth, IKI–, (3.4–)3.7–3.9(–4.2) × (1.8–)2.1–2.6(–2.9) µm, L = 2.8 µm, W = 2.4 µm, Q = 1.4 (Q ranges from 1.3–1.7) (n = 50).

Specimen examined: INDIA, Puducherry, Selli Amman Kovil, 12.18°20′25″N 79°92′18″E, on dead wood, 22 December 2022, *Elangovan Arumugam* (MUBL1138). Selli Amman Kovil, 12.17°19′23″N 79°90′14″E, on dead wood, 17 March 2023, *Malarvizhi Kaliyaperumal* (SAK2A/2).

Genbank: MUBL1138: PQ460313 (ITS), PQ460258 (LSU); SAK2A/2: PQ460314 (ITS), PQ460259 (LSU).

Notes: Phylogenetic analysis of ITS and nrLSU sequence data reveals that our collection MUBL1138 and SAK2A/2 are clustered with Central Africa specimens of *Phylloporia afrospathulata* with high statistical support (98% ML, 1.0 BPP) (Yombeni et al. 2015). Morphologically, our new collections are similar to *P. afrospathulata* from Central Africa by sharing annual, solitary, stipitate, concentrically sulcate

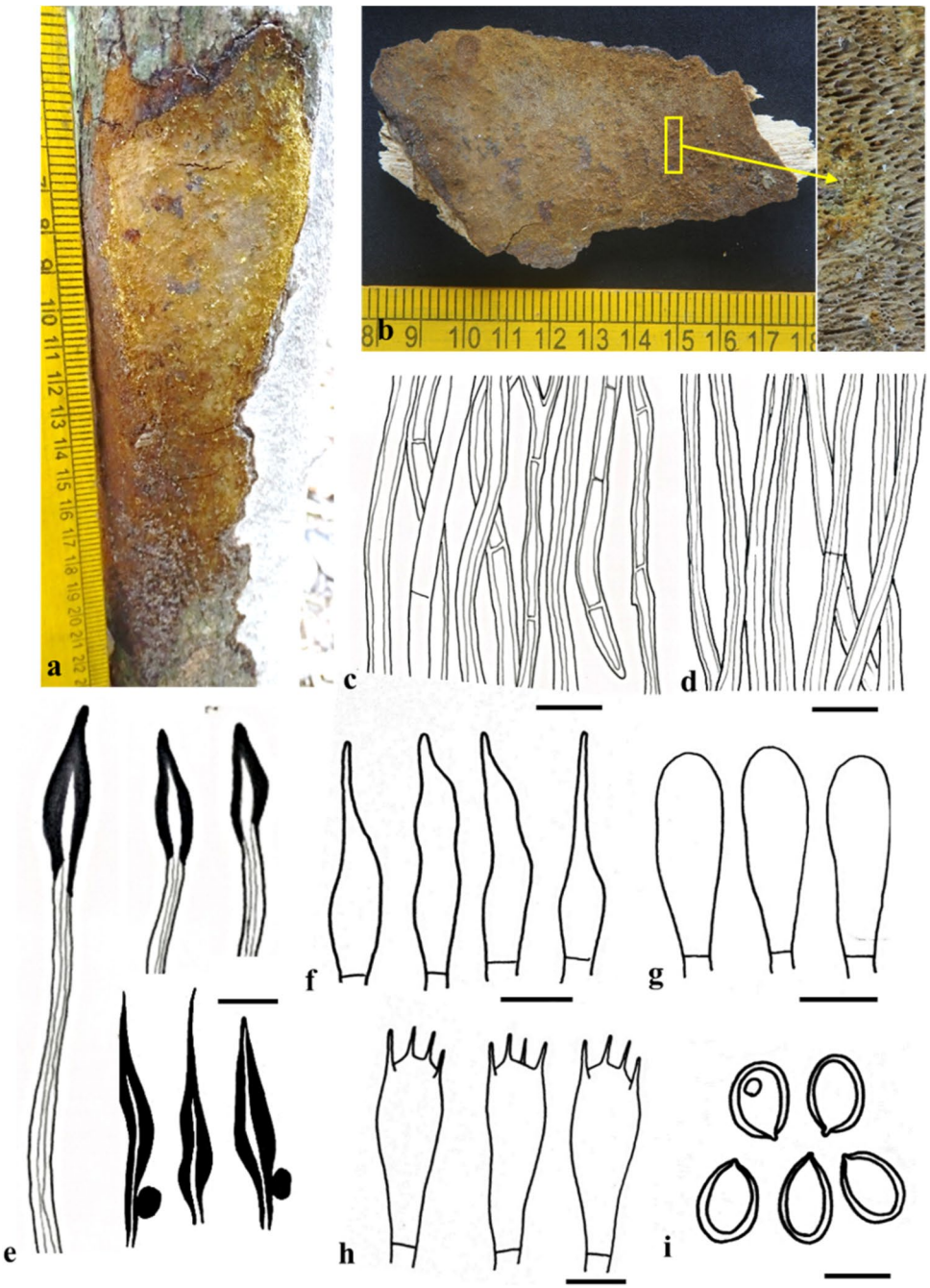


Fig. 124 ***Phellinus resupinatus (MUBL1126)*** ***a*** Basidiomata. **b** Pore surface and pores. **c** Contextual hyphae **d** Tramal hyphae. **e** Hymenial setae. **f** Cystidioles. **g** Basidioles. **h** Basidia. **i** Basidiospores. Scale bars: **c**–**i** = 5 µm

basidiomata, context (both pileus and stipe) duplex with thin black line between the upper tomentum and lower context, and pores (9–11 per mm). Hence, we identified our isolate to *P. afrospathulata*. This study is the first report with molecular evidence of *P. afrospathulata* from India.

Tropicoporus L.W. Zhou, Y.C. Dai & Sheng H. Wu.

Notes: Inonotus linteus complex was segregated into *Tropicoporus* L.W. Zhou, Y.C. Dai & Sheng H. Wu and *Sanghuangporus* Sheng H. Wu, L.W. Zhou & Y.C. Dai based on morphological and phylogenetic analyses (Zhou et al. 2015). *Tropicoporus* is distinctly characterized by annual to perennial, resupinate, effused-reflexed to pileate basidiomata, a homogeneous to duplex context, a monodimitic or strictly dimitic hyphal system, hymenial setae, presences or absences of cystidioles and slightly thin- to thick-walled, ellipsoid to subglobose, yellowish basidiospores (Zhou et al. 2015). There are 56 records of *Tropicoporus* listed in Index Fungorum (as of 29–10-2024). Species of *Tropicoporus* cause a white rot (Zhou et al. 2015).

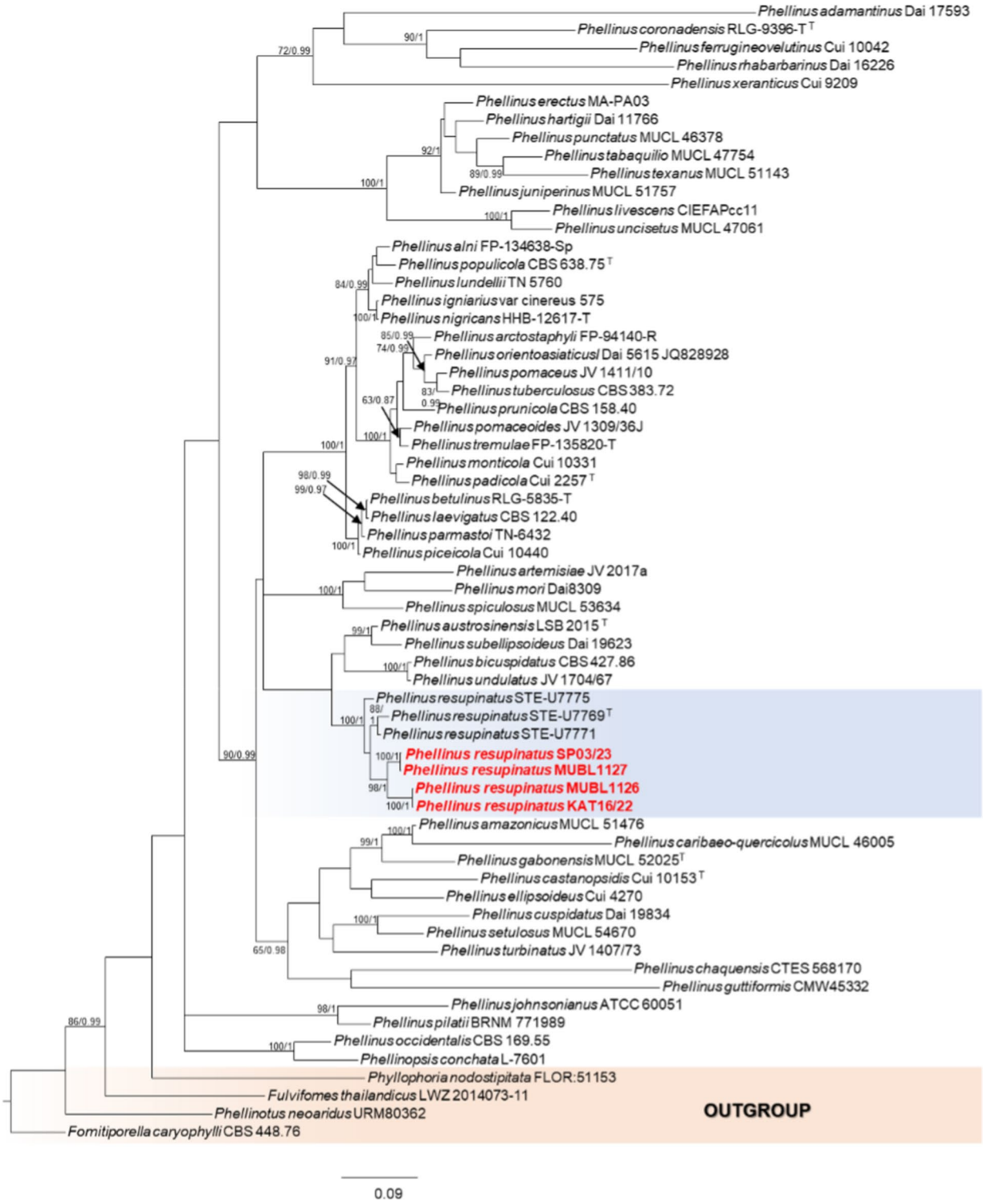


Fig. 125 Phylogenetic tree inferred from the combined ITS and LSU sequence alignments. The ITS and nLSU sequences were aligned separately in MEGA X v10.0.2 and edited manually to increase the similarity of the alignment (Kumar et al. 2018) and the same was used for the Maximum Likelihood (ML) analysis and Bayesian Posterior Probability (BPP) analysis using raxmlGUI 2.0 (Edler et al. 2021) and MrBayes 3.2.7a (Ronquist et al. 2012). Bootstrap support values for Maximum Likelihood (ML, first value) equal to or greater than 60% and Bayesian Posterior Probability (BPP, second value) equal to or greater than 0.8 are given above the nodes. The tree is rooted to *Fometiporella caryophylli* CBS 448.76. Ex-type strains are indicated with "T". The newly generated sequences are indicated in red and bold

Fig. 126 ***Phylloporia afrospathulata*** (MUBL1138). **a, b** Basidiomata. **c** (i) & (ii) Stipe and Pileus both showing duplex context with blackline respectively (Yellow arrow indicates thin black line between upper/external tomentum and lower/internal context). **d** Contextual hyphae. **e** Tramal hyphae. **f** Cystidioles. **g** Basidioles. **h** Basidia. **i** Basidiospores. Scale bars: **d**–**i** = 5 µm

Tropicoporus linteus (Berk. & M.A. Curtis) L.W. Zhou & Y.C. Dai, **new geographical record from India.**

Mycobank: MB 812159; *Facesoffungi*: FoF 17136; Figs. 128, 129

Basidiomata perennial, pileate, dimidiate, without odor or taste, hard corky to woody hard when fresh, become woody hard when dry. **Pilei** projecting up to 7 cm, 10 cm wide and 3 cm thick at base. Pilear surface golden brown (5D7) to yellowish brown (5E8) (Kornerup and Wanscher 1978), smooth to glabrous, weakly zonate, concentrically sulcate, pilei on maturation becoming rough, weakly cracked near attachment, grayish brown (6F3). **Margin** entire, obtuse to acute, velutinate, golden brown (5D7). **Pore surface** yellowish brown (5E7). **Pores** round, regular, 5–7 per mm. **Context** golden brown (5D7), up to 3.6 cm, homogeneous. **Tubes** yellowish brown (5D8), up to 1.4 cm, tube layers indistinct, up to 10 mm long.

Hyphal system monomitic in context, dimitic in trama; generative hyphae simple septate; tissue darkening and hyphae become swollen in KOH. **Context** generative hyphae varying from yellow to golden brown, slightly thick-walled to thick-walled with a distinct lumen, moderately branched, frequently with simple septa, regularly arranged, 3–5 µm in diam. **Trama generative hyphae** scanty, hyaline to yellowish, thin- to slightly thick-walled, occasionally branched and simple septate, 2–2.7 µm in diam; skeletal hyphae dominant, yellowish brown, thick-walled with a distinct lumen, unbranched, straight, subparallel along the tubes, 2.5–3.8 µm in diam. **Hymenial setae** frequent, ventricose or subulate, dark brown, thick-walled, 22–30 × 4–7 µm. **Cystidioles** fusoid, infrequently present 6–15.8 × 2.8 − 3.4 µm. **Basidia** barrel-shaped, with four sterigmata and a simple septum at the base, 9–12 × 4.5–6 µm. **Basidioles** barrel-shaped to subglobose, slightly smaller than basidia. Rhomboid crystals occasionally present. **Basidiospores** broadly ellipsoid to subglobose, yellowish and thick-walled, smooth, IKI–, CB–, (4.8–)5–5.3(− 5.5) × (3.9–)4–4.5(− 4.7) µm, Q = 1.21 (Q range 1.1–1.5).

Specimen examined: INDIA, Tamil Nadu, Salem district, Yercaud, on dead wood, 09 February 2018, *Kezhocuyi Kezo* (MUBL1137). Karadiyur, on dead wood, 22 January 2018, *Kezhocuyi Kezo* (MK-KA10). Salem district, on dead wood, 22 January 2018, *Malarvizhi Kaliyaperumal* (MK-KA10a/18). Namakkal district, Kolli hills, on dead wood, 03 March 2019, *Malarvizhi Kaliyaperumal* (KM-ASIII12).

GenBank: MUBL1137: PQ380935 (ITS), PQ380938 (LSU); MK-KA10: PQ380934 (ITS); MK-KA10a/18: PQ380936 (ITS); KM-ASIII12: PQ380937 (ITS).

Notes: The first report of *T. linteus* was as '*Polyporus linteus'* from Mesoamerica, Nicaragua (Berkeley and Curtis 1860). Later, a detailed description of based on type studies was published (Dai and Xu 1998). Then it has been reported from China, India, and the USA, on either dead angiosperm wood or living trees (Teng 1964; Sharma 1995; Tian et al. 2013). In India, this species has been reported as '*Phellinus linteus'* from different regions across different climatic conditions, viz. Himachal Pradesh, and Tamil Nadu (Kumari et al. 2021). Phylogenetic analysis of ITS and LSU sequence data revealed that our *T. linteus* is nested with other *T. linteus* from USA, with high statistical support (ML 100% and 1.00 BPP).

The morpho-microscopical characters of our Indian *Tropicoporus linteus* are consistent with an earlier report (Sharma 1995). Both Indian and American strains are sharing similar features like pileate, applanate to triquetrous basidiomata with concentrically sulcate, zonate pilear surface, 5–7 per mm, mono-dimitic hyphal system, presence of cystidioles, and basidiospore size (Tian et al. 2013). This study reveals the first molecular evidence of *T. linteus* from India.

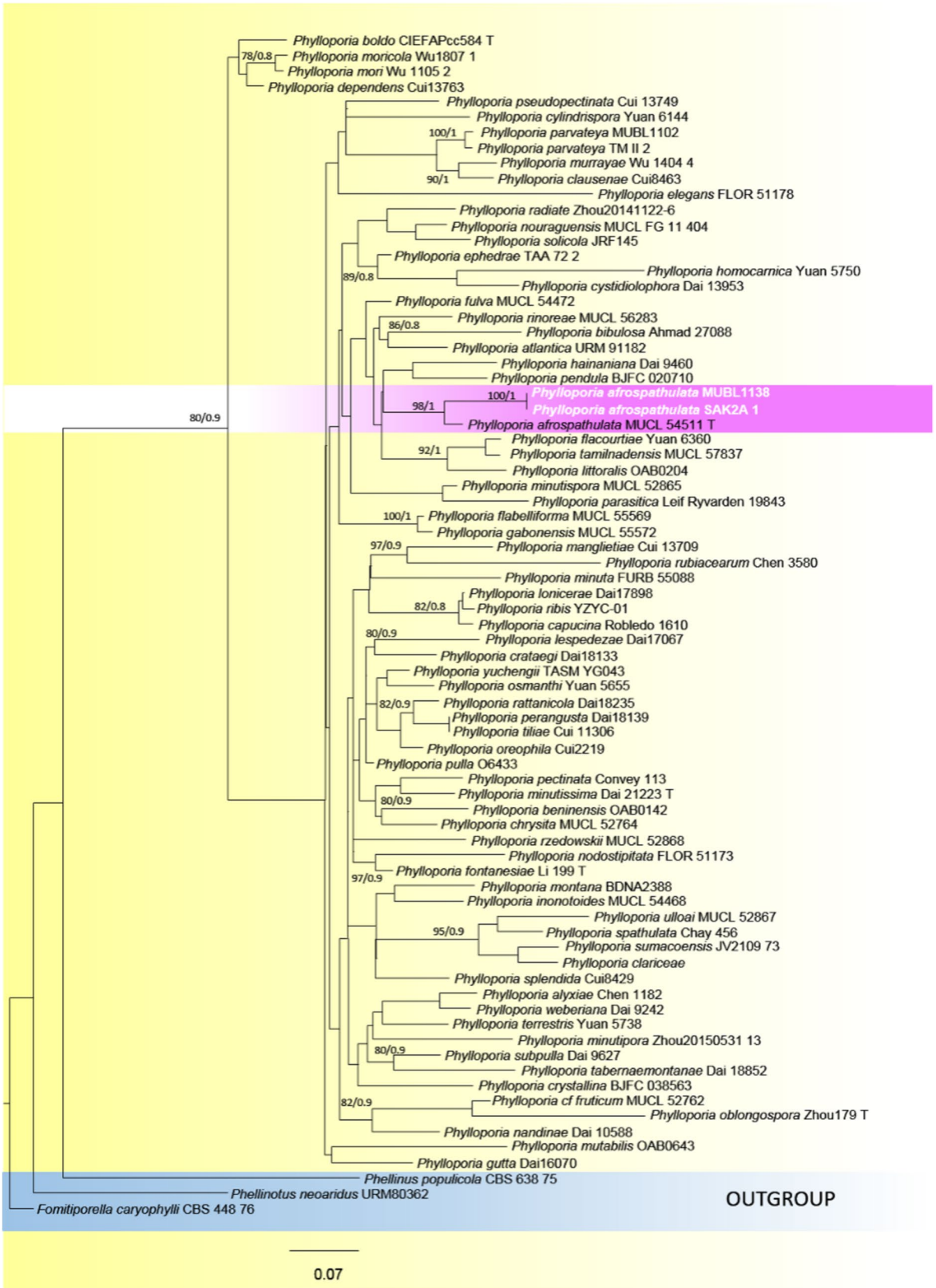
Hysterangiales K. Hosaka & Castellano.

Notes: Hysterangiales K. Hosaka & Castellano is an order of mostly hypogeous, entirely sequestrate fungi described by Hosaka et al. (2006). The Hysterangiales have an almost cosmopolitan distribution and is allied with the Phallales E. Fisch. and Gomphales Jülich (Hosaka et al. 2006). Hysterangiales contains two suborders, the saprotrophic Phallogastrinae Castellano, T. Lebel, Davoodian & K. Hosaka and the ectomycorrhizal Hysteranginae Castellano, T. Lebel, Davoodian & K. Hosaka (Davoodian et al. 2021). The former contains the family Phallogastraceae Castellano, T. Lebel, Davoodian & K. Hosaka, while the latter contains the families Gallaceaceae Locq. ex. P. M. Kirk, Hysterangiaceae E. Fisch, and Mesophelliaceae (G. Cunn.) Jülich. Mycophagy across a broad range of Hysterangiales taxa by marsupials and small mammals is well-documented (e.g. Lamont et al. 1985; Claridge and May 1994).

Mesophelliaceae (G. Cunn.) Jülich.

Notes: Mesophelliaceae is a family of sequestrate, hypogeous fungi endemic to Australia and likely Papua New Guinea as well. Many Mesophelliaceae taxa are known food sources for mycophagous marsupials and rely on these animals for dispersal of spores (Lamont et al. 1985). Their ectomycorrhizal physiology is critical to nutrient cycling in Australia's ancient, nutrient poor soils. The Mesophelliaceae assist in plant regeneration after fire via established mycorrhizal networks while also providing nutrition for mycophagous mammals in post-fire environments.

Davoodian et al. (2021) identified at least 10 new genera and many novel species awaiting description, and also determined that recircumscription of *Mesophellia* and *Chondrogaster* is required, as the current broad application of these names on herbarium specimens is not monophyletic.


Phylloporia boldo CIEFAPcc584 T
78/0.8
Phylloporia moricola Wu1807 1
Phylloporia mori Wu 1105 2
Phylloporia dependens Cui13763
Phylloporia pseudopectinata Cui 13749
Phylloporia cylindrispora Yuan 6144
100/1
Phylloporia parvateya MUBL1102
Phylloporia parvateya TM II 2
Phylloporia murrayae Wu 1404 4
90/1
Phylloporia clausenae Cui8463
Phylloporia elegans FLOR 51178
Phylloporia radiate Zhou20141122-6
Phylloporia nouraguensis MUCL FG 11 404
Phylloporia solicola JRF145
Phylloporia ephedrae TAA 72 2
89/0.8
Phylloporia homocarnica Yuan 5750
Phylloporia cystidiolophora Dai 13953
Phylloporia fulva MUCL 54472
Phylloporia rinoreae MUCL 56283
86/0.8
Phylloporia bibulosa Ahmad 27088
Phylloporia atlantica URM 91182
Phylloporia hainaniana Dai 9460
Phylloporia pendula BJFC 020710
100/1
Phylloporia afrospathulata MUBL1138
98/1
Phylloporia afrospathulata SAK2A 1
80/0.9
Phylloporia afrospathulata MUCL 54511 T
Phylloporia flacourtiae Yuan 6360
92/1
Phylloporia tamilnadensis MUCL 57837
Phylloporia littoralis OAB0204
Phylloporia minutispora MUCL 52865
Phylloporia parasitica Leif Ryvarden 19843
100/1
Phylloporia flabelliforma MUCL 55569
Phylloporia gabonensis MUCL 55572
97/0.9
Phylloporia manglietiae Cui 13709
Phylloporia rubiacearum Chen 3580
Phylloporia minuta FURB 55088
Phylloporia lonicerae Dai17898
82/0.8
Phylloporia ribis YZYC-01
Phylloporia capucina Robledo 1610
80/0.9
Phylloporia lespedezae Dai17067
Phylloporia crataegi Dai18133
Phylloporia yuchengii TASM YG043
Phylloporia osmanthi Yuan 5655
82/0.9
Phylloporia rattanicola Dai18235
Phylloporia perangusta Dai18139
Phylloporia tiliae Cui 11306
Phylloporia oreophila Cui2219
Phylloporia pulla O6433
Phylloporia pectinata Convey 113
Phylloporia minutissima Dai 21223 T
80/0.9
Phylloporia beninensis OAB0142
Phylloporia chrysita MUCL 52764
Phylloporia rzedowskii MUCL 52868
Phylloporia nodostipitata FLOR 51173
Phylloporia fontanesiae Li 199 T
97/0.9
Phylloporia montana BDNA2388
Phylloporia inonotoides MUCL 54468
Phylloporia ulloai MUCL 52867
95/0.9
Phylloporia spathulata Chay 456
Phylloporia sumacoensis JV2109 73
Phylloporia clariceae
Phylloporia splendida Cui8429
Phylloporia alyxiae Chen 1182
Phylloporia weberiana Dai 9242
Phylloporia terrestris Yuan 5738
Phylloporia minutipora Zhou20150531 13
80/0.9
Phylloporia subpulla Dai 9627
Phylloporia tabernaemontanae Dai 18852
Phylloporia crystallina BJFC 038563
82/0.9
Phylloporia cf fruticum MUCL 52762
Phylloporia oblongospora Zhou179 T
Phylloporia nandinae Dai 10588
Phylloporia mutabilis OAB0643
Phylloporia gutta Dai16070
Phellinus populicola CBS 638 75
Phellinotus neoaridus URM80362
Fomitiporella caryophylli CBS 448 76
OUTGROUP
0.07

◂**Fig. 127** Phylogenetic tree inferred from the combined ITS and nrLSU sequence alignments. The ITS and nrLSU sequences were aligned separately in MEGA X v10.0.2 and edited manually to increase the similarity of the alignment (Kumar et al. 2018) and the same was used for the Maximum Likelihood (ML) analysis and Bayesian Posterior Probability (BPP) analysis using raxmlGUI 2.0 (Edler et al. 2021) MrBayes 3.2.7a (Ronquist et al. 2012). Bootstrap support values for Maximum Likelihood (ML, first value) equal to or greater than 60% and Bayesian Posterior Probability (BPP, second value) equal to or greater than 0.8 are given above the nodes. The tree is rooted to *Fometiporella caryophylli* CBS 448.76. Ex-type strains are indicated with "[T]". The newly generated sequences are indicated in white and bold

Fusicastoreum R.A. Day, Davoodian, T. Lebel & Castellano, **gen. nov.**

Mycobank: MB 853778; *Facesoffungi*: FoF 17092; Figs. 130, 131, 132, 133, 134, 135, 136

Etymology: Refers to the fusoid spores, and the morphological resemblance of the basidiomata to the related genus *Castoreum* (Mesophelliaceae).

Type species: *Fusicastoreum pisiglareum* R.A. Day, Davoodian, T.W. May, T. Lebel & Castellano.

Basidiomata globose to subglobose; peridial surface brown, black or white, encrusted with roots, soil particles and debris, surface somewhat lumpy from debris to more or less even, base sometimes flattened, without conspicuous attachment or emanating hyphae. **Peridium** composed of three layers; epicutis brown to black and white, melanised, incorporating soil and debris and occasionally plant roots; mesocutis off-white to pale brown, occasionally staining pinkish-brown, often incorporating plant roots, plant roots appearing to be flanked by brown-colored filaments; subcutis the thinnest of the three layers and colored deep brown to black. **Gleba** pale yellow-beige to sienna in color, locules spherical to sinuous during development, becoming elongate at maturity and powdery. **Trama** narrow, pale cream strands in young basidiomata, indistinct in mature basidiomata. **Odor** camphor or naphthalene, occasionally fungoid, sweet, or acetone.

Epicutis dark brown, nearly opaque; occasionally incorporating soil particles; of hardened, melanised hyphae in a melanised matrix; hyphae, densely packed, arrangement difficult to ascertain given degree of melanisation, though where apparent appearing as tangled hyphae, compactly woven to well-spaced, organised in rough bundles. **Mesocutis** hyaline; hyphae compactly interwoven, ± parallel to outer surface, terminal cells occasionally appearing inflated; incorporating plant roots among hyphae. Hyphal coils occasionally present. **Subcutis** of hardened, melanised hyphae; colored as epicutis above though slightly less melanised; hyphae very densely packed to loosely interwoven, arranged in variously oriented bundles to somewhat radially arranged. **Trama** hyaline to whitish; hyphae tangled.

Basidia two-spored; sterigmata inconspicuous to small. **Spores** fusoid, smooth; base truncate, apex acuminate; hyaline to faint yellow-beige in color. **Utricle** absent.

Habit and Habitat: *Fusicastoreum* is hypogeal, solitary, sometimes caespitose, scattered or in groups beneath leaf litter and up to 10–15 cm of topsoil. *Fusicastoreum* species occur in a variety of open eucalypt woodlands including young to medium age stands of *Eucalyptus sieberii* [SAY (Stand Age Young) = 5–15yrs; SAM (Stand Age Mature) = 20–30yrs], mallee eucalypt (Kangaroo Island, South Australia), *Eucalyptus globulus* (Tasmania), *Eucalyptus diversicolor* and *Eucalyptus marginata* (Western Australia).

Notes: In reporting results of a study of ectomycorrhizal fungi on rehabilitated bauxite mines in the Jarrahdale region of Western Australia, Gardner and Malajczuk (1988) listed "*Castoreum camphoratum* Trappe & Malajczuk sp. nov." without further information. This designation was also used by Hilton (1989). Dell et al. (1990) described in some detail the morphology of mycorrhizal associations between Eucalypts and certain sequestrate fungi, including "*Castorium* [sic] *camphoratum* nom. ined." Claridge et al. (2000) described the diversity of sequestrate fungi in an area of south-eastern Australia finding more than 200 species in numerous genera, amongst which 18 were undescribed. The novel genera were "tentatively" referred to by designations, one of which was "*Fusicastoreum*" which was listed as containing one novel species (un-named). Consequently, various collections in Australian fungaria are labelled as either "*Castoreum camphoratum*", "*Fusicastoreum*" sp. or "*Fusicastoreum camphoratum*". None of these fungarium names were validly published, as they lacked a description or a diagnosis and citation of a type specimen.

A recent phylogenetic study of the Hysterangiales by Davoodian et al. (2021) distinguished approximately 30 novels but un-named genera worldwide. In this study, specimens from three collections labelled as "*Castoreum camphoratum*" and one labelled "*Castoreum* sp." fell within a novel genus designated as provisional genus 3; two further "*Castoreum* sp." collections from New South Wales fell within the sister clade of provisional genus 26. Following examination of additional fungarium collections from a broader geographic area, and subsequent analyses of morphology and molecular data, provisional genus 26 was found to sit within a clade that we formally recognize as *Fusicastoreum* gen. nov. This new genus incorporates collections originally placed under the provisional genera 3 and 26.

Fusicastoreum can be distinguished from the genus *Castoreum* by the lack of gummy hyphae within the peridium, the lack of a robust basal rhizoid (which is often present in *Castoreum*), generally smaller basidiomata, a strong odor (of

Fig. 128 ***Tropicoporus linteus*** (MUBL1137). **a** Basidiomata. **b** Pore surface. **c** Tramal hyphae. **d** Skeletal hyphae. **e** Contextual hyphae. **f** Cystidiole. **g** Hymenial setae. **h** Basidioles. **i** Basidia. **j** Basidiospores. Scale bars: **c**–**j** = 5 µm

naphthalene or camphor), and fusoid, smooth spores lacking an utricle.

Key to the species of *Fusicastoreum*

1: Mesocutis 240–450 µm thick; peridium even in thickness and arrangement surrounding gleba; occurring on Kangaroo Island, South Australia.—*F. arenarium.*
1: Mesocutis 400–1500 µm thick; peridium uneven in thickness surrounding gleba; occurring in other regions of Australia.—**2.**
2: Mesocutis containing hyphal coils towards interior; mean spore length 10.8 µm; occurring in southern Western Australia.—*F. occidentale.*
2: Mesocutis without hyphal coils; mean spore length > 11.5 µm; occurring in southeastern Australia.—**3.**
3: Mean spore length 11.6 µm; peridium distinctly wavy in cross section; subcutis 60–90 µm thick; glebal locules spherical to sinuous when young.—*F. pisiglareum.*
3: Mean spore length 12.1 µm; peridium somewhat wavy; subcutis 30–50 µm thick; glebal locules appearing as wavy, elongate, recessed striae radiating from gleba center.—*F. trappei.*

Fusicastoreum arenarium R.A. Day, Davoodian, T. Lebel & Castellano, **sp. nov.**

Mycobank: MB 853829; *Facesoffungi*: FoF 17137; Figs. 130b, 132c, d, 133b, 134b

Etymology: The specific epithet refers to the sandy substrate that is incorporated in the peridium of the type collection.

Holotype: MEL2389702.

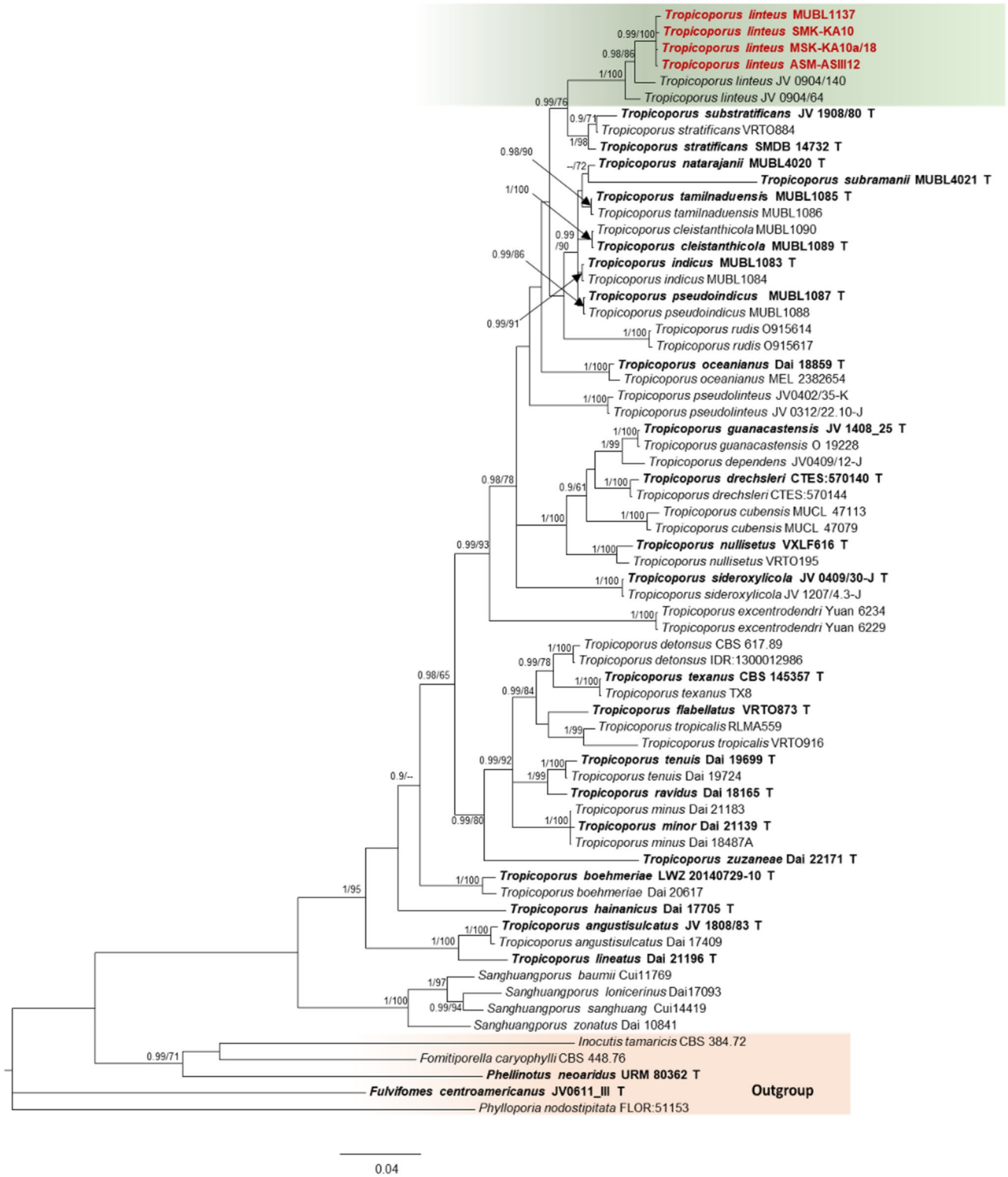


Fig. 129 Phylogenetic tree inferred from the combined ITS and LSU sequence alignments. The ITS and nLSU sequences were aligned separately in MEGA X v10.0.2 and edited manually to increase the similarity of the alignment (Kumar et al. 2018) and the same was used for the Maximum Likelihood (ML) analysis and Bayesian Posterior Probability (BPP) analysis using raxmlGUI 2.0 (Edler et al. 2021) MrBayes 3.2.7a (Ronquist et al. 2012). and Bayesian Posterior Probability (BPP, first value) equal to or greater than 0.9 and Bootstrap support values for Maximum Likelihood (ML, second value) equal to or greater than 60% are given above the nodes. The tree is rooted to *Fometiporella caryophylli* CBS 448.76. Ex-type strains are indicated with "[T]". The newly generated sequences are indicated in red and bold

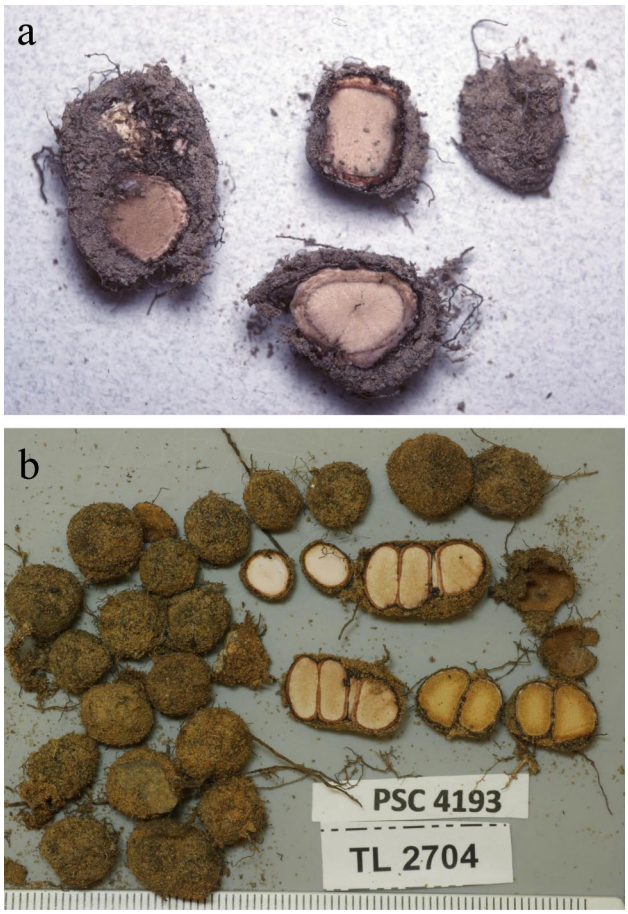


Fig. 130 Basidiomata of *Fusicastoreum* spp. showing pinkish-brown staining of mesocutis. **a** gleba and peridium of mature basidiomata *F. pisiglareum* (MEL2063469). **b** gleba and peridium of immature basidiomata *F. arenarium* (MEL2389702, **holotype**). Scale = 1 mm. Credit: Teresa Lebel (**a**), David Catcheside (**b**)

Basidiomata subglobose, 8–11 mm wide × 6–8 mm tall; peridial surface brown, surface ± even; encrusted with soil particles and debris up to 1 mm thick (multiple layers of soil and debris apparent); base slightly flattened, no conspicuous point of attachment, carbonised layer beneath soil debris. **Peridium in cross-section** even in width and arrangement around spherical gleba; three-layered; epicutis dark brown to black; mesocutis slightly thicker than epicutis, off-white, staining pinkish brown, incorporating plant roots; subcutis dark brown, pigmentation gradually paler towards mesocutis. **Gleba** initially white and finely loculate in appearance, locules eventually developing into meandering hollow tubes; large fissures emerging with maturity and segregating gleba into large sections; maturing spore mass becoming powdery and pale sandy brown to tan brown sienna in color; overall ± round in gross cross-section. **Trama** white, narrow strands. **Odor** strongly naphthalene/acetone-like.

Epicutis 100–170 µm thick; deep brown, melanised; rough, irregular texture, incorporating soil particles; hyphae compactly interwoven, 3–5 µm wide, appearing tangled. **Mesocutis** 240–450 µm thick, hyaline; hyphae interwoven, 4–7 µm wide. **Subcutis** 70–90 µm thick, dark brown; grading to more transparent towards mesocutis; hyphae interwoven, 10–25 µm wide. **Trama** hyaline; hyphae tangled, ± 4 µm wide. **Basidia** not observed. **Spores** fusoid, smooth, 9–11.1–13 × 3.5–3.9–4 µm, Q = 2.20–2.89–3.73; base truncate, apex acuminate; hyaline to faint yellow-beige in color. **Utricle** absent.

Habitat and Habit: *Fusicastoreum arenarium* has a sequestrate, hypogeous habit and is solitary or sometimes caespitose, found scattered or in groups beneath leaf litter and 10–15 cm of topsoil. Presumed ectomycorrhizal with *Eucalyptus* spp. Associated with mallee *Eucalyptus* and *Acacia* dominated vegetation in mineral/sandy soil.

Material examined: AUSTRALIA, South Australia, Kangaroo Island, Ravine des Casoars, site 2, between old and new car parks, on roadside, -35°57′ 136°42', 22 Jun 2015, *D. Catcheside, T. Lebel*, *Lebel 2704* (MEL2389702, **holotype**).

GenBank: MEL2389702: PP723091 (LSU), MW417408 (*atp6*), MW302241 (*tef1*).

Notes: Known from a single collection of several basidiomata. This taxon has not been recollected in spite of extensive searching for sequestrate fungi over 20 years on Kangaroo Island and the Fleurieux Peninsula (P. Catcheside pers. comm.).

Fusicastoreum arenarium differs from other species of *Fusicastoreum* by its peridium, which is even in thickness and arrangement where other species have a peridium varying in thickness with a wavy arrangement. *Fusicastoreum arenarium* also has a thinner mesocutis (< 450 µm as opposed to up to 400–1500 µm).

Fusicastoreum occidentale R.A. Day, Davoodian, T.W. May, T. Lebel & Castellano, **sp. nov.**

Mycobank: MB 853837; *Facesoffungi*: FoF 17138; Figs. 131d, 132g, h, 133d, 134d

Etymology: The specific epithet refers to the Western Australian distribution of the collections, relative to other members of *Fusicastoreum*.

Holotype: PERTH08563969.

Basidiomata sequestrate, subglobose, 8–16 mm wide × 8 mm tall; peridial surface deep brown to black; encrusted with soil particles and debris; somewhat more flattened at the base, no conspicuous point of attachment. **Peridium in cross-section** slightly wavy; three-layered; epicutis pigmented dark brown; mesocutis is the thickest layer of the three, white to fawn, incorporating plant roots, bruising pink; subcutis layer thinnest of the layers, dark brown in color. **Gleba** fawn to sandy brown in color; elliptical in gross cross-section in juvenile basidiomata. **Glebal locules** elongate, cylindrical, radiating from gleba

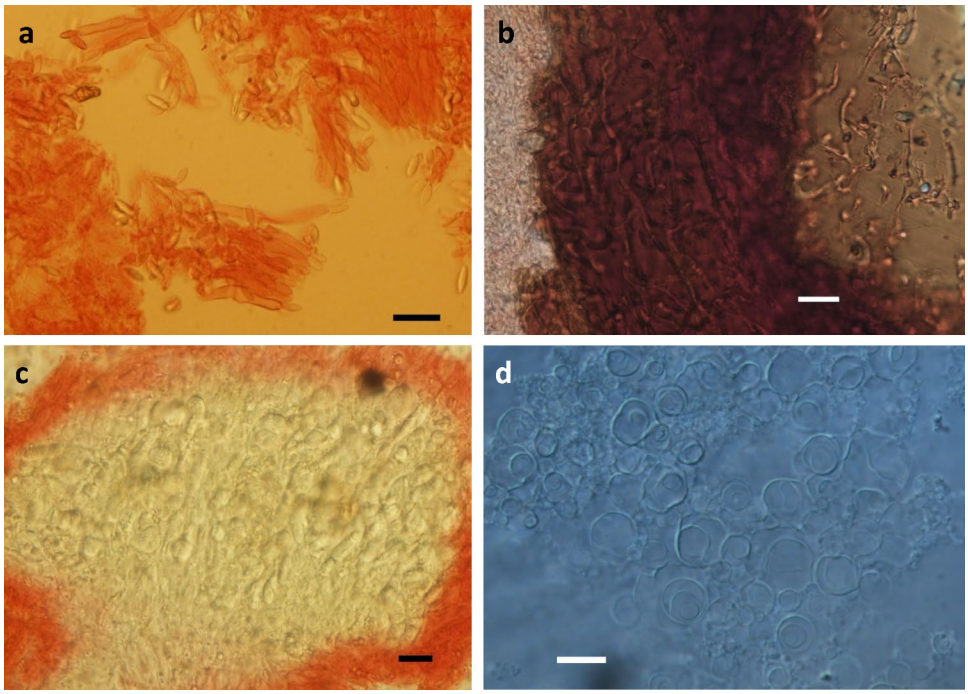


Fig. 131 Selected microscopic characters of *Fusicastoreum* in 5% KOH. **a** Basidia and spores of *F. pisiglareum* stained with Congo Red, MEL2063469. **b** Epicutis cross-section of *F. trappei*, showing melanised hyphae, MEL2063470. **c** Inflated mesocutis cells of *F. pisiglareum* stained with Congo Red, MEL2238635 (**holotype**). **d** Hyphal coils in mesocutis of *F. occidentale*, PERTH07634390. Scale bars: **a, b, c** = 20 µm, **d** = 10 µm. Credit: Rory Day (**a, c**), Teresa Lebel (**b, d**)

center. **Columella** not seen. **Trama** not observed. **Odor** sweet camphor.

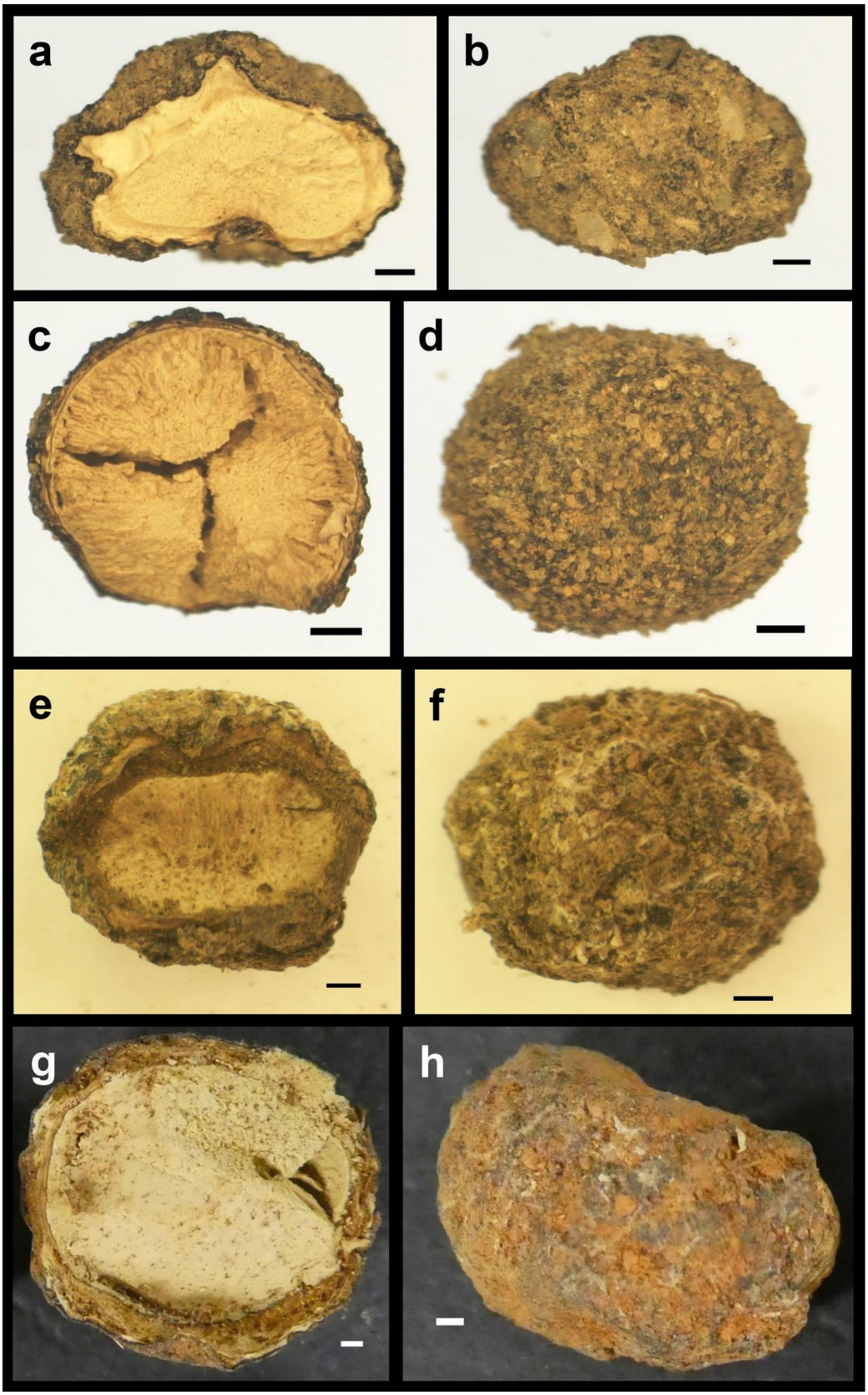
Epicutis 100–350 µm thick; very dark brown, nearly opaque; somewhat uneven across peridium; occasionally incorporating soil particles; of well-spaced hyphae 3–5 µm wide, embedded in a melanised and hardened matrix, hyphae often obscured due to intensity of melanisation, matrix possibly formerly gelatinized before hardening. **Mesocutis** 400–1250 µm thick, hyaline; hyphae tightly interwoven, somewhat parallel to outer surface, 2–6 µm wide, becoming wider towards subcutis; some hyphal terminals inflated, 8–18 µm wide, more common towards subcutis; hyphal coils present near subcutis; incorporating plant roots among hyphae. **Subcutis** 15–90 µm thick, very dark brown; of melanised hyphae, slightly less melanised than epicutis; hyphae densely packed, arranged in variously oriented bundles, hyphae approximately 4 µm wide. **Trama** hyaline to whitish; hyphae tightly coiled and interwoven, compressed, irregular, approximately 3–6 µm wide. **Basidia** two-spored, other characters undiscernable. **Spores** fusoid, smooth, 9.0–10.8–12.5 µm × 2.5–3.6–4.5 µm, Q = 2.41–3.03–4.23; base truncate, apex acuminate; hyaline, faintly dextrinoid in Melzer's reagent. **Utricle** absent.

Habitat and Habit: *Fusicastoreum occidentale* has a hypogeous habit, with basidiomata occurring gregariously. It is presumed to be ectomycorrhizal with *Eucalyptus* spp., with collections associated with *E. marginata* and *E. diversicolor* forests. Thus far only known from Western Australia.

Material examined: AUSTRALIA, Western Australia, Winnejup, Greater Kingston National Park, -34°2′46" 116°22′51", 24 Apr 2009, *K. Zosky, WDP1337* (PERTH08563969, **holotype**); Western Australia, Boranup, Point Rd, -34°5′ 115°, 21 Jun 1989, *J. Eyres* (PERTH07658044); Western Australia Pemberton, -34°26′ 116°2', 12 Dec 1979, *N. Malajczuk* (PERTH07634390); Western Australia, Manjimup, Pine Creek Rd, -34°14′ 116°8', 1 Nov 1978, *T.S. Grove, Trappe 5535* (PERTH07552351); Western Australia, East of Dwellingup, Murray River Rd, Plavins Forest Block, -32°50′ 116°13′50", 1 Aug 1995, *B. Dunstan* (PERTH07584377); Western Australia, Manjimup, Pine Creek Rd, Site 1, -34°13′ 115°54', 26 Jun 1986, *N. Malajczuk* (PERTH07613628).

GenBank: PERTH08563969: PP626890 (ITS), PP723094 (LSU), PP736586 (*atp6*), OP572242 (*tef1*); PERTH07658044: PP723095 (LSU), OP572241 (*tef1*); PERTH07634390: PP626891, PP626892 (ITS – intragenomic variants), PP723098 (LSU), PP736588 (*atp6*), OP572240 (*tef1*); PERTH07552351: PP626889 (ITS), PP723099 (LSU), OP572236 (*tef1*); PERTH07584377: PP626888 (ITS), PP723096 (LSU), PP736587 (*atp6*), OP572237 (*tef1*); PERTH07613628: PP723097 (LSU), PP736585 (*atp6*), OP572238 (*tef1*).

Notes: In comparison to the three Eastern Australian species of *Fusicastoreum*, the Western Australian *F. occidentale* has a sweeter camphor odor rather than the stronger chemical odor of naphthalene. Collections of *F. occidentale* also displayed hyphal coils (Fig. 131d) in the mesocutis that were not seen in other species. The identification of other


a
b
c
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e
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h

◂**Fig. 132** Basidiomata cross-sections and exteriors of *Fusicastoreum* spp. **a, b** *F. pisiglareum* (MEL2063469). **a** Basidiomata cross-section. **b** Basidiomata exterior. **c, d** *F. arenarium* (MEL2389702, **holotype**). **c** Basidiomata cross-section. **d** Basidiomata exterior. **e, f** *F. trappei*, (MEL2238626). **e** Basidiomata cross-section. **f** Basidiomata exterior. **g, h** *F. occidentale* (PERTH07613628). **g** Basidiomata cross-section. **h** Basidiomata exterior. Scale bars = 1 mm. Credit: Rory Day (**a, b, c, d**), Naveed Davoodian (**e, f**), Teresa Lebel (**g, h**)

collections labelled either '*Fusicastoreum* sp.' or '*Fusicastoreum camphoratum'* accessioned in the PERTH herbarium awaits confirmation; they may likely be *F. occidentale*.

In addition to the different geographic distribution and the presence of hyphal coils in the mesocutis, *F. occidentale* has smaller spores than other species of *Fusicastoreum* (mean spore length = 10.8 µm as opposed to 11.6 µm, 11.1 µm and 12.1 µm for *F. pisiglareum*, *F. arenarium* and *F. trappei*, respectively).

Fusicastoreum pisiglareum R.A. Day, Davoodian, T.W. May, T. Lebel & Castellano, **sp. nov.**

Mycobank: MB 853779; *Facesoffungi*: FoF 17139; Figs. 130a, 131a, c, 132a, b, 133a, 134a

Etymology: The specific epithet is derived from Latin *pisi*, meaning 'pea', and *glareum* meaning 'gravel', referring to the resemblance of the basidiomata to pea gravel.

Holotype: MEL2238635.

Basidiomata irregularly subglobose to orbicular, 10–21 mm wide × 6–15 mm tall; peridial surface brown, somewhat lumpy from encrusted soil particles and debris; somewhat flattened at base, no conspicuous point of attachment. **Peridium in cross-section** wavy, of irregular thickness around radius; three-layered; epicutis dark brown to black; mesocutis thickest layer of the three, white to pale beige, staining pinkish brown, incorporating plant roots; subcutis thinnest layer, dark brown to black in color. **Gleba** breaking up into verrucae-like portions with age, beige to pale brown in color; overall subreniform in gross cross-section in juvenile basidiomata, becoming elliptical at maturity. **Glebal locules** spherical to sinuous when young, becoming deeply fissured and elongate to roundish with development; powdery. **Trama** white to pale cream narrow strands in young basidiomata. **Odor** camphor or naphthalene, occasionally fungoid or sweet.

Epicutis 120–350 µm thick, dark brown, nearly opaque; occasionally incorporating soil particles; of densely packed, hardened, melanised hyphae in a melanised matrix; hyphae 3–5 µm wide, arrangement difficult to ascertain given degree of melanisation, though where apparent appearing as tangled hyphae organised in rough bundles. **Mesocutis** 570–1500 µm thick; hyaline; hyphae densely interwoven, ± parallel to outer surface, 3.5–4.5 µm wide, some terminal cells appearing inflated, 12–15 µm wide; incorporating plant roots among hyphae. **Subcutis** 60–90 µm thick; of densely packed, hardened, melanised hyphae; colored as epicutis above though slightly less melanised; more or less radially arranged, 2.5–4.5 µm wide. Trama hyaline to whitish; hyphae somewhat bundled to tangled, 3–6 µm wide. **Basidia** two-spored, 48–54(–63) µm × 5–7 µm; sterigmata inconspicuous to small, usually < 2 µm long. **Spores** fusoid, smooth, (8.5–)10–11.6–14(–14.5) µm × 3.5–3.9–4.5 µm, Q = (2.32–)2.59–3.09–3.58(–4.19); base truncate, apex acuminate: hyaline to faint yellow-beige in color. **Utricle** absent.

Habit and Habitat: *Fusicastoreum pisiglareum* has a sequestrate, hypogeous habit, occurring solitarily or gregariously. It is presumed ectomycorrhizal with *Eucalyptus* spp. Collection MEL2063469 collected from *Eucalyptus sieberi* dominated forest. Thus far only known from southern New South Wales (Nungatta) and eastern Tasmania.

Material examined: AUSTRALIA, New South Wales, South Coast, Southern Forests district, near Bombala, Off Monaro Hwy, to north side of road, long axis more or less perpendicular to Laings Rd, c. 400 m east of SAM5, -37°9′3" 149°23′16", 03 Oct 2002, *J. Ritson, Lebel 1636* (MEL2238635, **holotype**); New South Wales, South Coast, Southern Forests district, near Bombala, off Monaro Hwy, off Laings Rd central. Near junction with Reef Rd east. c. 120 m in from roadside, -37°9′8" 149°26′20", 18 Oct 2000, *T. Lebel 330* (MEL2063470); New South Wales, Southern Forests District, roughly between Bombala and Eden, off Nungatta Creek Rd, 3.5 km from junction of Imlay Rd and Nungatta Creek Rd, site SAY 4.2 (between SAY 4 & 5), -37°9′7" 149°26′20", 15 Nov 2000, *T. Lebel, Lebel 327* (MEL 2063469); New South Wales, South Coast, Southern Forests district, roughly between Bombala and Eden, off Nungatta Rd, 3.35 km from junction with Imlay Rd, off small track to east (runs between SAY4 and SAY5), long axis more or less parallel to Nungatta Rd (SAY 5.2), -37°9′8" 149°26′30", 30 Sep 2002, *T. Lebel*, *Lebel 1440* (MEL2238627); New South Wales, South Coast, Southern Forests district, roughly between Bombala and Eden, off Nungatta Rd, 3.2 km south from junction with Imlay Rd, off small track to east (runs between SAY4 and SAY5), long axis more or less parallel to Nungatta Rd (SAY 7.5), -37°9′4" 149°26′27", 03 Oct 2002, *J. Ritson, Lebel 1628* (MEL2238637); New South Wales, South Coast, Southern Forests district, off Reef Rd West, c. 150 m from junction with Laings Rd West, east side of road, long axis runs c. parallel to Reef Rd (SAY 8.3), -37°09′11" 149°22′07", *T. Lebel, J. Zdravevski, Lebel 1901* (MEL2356170); Tasmania, South of Swansea, 02 May 1990, *M.A. Castellano, N.L. Bougher* (PERTH07672942).

GenBank: MEL2238635: PP626897 (ITS), PP723086 (LSU), MW417404 (*atp6*), MW302231 (*tef1*); MEL2063470: PP626896 (ITS), MW449877 (*atp6*), MW302233 (*tef1*); MEL2063469: PP626898 (ITS),

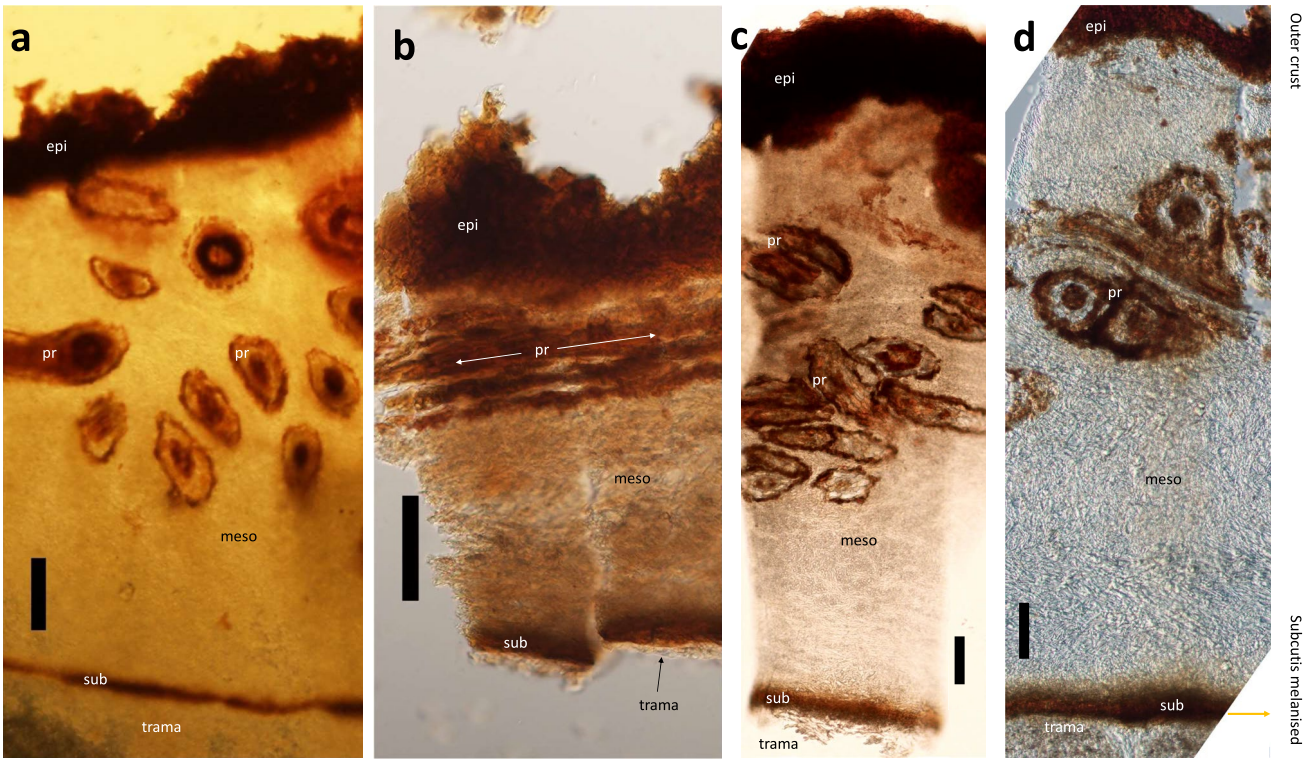


Fig. 133 Comparison of peridia of different *Fusicastoreum* spp. in 5% KOH. **a** *F. pisiglareum* (MEL2063469). **b** *F. arenarium* (MEL2389702, **holotype**). **c** *F. trappei* (OSC-M-002284, **holotype**). **d** *F. occidentale* (PERTH07613628). Epicutis, mesocutis, and subcutis labelled as 'epi', 'meso', and 'sub' respectively. Plant roots labelled as 'pr'. Scale bars: **a** = 200 µm, **b, c, d** = 100 µm. Credit: Rory Day (**a, b**), Teresa Lebel (**c, d**)

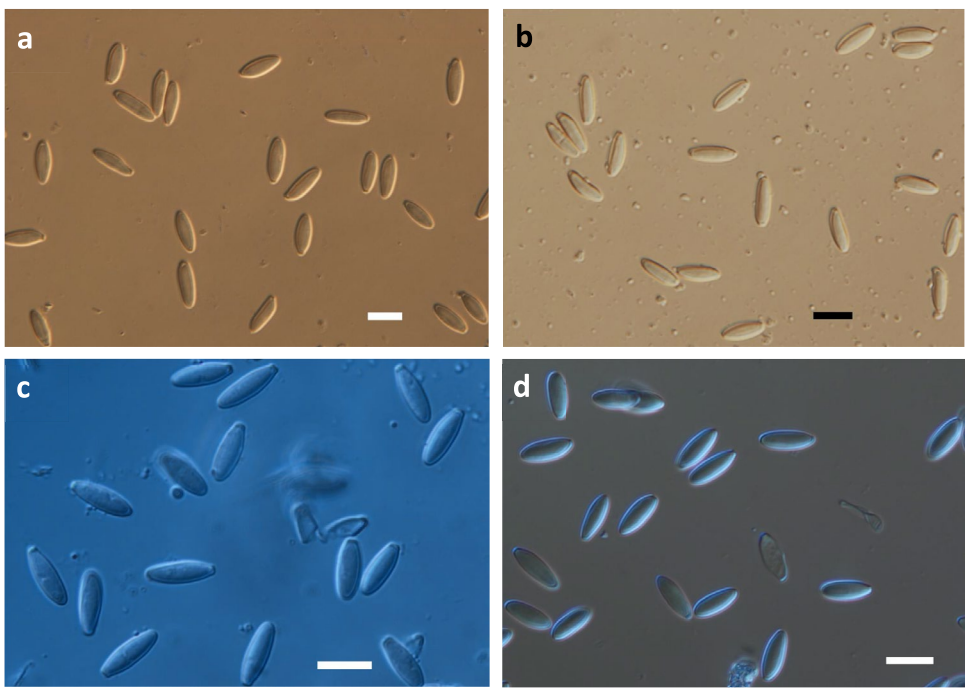


Fig. 134 Spores of different *Fusicastoreum* spp. in 5% KOH. **a** *F. pisiglareum* (MEL2238635, **holotype**). **b** *F. arenarium* (MEL2389702, **holotype**). **c** *F. trappei* (OSC-M-002284, **holotype**). **d** *F. occidentale* (PERTH08563969, **holotype**). Scale bars = 10 µm. Credit: Rory Day (**a, b**), Teresa Lebel (**c, d**)

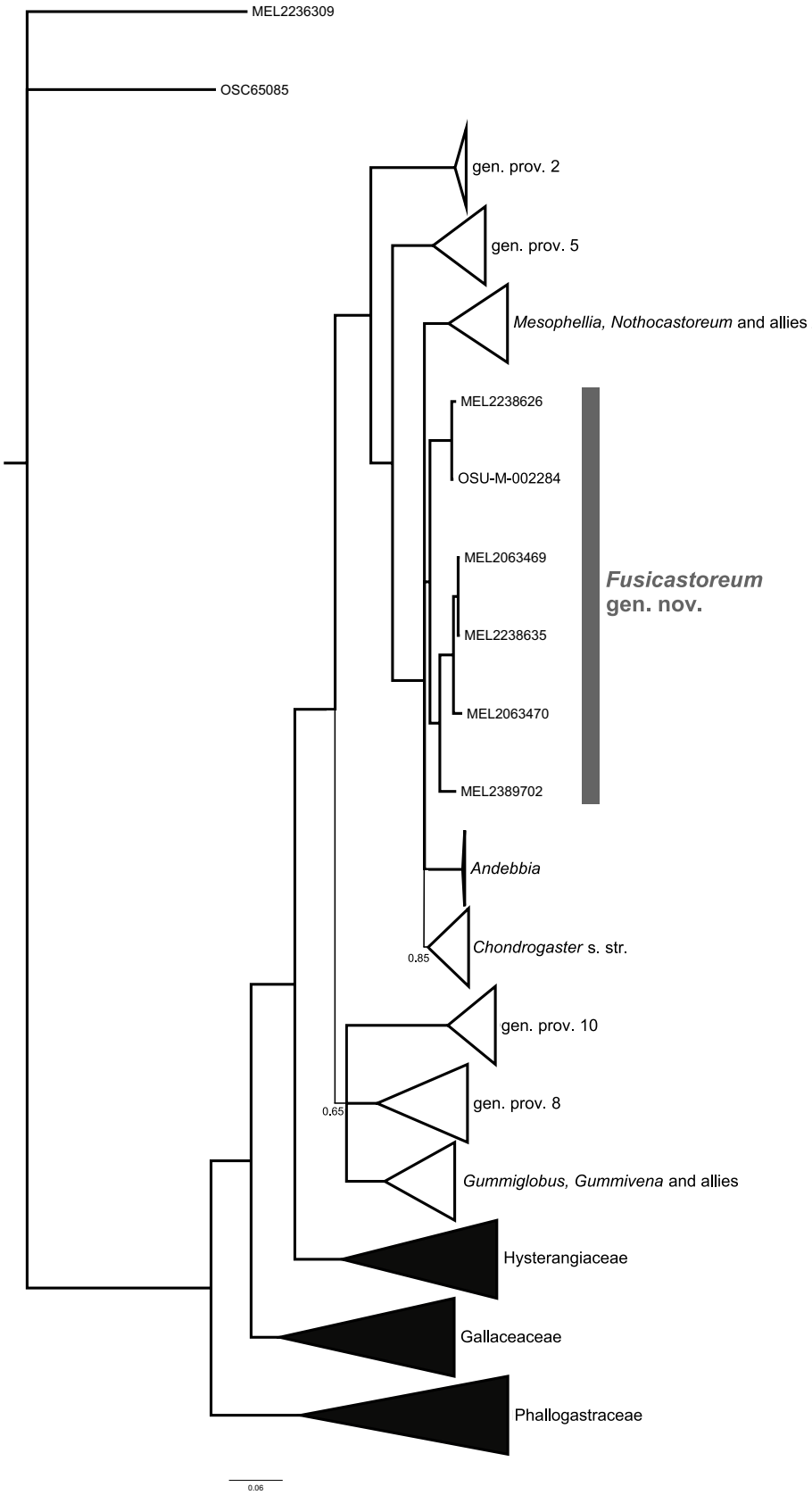


Fig. 135 Phylogram of Hysterangiales specimens produced from Bayesian inference of concatenated *atp6*, *tef1*, and LSU DNA sequences. Mesophelliaceae family expanded, showing major clades alongside *Fusicastoreum* (labelled). All nodes > 0.99 Bayesian posterior probability (bpp), otherwise labelled. Branches with > 0.95 bpp thickened. Scale bar shows substitutions per site

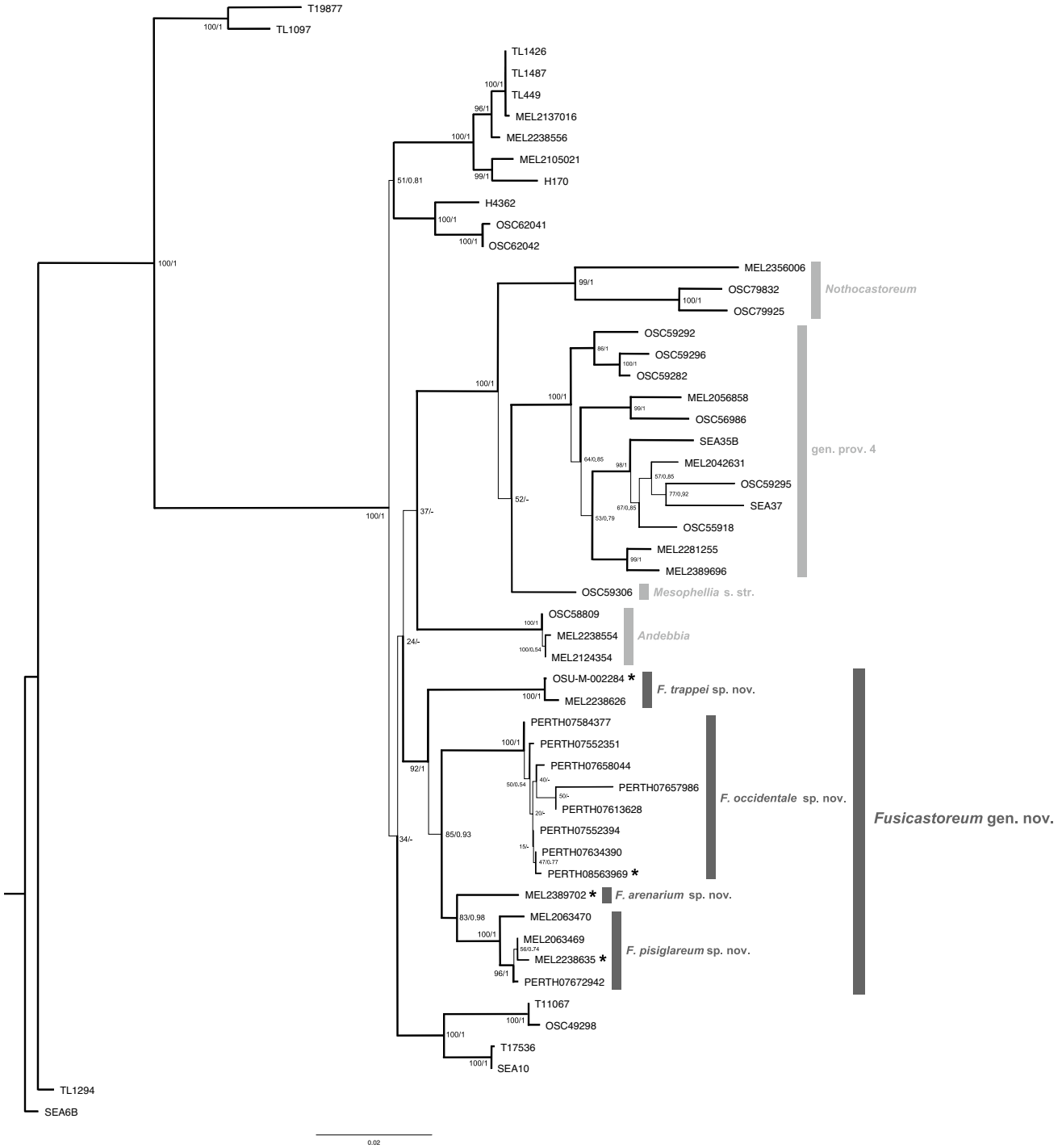


Fig. 136 Phylogram of *Fusicastoreum* and allies produced from Maximum Likelihood and Bayesian inference of *atp6*, *tef1*, and LSU DNA sequences. Maximum Likelihood (ML) bootstrap values / Bayesian posterior probabilities (bpp) labelled at nodes. Branches with > 70 ML and > 0.95 bpp thickened. Nodes with '-' for bpp were not recovered in Bayesian inference. *Fusicastoreum* and related genera are labelled sensu Davoodian et al. (2021). Scale bar shows substitutions per site. Holotypes indicated by an asterisk. *Fusicastoreum* was recovered with 92 ML and > 0.99 bpp; each species of *Fusicastoreum* represented by multiple samples was recovered with 100 ML and > 0.99 bpp

PP723087 (LSU), MW417404 (*atp6*), MW302231 (*tef1*); MEL2238627: PP723088 (LSU); MEL2238637: PP626899 (ITS), PP574415 (*tef1*), PP723089 (LSU); MEL2356170: PP723090 (LSU); PERTH07672942: PP626895 (ITS), PP736589 (*atp6*), OP379654 (*tef1*).

Notes: The holotype (MEL2238635) consists of a single, mature basidiomata, however it was thought better to stabilise the taxon on the mature rather than immature characters of other collections such as MEL2063469 (Fig. 132a, b). The collection MEL2063470 has a much wider mesocutis (1000–1500 µm thick), compared to 570–700 µm thick observed in the other available material (such as MEL2063469, MEL2238635, PERTH07672942). MEL2063470 also varies in the ITS sequence from the other two Nungatta area specimens (MEL2063469 and MEL2238635) by 1.59% (7 bases out of 440). However, the low genetic divergence and single anomalous morphological character do not warrant segregation of MEL2063470 from *F. pisiglareum*.

Fusicastoreum pisiglareum differs from other species of *Fusicastoreum* by its distinctly wavy peridium, which has a varying thickness surrounding the basidiomata. *Fusicastoreum pisiglareum* most closely resembles *F. trappei* morphologically, and occurs in the same locations. These two species differ by the thicker epicutis and subcutis in *F. pisiglareum* (120–350 µm and 60–90 µm, respectively) than in *F. trappei* (150–200 µm and 30–50 µm, respectively).

Fusicastoreum trappei R.A. Day, Davoodian, T.W. May, T. Lebel & Castellano, **sp. nov.**

Mycobank: MB 853836; *Facesoffungi*: FoF 17140; Figs. 131b, 132e, f, 133c, 134c

Etymology: The specific epithet refers to James M. Trappe of Corvallis, Oregon, preeminent truffle expert, who has made significant contributions to our understanding of the Australian truffle mycota.

Holotype: OSC-M-002284.

Basidiomata subglobose and somewhat flattened, 11 mm wide × 9 mm tall; peridial surface brown, black, and white, somewhat lumpy; encrusted with soil particles and debris; somewhat more flattened at the base, no conspicuous point of attachment. **Peridium in cross-section** slightly wavy, of irregular thickness around radius; three-layered; outermost layer dark brown; middle layer is thickest layer of the three, white to fawn, incorporating plant roots; innermost layer thinnest, dark brown in color. **Gleba** beige to sandy brown in color; elliptical in gross cross-section in juvenile basidiomata. **Glebal locules** appearing somewhat wavy, elongate, with recessed striae radiating from the gleba center. **Trama** not observed. **Odor** camphor or naphthalene.

Epicutis 150–200 µm thick, very dark brown, nearly opaque; fairly uniform across peridium; occasionally incorporating soil particles; of well-spaced, solitarily to sometimes branching hyphae 3–5 µm wide, embedded in a melanised and hardened matrix, hyphae often obscured due to intensity of melanisation, matrix possibly formerly gelatinized before hardening. **Mesocutis** 1100–1400 µm thick, of hyaline hyphae 3–4 µm wide, tightly interwoven, somewhat parallel to outer surface; some hyphae inflated, 7–10 µm wide, inflated hyphae more common towards subcutis; incorporating plant roots among hyphae. **Subcutis** 30–50 µm thick, very dark brown; of melanised hyphae, though slightly less melanised than epicutis; hyphae very densely packed, arranged in variously oriented bundles, hyphae approximately 4 µm wide. **Trama** hyaline to whitish; hyphae somewhat bundled to tangled, hyphae approximately 4 µm wide. **Basidia** two-spored, 50–56–64 µm × 5.5–5.7–7 µm; sterigmata small, up to 1 µm long. **Spores** fusoid, smooth, 10.5–12.1–13.5 µm × 3.5–3.9–4.5 µm, Q = 2.51–3.07–3.81; base truncate, apex acuminate; hyaline. **Utricle** absent.

Habitat and Habit: *Fusicastoreum trappei* has a hypogeous habit and solitary basidiomata. It is likely ectomycorrhizal with *Eucalyptus* spp. Thus far only known from near Nungatta, New South Wales.

Material examined: AUSTRALIA, New South Wales, Southern Forests District, near Nungatta, off Imlay Rd, near junction with Pericoe Rd, west side of track running north of Imlay Rd. long axis more or less perpendicular to Imlay Rd, -37°8′50" 149°31′49", 27 Sep 2001, *T. Lebel, Lebel 1051* (MEL2238626); New South Wales, Bondi State Forest, Nungatta rd., 1.8 km southeast of Imlay Rd., Claridge site 24,

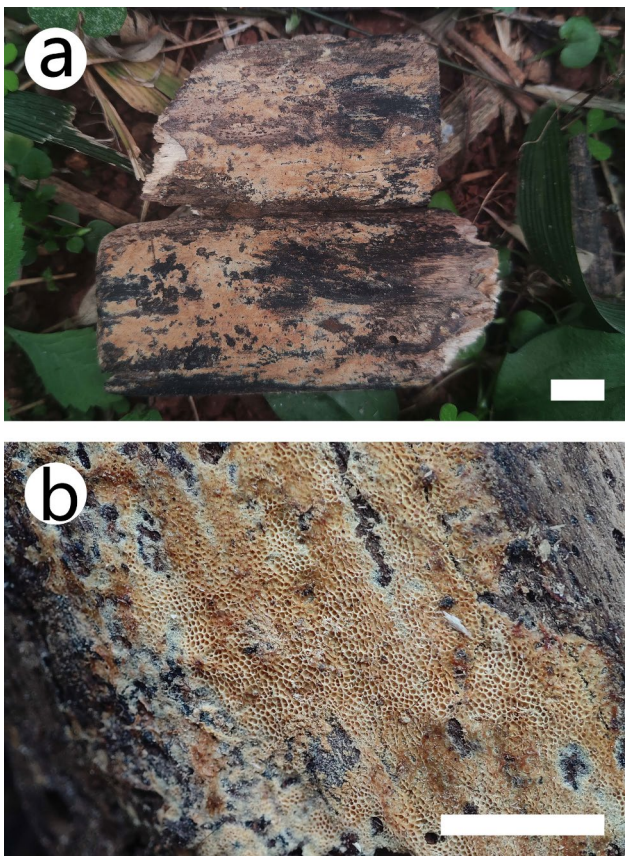


Fig. 137 Basidiomata of ***Ceriporia yunnanensis***. **a, b** CLZhao 22,387 (**holotype**). Scale bars: **a** = 1 cm, **b** = 0.5 cm

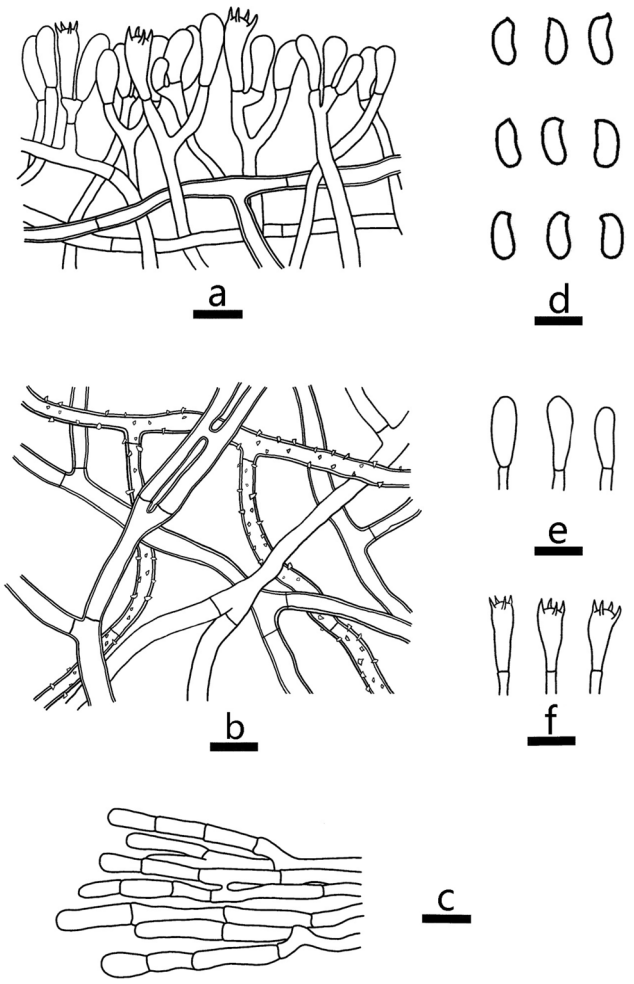


Fig. 138 Microscopic structures of ***Ceriporia yunnanensis*** (CLZhao 22,387, **holotype**). **a** Section of hymenophore trama. **b** Hyphae from context. **c** Section of hyphal ends in the basidial layer. **d** Basidiospores. **e** Basidioles. **f** Basidia. Scale bar: **a–c**, **e–f** = 10 µm, **d** = 20 µm

-37°8′51" 149°25′56", 580 m asl. 5 Jun 1996, *A. Jumpponen, Trappe 18,910* (OSC-M-002284, **holotype**).

GenBank: OSC-M-002284: PP626893 (ITS), PP723092 (LSU), MW417409 (*atp6*), MW302230 (*tef1*); MEL2238626: PP626894 (ITS), PP723093 (LSU), MW449869 (*atp6*), MW302229 (*tef1*).

Notes: Collection MEL2238626 is of immature basidiomata, clearly showing young locules in development and basidia and spores. Gross morphology of *Fusicastoreum trappei* is more similar to *F. pisiglareum* than *F. arenarium*. The OSC-M-002284 site coordinates were originally recorded as Easting 712,600 / Northing 5,899,100, likely by mistake since those are the coordinates for Claridge site 25 (Claridge et al. 2000), rather than 24 (Claridge site 25 lies north of Imlay Rd; Claridge site 24 lies south of Imlay Rd).

At least two *Fusicastoreum* species (*F. pisiglareum* and *F. trappei*) occur in the same localities in eastern Australia, with very few morphological differences ascertainable. Both species are strongly supported by molecular data (Fig. 136). A potential explanation for sympatric species that have slight differences in morphology is host specificity. Future studies examining plant root DNA sequences from basidiomata (i.e. from root matter occurring in mesocutis) may determine if different species of *Fusicastoreum* associate with different species of *Eucalyptus* or other potential ECM hosts.

Fusicastoreum trappei can be distinguished from other species of *Fusicastoreum* by its somewhat wavy peridium, eastern Australian distribution, and thin subcutis (30–50 µm as opposed to up to 90 µm in other species). It most resembles *F. pisiglareum*, but has a thinner epicutis (150–200 µm in *F. trappei* as opposed to 120–350 µm in *F. pisiglareum*) and slightly larger spores (mean spore length = 12.1 µm in *F. trappei* as opposed to 11.6 µm in *F. pisiglareum*).

Polyporales Gäum.

Notes: Polyporales is a large group of Agaricomycetes, accommodating more than 2700 species (He et al. 2019; Wu et al. 2022b; Mao et al. 2023; Wang et al. 2024b; Zhao et al. 2024b). This order includes variety of basidiomata morphologies from pileate, effused to resupinate; sessile, imbricate, flabellate to stipitate. The hymenophore differs from smooth, poroid to lamellate, daedaleoid to hydnoid. Hyphal system includes monomitic, pseudodimitic, dimitic to trimitic with basidiospores shape ranging from globose, subglobose, ellipsoid, to cylindrical, usually smooth, some with ornamentation (Cui et al. 2019; Zhou et al. 2021). The latest treatments and updated accounts of Polyporales are followed in Justo et al. (2017), He et al. (2019), and Wijayawardene et al. (2022).

Irpicaceae Spirin & Zmitr.

Notes: Irpicaceae was established by Spirin (2003), and it is a well-supported clade which currently comprises 12 genera (*Byssomerulius*, *Ceriporia*, *Cytidiella*, *Efibula*, *Emmia*, *Flavodon*, *Gloeoporus*, *Hydnopolyporus*, *Irpex*, *Leptoporus*, *Meruliopsis* and *Trametopsis*) (Justo et al. 2017; Luo et al. 2022; Wang et al. 2023b; Zhao et al. 2023b), and an additional genus *Crystallicutis* was added to subsequent study (El-Gharabawy et al. 2021). The family comprises of the corticioid species with the characters of the resupinate or pileate basidiomata, and the hyphal system is usually mono-, rarely dimitic, and the generative hyphae are usually simple-, rarely nodose-septate and basidiospores are usually thin-walled, smooth and colorless (Chen et al. 2021).

Ceriporia Donk.

Notes: The genus *Ceriporia* was established by Donk (1933) with *Polyporus viridans* Berk. & Broome (≡ *C. viridans* (Berk. & Broome) Donk) as the type species. It is a poroid genus composed of species that possess seasonal,

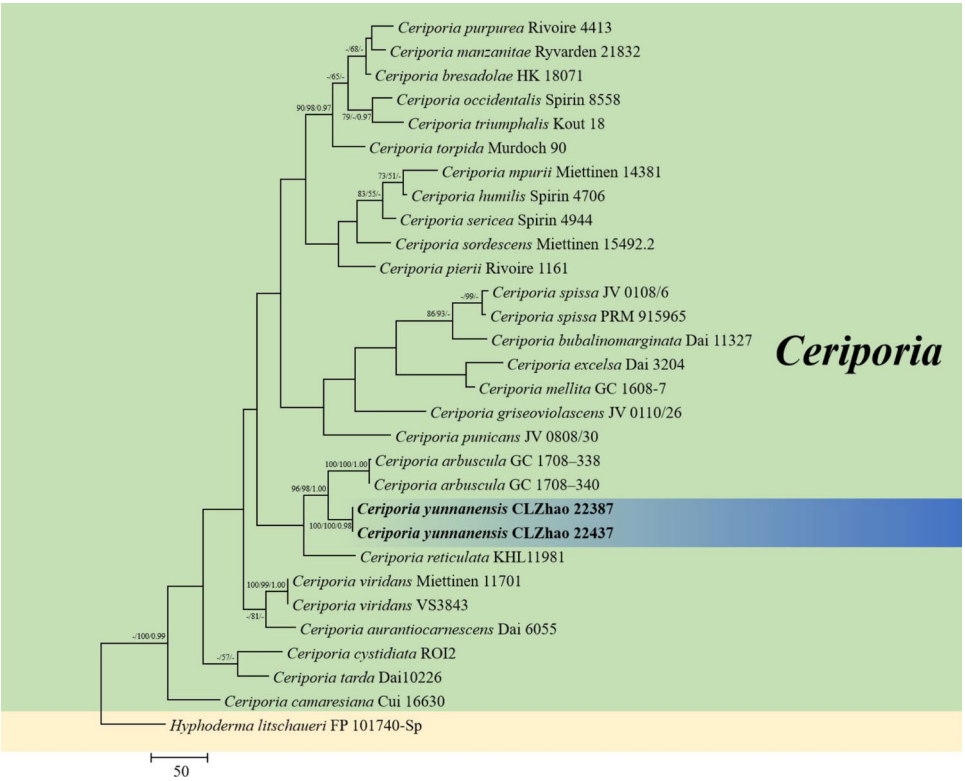


Fig. 139 Maximum Parsimony strict consensus tree illustrating the phylogeny of the new species of *Ceriporia* based on ITS sequences. Branches are labeled with Maximum Likelihood bootstrap values > 70%, parsimony bootstrap values > 50% and Bayesian posterior probabilities > 0.95. The new species are in bold

thin, and resupinate Basidiomata, which vary in color and are soft when fresh. The samples become fragile as they dry. When viewed microscopically, most species of this genus have a monomitic hyphal structure with simple septa on generative hyphae, a lack of cystidia in most species, and colorless, thin-walled basidiospores which are negative in Cotton Blue and Melzer's reagent, and cause a white rot (Gilbertson and Ryvarden 1986; Jia et al. 2014; Ryvarden and Melo 2017; Chen et al. 2020). Currently, approximately 71 *Ceriporia* species have been recorded worldwide, which includes 31 species from China (Spirin et al. 2016; Yuan et al. 2017b; Ryvarden 2018, 2020; Chen et al. 2022; Wang et al. 2023b).

Ceriporia yunnanensis Y. Yang & C.L. Zhao, **sp. nov.**

Mycobank: MB 851380; *Facesoffungi*: FoF 17141; Figs. 137, 138, 139

Etymology: refers to Yunnan Province, the locality of the type specimen.

Holotype: CLZhao 22,387 (SWFC).

Basidiomata annual, resupinate, soft when fresh, brittle when dry, up to 10 cm long, 4 cm wide, and 1 mm thick at the center. **Pore surface** cream to buff when fresh, salmon to clay-buff when dry; pores angular, 5–7 per mm; dissepiment thin, lacerate. Margin thin, flesh-pink to salmon, up to 1 mm wide. **Subiculum** salmon, fragile when dry, up to 0.1 mm thick. **Tubes** concolorous with pore surface, brittle when dry, up to 1 mm long.

Hyphal system monomitic; generative hyphae with simple septa, IKI −, CB +; tissues unchanged in KOH, hyphal ends frequently present in the basidial layer. Generative hyphae in subiculum colorless, thin- to thick-walled, frequently branched, interwoven, 2.5–4.5 µm in diameter abundant crystals. Generative hyphae in tubes colorless, thin-walled, frequently branched, subparallel along tube to loosely interwoven, 1.5–3 µm in diameter. **Cystidia** and **cystidioles** absent. **Clamp connections** absent. **Basidia** short clavate with four sterigmata and a simple basal septum, 9–16 × 2.5–5.5 µm; basidioles similar in shape to basidia, but slightly smaller. **Basidiospores** allantoid, colorless, thin-walled, smooth, IKI −, CB −, (2–)2.5–5.5(–6) × 1–3 µm, L = 4.11 µm, W = 1.95 µm, Q = 2.02–2.22 (n = 60).

Material examined: CHINA, Yunnan Province, Dali, Weishan County, Qinghua Township, Green Peacock Reserve, Jiangzui Village, 25°01′N 100°11′E, 1500 m asl, 18 July 2022, *Changlin Zhao*, **holotype** CLZhao 22,387; *Changlin Zhao*, CLZhao 22,437.

GenBank: CLZhao 22,387: OR149907 (ITS); CLZhao 22,437: OR149908 (ITS).

Notes: *Ceriporia yunnanensis* belongs to the genus *Ceriporia*, which is represented by two specimens from Dali of Yunnan Province, China, in a well-supported clade, and is phylogenetically related to *C. arbuscula* C.C. Chen & Sheng H. Wu and *C. reticulata* (Hoffm.) Domański (Fig. 139). However, there are clear morphological differences, *C. arbuscula* differs in its yellowish brown to pale brown pore

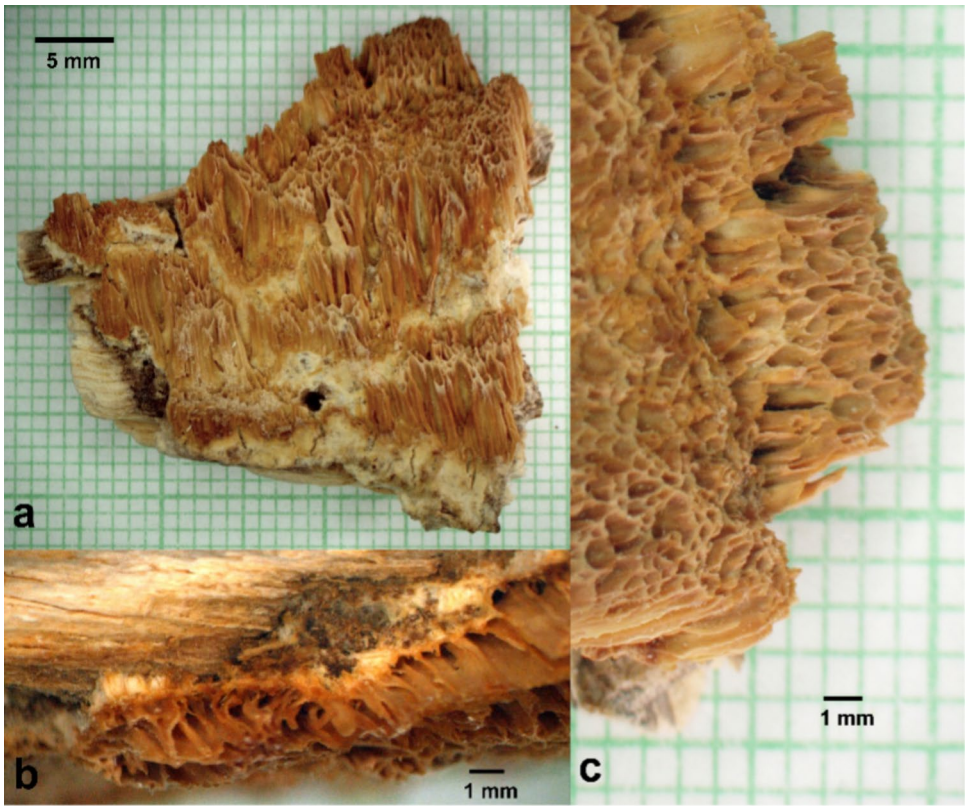


Fig. 140 Basidiomata of ***Bjerkandera meridionalis*** (BRNM 844459, **isotype**). **a** General view of basidiomata**. b** Subiculum and tubes. **c** Tubes

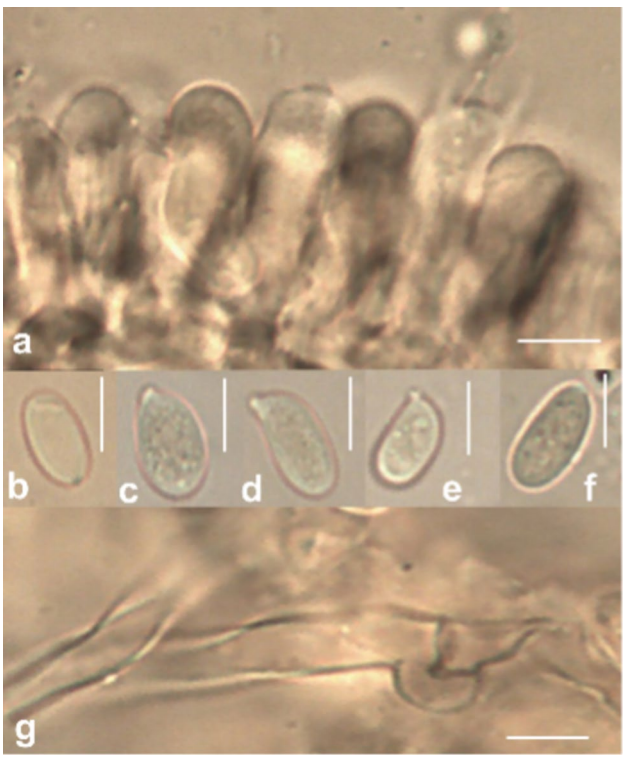


Fig. 141 ***Bjerkandera meridionalis*** (MJ 2889, **holotype**). **a** Hymenium. **b–f** basidiospores. **g** Generative hyphae**.** Scale bars: **a–g** = 5 µm

surface and cylindrical basidiospores (Chen et al. 2020). Another species *C. reticulata* is separated from *C. yunnanensis* by the white to gray pore surface, the bigger pores (3–4 per mm), and longer basidiospores (7–10 × 2.5–3.5 µm) (Pieri and Rivoire 1997).

Phanerochaetaceae Jülich.

Notes: Family includes mostly resupinate corticioid genera, but also some resupinate-pileate polyporoid or hydnaceous thats. The hyphal system is usually monomitic, rarely dimitic; the generative hyphae are simple-septate or with clamp connections. Cystidia are present or absent, and basidiospores are usually smooth, thin-walled, and colorless. According to Justo et al. (2017), the nuclear behavior of the respective genera is usually heterocytic (rarely astatocoenocytic) and the mating system is bipolar. The ecology is rather uniform, the genera include wood-decaying saprothrophs causing a white rot in most forest ecosystems (Luo et al. 2024). According to Chen et al. (2021), 23 genera are placed in Phanerochaetaceae, e.g. *Bjerkandera* P. Karst., *Donkia* Pilát, *Hapalopilus* P. Karst., *Hyphodermella* J. Erikss. & Ryvarden, *Phanerochaete* P. Karst., *Phlebiopsis* Jülich, *Pirex* Hjortstam & Ryvarden, *Porostereum* Pilát or *Terana* Adans.

Bjerkandera P. Karst.

Notes: Currently eleven species of *Bjerkandera* are recognised, type species is *B. adusta* (Willd.) P. Karst.

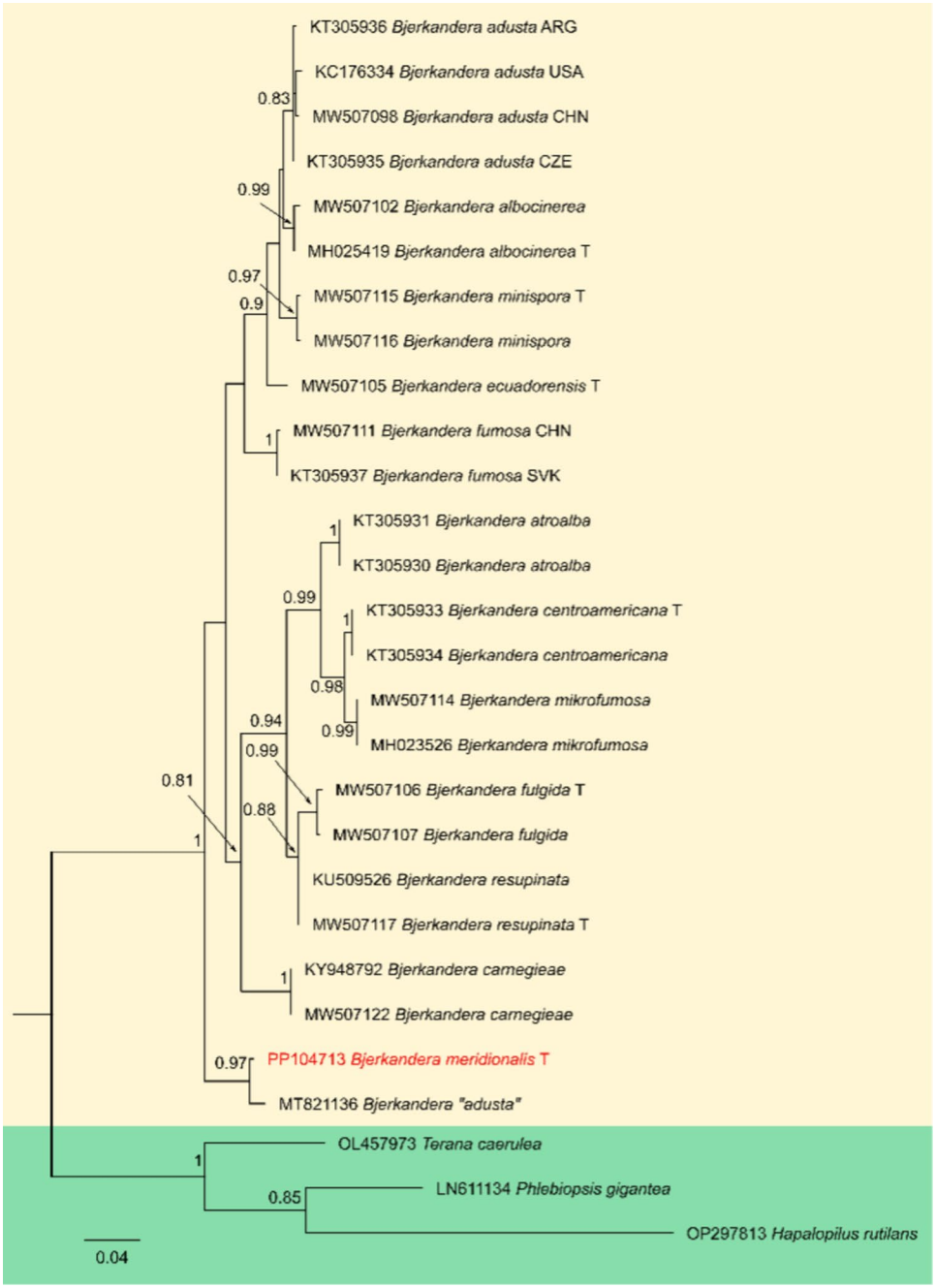


Fig. 142 Maximum Likelihood tree based on ITS sequences, bootstrap values greater than 75% are shown around nodes. The bar indicates the number of expected substitutions per position. New species is shown in red. "T" refers to a type specimen

Basidiomata are resupinate, effused to pileate, hymenophore is poroid. The pileate species are characterized with a dark line separating the tube layer from the context. Hyphal system is monomitic, generative hyphae with clamp connections, cystidia are absent, basidiospores are smooth and negative in Melzer's reagent. Wood-decaying fungi causing white rot, saprotrophs or facultative parasites on wounded or damaged trees with endophytic stage. Asexual morph Asexual morph was described as *Geotrichopsis* (Stalpers et al. 2021). Genus is distributed globally in forest biomes only *B. carnegieae* is associated with woody Cactaceae in desert areas of South West USA (Arizona) and Mexico (Robledo et al. 2021). Phylogenetic relationships of *Bjerkandera* were studied by Westphalen et al. (2015), Motato-Vásquez et al. (2020), Robledo et al. (2021) and Wang et al. (2021b).

Bjerkandera meridionalis Tomšovský, **sp. nov.**

Index Fungorum: IF 901612; *Facesoffungi*: FoF 15350; Figs. 140, 141, 142, 143

Etymology: *meridionalis* (Lat.), referring to the southern distribution in Europe.

Holotype: MJ 2889; *Isotype*: BRNM 844459.

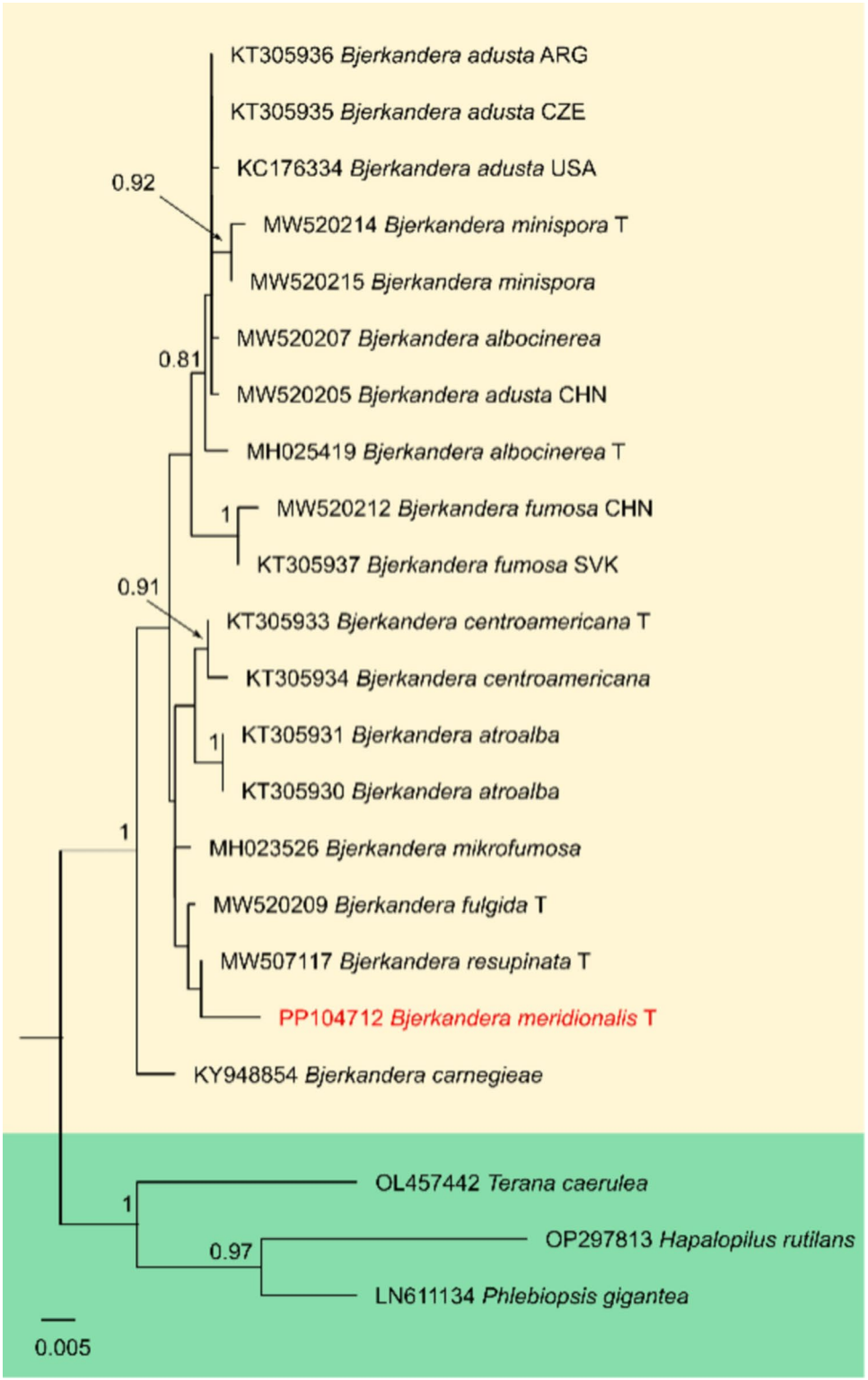


Fig. 143 Maximum Likelihood tree based on LSU sequences, bootstrap values greater than 75% are shown around nodes. The bar indicates the number of expected substitutions per position. New species is shown in red. "T" refers to a type specimen

Diagnosis: Differs from temperate *Bjerkandera* spp. by resupinate basidiomata. Similar *Bjerkandera carnegieae* and *B. resupinata* have different basidiospores and DNA sequences of ITS and LSU regions of ribosomal RNA gene.

Basidiomata. Annual, resupinate, adnate, corky, up to several cm long, 3 cm wide, 0.5 mm thick at base. Pore surface yellow ochre to yellowish brown (5C6, 5C7, 5E8) when dry, sterile margin thin pale cream (4A3); pores round to angular, 1–3 per mm; dissepiments thin, entire to lacerated.

Subiculum pale cream (4A3); up to 0.2 mm thick with a distinct contrast zone between subiculum and tubes. Tubes up to 3 mm long, concolorous with the pore surface (5C6, 5C7), becoming dark in KOH.

Spores (5.5–)5.7–6.8–8(–8.3) × (3.4–)3.5–3.8–4.2(–4.9) µm, ellipsoid, thin-walled Q = (1.49–)1.56–1.81–2.03(–2.14); negative in Melzer's reagent (n = 35). **Basidia** 14.4–21.5 × 4.6–6.5 µm, clavate, 4-spored; basidioles similar 3.3–5.1 µm wide. **Cystidia and cystidioles** absent. **Hyphal system** monomitic**,** generative hyphae with clamp connections, smooth, colorless; hyphae of subiculum thick-walled with a wide lumen, rarely branched, 3.5–4.9 µm in diam; hyphae of tubes thin- to slightly thick-walled, frequently branched, 2.3–3.6 µm in diam.

Material examined: CZECHIA, South Moravian Region, Bulhary, dead arm of the Dyje river, alluvial forest NE of the village, 10 km BW of Břeclav, *Acer campestre* – on fallen trunk, coordinates approximately 48.8348564N 16.7571736E, 170 m a.s.l., 04 May 1993, *Petr Vampola*, *P. Vampola 134/93* (MJ 2889, **holotype**; BRNM 844459, isotype).

GenBank: MJ 2889: PP104713 (ITS), PP104712 (LSU).

Notes: *Bjerkandera meridionalis* is similar to *Raduliporus aneirinus (Ceriporiopsis aneirina).* The two species differ in size of basidia and DNA sequences, while the dimensions of basidiospores and pores overlap. Other similar polypore occurring in the same habitat is *Pouzaroporia subrufa* having distinctly dimitic hyphal system. The color of *B. meridionalis* basidiomata is close to that of *B. carnegieae* but the species differ in ecology and basidiospore dimensions. The phylogenetic analyses including all currently distinguished *Bjerkandera* spp. were conducted with PhyML software (Maximum Likelihood) available at https://www.phylogeny.fr using GTR nucleotide substitution model and 100 bootstrap replicates. The results of ITS analysis (Fig. 142) indicate the basal position of *B. meridionalis* within all *Bjerkandera spp*. On the contrary, the LSU phylogram revealed proximity of the new species to *B. fulgida* and *B. resupinata* (Fig. 143). The description of *B. meridionalis* is based only on the old herbarium specimen (collected in 1993) and no fresh basidiomata of the species has been found recently in the type locality. Nevertheless, the wider distribution of *B. meridionalis* in Europe and broader spectrum of its woody hosts is confirmed by the ITS sequence (GenBank no. MT821136) from roots of *Olea europea* (cultivar Picual) in Spain. The ITS1 sequence of *B. meridionalis* matchs some records of the Global Fungi database (Větrovský et al. 2020), the species was revealed among airborne mycobiota sequences of cropland (rice field) in North Italy (Franco Ortega et al. 2020).

Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David.

Notes: The Russulales form a large, morphologically diverse order within the Agaricomycetes. It contains 12 families, with 98 genera and 4436 species, including agaricoid, discoid, clavarioid, polyporoid, corticioid and sequestrate representatives. Their ecological strategies range from mainly saprotrophic to ectomycorrhizal, plant pathogenic

Fig. 144 Basidiomata. **a, b** *Lactifluus aureoelephanti* (BRI: AQ808487 **paratype**). **c** *Lactifluus croceivillus* (BRI: AQ794270, **holotype**). Scale bars = 10 mm

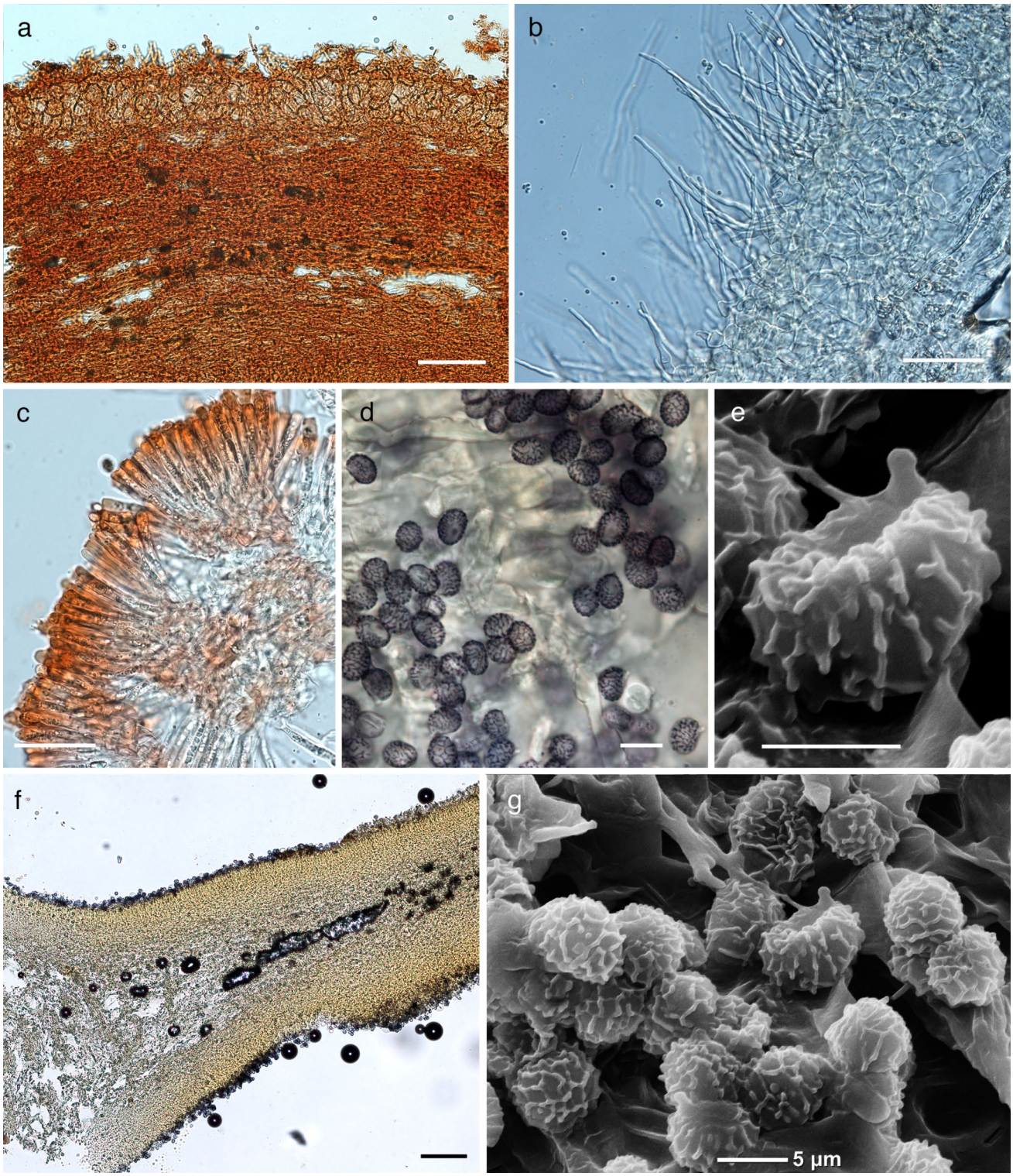


Fig. 145 ***Lactfluus aureoelephanti*** (BRI: AQ794627 **holotype**). **a** Lampropalisade pileipellis, subpellis (sp) and terminal elements (te), heteromerous context (hc). **b** Pileipellis terminal elements (te) and subpellis (sp). **c** Basidia and subhymenium. **d** Basidiospores. **e** SEM of basidiospores. **f** Hymenial trama and pleurocystidia. **g** SEM of basidiospores. Scale bars: **a–c** = 50 µm, **d** = 10 µm, **e** = 5 µm, **f** = 100 µm, **g** = 5 µm

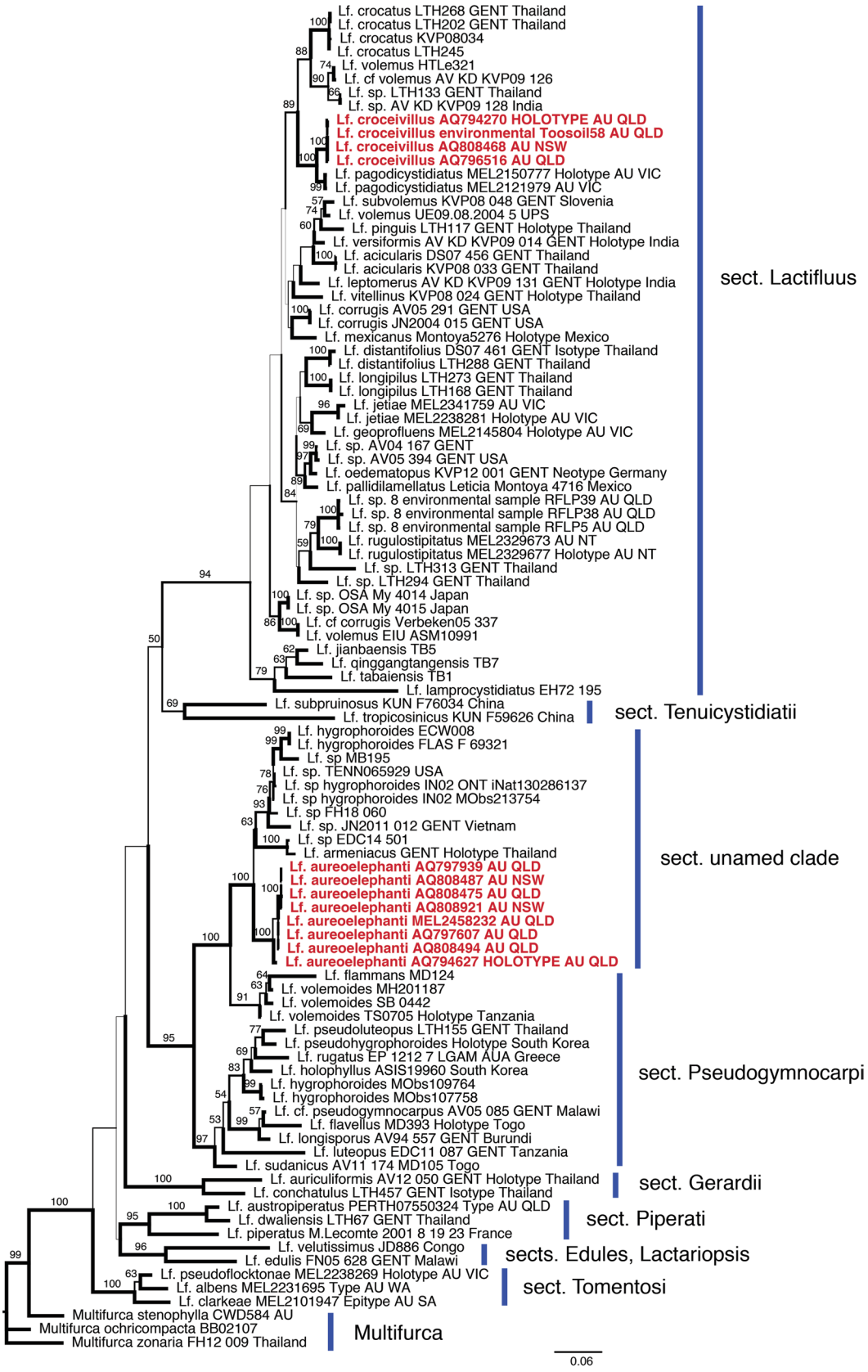
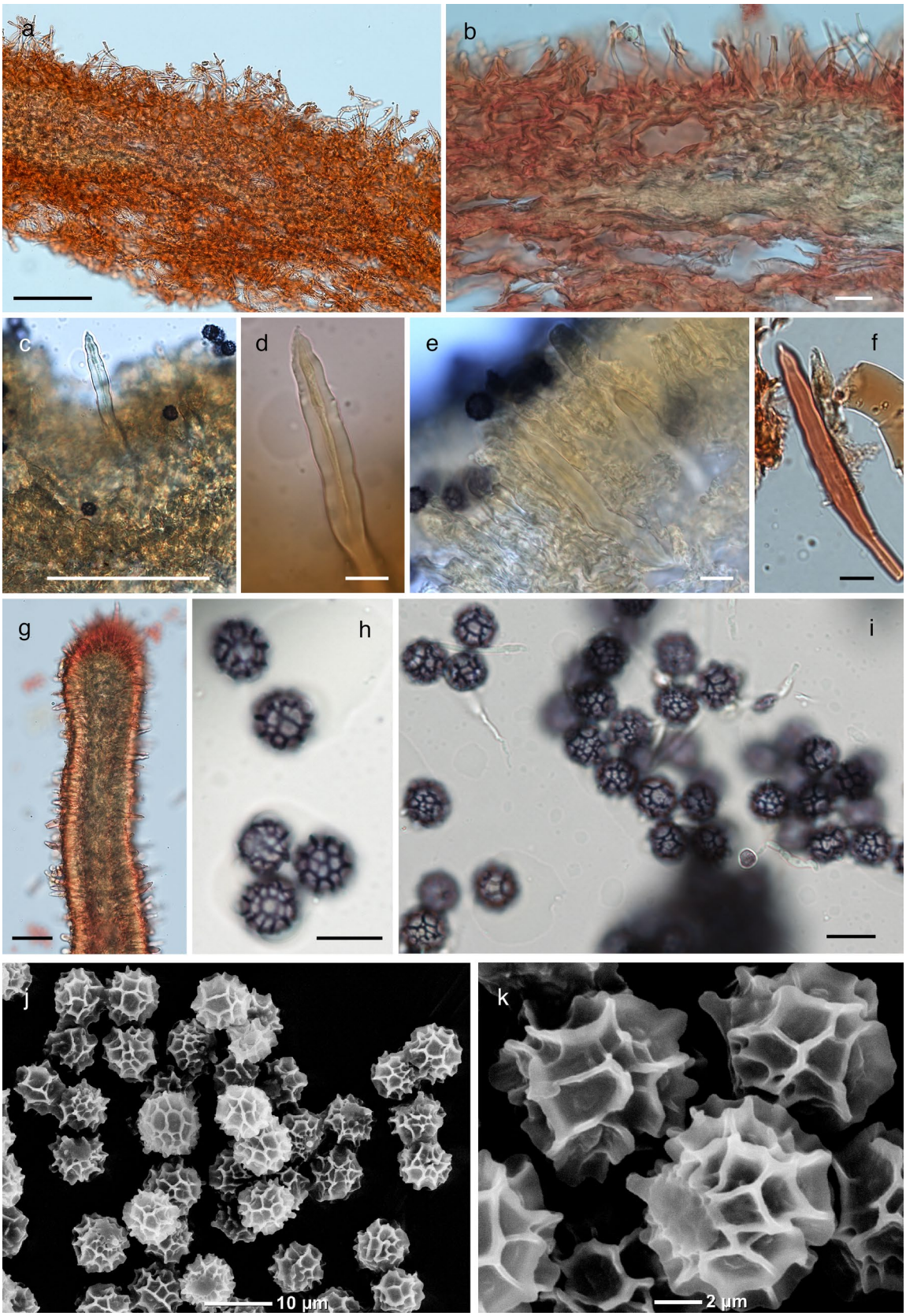


Fig. 146 Maximum Likelihood tree based on ITS and LSU sequences, bootstrap values greater than 50% are shown around nodes and bold lines indicate ML support > 90%. New species are shown in red. Sections within *Lactifluus* are indicated


a
b
c
d
e
f
g
h
i
j
10 µm
k
2 µm

◂**Fig. 147** ***Lactifluus croceivillus*** (BRI: AQ794270 **holotype**). **a** Lampropalisade pileipellis, subpellis (sp) and terminal elements (te), heteromerous context (hc). **b** Pileipellis terminal elements and subpellis (sp). **c, d** Hymenial elements and pleurocystidia. **e, f** Hymenial elements and cheilolamprocystidia. **g** Hymenium with abundant lamprocystidia. **h, i** Basidiospores. **j, k** SEM of basidiospores. Scale bars: **a**, **c** = 100 µm, **b** = 20 µm, **d–f**, **h–j** = 10 µm, **g** = 50 µm, **k** = 2 µm

and entomogenous (Hibbett et al. 2014; He et al. 2019). Molecular analyses have helped clarify the evolutionary relationships between families and genera (Larsson and Larsson 2003; Miller et al. 2006; Buyck et al. 2008; De Crop et al. 2017; Wang et al. 2018a; Vidal et al. 2019; Wu et al. 2020; Zhou et al. 2025).

Russulaceae Lotsy.

Notes: Russulaceae was established by Lotsy (1907) based on the genera *Russula* and *Lactarius* with *Russula* as the type. The family is one of the most speciose in the order, with over 4000 species represented. The four mushroom forming genera, *Lactarius*, *Lactifluus*, *Multifurca* and *Russula*, along with several nested sequestrate genera form a monophyletic ectomycorrhizal lineage arising from a small group of saprotrophic genera (Buyck et al. 2008, 2018; Vial et al. 2019).

Lactifluus (Pers.) Roussel.

Notes: The genus *Lactifluus* was separated from *Lactarius* based on multigene phylogenies of Russulaceae (Buyck et al. 2008; Verbeken and Nuytinck 2013). While *Lactifluus* is not easily distinguished from *Lactarius* by macroscopic morphology, its species tend to have thicker-walled terminal elements in the pileipellis and stipitipellis, as well as abundant sphaerocytes in hymenophoral, pileus and stipe trama tissues (Verbeken and Nuytinck 2013; De Crop et al. 2021). The majority of species are found in subtropical to tropical regions, but also in temperate areas, in a wide range of vegetation types. Basidiomata forms range from agaricoid, pleurotoid, to rarely sequestrate (Lebel et al. 2021). In the latest global molecular based classification of the genus, De Crop et al. (2017) divided *Lactifluus* into four subgenera—*Lf.* subg. *Gymnocarpi, Lf.* subg. *Lactariopsis, Lf.* subg. *Lactifluus, and Lf.* subg. *Pseudogymnocarpi*, with each subgenus further divided into four or more sections.

Lactifluus aureoelephanti T. Lebel, Nuytinck & Cooper, **sp. nov.**

Mycobank: MB 851472; *Facesoffungi*: FoF 17142; Figs. 144, 145, 146

Etymology: refers to the overall color and wrinkly, felted texture of the pileus. L = golden (aureo) elephant (elephanti).

Holotype: BRI: AQ794627.

Basidiomata gregarious or solitary. **Pileus** with deeply depressed center, even in young basidiomata, 30–75(–90) mm diam., center sienna (11; Royal Botanic Gardens Edinburgh color chart) to dark brick (20) shading to cinnamon (10) to rusty tawny orange (14) or saffron with paler margins (pale ochre (9H)) in some basidiomata, smooth to somewhat wrinkled or very finely felted, margins sometimes uplifted, irregularly; context pale cream to buff ochre, unchanging. **Lamellae** 2–6 mm deep, adnate to subdecurrent, occasionally forking, white to cream, moderately to distantly spaced, with 3–4 tiers lamellulae, colored brown where latex dries; edges concolorous and even. **Stipe** 25–40 × 8–15(–17) mm, rust (13) to sienna (11), sometimes white at apex of stipe and base, longitudinally streaked, stuffed or solid in younger material; context white. **Spore print** cream. **Latex** white drying dark brown, copious; taste mild to slightly astringent but not hot. **Odor** not distinctive. **Taste** mild. **Chemical tests**: phenol faintly violet-pink after 5–10 min; FeSO4 greenish gray slowly; KOH cuticle olive, flesh yellow.

Basidiospores (7.0–)7.5–8.95–9.0(–10.0) × 5.0–6.01–6.5(–7.0) µm, subglobose to ellipsoid Q = 1.18–1.43–1.54; ornamentation a fine partial to almost complete reticulum of low lines and a few scattered isolated elements 0.5–1.0 µm high; plage inamyloid; hilar appendix up to 2.5 µm. **Basidia** 35–53.23–58(–62) × 6–9.78–10.5(–11.5) µm, 2–5 µm wide at base, narrowly clavate to subfusiform, mostly 4-spored, sometimes 2-spored; sterigmata 2–6 × 1–3 µm; basidioles 20–41.65–47 × 6–10.11–12 µm, 3–5 µm wide at base, cylindrical to narrowly clavate. **Pleurolamprocystidia** 48–65.03–80 × 5–6.97–9 µm, 2–4 µm at base, narrow-cylindrical to narrow-subfusiform, tapering toward apex and base with widest point (5–9 µm) two thirds of the way towards apex, apex obtuse or capitate, emergent above hymenium and sometimes arising from subhymenium or hymenophoral trama, moderately abundant, outline sinuous or wavy. **Pleuropseudocystidia** 3–5.10–9 µm diam., flexuose and cylindrical to fusiform, apex obtuse, rarely emergent above hymenium, scarce. **Cheilolamprocystidia** absent. **Hymenophoral trama** consisting of interwoven hyphae 2–4 µm diam., sinuous laticiferous hyphae 2–8 µm diam., and abundant sphaerocytes 13–23.01–32 × 8–18.11–26 µm; subhymenium 15–32 µm wide, 3–5 layers of interconnected polygonal cells 6–8.21–11 × 4–6.47–9 µm, angular to irregular, thin-walled. **Pileipellis** a lampropalisade; subpellis 48–75(–85) µm wide, composed of 3–5 tiers of closely interconnected rounded, angular, or elongated thick-walled polygonal cells (9–) 14–19.40–28 × (7–)11–15.68–23 µm; terminal elements 28–34.79–50(–65) × 3–11.86–5.5(–8) µm, 2–5 µm wide at base, narrow-subcylindrical to fusiform or narrowly clavate, apex obtuse or acuminate, thick-walled; pileus trama consisting of interwoven hyphae 2–4 µm diam., abundant laticiferous hyphae 2–8 µm diam., and rare sphaerocytes 11–30 × 8–24 µm.

Material examined: AUSTRALIA, Queensland, Mt Tambourine National Park, Palm Groves Track, in Eucalyptus forest, 1 Mar. 2009, *K. Querengasser, M. Prance, R. Thomson* (BRI: AQ794627, **holotype**); Great Sandy National Park, Cooloola, Freshwater Rd, growing in association with *Melaleuca* and *Eucalyptus* sp., 23 May 2011, *R.E. Halling, T. Baroni, N.A. Fechner REH 9539* (BRI: AQ797939); Great Sandy National Park, Fraser Island, Pile Valley Walking Track, 12 Feb. 2009, *N. Fechner 12,209–26* (BRI: AQ797607); Wide Bay District, Dilkusha Nature Refuge, Maleny, Hoya Track, under Eucalyptus and regenerating subtropical rainforest understorey, 22 Mar. 2018, *F.E. Guard FG2018031* (MEL 2458232); Taromeo, Playstowe Rd, 21 May 1989, *A. Young & D. Young 1457* (BRI: AQ 808494); D'Aguilar National Park, Mount Mee, 3 Mar. 1990, *A. Young 1525* (BRI: AQ808475); New South Wales, Watagan National Park, in Eucalyptus woodland, 11 Apr. 1983, *A. Young 731* (BRI: AQ808921); Watagan National Park, in Eucalyptus woodland, 11 Apr. 1983, *A. Young* (BRI: AQ808487).

GenBank: BRI AQ797939: PP028773 (ITS), MW128164 (LSU); BRI AQ794627: MW134821 (ITS), MW128166 (LSU); BRI AQ797607: PP028774 (ITS), PP028766 (LSU); MEL2458232: MW134820 (ITS), MW128165 (LSU); BRI AQ808475: PP028775 (ITS), PP028767 (LSU); BRI AQ808921: PP028776 (ITS), PP028768 (LSU); BRI AQ808487: PP028777 (ITS), PP028769 (LSU); BRI AQ 808494: PP028778 (ITS), PP028770 (LSU).

Notes: *Lactifluus aureoelephanti* falls within a broader clade with *Lf. armeniacus* from Thailand, *Lf. volemoides* from Tanzania, *Lf. flammans* from Togo, and singleton sequences from Vietnam and multiple sequences from the USA, forming a potential new section within subg. *Pseudogymnocarpi* (Fig. 146). A description and photograph of basidiomata was provided in Lebel et al. (2021) as "*Lf.* sp7", but no microscopic characters were described nor figures included. A further two collections are added here, expanding the known distribution into northern New South Wales.

The pileus surface of *Lf. armeniacus* is also wrinkled, with an undulate margin and pruinose texture, and thus similar in morphology to *Lf. aureoelephanti* (Fig. 144a, b). The pileus is more orange-yellow tinged than *Lf. croceivillus*, the lamellae white to cream rather than tinged orange, and the spore ornamentation a fine low (0.5–1 µm high) partial to almost complete reticulum rather than robust (1.5–2 µm high) reticulum. Pileipellis terminal element turf is not as dense and hymenial cystidia scarcer than in many other Australian orangeish *Lactifluus clarkeae* complex species. *Lf. aureoelephanti* is associated with *Eucalyptus* and *Melaleuca* spp. dominated vegetation in open woodland, with an understorey of scattered *Allocasuarina* spp and *Leptospermum* spp or sometimes regenerating subtropical rainforest in southern QLD and northern NSW.

Lactifluus croceivillus T. Lebel, Nuytinck & Cooper, **sp. nov.**

Mycobank: MB 851473; *Facesoffungi*: FoF 17143; Figs. 144, 146, 147

Etymology: refers to the saffron color and velvety texture of the pileus. L = saffron (croceus), velvety (villus).

Holotype: BRI: AQ794270.

Basidiomata gregarious or solitary. **Pileus** 35–70(–110) mm diam., plano-convex becoming depressed on the disc, then with uplifted margin, dry, matte to very finely subvelutinous, dark brown to dark reddish brown brick (20), becoming saffron brown to reddish orange, cracking/ coarsely areolate with age and drying in situ, with margin incurved to decurved, rarely with a circumferential ridge and somewhat rugulose to subcorrugate; context pale creamy white (4A3), staining pale brownish. **Lamellae** 3–7 mm deep, broadly adnate to nearly subdecurrent, crowded, light yellow (F6 to 8G) to light orange (5A5) at first, paler with age, staining brown from latex. **Stipe** 30–45(–60) × 10–25 mm, equal to tapered toward base, dry, matte, sometimes with a hoary aspect, dark brown to dark reddish brown, to pale brownish orange, white at base, with interior as in pileus. Extremely tough textured. **Spore print** not observed. **Latex** white, copious, staining tissues brown. **Taste** mild. **Odor** very slightly fishy-prawn with age. **Chemical tests:** FeSO4 rapidly gray green on cap; phenol on context slowly wine brown.

Basidiospores 7.5–8.03–8.5 × 7.5–7.87–8.0 µm, globose to subglobose, Q = 1.01–1.05–1.09, ornamentation a robust almost complete reticulum with ridges up to 1.8 µm high, walls between ridges mostly amyloid; plage distally to completely amyloid; hilar appendix up to 2.5 µm. **Basidia** 32–50.07–59 × 8.5–10.37–12 µm, 2–5 µm wide at base, clavate to subfusiform, mostly 4-spored; sterigmata 5–7.01–8 × 2–2.60–4 µm; basidioles 18–29.15–36 × 5–8.91–11 µm, 3–4.5 µm wide at base, cylindrical to clavate. **Pleurolamprocystidia** 45–71.38–86.5 × 5–7.13–11 µm, 2–5 µm at base, thick-walled, narrow-cylindrical to narrow-subfusiform, tapering toward apex and base with widest point two thirds of the way towards apex, apex constricted or somewhat strangulated and tapering, emergent above hymenium and often arising from subhymenium or hymenophoral trama, abundant, outline sinuous or wavy. **Pleuropseudocystidia** 3–5.73–8 µm diam up to 38 µm long, flexuose and cylindrical to fusiform, apex obtuse, rarely emergent above hymenium, scarce. **Cheilolamprocystidia** 65–91.40–125 × 5–7.35–9 µm, 7–9 µm wide centrally, thick-walled, narrow cylindrical to fusiform, occasionally somewhat pagodaform and tapering toward apex in narrowing tiers, apex acuminate, distinctly emergent above basidia, abundant. **Hymenophoral trama** consisting of interwoven hyphae 2–4 µm

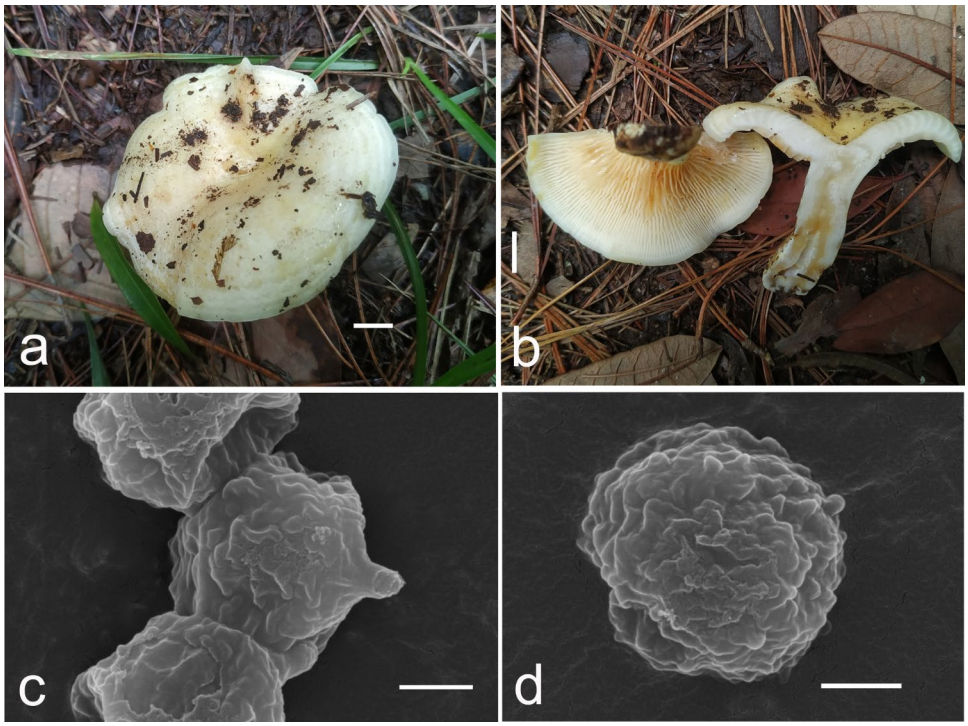


Fig. 148 *Multifurca pseudofurcata*. **a, b** Basidiomata. **c**, **d** SEM photograph of basidiospores. Scale bars: **a, b** = 1 cm, **c, d** = 1 µm

diam, laticiferous hyphae 2–8 µm diam, and sphaerocytes 12–18.71–23 × 8–14.21–20 µm; subhymenium 20–35 µm wide, 2–4 layers of interconnected polygonal cells 7–9.71–12 × 5–7.14–11 µm, angular to almost spherical. **Pileipellis** a lampropalisade; subpellis 25–50 µm wide, composed of 3–6 tiers of closely interconnected rounded, angular, or elongated thick-walled polygonal cells 18–20.50–29 × 6–11.23–12(–15) µm; terminal elements 20–43.29–65 × 2–5 µm, subcylindrical to fusiform or narrowly clavate, tapering toward apex, apex acute or obtuse, thick-walled, contents in narrow thread when present; pileus trama consisting of interwoven hyphae 2–4 µm diam, laticiferous hyphae 2–8 µm diam, and sphaerocytes 18–35 × 13–26 µm.

Material examined: AUSTRALIA, Queensland, Wide Bay District. Great Sandy National Park, Fraser Island, Cathedral Beach. Alt. 40 m., 18 May 2010, *R.E. Halling, N. Fechner, & M. Castellano REH9320* (BRI: AQ794270, **holotype**); North Maleny, Baroon Pocket Dam, Obi Obi Gorge track, 2 Oct. 2010, *P. Leonard 31,010* (BRI: AQ796516); Brisbane, Toohey Forest Conservation Park, off Nathan Ridge Track, in *Eucalyptus curtisii*, *E. planchoniana, E. microcorys, E. maculata, E. trachyphloia, E. umbra, E. henryi, E. drepanophylla, E. resinifera, E. baileyana, E. siderophloia,* Dec. 2011 (estimate)*, E.Greenway toosoil 58*. New South Wales, Watagan National Park, in *Eucalyptus* woodland, 11 Apr. 1983, *A. Young 722* (BRI: AQ808468).

GenBank: BRI: AQ794270: KR364096 (ITS), KR364228 (LSU); Toosoil 58: KC222838 (ITS); BRI AQ796516: PP028779 (ITS), PP028771 (LSU); BRI AQ808468: PP028780 (ITS), PP028772 (LSU).

Notes: *Lactifluus croceivillus* is sister to *Lf. pagodicystidiatus*, in a sub-clade within subg. *Lactifluus* with unnamed species from Thailand/India, and *Lf. crocatus* from Thailand. The stocky basidiomata of *Lf. croceivillus* and *Lf. pagodicystidiatus* are more reddish-orange-brown tinged than the yellow brown to orange-brown of *Lf. crocatus* but are otherwise very similar in shape and texture. The two species are associated with quite different vegetation, *Lf. crocatus* is found in rainforest with *Castanopsis, Lithocarpus echinops* and *Quercus*, while *Lf. croceivillus* and *Lf. pagodicystidiatus* are associated with *Eucalyptus pilularis* woodland or wet sclerophyll forest. *Lf. croceivillus* differs from *Lf. pagodicystidiatus* in the more robust and taller (1.8 versus < 1 µm) spore ornamentation, and the less strangulated form (pagodaform) of the hymenial cystidia. *Lf. pagodicystidiatus* is currently only known from Victoria, Australia, so the distributions of these two species do not overlap.

A description and photograph of basidiomata was provided in Lebel et al. (2021) as "*Lf.* sp9", but no microscopic characters were described nor figures included. The sequences from REH9320 (BRI: AQ794270) were published in De Crop et al. (2017). The deep dark brown, reddish-orange-brown to saffron brown-orange pileus of *Lf. croceivillus* is generally redder tinged than *Lf. aureoelephanti*, and the lamellae light orange rather than white to creamy. The collection (BRI: AQ808468) is here confirmed as *Lf.*

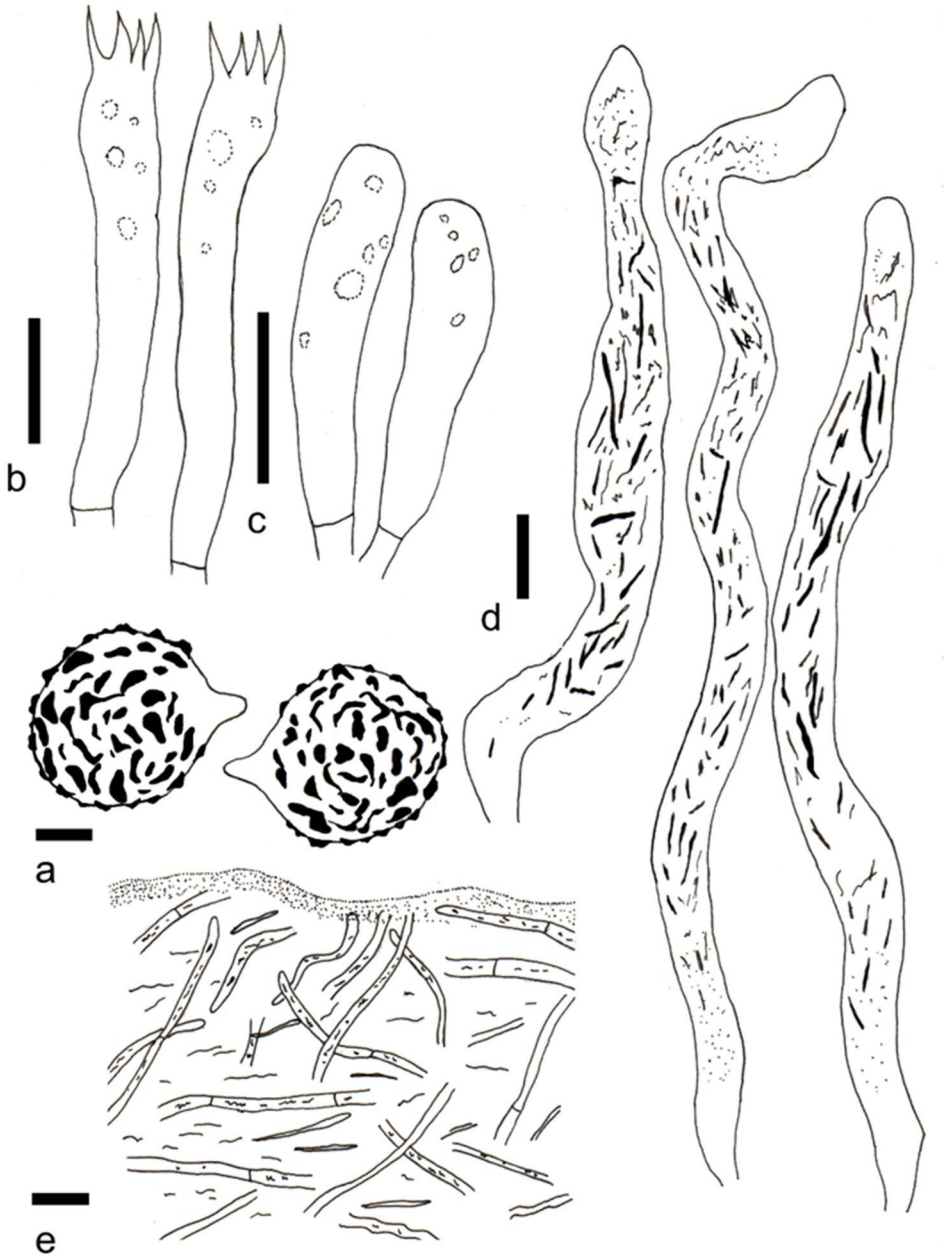


Fig. 149 ***Multifurca pseudofurcata*** (GUBH 20460). **a** Basidiospores. **b** Basidia. **c** Basidioles. **d** Pseudocystidia. **e** Pileipellis. Scale bars: **a** = 1 µm, **b–d** = 10 µm, **e** = 20 µm

croceivillus, expanding the known distribution into northern New South Wales.

Multifurca Buyck & V. Hofst.

Notes: In 2008, Buyck and V. Hofst established the genus *Multifurca* to include species that possess characteristics from both *Russula* and *Lactarius* species. The type species for this genus is *Multifurca ochricompacta*. There are 12 described species of the genus reported to date. The genus has been classified into two subgenera, namely *M.* subg. *Furcata* Buyck & X.H. Wang and *M.* subg. *Multifurca* Buyck & V. Hofst., based on phylogenetic relationships determined using three genetic markers (ITS, LSU, and *rpb2*). *Multifurca* subg. *Furcata* exclusively consists of species with lactaroid characteristics, while *M.* subg. *Multifurca* includes species with russuloid habit (Buyck et al. 2008; Wang et al. 2018a).

Multifurca pseudofurcata X.H. Wang, **new geographical record from India.**

Fungal Names: FN 554372; *Facesoffungi*: FoF 15274; Figs. 148, 149, 150

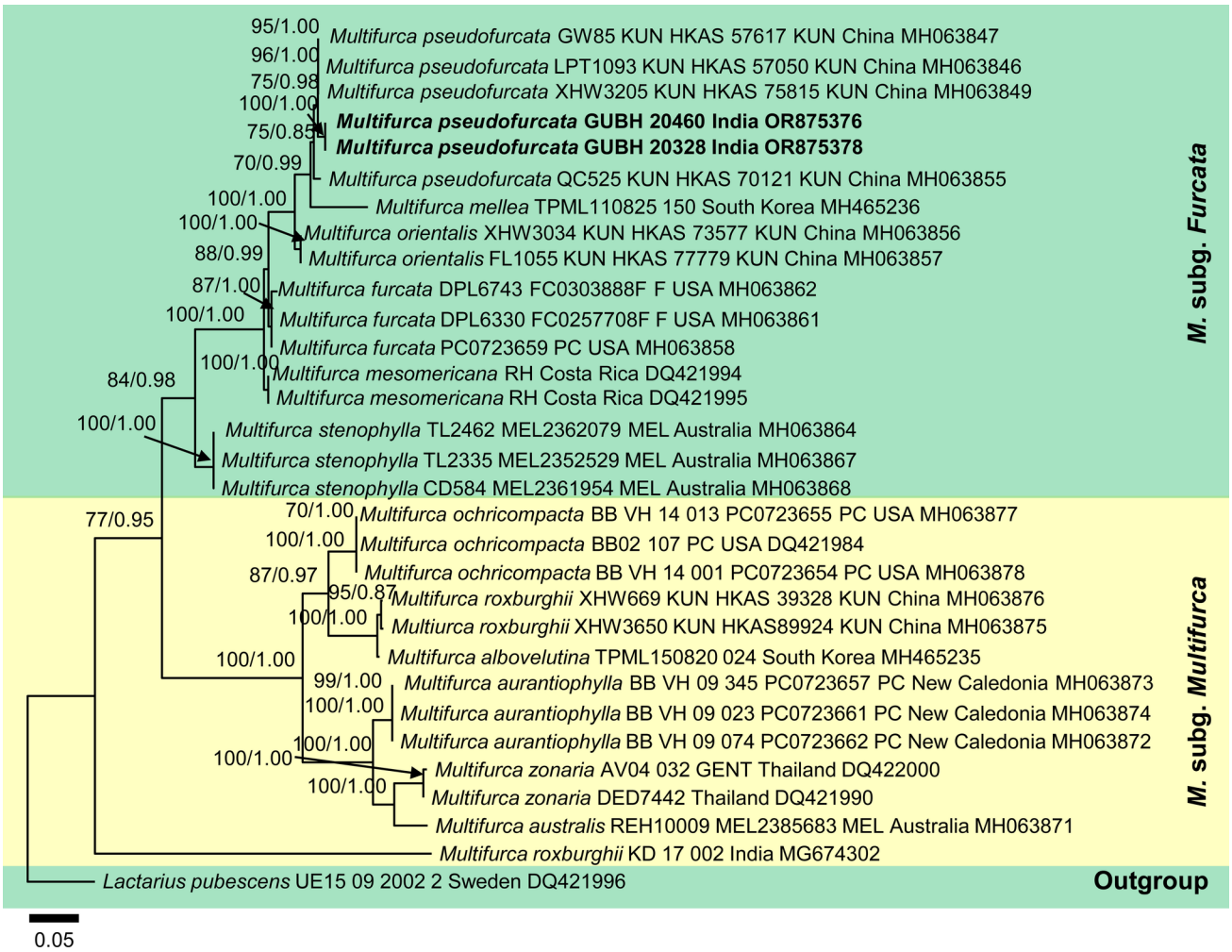


Fig. 150 Maximum Likelihood tree (– *InL* = 3600.818043) generated using the GTR + G model of nucleotide evolution. Values to the left of '/' are MLBS support, and those to the right of '/' indicate Bayesian posterior probabilities (PP) support. MLBS values ≥ 70% and PP values ≥ 0.80 are shown above or below the nodes. Sequences generated for this study are in bold. Specimen voucher number, Country of origin and GenBank accession numbers are indicated after each taxon name

Pileus medium-sized, 30–70 mm diam., rigid and thick, at first convex at young stage, plano-convex to umbilicate with a central depression when matured, with strongly inrolled margin when young to slightly an inrolled margin at age; surface dry to slightly gelatinous, smooth, not cracking, sometimes translucent, sometimes pithy at the center, scrobicules present, circular to ellipsoid patches present elsewhere, zonate with about 14–16 concentric rings, cartilaginous, surface turning pale yellowish with KOH, no change was observed with guaiacol, sulfovanillin, $FeSO_4$ and phenol, grayish yellow (1B4) towards the center and pale yellow (1A3) towards the margin. **Lamellae** 2–4 mm deep, adnate with tooth to sub-decurrent, forking multiple times with short lamellulae, margin wavy, edge entire, turning red with sulfovanillin, no change observed with KOH, guaiacol, $FeSO_4$ and phenol, concolorous, grayish champagne yellow (4B4) towards the center and yellowish white (4A2) towards the margin. **Stipe** 20–35 × 10–13 mm, equal sometimes tapering towards the end, central, cylindrical, solid, surface turning pinkish red with sulfovanillin, no change observed with KOH, guaiacol, $FeSO_4$ and phenol, smooth sometimes with scrobicules, stipe base covered with adhering soil, slightly hollow at the base, yellowish white (4A2). **Context** 2–8 mm thick, firm, zoned concentrically above the lamellae, turning fainted pink with sulfovanillin, no change observed with KOH, guaiacol, FeSO4 and phenol, white (4A1). **Latex** white, does not change on exposure. **Taste** acrid. **Odor** not recorded. **Spore print** white.

Spores (2.0–)2.5–3.7–4.6(–5.6) × (1.5–)2.0–2.9–3.0(–4.6) µm, Q = (1.1–)1.17–1.3–1.5(–1.6), subglobose to ellipsoid; ornamentations of low and faint isolated [15–20(–28) in a 3 µm in diam. in a circle] irregular amyloid warts, which are 0.1–0.25(–0.3) µm high, sometimes isolated and more often fused [2–5(–7) fusions in a circle], rarely

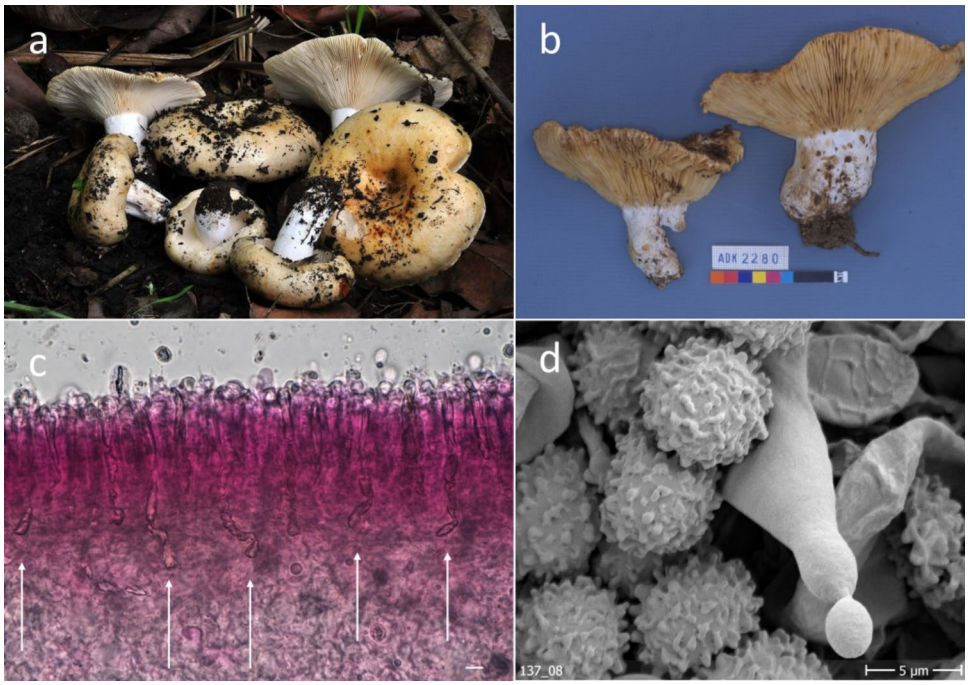


Fig. 151 ***Russula afroscrobiculata***. **a** Field habit (EDC 12–031) (photo: Eske De Crop). **b** Scrobicule-like spots on the stipe of the type specimen (ADK 2280) (photo: André De Kesel). **c** Pleuropseudocystidia-like cells in sulfovanillin, 40 × 10x, EDF stacking, arrows indicate the basal part of the pleurocystidia bending in the trama (MD 335), scale bar = 10 µm. **d** Pleurocystidium and spores, SEM

connected by lines; apiculus 0.2–0.4 µm high, suprahilar spot inamyloid. **Basidia** (25–)27–30–32(–41) × (5–)5.5–6.6(–7.6) µm, subcylindrical to clavate, thin-walled, hyaline, 4-spored, sterigmata 0.5–1.2 µm high. **Basidioles** 20–22.5 × 4.5–5.5 µm, clavate, thin-walled, hyaline. **Hymenial macrocystidia** absent. **Marginal cells** not differentiated. **Pseudocystida** abundant, 3.8–9.0(–12) µm wide, common, mostly with a blunt rounded apex, rarely acute apex, with dense brownish contents reacting with sulfovanillin, projecting mostly beyond the basidia. Lamellae edge sterile. **Pileipellis** an ixocutis, 150–310 µm deep, consisting of densely interwoven hyphae and yellowish brown laticifers, near the surface, hyphae 2–5 µm in diam., hyphae often shriveled and not usually gelatinous. **Stipitipellis** an ixocutis, 80–130 µm deep; hyphae 1.5–3.0(–5.0) µm wide, gelatinized and compactly arranged. Lamellar trama consisting of laticifers and hyphae, consisting of yellowish-brown contents upon reaction with sulfovanillin, lacking spherocytes. **Pileus and stipe trama** consisting with many rossettes. Hyphal incrustations and clamp-connections absent from all tissues.

Habit and habitat: Solitary, scattered, under *Pinus kesiya*.

Material examined: INDIA, Meghalaya, Shillong, Rhododendron Trek, 25°33′54″N 91°51′33″E, 1602 m asl., under *Pinus kesiya* tree, 11 Jun 2022, *N. Roy*, *A.K. Dutta* and *P. Chattopadhyay*, GUBH 20460; Meghalaya, Shillong, Lummawbah, 25°33′38″N 91°51′20″E, 1652 m asl., under *Pinus kesiya* tree, 15 Jun 2022, *N. Roy*, *A.K. Dutta* and *P. Chattopadhyay*, GUBH 20328.

GenBank: GUBH 20460: OR875376 (ITS); GUBH 20328: OR875378 (ITS).

Notes: *Multifurca pseudofurcata*, a species classified under the *Multifurca* subg. *Furcata*, is found in two collections from Meghalaya, India. It forms a highly supported clade (MLBS = 100%, PP = 1.00; Fig. 150) along with other members of the *M.* subg. *Furcata*. The newly generated sequences of *M. pseudofurcata* cluster with the type specimens *Multifurca pseudofurcata* (GenBank MH063849), *M. mellea* (GenBank MH465236), and *M. orientalis* (GenBank MH063856 and MH063857). However, morphologically, *M. orientalis* is distinguished from *M. pseudofurcata* by its latex, which turns a dull yellowish white when dried, and by the narrow pseudocystidia, which measure 4–8 µm in width (Wang et al. 2018b). The South Korean species *Multifurca mellea* is distinct in its characteristics, as described in its type description. *Multifurca mellea* is characterized by having a pileus surface without distinct zones and a pileipellis that resembles a cutis, according to Verbeken et al. (2018). However, Das et al. (2018) argues that *M. mellea* is synonymous with either *M. orientalis* or *M. pseudofurcata*. *Multifurca pseudofurcata*, initially confused as *M. furcata* and then validly published in China, has now been recorded in India for the first time. This is the second species of the *Multifurca* genus found in the Indian geographic region.

Russula Pers.

Notes: With around 1350 species described and potentially around 3000 species in the northern hemisphere alone, *Russula* is the largest genus within the Russulales and one of the largest within the Agaricomycetes (He et al. 2019; Bhunjun et al. 2022; Wang et al. 2024c). It is an important ectomycorrhizal clade in temperate and tropical ecosystems

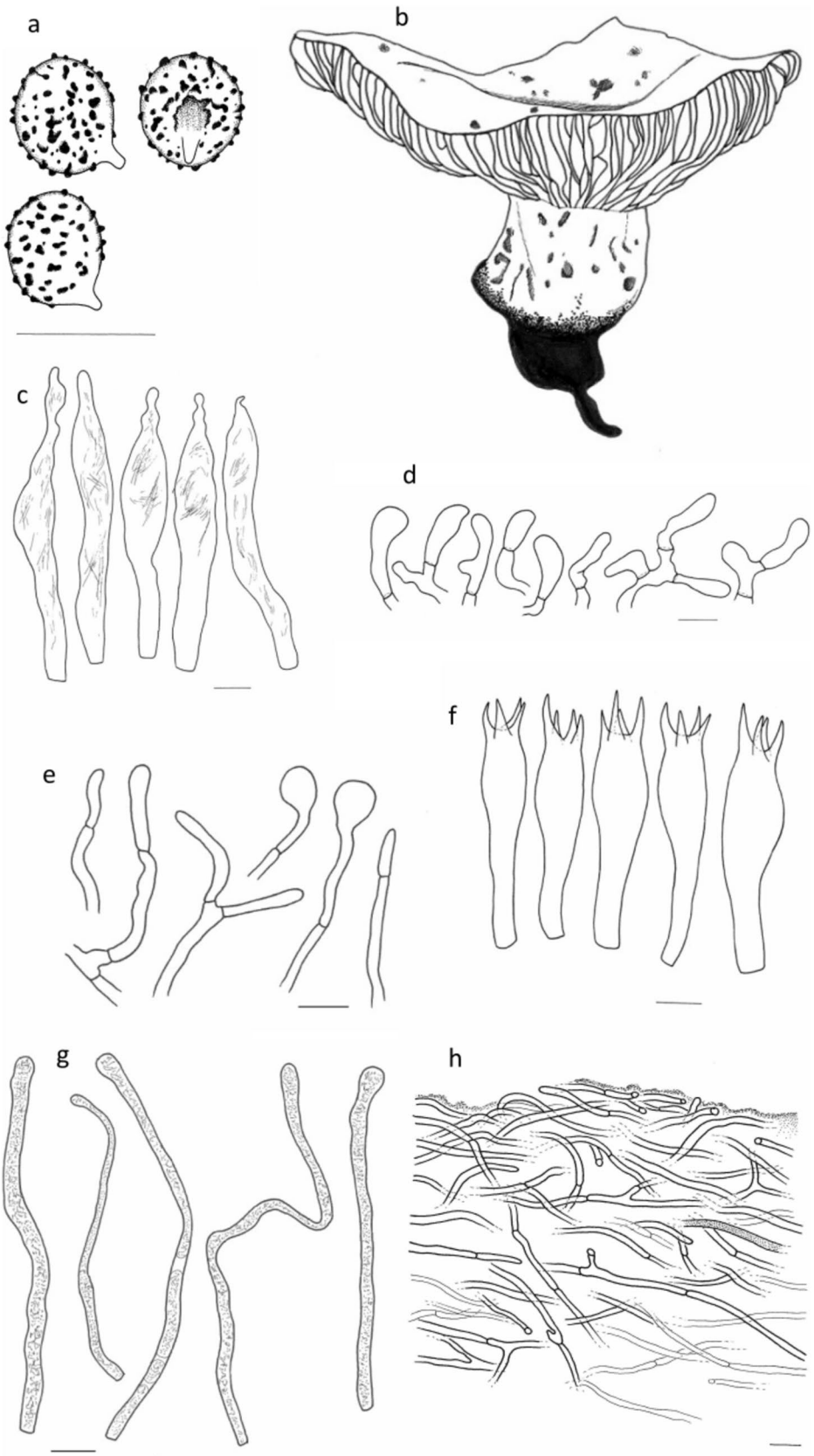


Fig. 152 ***Russula afroscrobiculata***. **a** Spores (ADK 2880). **b** Basidioma (ADK 2880). **c** Pleurocystidia (ADK 2880). **d** Hyphal terminations of the hymenium (ADK 2880). **e** Hyphal terminations of the pileipellis (AV 19–003). **f** Basidia (ADK 2880). **g** Pileocystidia (AV 19–003). **h** Section through pileipellis (ADK 2880). Scale bars = 10 µm. Adapted from Van Rooij et al. (2003)

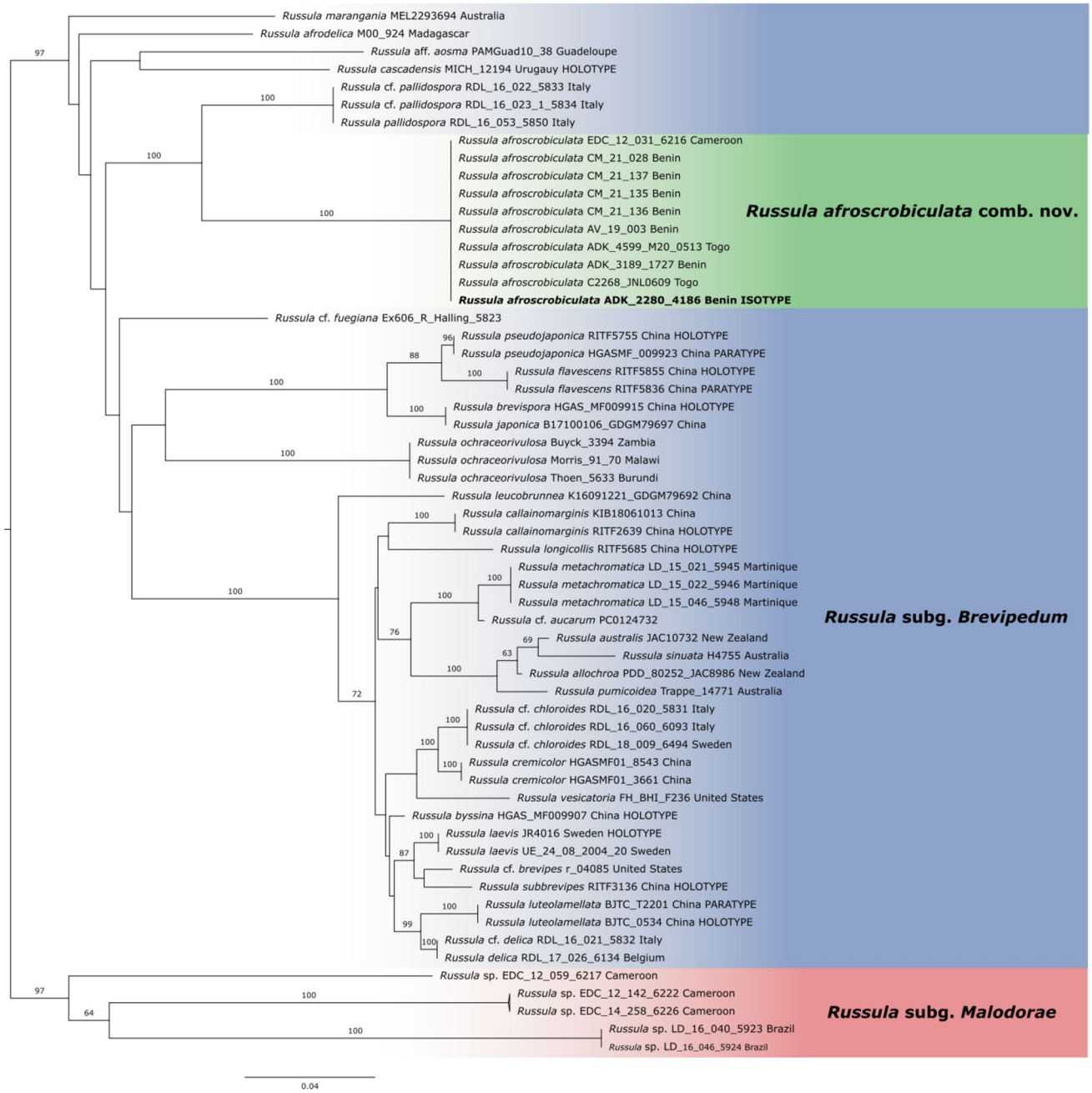


Fig. 153 Phylogram generated from ML analysis with standard bootstrapping (1000 replicates), based on combined ITS, LSU, *rpb2* and *tef1* sequence data for *Russula* subg. *Brevipedum*. The combined dataset contains 54 samples and 5 samples from *R.* subg. *Malodorae* as an outgroup, with 3227 characters including gaps. 103 sequences, of which 31 of *R. afroscrobiculata*, were newly generated in this study and deposited in Genbank. ML bootstrap values ≥ 60 are shown

and is divided into nine subgenera: *Archaeae* Buyck & V. Hofst., *Brevipedum* Buyck & V. Hofst., *Compactae* (Fr.) Bon, *Crassotunicatae* Buyck & V. Hofst., *Glutinosae* Buyck & X.H. Wang, *Cremeo-ochraceae* Buyck & X.H. Wang, *Heterophyllidiae* Romagn., *Malodorae* Buyck & V. Hofst., *Russula* Buyck & V. Hofst (Buyck et al. 2018, 2020, 2024; Adamčík et al. 2019).

Russula afroscrobiculata (Verbeken & Van Rooij) Tondeleir & Lagaet, **comb. nov.**

Mycobank: MB 851194; *Facesoffungi*: FoF 15301; Figs. 151, 152, 153

Basionym: *Lactarius afroscrobiculatus* Verbeken & Van Rooij, Nova Hedwigia 77: 226 (2003).

Type: *ADK 2280* (holotypus BR, isotypus GENT).

Pileus 64–108 mm diam., planoconcave to concave; cuticle sticky and smooth, not peeling, pale yellow to yellowish brown (4A45–5C87), with brown spots when bruised; margin regular when young, undulate when older, very thin, membranaceous and white in some collections. Flesh 10 mm thick at half radius. **Stipe** 12–36 × 15–33 mm, short, thick, firm, cylindric to clavate; cuticle pale white and sometimes scrobiculate, if so, then pits yellow–brown to dark-brown, small and not very abundant, concentrated in upper half of the stipe, small and irregularly shaped. **Lamellae** very brittle, decurrent, very dense (13–16 L + l/cm), often with anastomosing veins at the pileus margin; lamellulae 1 l/L, very short, light yellow or darker (4A45), turning brownish yellow when bruised and aged. **Context** very firm, thick in pileus, chambered to fistulous in stipe; taste first mild to acrid, sometimes becoming bitter, faint resin-like; smell fruity, in older specimens somewhat fish-like. Reaction with guaiac after 8–10 s negative to very weakly positive on stipe and weakly positive on lamellae surfaces, negative with $FeSO_4$ and KOH. **Spore print** not observed.

Spores broadly ellipsoid, sometimes subglobose or ellipsoid, (6.4–)7.3–7.9(–8.8) × (5.3–)6.1–6.6(–7.4) µm, Q = (1.06–)1.17–1.21(–1.35); ornamentation amyloid, composed of irregular warts, up to 1 µm high, subconical to subspherical, moderately dense [4–5 in a 3 µm diam. circle], mostly isolated, seldom connected with fine lines or aligned [0.5 in a 3 µm diam. circle], size 0.7 µm; suprahilar spot smooth, slightly amyloid. **Basidia** 45–53 × 5–14 µm, subclavate, with long (7–12 × 2–3 µm) and sharp sterigmata, thin-walled to slightly thickened, 4-spored, contents seldom with oil-like droplets, not reactive in sulfovanillin. **Pleurocystidia** abundant (700–1000/mm^2), 60–90 × 10–15 µm, subcylindrical, highly variable in shape: from tapering upwards to mucronate to slightly clavate, slightly emergent, with contents needle-like and granular, reactive in sulfovanillin (gray), slightly thick-walled, sometimes extending deep into the subhymenium and trama, then 5–8 µm diam., irregularly cylindric, with refractive contents. **Lamella edge** sterile, cystidia lacking; **marginal cells** 12–21 × 2–6 µm, clavate to irregularly cylindric, sometimes branched, thin-walled, hyaline. **Pileipellis** ortochromatic in Cresyl Blue, sharply delimited from underlying context, strongly gelatinized, 120 µm thick, composed of densely interwoven recumbent or ascending hyphae, 2–5 µm diam. No difference between supra- and subpellis. **Oleiferous hyphae** present in subpellis and hymenophoral trama. **Cystidioid hyphae** present in both subpellis and hymenophoral trama; their contents finely crystalline. **Hyphal terminations near pileus margin** densely arranged, rarely branched, hyaline, slightly thick-walled. Terminal elements (20–)23(–26) × (2–)4.5(–7) µm, subclavate to irregularly cylindric, sometimes clavate, then (4–)9(–14) µm wide. Subterminal elements 3–4 µm wide, regularly cylindric, sometimes slightly tortuous, aseptate. **Hyphal terminations near pileus center** similar in shape, but less densely arranged and terminal elements shorter: (14.5–)19(–23.5) × (3.5–)4.5(–5.5) µm. **Pileocystidia at margin abundant**, (58–)92(–125) × (4–)5.5(–7) µm, thin-walled, cylindric to subcapitate, slightly tortuous, with finely crystalline contents, slightly reactive in sulfovanillin (gray). **Pileocystidia near pileus center** similar in size and shape, but less abundant. **Acid-resistant incrustations** absent. **Clamp connections** absent in all parts.

Material examined: BENIN, Borgou Province: Wari Maro, 9°09.485N 2°08.846E, 20 Sept. 1998, leg. *A. De Kesel* (*ADK 2280*, **holotype** BR, **isotype** GENT); Ibid., 9°10.782N 2°09.860E, 25 Sept. 1998, leg. *A. De Kesel* (*ADK 2337*, BR); Ibid., 9°10.617N 2°09.932E, 13 Sept 2001, leg. *A. De Kesel* (*ADK 3160*, BR); Ibid, Savanna with shrubs and trees like *Isoberlinia doka* and *Uapaca togoensis*, 9°08.110N 2°10.215E, 9 Oct. 2001, leg. *A. De Kesel* (*ADK 3189*, BR); Ibid., Savanna with trees, open canopy with *Isoberlinia doka* and *Uapaca* sp., 9°09.541N 2°9.305E, 23 Sept. 2001, leg. *A. De Kesel* (*ADK 3236*, BR); Ibid., on sandy soil with *Isoberlinia doka*, 310 m elevation, 17 July 2021, leg. *C. Manz*, *F. Hampe* and *G. Abohoumbo* (*CM 21–135*); Ibid., on sandy soil with *Isoberlinia doka*, 310 m elevation, 17 July 2021, leg. *C. Manz*, *F. Hampe* and *G. Abohoumbo* (*CM 21–136*); Borgou Province: Doguè, 9°07.249N 1°54.839E, 10 Oct 2001, leg. *A. De Kesel* (*ADK 3216*, BR); Borgou Province: Gando, in deciduous woodlands dominated by *Isoberlinia tomentosa*, *Isoberlinia doka*, and *Uapaca togoensis*, 7 July 2013, leg. *D. Maba* (*MD 335*); Borgou Province: Forêt Classée de N'Dali, on sandy soil with *Isoberlinia doka*, 375 m elevation, 18 July 2021, leg. *C. Manz*, *F. Hampe* and *G. Abohoumbo* (*CM 21–137*); Collines Province: Okpara Forest Park, in Sudanian woodland with *Isoberlinia doka*, 11 Sept. 2019, leg. *A. Verbeken* (*AV 19–003*, GENT); Ibid., on sandy soil with *Isoberlinia doka*, 374 m elevation, 27 June 2021, leg. *C. Manz*, *F. Hampe* and *A. Boukary* (*CM 21–028*). CAMEROON, Western region: Noun division, Foumban subdivision, Mambouo village, in a gallery forest in the savanna region, with *Uapaca guineensis*, 879 m elevation, 5.6769°N 10.9369°E, 9 May 2012, leg. *E. De Crop* (*EDC 12–031*, GENT). TOGO, Centrale region: Parc National Fazao, 16 Jun 2007, leg. *A. De Kesel* (*ADK 4387*, BR); Forêt Classée d'Alédjo, 29 May 2008, leg. *A. De Kesel* (*ADK 4577*, BR); Ibid., 31 May 2008, leg. *A. De Kesel* (*ADK 4599*); lbid., 2008, leg. *A. Guelly* (*C 2268*).

GenBank: ADK 2280: PP028827 (ITS); EDC 12–031: PP028823 (ITS), PP028849 (LSU), PP033807 (*rpb2*); CM 21–137[1]: PP028844 (ITS), PQ249297(LSU), PP033847 (*tef1*), PP033826 (*rpb2*); CM 21–136: PP028843 (ITS), PQ249296 (LSU), PP033846 (*tef1*), *PP033825* (*rpb2*); CM 21–135: PP028842 (ITS), PQ249298 (LSU), PP033845 (*tef1*), PP033824 (*rpb2*); CM 21–028: PP028841 (ITS), PQ249295 (LSU), PP033844 (*tef1*), PP033823 (*rpb2*); AV

Fig. 154 Basidiomata. **a, b** *Russula gaoligongensis* (HMAS 287500, **holotype**). **c** *Russula gaoligongensis* (HMAS 287502). **d** *Russula gaoligongensis* (HMAS 287501). **e** *Russula guilinensis* (HMAS 287503, **holotype**). **f** *Russula guilinensis* (HMAS 287504). Scale bars = 1 cm

19–003: PP028838 (ITS), PP028863 (LSU), PP033820 (*rpb2*); C 2268: PP028828 (ITS), PP028853 (LSU); ADK 4599: PP028839 (ITS), PP028864 (LSU), PP033821 (*rpb2*); ADK 3189: PP028840 (ITS), PP028865 (LSU), PP033822 (*rpb2*).

Notes: *Russula afroscrobiculata* comb. nov. was originally described as *Lactarius afroscrobiculatus* by Van Rooij et al. (2003). Two synapomorphies of milkcaps (*Lactarius* & *Lactifluus*) are the presence of latex and pleuropseudocystidia, aseptate extensions of the lactifers in the hymenium. In *Lactarius afroscrobiculatus*, no latex was observed. However, in tropical environments, less latex can be produced with respect to temperate areas, which could have been an argument to initially describe the species within *Lactarius*. The pleuropseudocystidia were stated to be very rare (Van Rooij et al. 2003; Verbeken and Walleyn 2010). In none of the collections examined for this study, true pleuropseudocystidia were observed. However, some hymenial cystidia do contain needle-like and granular, refractive structures similar to the appearance of latex. Although these cystidia are differently shaped compared to the 'regular' pleurocystidia, and sometimes extend very deep into the subhymenium, we were unable to reject the presence of a septum. Since the pleurocystidia that penetrate deep into the subhymenium are hard to see clearly and the oleiferous hyphae are obvious and abundant in the trama, it is easy to see how some pleurocystidia could have been interpreted as pseudocystidia. On top of that, the most basal part of the pleurocystidia sometimes seems to extend and bend in the trama (Fig. 151c), like in typical pseudocystidia in milkcaps.

Another characteristic that gives *Russula afroscrobiculata* its *Lactarius*-like appearance is the scrobiculate stipe. This would be the first species in *Russula* that contains scrobicules, but it is also not common for African milkcaps to have this trait. However, spotty depressions, which could easily be identified as scrobicules, are described from *R.*

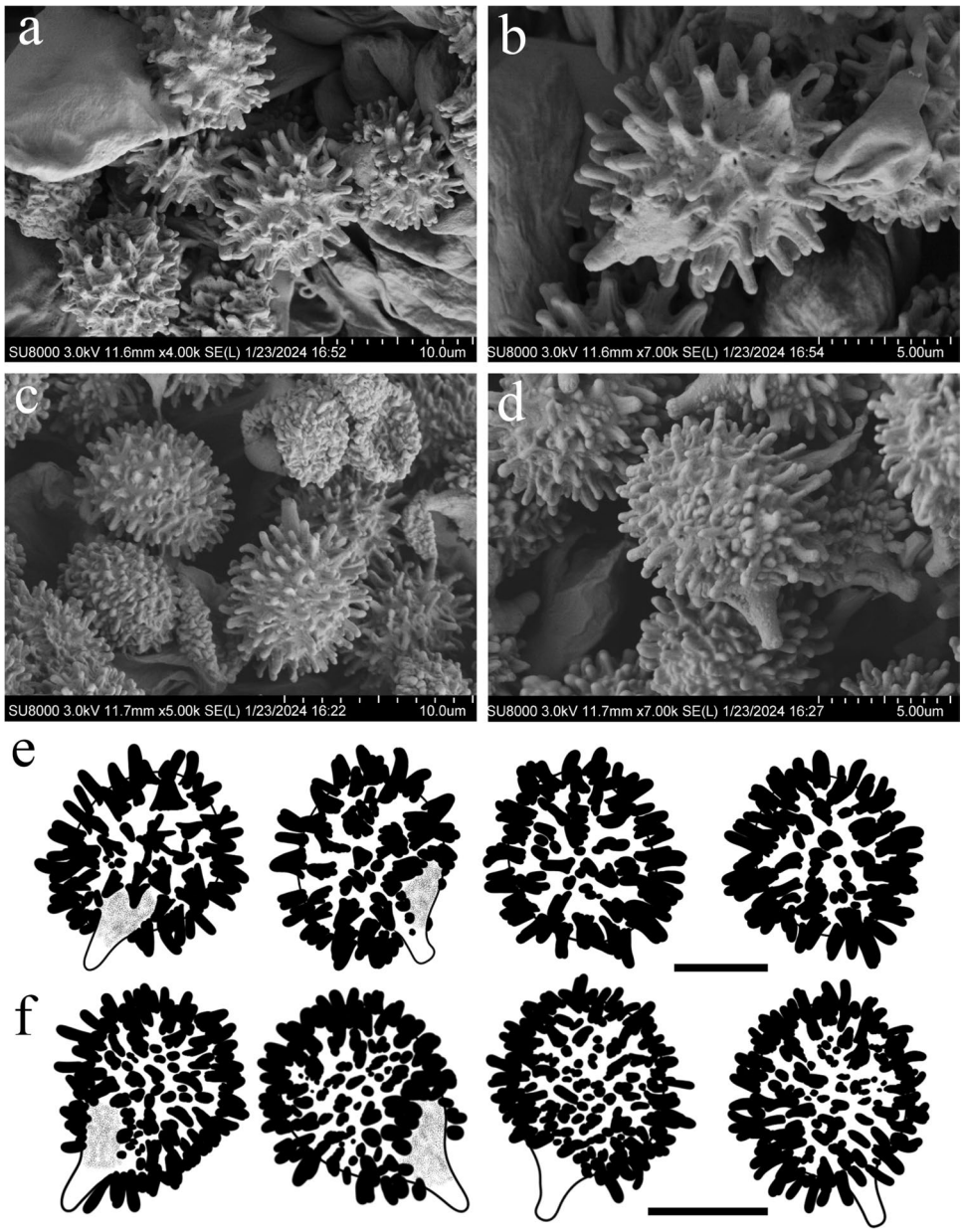


Fig. 155 Basidiospores. **a, b** Basidiospores of *Russula gaoligongensis* (HMAS 287500, **holotype**) under scanning electron microscope. **c, d** Basidiospores of *Russula guilinensis* (HMAS 287503, **holotype**) under scanning electron microscope. **e** Spore drawings of *Russula gaoligongensis* (HMAS 287500, **holotype**) showing ornamentation in Melzer's reagent. **f** Spore drawings of *Russula guilinensis* (HMAS 287503, **holotype**) showing ornamentation in Melzer's reagent. Scale bars: **e, f** = 5 µm

pallidospora J. Blum ex Romagn., which is sister to this species (Fig. 153). It thus begs the question if these structures are true scrobicules.

The phylogenetic analyses revealed that this species indeed does not belong in the genus *Lactarius* (Fig. 153), but rather it is a member of *Russula* subg. *Brevipedum* Buyck & V. Hofstetter. Although deep nodes show low bootstrap values, *Russula afroscrobiculata* forms a well-supported clade with its sister species *Russula pallidospora*. Some morphological characters also support this placement in the genus *Russula*: the absence of latex, and the spores with an ornamentation consisting of warts. The decurrent gills and dull cap colors are typical characteristics for subg. *Brevipedum.* As previously mentioned, it shares some characteristics with its sister species, *R. pallidospora*, such as a 'scrobiculate' stipe, spores with low, isolated warts, cream-colored lamellae. The unusual pleuropseudocystidia-like cells are however absent in this species.

Remarkable is the lack of any closely related African species. Two morphologically similar, unsequenced African *Russula* species are *R. pallidorimosa* Buyck and *R. terrena* Buyck, known from DR Congo and Zimbabwe respectively. However, some microscopical differences can be discerned, such as the higher spore ornamentation of *R. pallidorimosa*. *R. terrena* in its turn has larger spores, undifferentiated marginal cells and lacks lamellulae. Likewise, *R. afrodelica* Buyck (DR Congo) and *R. ochraceorivulosa* Buyck (Burundi) are also morphologically similar, but are

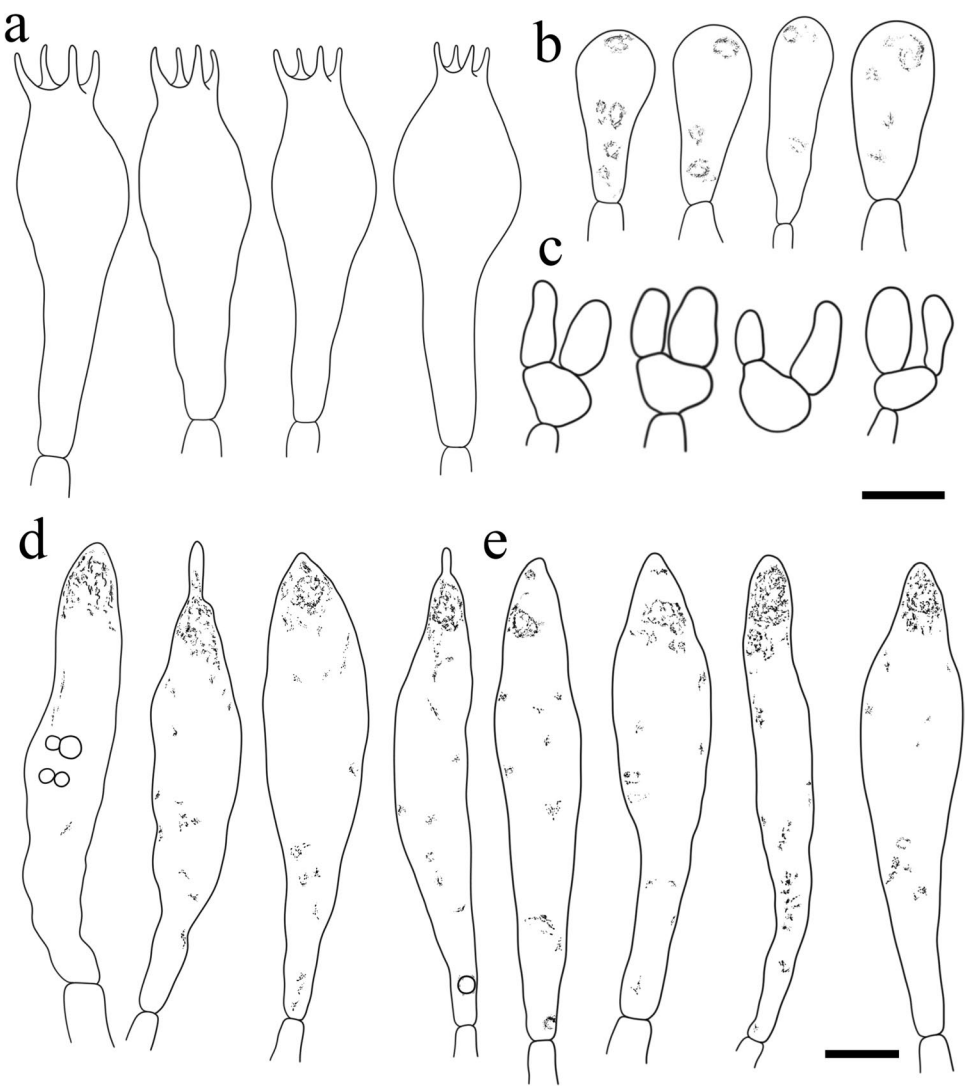


Fig. 156 ***Russula gaoligongensis*** (HMAS 287500, **holotype**), hymenium. **a** Basidia. **b** Basidioles. **c** Marginal cells on the lamella edges. **d** Hymenial cystidia near the lamella sides. **e** Hymenial cystidia on the lamella edges. Cystidia with contents as observed in Congo Red. Scale bars = 10 µm

delimited from *R. afroscrobiculata* based on molecular data (Fig. 153). Moreover, these species have different spore sizes and ornamentation.

The species occurs in extensively pastured savanna woodlands dominated by *Burkea africana* and *Isoberlinia doka*, as well as in savannas dominated by *Isoberlinia tomentosa*, *Uapaca togoensis* and/or *Detarium* sp. and in gallery forests in the savanna region with *Uapaca guineensis*. Only known from Benin, Cameroon and Togo.

Russula gaoligongensis R.L. Zhao, B. Cao & S.H. Wang, **sp. nov.**

Fungal Names: FN 571918; *Facesoffungi*: FoF 17144; Figs. 154, 155, 156, 157, 158, 159

Etymology: refers to Gaoligongshan National Nature Reserve, the locality of the type specimen.

Holotype: HMAS 287500.

Pileus medium-sized to large, 70–100 mm diam., plane, slightly depressed in the center; margin deflexed, cuticle rough sometimes lubricous, sticky to slightly viscid, shiny when wet, sometimes margin inconspicuous striation, pinkish white (10A2) to brownish red (10C6), in the center variegated, e.g. yellowish white (3A2), pale yellow (4A3), dull yellow (3B3), grayish yellow (4B3), orange white (6A2), sometimes light yellow (4A4) to orange yellow (4A6–4B7) when cracked with dry. **Lamellae** 3–5 mm deep, adnate to slightly decurrent, dense, white (1A1) when young, becoming yellowish white (1A2) when mature; lamellulae and furcations absent; edges concolorous and even. **Stipe** 71–100 × 12–19 mm, usually slightly narrowing upwards, white (1A1) to yellow white (1A2), sometimes slightly pale red (11A3) to grayish rose (11B4). **Context** 1–2 mm thick in a half of the pileus radius, white (1A1), yellowish white (1A2) when mature. **Spore print** not observed.

Spores (7.0–)7.6–8.2–8.7(–9.5) × (5.2–)6.2–6.8–7.3(–7.8) µm, broadly ellipsoid, Q = (1.1–)1.14–1.21–1.28(–1.4); ornamentation of large, distant [2–3(–3) in a 3 µm diam. circle] amyloid spines or warts, which are

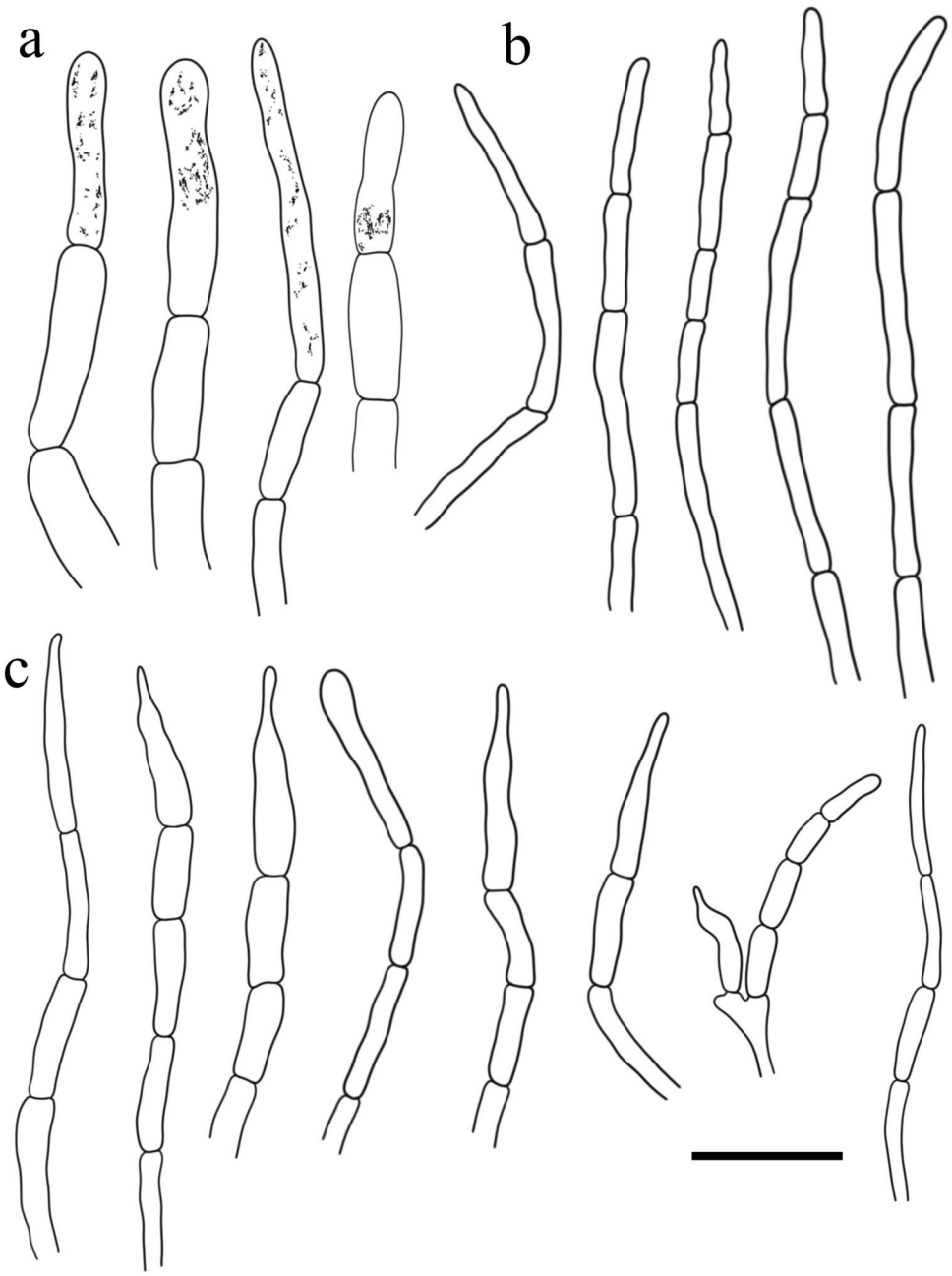


Fig. 157 *Russula gaoligongensis* (HMAS 287500, **holotype**), pileipellis. **a** Pileocystidia near the pileus center. **b** Hyphal terminations near the pileus center. **c** Pileocystidia near the pileus margin. Cystidial contents as observed in Congo Red. Scale bar = 10 µm

(1.1–)1.3–1.6–1.9(–1.9) µm high, isolated or fused in pairs or short chains [0–1(–1) fusions in the circle]; line connections absent. **Basidia** (41–)42–45–48(–50) × (14–)14–15–16(–16) µm, clavate, 4-spored; basidioles first cylindrical, then clavate, 11.3–13.4 µm wide. **Hymenial cystidia** (64–)69–78–87(–94) × (11–)12–15–17(–18) µm, mainly clavate or fusiform, apically acute or mucronate with a 0–5 µm long appendage, originating in subhymenium, thin-walled; contents in most whole volume optically empty and only apically granulose-crystalline; abundant near the lamellae edges, (68–)84–94–104(–104) × (11–)13–15–18(–18) µm, similar to those on the sides. **marginal cells** (12–)18–22–26(–28) × (5–)6–7–8(–9) µm, clavate or cylindrical, obtuse, usually branched. **Acid-resistant incrustations** absent. Hyphal terminations near the pileus margin normally attenuated, occasionally inflated, thin-walled; terminal cells (11–)15–23–30(–33) × (1.9–)2.6–3.4–4.1(–5.0) µm, cylindrical, apically obtuse or slightly constricted; subterminal cells usually equally long and wide. Hyphal terminations near the pileus center similar, terminal cells even narrower, (8–)9–17–24(–29) × (1.2–)1.5–2.0–2.4(–2.6) µm; subterminal cells scarcely branched, occasionally flexuous. **Pileocystidia** near the pileus margin absent. Pileocystidia near the pileus center mainly 1(–2)-celled; terminal cells (11–)15–23–30(–

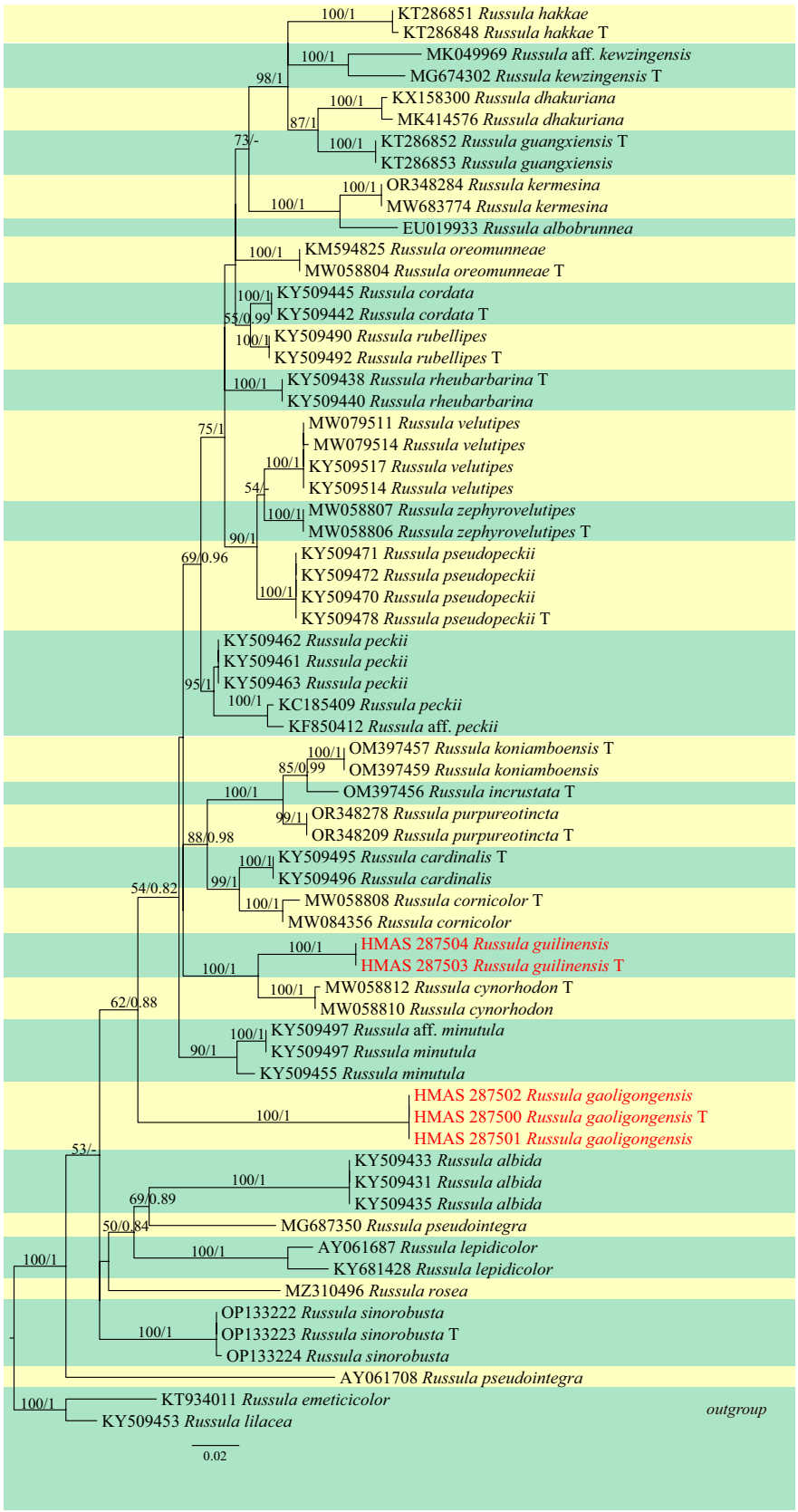


Fig. 158 Maximum Likelihood tree of subsect. *Roseinae* based on ITS sequences, bootstrap values greater than 50% are shown around nodes. New species are shown in red. "T" refers to a type specimen

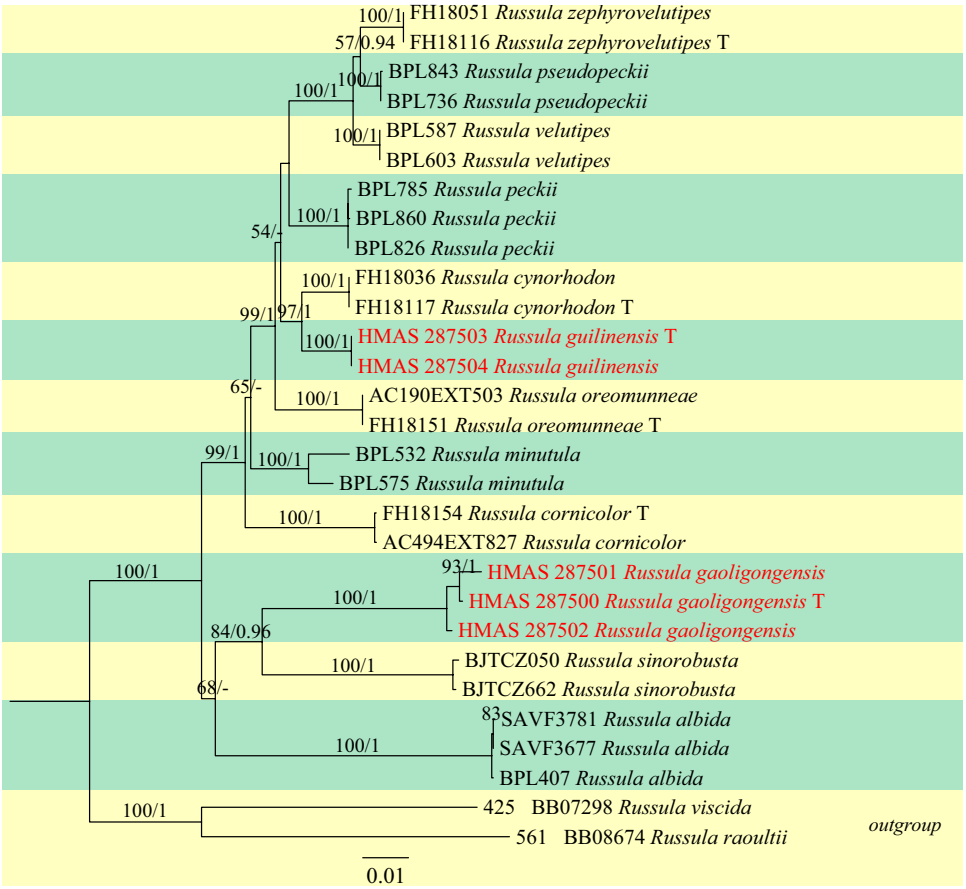


Fig. 159 Maximum Likelihood tree of subsect. *Roseinae* based on 3-locus (*rpb1-rpb2-tef1*) combined sequences, bootstrap values greater than 50% are shown around nodes. New species are shown in red. "T" refers to a type specimen

33) × (2.0–)2.3–3.1–3.9(–4.5) µm, mostly subclavate, cylindrical, apically obtuse. **Cystidioid hyphae** in subpellis and context dispersed, with heteromorphousgranulose contents, oleiferous hyphae frequent in the lower part of subpellis and context.

Material examined: CHINA, Yunnan Province, Baoshan Municipality, Tengchong Municipality, Gaoligongshan National Nature Reserve, 25°33′N 98°35′E, 1898 m asl, 6 Jul 2018, *Bin Cao*, *Hui-Jun Wang*, *Rui-Lin Zhao*, *ZRL20180305* (HMAS 287502), *ZRL20180569* (HMAS 287501) and *ZRL20180751* (HMAS 287500, **holotype**).

GenBank: HMAS 287500: PP716404 (ITS), PP716409 (LSU), PP723166 (mitSSU), PP723235 (*rpb1*), PP723240 (*rpb2*), PP723245 (*tef1*); HMAS 287502: PP716402 (ITS), PP716407 (LSU), PP723164 (mitSSU), PP723233 (*rpb1*), PP723238 (*rpb2*), PP723243 (*tef1*); HMAS 287501: PP716403 (ITS), PP716408 (LSU), PP723165 (mitSSU), PP723234 (*rpb1*), PP723239 (*rpb2*), PP723244 (*tef1*).

Notes: *Russula gaoligongensis* belonging to subsection *Roseinae*. On the phylogenetic tree (Fig. 158), this species forms a separate branch that can be well separated from other known species. Morphologically *R. gaoligongensis* and *R. cornicolor* Manz & F. Hampe are similar, but phylogenetically they can be well separated (Manz et al. 2021).

Russula guilinensis R.L. Zhao, B. Cao & S.H. Wang, **sp. nov.**

Fungal Names: FN 571919; *Facesoffungi*: FoF 17145; Figs. 154, 155, 158, 159, 160, 161

Etymology: refers to Guilin Municipality, the locality of the type specimen.

Holotype: HMAS 287503.

Pileus medium-sized, 67–77 mm diam., applanate with deeply indented center; margin smooth or slightly striate; cuticle matt, velvety smooth, dark red (11C8) in the center, red (11A6–11B7) towards the margin, violet brown (10E7–10F7) when wet. **Lamellae** 4–6 mm deep, adnate to slightly decurrent, dense, white (1A1) when young, becoming yellowish white (1A2) when mature; lamellulae and furcations absent; edges concolorous and even. **Stipe** 45–60 × 11–16 mm, usually slightly narrowing upwards, white (1A1), olive yellow (2D6–8) when old; medulla stuffed and becoming hollow when mature. **Context** 1–2 mm thick in a half of the pileus radius, white

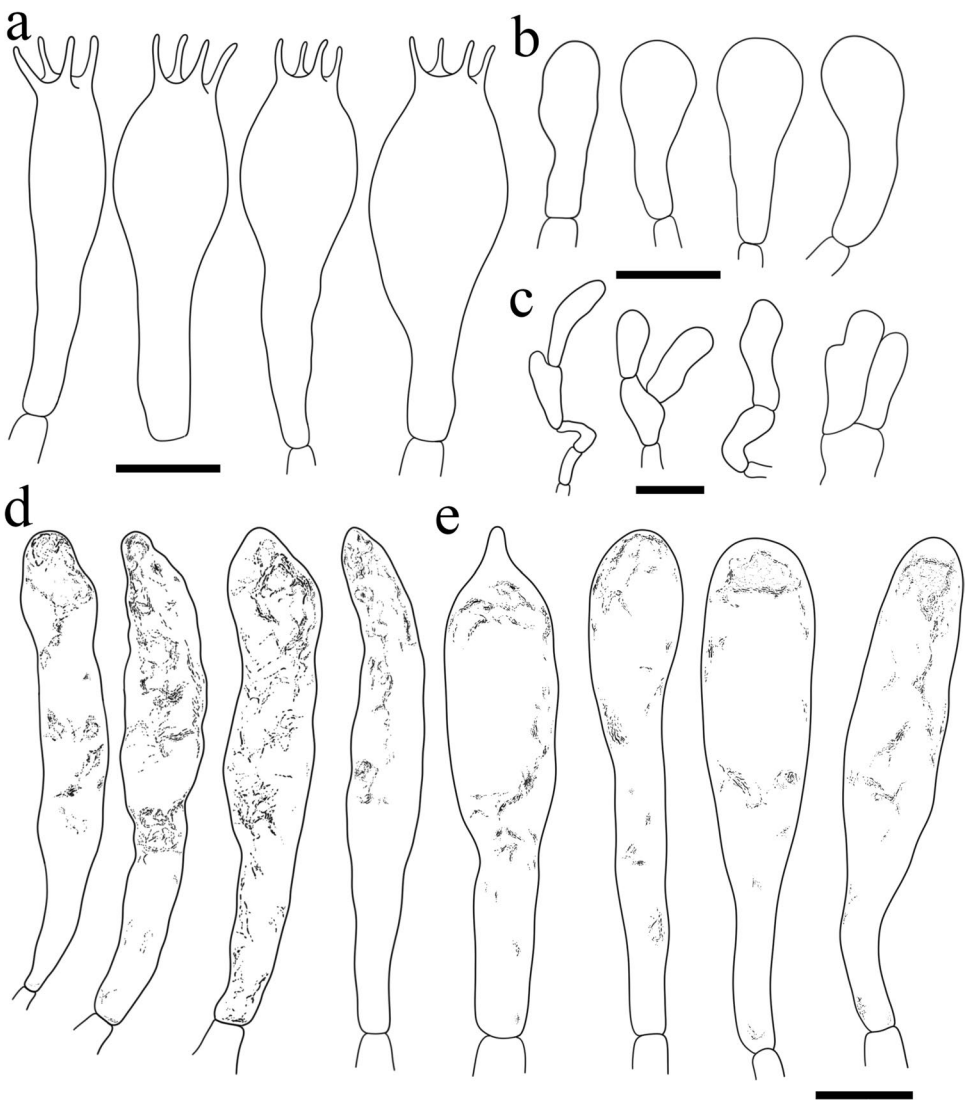


Fig. 160 *Russula guilinensis* (HMAS 287503, **holotype**), hymenium. **a** Basidia. **b** Basidioles. **c** Marginal cells on the lamella edges. **d** Hymenial cystidia near the lamella sides. **e** Hymenial cystidia on the lamella edges. Cystidia with contents as observed in Congo Red. Scale bars = 10 µm

(1A1), yellowish white (1A2) when mature. **Spore print** not observed.

Spores (6.5–)6.8–7.2–7.6(–8.0) × (5.5–)5.6–5.9–6.3(–6.9) µm, broadly ellipsoid, Q = (1.11–)1.16–1.21–1.27(–1.34); ornamentation of large, distant to moderately distant [3–5(–6) in a 3 µm diam. circle] amyloid spines or warts, which are (0.5–)0.8–1.0–1.3(–1.6) µm high, isolated or fused in pairs or short chains [0–1(–2) fusions in the circle]; line connections absent. **Basidia** (29–)31–33–35(–36) × (10–)11–12–12(–13) µm, clavate, 4-spored; basidioles first cylindrical, then clavate, 8–11 µm wide. **Hymenial cystidia** (41–)45–51–57(–62) × (7–)7–8–9(–11) µm, clavate, apically obtuse or mucronate with a 0–6 µm long appendage, originating in subhymenium, thin-walled; contents partly heteromorphous, granulose or seldom crystalline; abundant near the lamellae edges, (47–)49–55–62(–67) × (6–)7–9–11(–12) µm, similar to those on the sides. **marginal cells** (21–)24–31–39(–47) × (2–)3–5–6(–7) µm, clavate or obpyriform, obtuse. **Acid-resistant incrustations** absent. Hyphal terminations near the pileus margin occasionally narrow, thin-walled; terminal cells (7–)7–17–27(–47) × (3.1–)3.5–4.2–4.9(–5.4) µm, cylindrical, apically obtuse or slightly constricted; subterminal cells usually equally long and wide, but often also shorter and wider, 4–5 µm wide. Hyphal terminations near the pileus center similar, (7–)11–17–28(–36) × (2.8–)3.3–3.8–4.4(–4.6) µm; subterminal cells occasionally branched and imbedded in intricate hyphae of the subpellis. **Pileocystidia** near the pileus margin typically 1–2-celled, sometimes 2–3-celled, usually clavate, occasionally slightly flexuous, thin-walled, terminal cells variable in length, (23–)31–41–51(–54) × (3.1–)3.4–3.9–4.3(–4.7) µm, mostly subcylindrical or narrowly clavate, apically mainly obtuse, contents heteromorphous, usually granulose. Pileocystidia near the pileus center slightly longer; terminal cells (33–)32–51–71(–86) × (3.1–)3.4–3.9–4.4(–4.6) µm, mostly subclavate or cylindrical, apically obtuse. **Cystidioid hyphae** in subpellis

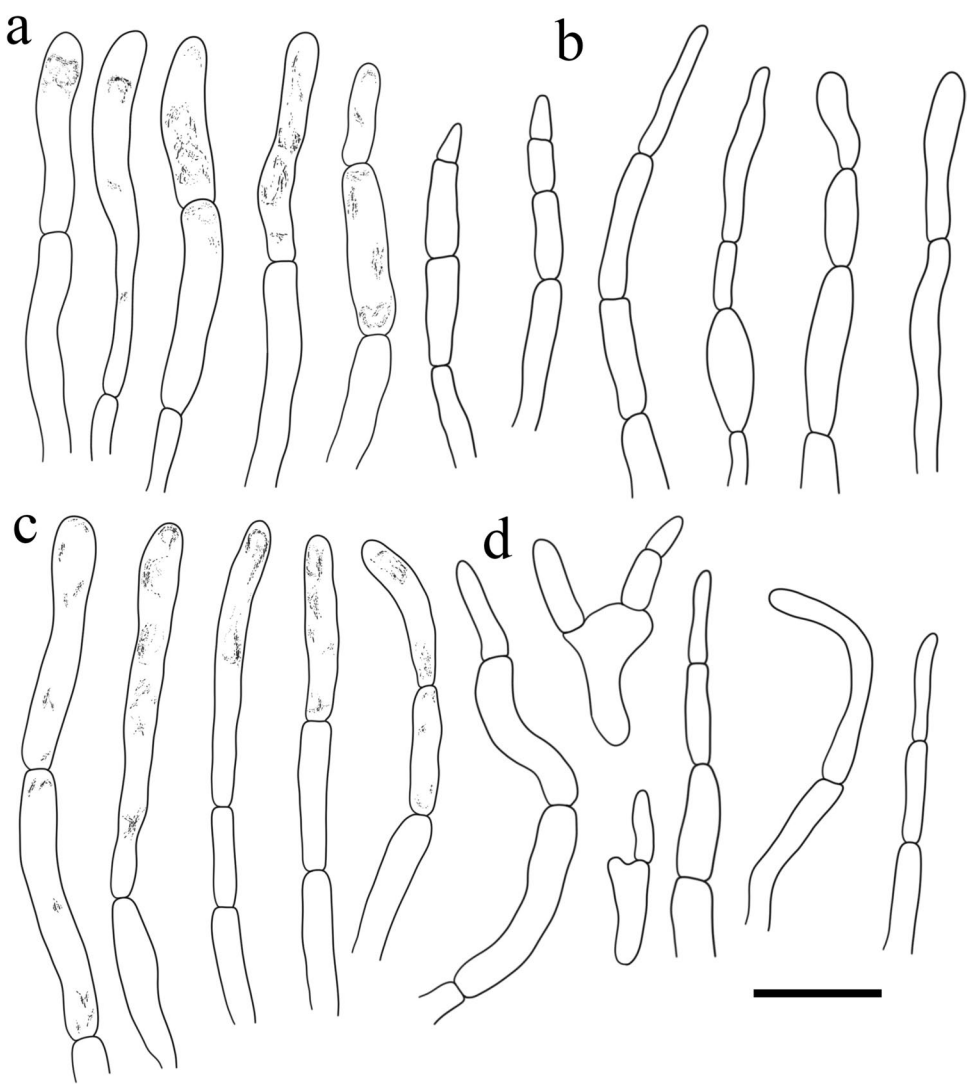


Fig. 161 ***Russula guilinensis*** (HMAS 287503, **holotype**), pileipellis. **a** Pileocystidia near the pileus center. **b** Hyphal terminations near the pileus center. **c** Pileocystidia near the pileus margin. **d** Hyphal terminations near the pileus margin. Cystidial contents as observed in Congo Red. Scale bar = 10 µm

and context dispersed, with heteromorphousgranulose contents, oleiferous hyphae frequent in the lower part of subpellis and context.

Material examined: CHINA, Guangxi Zhuang Autonomous Region, Guilin Municipality, Xing'an County, Mao'er Mountain Nature Reserve, Yeren Lake, 25°53′N 110°26′E, 2100 m asl, 1 Aug 2017, *An-Qi Liu*, *Guo-Jie Li*, *Hu-Sheng Ma*, *Ming-Zhe Zhang*, *Qi-Hui Mo*, *Xin-Zhan Liu*, *Yan-Lei Ding*, *Zhi-Lin Ling*, *GX20172286* (HMAS 287503, **holotype**), *GX20172514* (HMAS 287504).

GenBank: HMAS 287503: PP716400 (ITS), PP716405 (LSU), PP723162 (mitSSU), PP723231 (*rpb1*), PP723236 (*rpb2*), PP723241 (*tef1*); HMAS 287504: PP716401 (ITS), PP716406 (LSU), PP723163 (mitSSU), PP723232 (*rpb1*), PP723237 (*rpb2*), PP723242 (*tef1*).

Notes: Russula guilinensis belonging to subsection *Roseinae*. On the phylogenetic tree, *R. guilinensis* and *R. cynorhodon* are close (Figs. 158, 159), but they can be distinguished morphologically. The diameter of the pileus of *R. guilinensis* (67–77 mm) is larger than *R. cynorhodon* (14–49 mm). Not only that, when matures, the edge of the pileus of *R. guilinensis* is usually upturned, and the edge of the pileus of *R. cynorhodon* is usually inrolled (Manz et al. 2021). Morphologically, *R. guilinensis* is similar to *R. cordata* Looney, *R. pseudopeckii* Fatto and *R. velutipes* R. Heim, but phylogenetically they can be well distinguished (Sarnari 2005; Looney et al. 2022).

Russula pseudovirescens N. Roy, A.K. Dutta & Tanti, **sp. nov.**

MycoBank: MB 851248; *Facesoffungi*: FoF 15275; Figs. 162, 163, 164

Etymology: "*pseudovirescens*" refers to the morphological similarity to *R. virescens*.

Holotype: GUBH 20322.

Pileus small to medium-sized, 42–65 mm diam., convex with a slight central depression when young, becoming applanate to plano-convex with a depression towards the

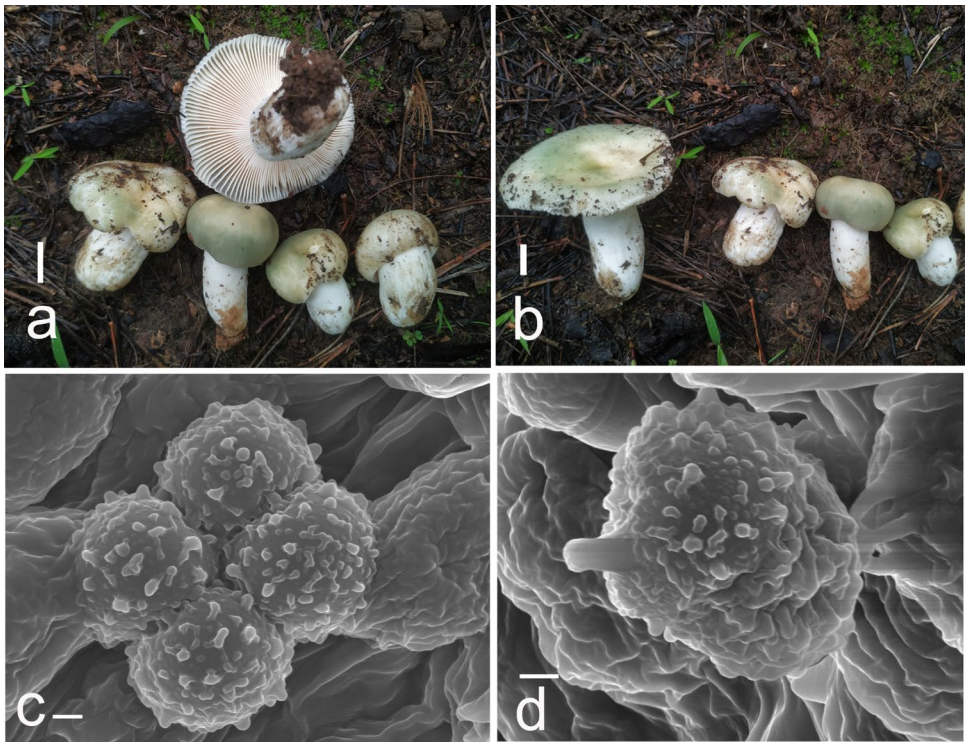


Fig. 162 *Russula pseudovirescens*. **a, b** Basidiomata. **c, d** SEM photograph of basidiospores. Scale bars: **a**, **b** = 1 cm, **c**, **d** = 1 µm

center to broadly convex with age; surface velvety, cracking to greenish patches, greenish green (27B5) to dull green (28D4) at the margin and viridine green (29A5) at the center when young to pastel green (27A4) at the margin to viridine green (29A5) towards the center when matured, unchanging on bruising and no reaction with KOH, very slowly turning red with guaiacol and unchanging with sulfovanillin, $FeSO_4$ and phenol; margin incurved, acute, translucent striate, not cracking on maturity; context ca.7 mm thick at the center, up to 3 mm thick at margin, white (1A1), unchanging with KOH, light red with guaiacol, unchanging with phenol, sulfovanillin and $FeSO_4$. **Lamellae** 3–5 mm broad, free, fragile, regular, distant with occasionally one series of lamellulae, white (6A1) to greenish white (28A2), discolors, pinkish red with sulfovanillin, orangish red with guaiacol, unchanging with KOH, phenol and $FeSO_4$. **Stipe** 35–42 × 18–25 mm, central, cylindrical with slightly tapered at base, straight to sometimes slightly curved, surface smooth, white (1A1), no changing on bruising and unchanging with KOH, slowly turning orange red to brick red with guaiacol, unchanging with sulfovanillin, phenol and $FeSO_4$; context stuffed, white, turning pale yellowish with KOH, light orangish red with guaiacol, unchanging with sulfovanillin, phenol and $FeSO_4$. **Spore-print** white. **Odor** sweet. **Taste** mild.

Spores (4.5–)5.0–6.4–6.5(–8.0) × (4.0–)4.5–6.0–6.5(–7.6) µm, globose to subglobose, hyaline, apiculus prominent, measuring 1.3 µm long, Q = 1.0–1.0–1.15; ornamentation small to medium sized, dense [(8–)10–12(–18) in a 3 µm diam. circle], composed of small amyloid conical warts, measuring 0.28–0.48 µm high, apex blunt, sometimes isolated, mostly fused (2–4 fusions in a circle), line connections (0–2 in a circle); suprahilar spot inamyloid. **Basidia** 36–48 × 7.5–10 µm, clavate, with oil droplets when viewed in KOH, thin-walled, 4-spored; sterigmata 1–1.5 µm long. **Basidioles** 28–38.5 × 6–10.0 µm, clavate, hyaline, thin-walled. Subhymenium pseudoparenchymatous. Lamellar trama mainly composed of spherocytes, measuring 36–43 × 9–15 µm. **Hymenial cystidia** dispersed, ca. 39.5–60 × 8.5–10 µm on gill sides, clavate to subclavate, thin-walled, apex obtuse or round to occasionally mucronate, mostly with heteromorphous contents towards the apex, not reacting with sulfovanillin, near gill edge ca. 33–52.5 × 5.5–9 µm, clavate to sphaeropedunculate, thin-walled, apically obtuse or round to occasionally mucronate, with heteromorphous contents towards to the apical part of the cystidium, no reaction with sulfovanillin. Lamellae edge consists of occasional basidia; **marginal cells** undifferentiated. **Pileipellis** a trichoderm, orthochromatic in Cresyl blue, sharply delimited from the underlying spherocytes of the context, up to 330–425 µm deep, disrupted towards the pileus margin, distinctly two layered, divided in a 25.5–46 µm deep suprapellis, composed of irregularly arranged, dense; subpellis comparatively less dense, consisting of irregularly arranged, hyaline hyphae measuring 5–10 µm broad. **Acid-resistant incrustations** absent. **Pileocystidia** arising from the hyphal terminations, towards the pileus margin measuring 30.5–47.5 × 2–5.5 µm, thin-walled, sub-cylindrical to fusiform, apically obtuse or acute, sometimes round or

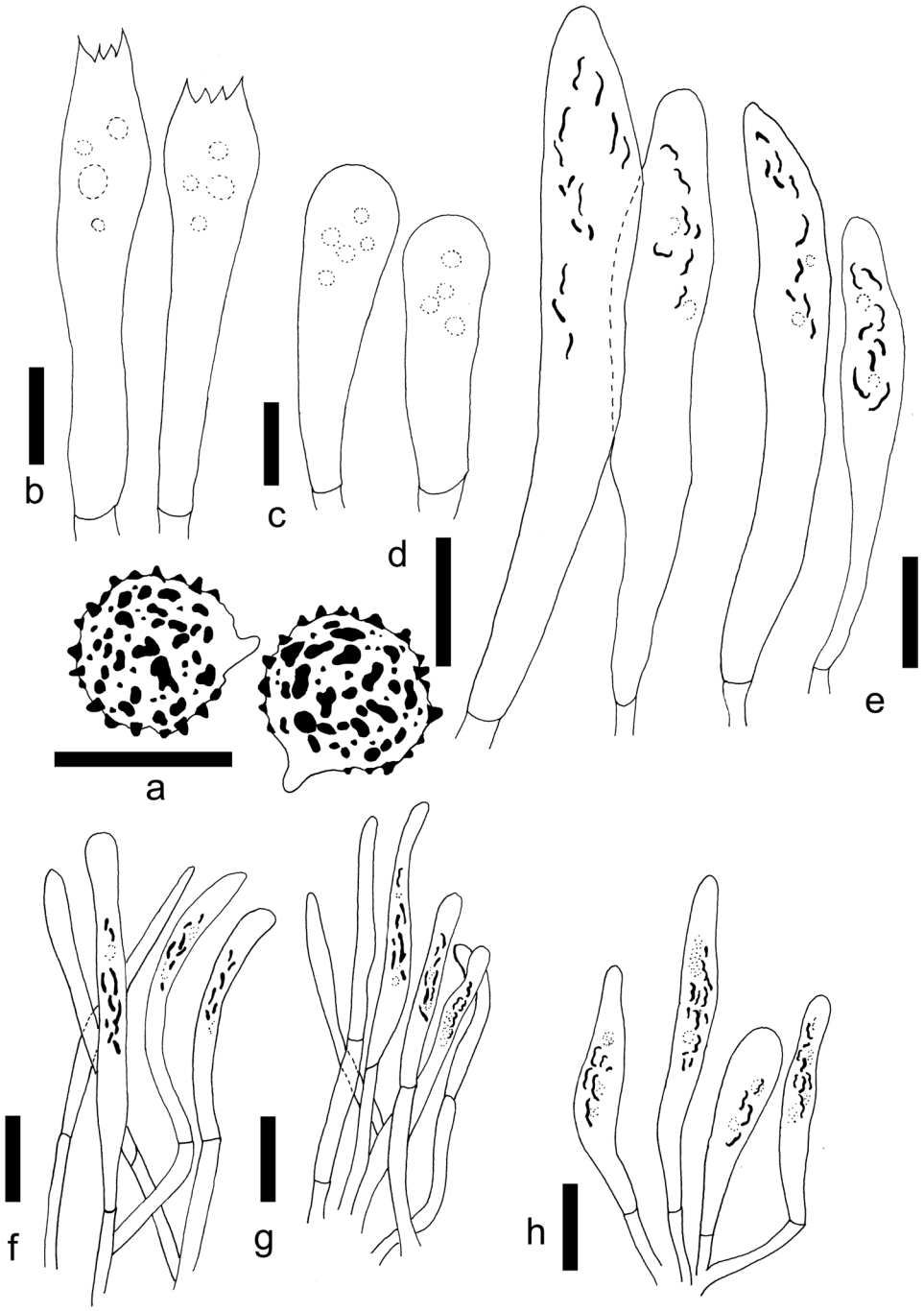


Fig. 163 ***Russula pseudovirescens*** (GUBH 20322, **holotype**). **a** Basidiospores. **b** Basidia. **c** Basidioles. **d** Hymenial cystidia near the lamella sides. **e** Hymenial cystidia on the lamella edges. **f** Pileocystidia with terminal cells near the pileus margin. **g** Pileocystidia with terminal cells near the pileus center. **h** Caulocystidia. Scale bars: **a** = 5 µm, **b**–**h** = 10 µm

mucronate, contents heteromorphous, not reacting with sulfovanillin, terminal cells towards the margin measuring 28–45 × 1.8–5 µm, thin-walled, sub-cylindrical, with a round apex; Pileocystidia towards the pileus center scarce, similar in shape, measuring 30–46 × 2.2–5 µm, thin-walled, sub-cylindrical to fusiform, apically obtuse or acute, sometimes round or mucronate, contents heteromorphous, not reacting with sulfovanillin, terminal cells towards the center similar in size and shape, measuring 30–40 × 2–4.5 µm, thin-walled, sub-cylindrical, with a round apex. **Stipitipellis** up to 146–160 µm thick, hyphae 1–2 µm broad, **Caulocystidia** 25.6–38.5 × 2.5–6.4 µm, thin-walled, ventricose to cylindrical in shape with a blunt apex. **Stipe trama** composed of subglobose spherocytes, measuring 15–38 × 9–19.0 µm. **Clamp-connections** absent in all tissues.

Habit and habitat: Solitary, scattered, under *Pinus kesiya*.

Material examined: INDIA, Meghalaya, East Khasi Hills District, Umshing Mawkynroh, 25°36′51"N, 91°53′30"E, 1365 m a.s.l., under *Pinus kesiya* tree, 15 Jun 2022, *N. Roy*, *B. Tanti & A.K. Dutta* (GUBH 20322, **holotype**);

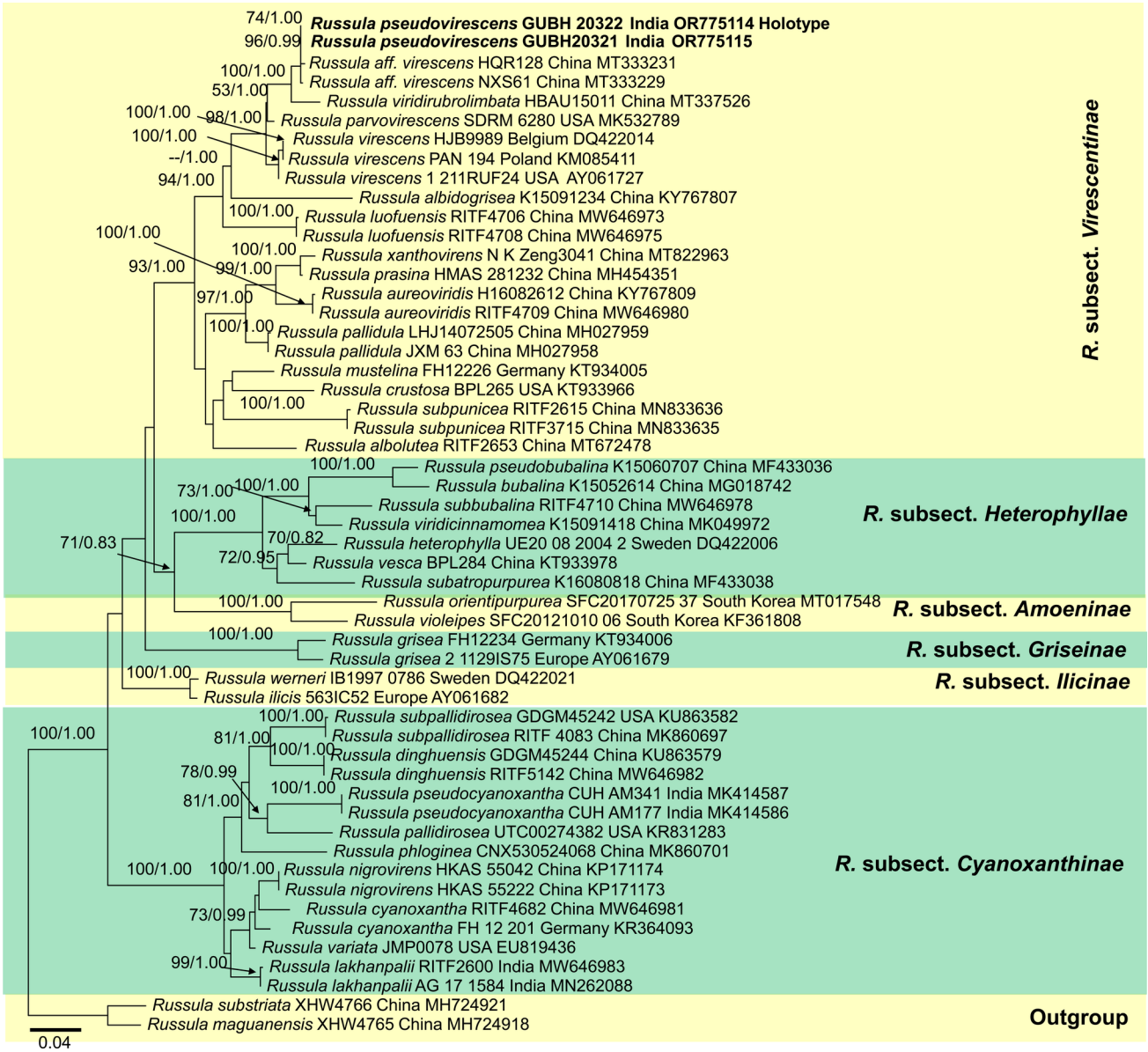


Fig. 164 Maximum Likelihood tree (−*InL* = 6185.166981) generated using GTR + I + G model of nucleotide evolution. Values to the left of '/' are MLBS support, and those to the right of '/' indicate Bayesian posterior probabilities (PP) support. MLBS values ≥ 70% and PP values ≥ 0.80 are shown above or below the nodes. Sequences generated for this study are in **bold**. Specimen voucher number, Country of origin and GenBank accession numbers are indicated after each taxon name

Meghalaya, East Khasi Hills District, Umshing Mawkynroh, 25°36′43"N, 91°53′38"E, 1436 m a.s.l., under *Pinus kesiya* tree, 15 Jun 2022, *N. Roy*, *B. Tanti & A.K. Dutta* (GUBH 20321).

GenBank: GUBH 20322: OR775114 (ITS); GUBH 20321: OR775115 (ITS).

Notes: *Russula pseudovirescens* is easily recognized by its small to medium-sized pileus with a greenish-green to viridine-green cracked surface towards the margin, which turns red with guaiacol; free lamellae with occasionally one series of lamellulae; a sweet smell; basidiospores with ornamentations composed of small, amyloid, conical warts; hymenial cystidia mostly clavate to subclavate in shape with an obtuse apex; and a trichoderm type of pileipellis composed of sub-cylindrical to fusiform pileocystidia.

In the phylogenetic tree (Fig. 164), *Russula pseudovirescens* group together with other well-known members of *R.* subsect. *Virescentinae* (MLBS = 93%, PP = 1.00), confirming its systematic position within the subsection. The newly generated two Indian sequences of *R. pseudovirescens* cluster together (MLBS = 96%, PP = 0.99) with two earlier deposited sequences from China in the GenBank database

after the name *Russula* aff. *virescens* (GenBank MT333229 and MT333231), suggesting all the sequences to be conspecific. However, there were no detailed descriptions available for *Russula* aff. *virescens*. Besides, the phylogenetic tree also confirms that the specimen is distinct from that of *Russula virescens* and is herein described as a new species (Fig. 164).

Apparently, *Russula pseudovirescens* can be confused with *R. virescens,* but *R. virescens* is primarily of European origin, whereas *R. pseudovirescens* is of Asian origin. Besides, *R. virescens* has a comparatively larger pileus (up to 125 mm diam.), sparsely forked and intervened lamellae, a larger stipe (40–90 × 20–45 mm), fusiform hymenial cystidia with a papillate or capitulate tip, and the absence of pileocystidia (Sarnari 2005).

Among other phylogenetically related taxa, *Russula viridirubrolimbata* differs from *R. pseudovirescens* by a larger pileus colored grass green at the center and darker red towards the margin and the presence of larger hymenial cystidia (78–107 × 8–10 µm) of fusiform to spindle-shaped (Deng et al. 2020). *Russula parvovirescens* has greenish brown to metallic bluish green or dark olive green pileus, the context of which discolors to ferruginous on exposure, somewhat larger basidiospores (mean of 7.5–8.0 × 6.4–6.5 µm vs. 6.4 × 6.0 µm in *R. pseudovirescens*), and longer hymenial cystidia (50–70 × 6–9 µm; Buyck et al. 2006).

Pucciniomycetes R. Bauer, Begerow, J.P. Samp., M. Weiss & Oberw.

Pucciniales Caruel.

Synonym: Pucciniales Clem. & Shear; Uredinales G. Winter.

Notes: Pucciniales (= Uredinales) has been known as rust fungi and one of the largest orders in fungi, containing about 8,000 species, more than 300 genera and 13 families (Cummins and Hiratsuka 2003; Aime 2006; Aime et al. 2006; Bauer et al. 2006; Aime et al. 2018a, b; Aime and McTaggart 2021). They are obligate parasites of vascular plants and have been reported worldwide. Each species is known to be parasitic on taxonomically narrow groups of plants (host specificity), which is suspected as the result of the co-evolution between rust fungi and their host plants. Many species cause serious plant diseases in agriculture and forestry. They have unique characteristics and produce five types of morphologically and functionally different spores (spermatium, aeciospore, urediniospore, teliospore, and basidiospore). Thick-walled urediniospore called amphispore is also produced in many species for wintering. Depending on the types of spores produced, six different rust fungi life cycles have been recognized. Furthermore, heteroecious species need two taxonomically different host plants to complete their life cycles, whereas autoecious species complete their life cycles on a single host plant (Cummins and Hiratsuka 2003; Aime 2006; Aime et al. 2017, 2018a; Aime and McTaggart 2021). After applying molecular phylogenetic approaches to rust fungi systematics, many new genera and changes to existing genera have been proposed. Aime and McTaggart (2021) proposed seven new suborders and 18 family systems mainly based on phylogenetic analyses. Zhao et al. (2021) also proposed an additional 3 families. These new family systems are different from the systems based on morphology, whereas still partially supported by morphological characters.

Pucciniaceae Chevall., **emend.** Aime & McTaggart.

Synonyms: Pucciniosiraceae (Dietel) Cummins & Y. Hirats.; Endophyllaceae Dietel.

Notes: Pucciniaceae was established by Chevallier (1826) and circumscribed by Cummins and Hiratsuka (2003) based on morphological characteristics. However, Aime and McTaggart (2021) emended this family based on the results of phylogenetic analyses. Spermogonia are type 4 (group V) of Cummins and Hiratsuka (2003), and aecia are aecidium types of Cummins and Hiratsuka (2003). Uredinia are mostly the uredo-type of Cummins and Hiratsuka (2003). Teliospores are borne singly, mostly pedicellate, and typically with 1 or 2 cells. Basidia are external. Most species are macrocyclic but many endocyclic and microcyclic species are as well. Life cycles are heteroecious or autoecious.

Puccinia Pers.

Notes: The genus *Puccinia* was described by Persoon (1801), but its description was simple and rough. Cummins and Hiratauka (2003) described this genus as follows: Spermogonia subepidermal, group V (type 4). Aecia subepidermal, erumpent, either *Aecidium*-type with peridium and catenulate and verrucose spores or *Uredo*-type with mostly echunulate spores borne singly on pedicels. Uredinia subepidermal, erumpent, without peridium, but may have paraphyses, *Uredo*-type or sometimes *Aecidium*-type; urediniospores borne singly on pedicels, mostly echinulate, germ pores various, or with peridium and catenulate and verrucose. Telia subepidermal, erumpent in most species, but remaining covered by epidermis and divided into locules by stromatic paraphyses in some species; teliospores typically 2-celled by transverse septum (but may have 1-celled and sometimes 3- or 4-celled spores in some species), borne singly on pedicels, basal sporogenous cells none to highly developed, spore wall mostly pigmented, but degree of pigmentation varies widely, smooth or variously sculptured, germ pore 1 in each cell, but not differentiated in a few species; basidia external. This genus is the largest genus of Pucciniales, with about 3,000 to 4,000 species. Both heteroecious and autoecious species occur in this genus. Because of morphological variations among species in this genus and difficulties in its delimitation, it has been suspected that *Puccinia* is a complex of

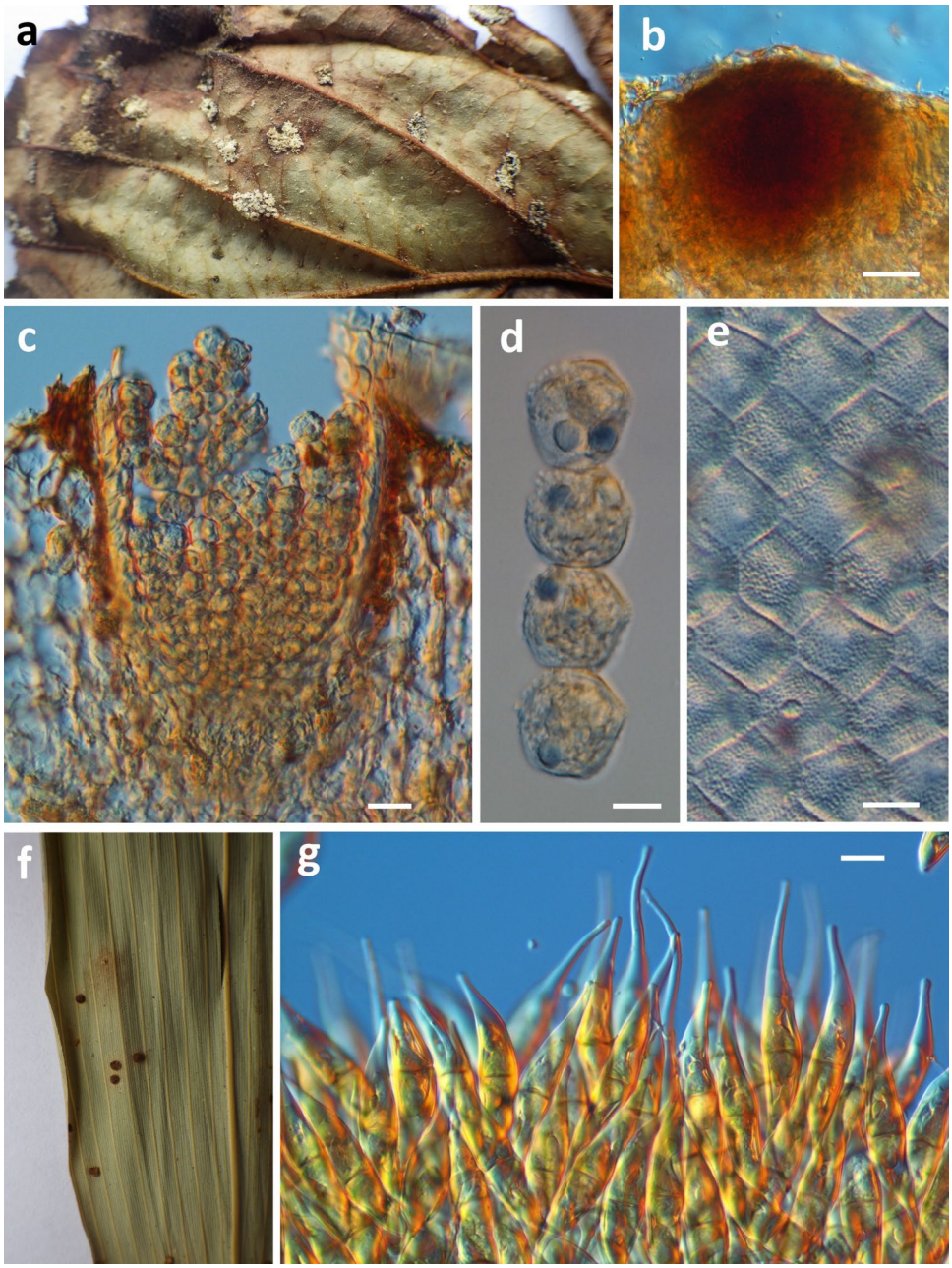


Fig. 165 ***Puccinia hamamelidis***. **a–e** Sermogonial and aecial specimen on *Hamamelis japonica* (TSH-R1601). **a** Aecia produced on the lower leaf surface. *b* Vertical section of a spermogonium. **c** Vertical section of an aecium. **d** Aeciospores with big granules on the surface. **e** Inner surfaces of peridial cells. **f, g** Telial specimen on *Sasa yahikoensis* (TSH-R0795, Epitype). **f** Telia produced on the lower leaf surface. **g** Teliospores. Scale bars: **b** = 100 µm, **c** = 25 µm, **d, e** = 10 µm, **g** = 30 µm

genera and a group of phylogenetically different taxons. Recently, 5 genera, *Puccorchidium* Beenken (Beenken and Wood 2015), *Austropuccinia* Beenken (Beeken 2017), *Neopuccinia* A. Martins Jr (Martins Junior et al. 2019), *Novopuccinia* Y.M. Liang & Y. Liu (Liu et al. 2021b) and *Pseudocerradoa* M. Ebinghaus & Dianese (Ebinghaus et al. 2022) were newly described and separated from *Puccinia*.

Twenty four species of *Puccinia* producing uredinia and/or telia on species of Bambusoideae (Poaceae) have been described until now, and they are distributed mainly in Asia: *P. aduncata* F. He & Kakish., *P. arundinariae* Schwein., *P. bambusarum* (Henn.) Arthur, *P. bambusicola* S.X. Wei & J.Y. Zhuang, *P. bracystachyicola* I. Hino & Katum., *P. corticioides* Berk, & Broome (= *Stereostratum corticioides* (Berk. & Broome) H. Magnus), *P. cymbiformis* F. He & Kakish., *P. deformata* Berk. & M. A. Curtis (= *P. amianthina* Syd. & P. Syd.), *P. deutziae* (Dietel) Kakish., K. Hosaka & Hosoya (= *P. kusanoi* Dietel), *P. flammuliformis* I. Hino et Katum., *P. hikawaensis* Hirats, f. & S. Uchida, *P. kwanhsienensis* F.L.Tai, *P. longicornis* Pat. & Har., *P. mitriformis* S. Ito, *P. neoporteri* I. Hino & Katum., *P. nigroconoidea* I. Hino & Katum., *P. phyllostachydis* Kusano, *P. sasae* Kusano, *P. sasicola* Hara ex I. Hino & Katum., *P. scabrida* F. He & Kakish., *P. sinarundinariae* J.Y. Zhung & S.X. Wei, *P. suzutake* Kakish. & S. Sato, *P. tenella* Hino & Katum., *P. xanthosperma* Syd. & P. Syd. (Ito 1950; Hino

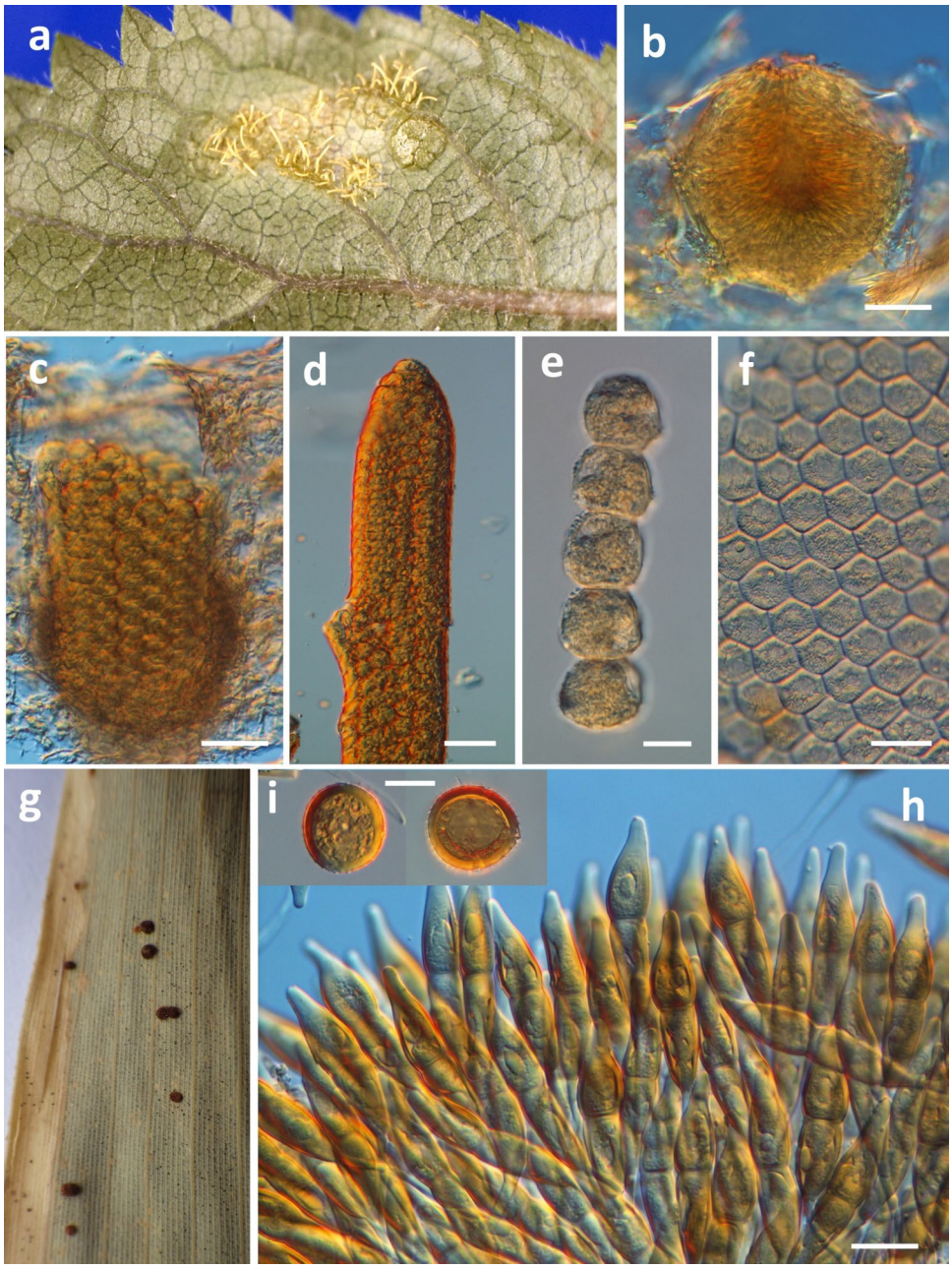


Fig. 166 ***Puccinia hydrangeicola.*** **a**–**f** Spermogonial and aecial specimen on *Hydrangea hirta* (TSH-R0305). **a** Aecia produced on lower leaf surface. **b** Vertical section of a spermogonium. **c** Vertical section of an aecium produced in host plant. **d** Upper part of an aecium. **e** Aeciospores with big granules on the surface. **f** Inner surfaces of peridial cells. **g**–**i** Uredinial and telial speciems on *Sasamorpha borealis* var. *borealis* (TSH-R0301, Epitype, Holotype of *P. suzutake*). **g** Telia produced on the lower leaf surface. **h** Teliospores. **i** Urediniospores. Scale bars: **b** = 150 µm, **c, d** = 50 µm, **e, h, i** = 20 µm, **f** = 40 µm

and Katumoto 1960; Hiratsuka 1960; Katumoto 1968; Cummins 1971; Tai 1979; Kakishima and Sato 1981; Wang and Wei 1983; Wei and Zhuang 1990; Hiratsuka and Chen 1991; Hiratsuka et al. 1992; Zhuang and Wei 1992; He et al. 1993; Zhuang et al. 1998; Azbukina 2015; Okane et al. 2021; Zhao et al. 2021; Kakishima et al. 2023). Among them, 4 species are required taxonomic reconsiderations following to International Code of Nomenclature for algae, fungi, and plants (ICNafp) (ICNafp Shenzhen Code, Turland et al. 2018). Three new combinations and 1 new name are proposed here.

Puccinia hamamelidis (Dietel) Jing X. Ji & Kakish., **comb. nov.**

MycoBank: MB 850294; *Facesoffungi*: FoF 14966; Fig. 165

Basionym: *Aecidium hamamelidis* Dietel, Botanische Jahrbücher für Systematik Pflanzengeschichte und Pflanzengeographie 27: 571, 1899 [MB 244817].

Homotypic synonym: *Novopuccinia hamamelidis* (Dietel) Y. Liu & Y.M. Liang, Frontiers in Microbiology 12 (no. 648890): 6, 2021 [MB 838359].

Heterotypic synonyms: *Aecidium hamamelidis* Magnus, Berichte der Deutschen Botanischen Gesellschaft 19: 297, 1901 [MB244522]; *Puccinia mitriformis* S. Ito, Journal of the Colledge of Agriculture, Tohaku Imperial University:

233, 1909 [MB 149329]; *Dicaeoma mitriforme* (S. Ito) Syd., Annales Mycologici 20 (3): 118, 1922 [MB 271424].

Type: **Lectotype** in Herbarium of Botanischer Garten, Berlin, Germany (B), Spermogonia and aecia on *Hamamelis japonica* Zieb & Zucc. (as *Hamamelidis japonicae* Zieb. & Zucc.), JAPAN, Tochigi Prefecture, Nikko, August 1895, *M. Miyoshi*, B700109001, MycoBank MBT10016651 (**Isolectotype** B700109002). **Epitype** in TSH, designated here because the holotype specimen has only spermogonia and aecia, and telia on epitype specimen are important characteristics to specify this species, Telia on *Sasa yahikoensis* Mak., JAPAN, Gunma Prefecture, Minakami, 16 May 1988, TSH-R0795, MycoBank MBT10016652.

Description: **Spermogonia** subepidermal, flask shaped, type 4 of Cummins and Hiratsuka (2003). **Aecia** pale yellow to brown, cylindrical with peridia; aeciospores catenulate, broadly obovoid or nearly globose, 22–30 × 20–26 µm, walls hyaline, verrucose with big granules, 1.5–2.5 µm thick. **Telia** phypophyllous, early exposed, brown to dark brown, teliospores long ellipsoid to fusiform, 90–130 × 16–25 µm, walls yellowish brown to pale brown, minutely rugose to smooth, thickness different in each side, 2–3 µm thick at the one sides, much thicker at the opposite sides, 40–70 µm thick at apices, 1-celled spores sometimes mixed, pedicels persistent, hyaline, long, up to 250 µm long.

Specimens examined: **Spermogonia and aecia** on *Hamamelis japonica* Sieb. & Zucc., JAPAN, Fukushima, Mt. Iimori, 6 August 1995, TSH-R1601. **Telia** on *Sasa yahikoensis* Mak., JAPAN, Gunma, Minakami, 18 April 1988, TSH-R0790; JAPAN, Gunma, Minakami, 16 May 1988, TSH-R0795 (Epitype), TSH-R0797.

Host plants and Distribution: **Spermogonia and aecia** on *Hamamelis japonica* Sieb. & Zucc. (JAPAN); *H. japonica* var. *obtusata* Matsum. (= *H. obtusata* Mak.) (JAPAN); *H. japonica* var. *obtusata* f. *discolor* Ohwi (= *H. obtusata* var. *discolor* Nakai) (JAPAN). **Telia** on *Sasamorpha borealis* (Hack.) Nakai var. *borealis* (JAPAN); *S. kohzegawana* Koidz. (JAPAN); *S. paniculata* var. *nobilis* Mak. & Uchida (= *S. nobilis* Nakai) (JAPAN); *S. kurilensis* (Rupr.) Mak. & Shibata (= *S. paniculata* var. *paniculata* Nakai) (JAPAN); *S. septentrionalis* Mak. (JAPAN); *S. yahikoensis* Mak. (JAPAN); *Sasa* sp. (CHINA) (Dietel 1899; Ito 1950; Hiratsuka 1960; Uchida 1965; Katumoto 1968; Hiratsuka and Sato 1970; Cummins 1971; Tai 1979; Hiratsuka et al. 1992; Zhuang et al. 1998; Liu et al. 2021b).

Notes: *Aecidium hamamelidis* is an anamorph (spermogonial and telial stages) of *P. mitriformis* because the life cycle of this species was clarified with inoculations by Hiratsuka and Sato (1970). Therefore, both species are identical and should be treated as the same species. *Aecidium hydrangeicola* is the legitimate earliest name of this species. Although *Aecidium* Pers. 1796 is a sanctioned former anamorphic genus name of rust fungi, *Puccinia* Pers. 1794 similarly sanctioned has its priority (Aime et al. 2018b). Therefore, we propose a new combination, *Puccinia hamamelidis* (Dietel) Jing X. Ji & Kakish. in *Puccinia* for this species under the ICNafp Shenzhen Code (Turland et al. 2018), to avoid taxonomic confusion. *Aecidium hamamelidis* was included in a new genus, *Novopuccinia* and treated as *N. hamamelidis* (Dietel) Y. Liu & Y.M. Liang by phylogenetic analyses (Liu et al. 2021b). However, this genus was phylogenetically included in a large clade of *Puccinia* and could not be considered as an independent lineage. Liu et al. (2021a, b) also reported that *Stereostratum corticioides* (Berk. & Broome) H. Magnus was phylogenetically close to this new genus, but this species was assigned to *Puccinia* as *Puccinia corticioides* Berk. & Broome by Okane et al. (2021) and Zhao et al. (2021) in their phylogenetic analyses. Therefore, we consider that *Aecidium hamamelidis* is a member of *Puccinia*. Specimens deposited in the Mycological Herbarium of Faculty of Life and Environmental Sciences, University of Tsukuba, Japan (TSH) were examined and photographed.

Puccinia hydrangeicola (Henn.) Jing X. Ji & Kakish., **comb. nov.**

MycoBank: MB 850296; *Facesoffungi*: FoF 14968; Fig. 166

Basionym: *Aecidium hydrangeicola* Henn., Botanische Jahrbücher für Systematik Pflanzengeschichte und Pflanzengeographie 28 (2): 264, 1900 [MB 631419].

Obligate synonym: *Aecidium hydrangiicola* Henn., 1900 [MB 235202].

Heterotypic synonym: *Puccinia suzutake* Kakish. & S. Sato, Transactions of the Mycological Society of Japan 22: 325, 1981 [MB 110061].

Type: **Holotype** in Herbarium of Botanischer Garten, Berlin, Germany (B), Spermogonia and aecia on *Hydrangea thunbergii* Sieb., JAPAN, Tochigi Prefecture, August 1896, M. Shirai, B700109004, MycoBank MBT10016656. **Epitype** in TSH, designated here because the neotype specimen has only spermogonia and aecia, and uredinia and telia on epitype specimen are important characteristics to specify this species, Uredinia and telia on *Sasamorpha borealis* (Hack.) Nakai var. *borealis*, JAPAN, Ibaraki Prefecture, Mt. Tsukuba, 15 April 1979, TSH-R0301 (Holotype of *P. suzutake*), MycoBank MBT10016657.

Description: **Spermogonia** amphigenous, subepidermal, flask-shaped, type 4 of Cummins and Hiratsuka (2003). **Aecia** hypophyllous or petiolicolous, pale yellow; aeciospores catenulate, subglobose to broadly ellipsoid, often angular, 24–32 × 20–28 µm, walls ca. 0.5 µm thick, hyaline, verrucose with big granules; inner surfaces of peridial cells densely verrucose. **Uredinia** hypophyllous, light brown to brown, with hyaline capitate paraphyses; urediniospores subglobose to obovoid, 36–43 × 33–40 µm, walls 3–5 µm thick, chestnut-brown, echinulate, 5 equatorial germ pores. **Telia**

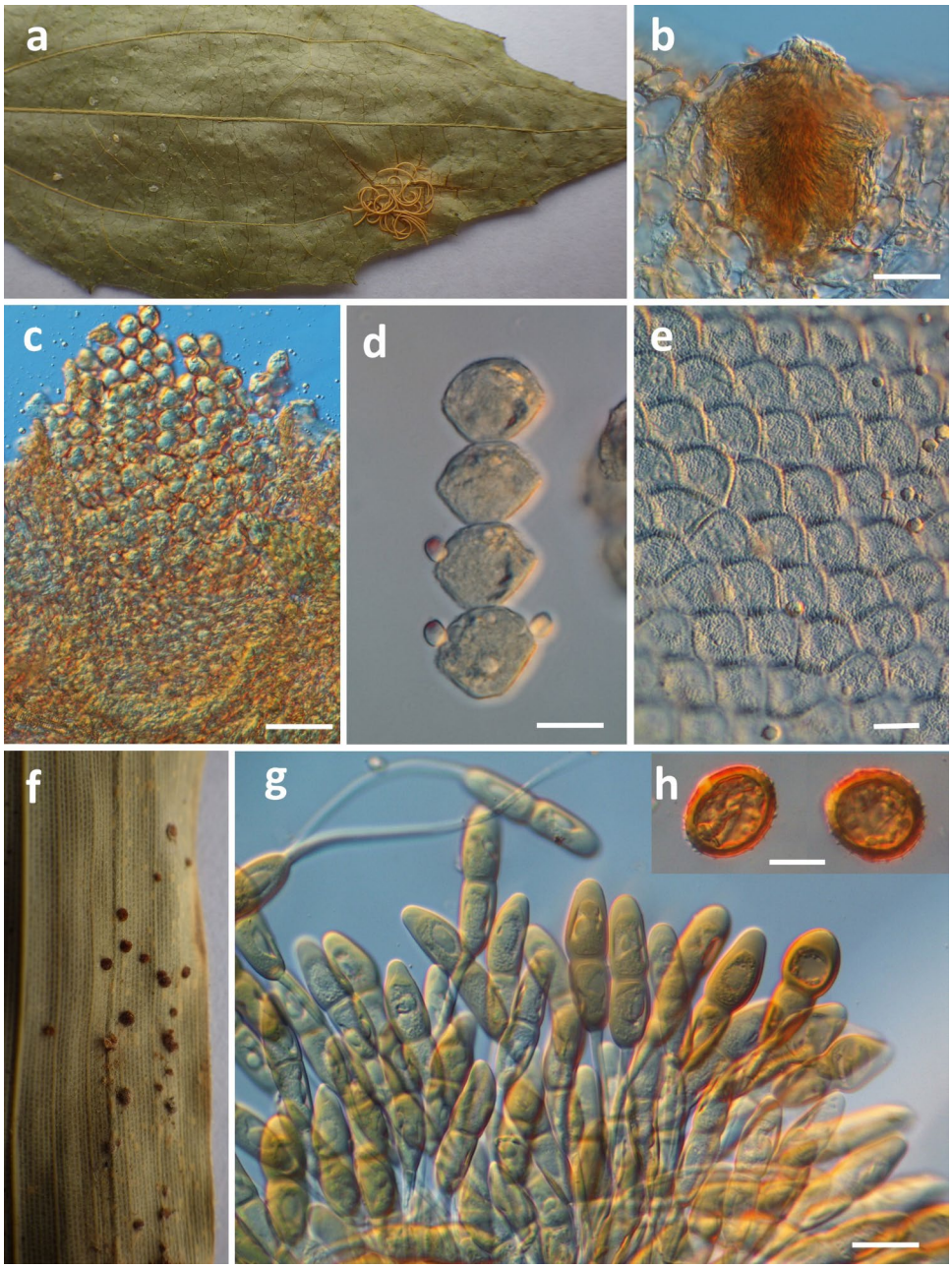


Fig. 167 ***Puccinia philadelphi***. **a–e** Spermogonial and aecial specimen on *Philadelphus satsumi* (TSH-R0522, Neotype). **a** Aecia produced on the lower leaf surface. **b** Vertical section of a spermogonium. **c** Vertical section of an aecium. **d** Aeciospores with big granules on the surface. **e** Inner surfaces of peridial cells. **f–h** Uredinial and telial specimen on *Sasamorpha borealis* var. *borealis* (TSH-R0519, Epitype). **f** Telia produced on the lower leaf surface. **g** Teliospores. **h** Urediniospores. Scale bars: **b** = 100 µm, **c** = 50 µm, **d** = 20 µm, **e, g, h** = 30 µm

hypophyllous, dark brown; teliospores fusiform to oblong-fusiform, constricted at septa, 52–96 × 11–22 µm, walls 1.5–2 µm thick at sides, 3–22 µm at apices, light brown to chestnut-brown, smooth; pedicels up to 80 µm long, pale yellow, persistent. A small number of broadly ellipsoid teliospores also present (40–64 × 18–26 µm).

Specimens examined: **Spermogonia and aecia** on *Hydrangea hirta* Sieb. et Zucc., JAPAN, Ibaraki, Mt. Tsukuba, 28 June 1979, TSH-R0305; JAPAN, Ibaraki, Tsukuba, 14 June 1979, TSH-R0307. **Uredinia and telia** on *Sasamorpha borealis* (Hack.) Nakai var. *borealis*, JAPAN, Ibaraki, Mt. Tsukuba, 15 April 1979, TSH-R0301 (Neotype, Holotype of *P. suzutake*).

Host plants and Distribution: **Spermogonia and aecia** on *Hydrangea angustipetala* Hayata (TAIWAN); *H. hirta* Sieb. & Zucc. (JAPAN); *H. longifolia* Hayata (JAPAN, TAIWAN); *H. macrophylla* var. *thunbergii* Mak. (= *H. thubergii* Sieb.) (JAPAN); *H. petiolaris* Sieb. & Zucc. (RUSSIAN FAR EAST); *H. umbellata* Rehdr (CHINA); *Hydrangea* sp. (CHINA). **Uredinia and telia** on *Sasa senanensis* (Fr. et Sav.) Rehder (RUSSIAN FAR EAST); *Sasamorpha borealis* (Hack.) Nakai var. *borealis* (= *Sasa borealis* Hack.) (JAPAN) (Hennings 1900b; Ito 1950; Hiratsuka 1960; Tai 1979; Kakishima and Sato 1981; Hiratsuka and Chen 1991; Hiratsuka et al. 1992; Zang et al. 1996; Azbukina 2015).

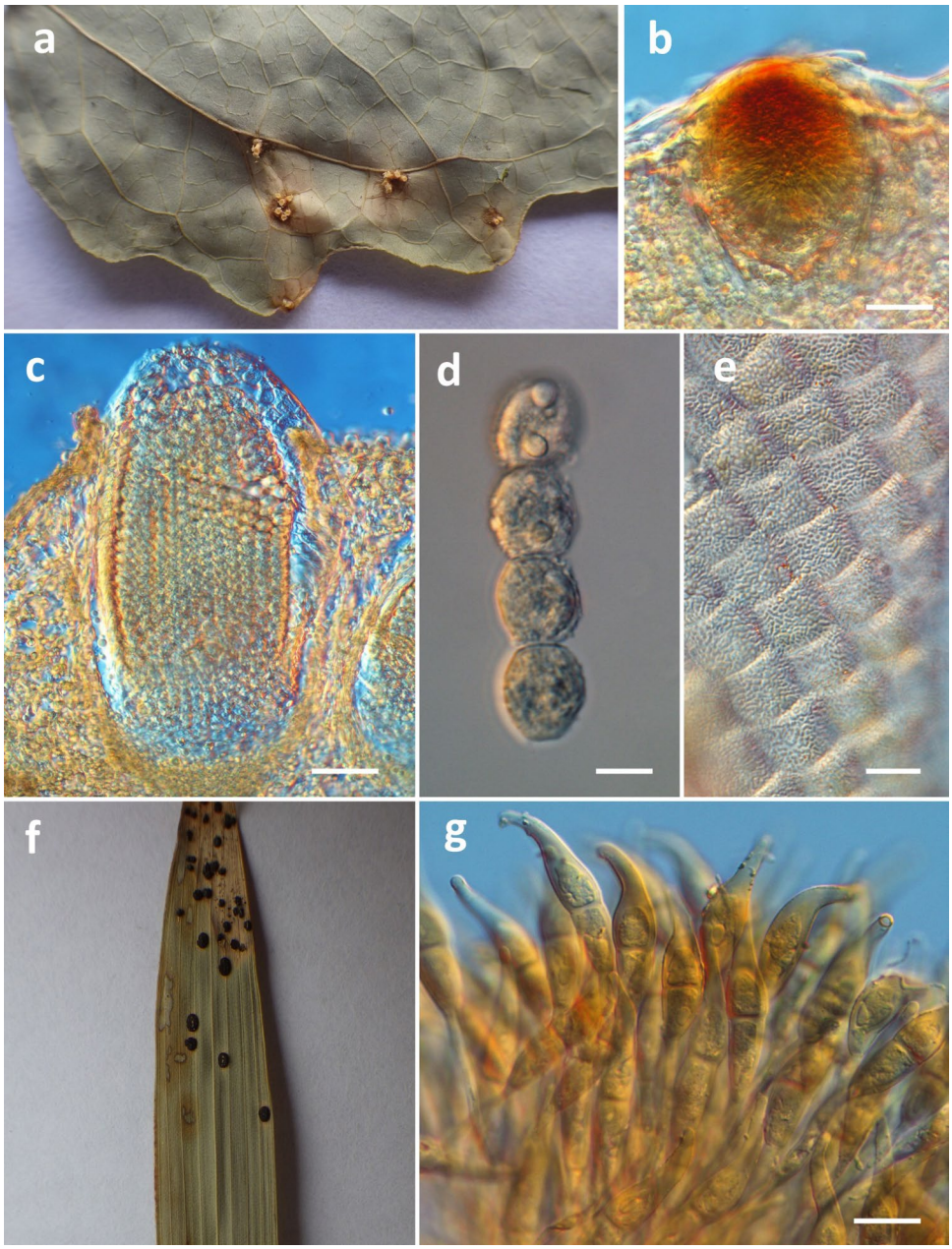


Fig. 168 ***Puccinia shojiana.*** **a–e** Spermogonial and aecial specimen on *Akebia quinate* (TSH-R3953). **a** Aecia produced on the lower leaf surface. **b** Vertical section of a spermogonium. **c** Vertical section of an aecium. **d** Aeciospores with big granules on the surface. **e** Inner surfaces of peridial cells. **f, g** Telial specimen on *Phyllostachys nigra* var. *henonis* (TSH-R18509, Epitype). **f** Telia produced on the lower leaf surface. **g** Teliospores. Scale bars: **b** = 100 µm, **c** = 50 µm, **d** = 20 µm, **e** = 30 µm, **g** = 40 µm

Notes: *Aecidium hydrangeicola* is an anamorph (spermogonial and telial stages) of *P. suzutake* because life cycle of this species was clarified with inoculations by Kakishima and Sato (1981). Therefore, both species are identical and should be treated as a same species. *Aecidium hydrangeicola* is the legitimate earliest name of this species. Although *Aecidium* Pers. 1796 is a sanctioned former anamorphic genus name of rust fungi, *Puccinia* Pers. 1794 similarly sanctioned has its priority (Aime et al. 2018b). Therefore, we propose a new combination, *Puccinia hydrangeicola* (Henn.) Jing X. Ji & Kakish in *Puccinia* for this species under the ICNafp Shenzhen Code (Turland et al. 2018) to avoid taxonomic confusion. Specimens deposited in Mycological Herbarium of Faculty of Life and Environmental Sciences, University of Tsukuba, Japan (TSH) were examined and photographed.

Puccinia philadelphi (Dietel) Jing X. Ji & Kakish., **comb. nov.**

MycoBank: MB 850295; *Facesoffungi*: FoF 14967; Fig. 167

Basionym: *Aecidium philadelphi* Dietel, Annales Mycologici 12 (1): 85, 1914 [MB 173969].

Heterotypic synonym: *Puccinia hikawaensis* Hirats. f. & S. Uchida, in Uchida, Mem. Mejiro Gakuen Woman's Jr College 2: 24, 1965 [MB 322030].

Type: **Neotype** in TSH, Designated here because holotype specimen on *Philadelphus satsumi* Sieb. ex Lindl. et Paxton (as *Philadelphus coronarius* L. var. *satsumi* Max.) collected in Nikko, Japan in June 1903 by N. Nambu (Dietel 1914) has not been found any herbarium in the world, Spermogonia and aecia on *Philadelphus satsumi* Sieb. ex Lindl. et Paxton, JAPAN, Nagano Prefecture, Minamisaku, Kawakami-mura, 8 August 1987, TSH-R0522, MycoBank MBT10016653. **Epitype** in TSH, designated here because the neotype specimen has only spermogonia and aecia, and uredinia and telia on epitype specimen are important characteristics to specify this species, Uredinia and telia on *Sasamorpha borealis* (Hack.) Nakai var. *borealis,* JAPAN, Nagano Prefecture, Minamisaku, Kawakami-mura, 29 April 1989, TSH-R0519, MycoBank MBT10016654.

Description: **Spermogonia** subepidermal, flask-shaped, type 4 of Cummins and Hiratsuka (2003). **Aecia** hypophyllous, pale yellow to brown, sparsely to loosely aggregate, minute, shortly cylindrical and fragile with peridia; aeciospores globose to ellipsoid, often angular, 25–34 × 20–28 µm, walls verrucose with big granules, hyaline,1.5 µm thick; peridial cells nearly cubic, outer walls finely striate, 5–7µ thick, inner walls verrucose, 3–4 µm thick. **Uredinia** hypophyllous, dark brown, with capitate paraphyses; urediniospores 28–39 × 28–32 µm, mostly broadly obovoid; walls chestnut brown, echinulate, 3–5 µm thick, germ pores 4 or 5, equatorial. **Telia** hypophyllous, cinnamon-brown; teliospores 45–67 × 16–28 µm, fusiform, walls yellow to brown, smooth, 3–5 µm thick at sides, 6.5–9 µm at apices; pedicels hyaline, thick-walled, persistent, up to 90 µm long.

Specimens examined: **Spermogonia and aecia** on *Philadelphus satsumi* Sieb. ex Lindl. et Paxton, JAPAN, Nagano, Minamisaku, Kawakami-mura, 8 August 1987, TSH-R0522 (Neotype); JAPAN, Ibaraki, Tsukuba, 6 July 1989, TSH-R0523. **Uredinia and telia** on *Sasamorpha borealis* (Hack.) Nakai var. *borealis,* JAPAN, Nagano, Minamisaku, Kawakami-mura, 29 April 1989, TSH-R0519 (Epitype).

Host plants and Distribution: **Spermogonia and aecia** on *Philadelphus tenuifolius* Rupr & Maxm. (KOREA); *P. satsumi* Sieb. ex Lindl. & Paxton (= *P. coronarius* var. *satsumi* Maxim.) (JAPAN); *P. schrenkii* Rupr. (KOREA). **Uredinia and telia** on *Sasa kesuzu* Muroi & Okam. (= *Sasamorpha mollis* Nakai) (JAPAN); *Sasamorpha borealis* (Hack.) Nakai var. *borealis* (JAPAN) (Dietel 1914; Uchida 1965; Ito 1950; Hiratsuka 1960; Kim 1963; Katumoto 1968; Cummins 1971; He et al. 1989; Hiratsuka et al. 1992; Ono 2019).

Notes: *Aecidium philadelphi* is an anamorph (spermogonial and telial stages) of *P. hikawaensis* because life cycle of this species was clarified with inoculations by He et al. (1989). Therefore, both species are identical and should be treated as a same species. *Aecidium philadelphi* is the legitimate earliest name of this species. Although *Aecidium* Pers. 1796 is a sanctioned former anamorphic genus name of rust fungi, *Puccinia* Pers. 1794 similarly sanctioned has its priority (Aime et al. 2018b). Therefore, we propose a new combination, *Puccinia philadelphi* (Dietel) Jing X. Ji & Kakish. in *Puccinia* for this species under the ICNafp Shenzhen Code (Turland et al. 2018) to avoid taxonomic confusion. Specimens deposited in Mycological Herbarium of Faculty of Life and Environmental Sciences, University of Tsukuba, Japan (TSH) were examined and photographed.

Puccinia shojiana Jing X. Ji & Kakish., **nom. nov.**

MycoBank: MB 850297; *Facesoffungi*: FoF 14965; Fig. 168

Basionym: *Aecidium akebiae* Henn., Hedwigia Beiblätter 39: 154, 1900 [MB 226281].

Heterotypic synonym: *Puccinia cymbiformis* F. He & Kakish., Transactions of the Mycological Society of Japan 34 (1): 133, 1993 [MB 360073].

Competing homonym: *Puccinia akebiae* Y.Z. Wang & S.X. Wei, Acta Microbiologica Sinica 20 (1): 18, 1980 [MB 113979].

Etymology: Name after the late Dr. Shoji Sato, a Japanese mycologist working on rust fungi.

Type: **Holotype** in Herbarium of Botanischer Garten, Berlin, Germany (B), Spermogonoa and aecia on *Akebia quinata* (Thunb.) Decaisne, JAPAN, Kochi Prefecture, Kawauchi-mura, June 1900, T. Inouye. B700109003, MycoBank MBT10016658. **Epitype** in TSH, designated here because the neotype specimen has only spermogonia and aecia, and telia on epitype specimen are important characteristics to specify this species, Telia on *Phyllostachys nigra* var. *henonis* (Bean) Stapf., JAPAN, Tottori Prefecture, Kokoge, 16 March 1976, TSH-R18509, MBT10016659.

Description: **Spermogonia** amphigenous, subepidermal, yellow to pale brown, aggregated, flask-shaped, type 4 of Cummins and Hiratsuka (2003). **Aecia** hypophyllous or petiolicolous, aggregated in small groups, pale yellow; aeciospores catenulate, globose to subglobose to broadly ellipsoid, often angular, 20–32.5 × 17.5–32 µm, walls ca. 0.5 µm thick, hyaline, verrucose with big granules; inner surfaces of peridial cells densely verrucose. **Telia** hypophyllous, erumpent, pale yellow to dark brown; teliospores fusiform to cymbiform with long and cylindrical apices, constricted at septa, 53–95 × 12–20 µm, walls 1.5–3.5 µm thick at sides, 14–34.5 µm at apices, brown, smooth; pedicels hyaline, persistent.

Specimens examined: **Spermogonia and aecia** on *Akebia quinata* (Thunb.) Decaisne, JAPAN, Shizuoka, Ikawa, 1 July 1998, THS-R3953; *A. trifoliata* (Thunb.) Koidz. JAPAN, Shizuoka, Ikawa, 1 July 1998, TSH-R3954. **Telia**

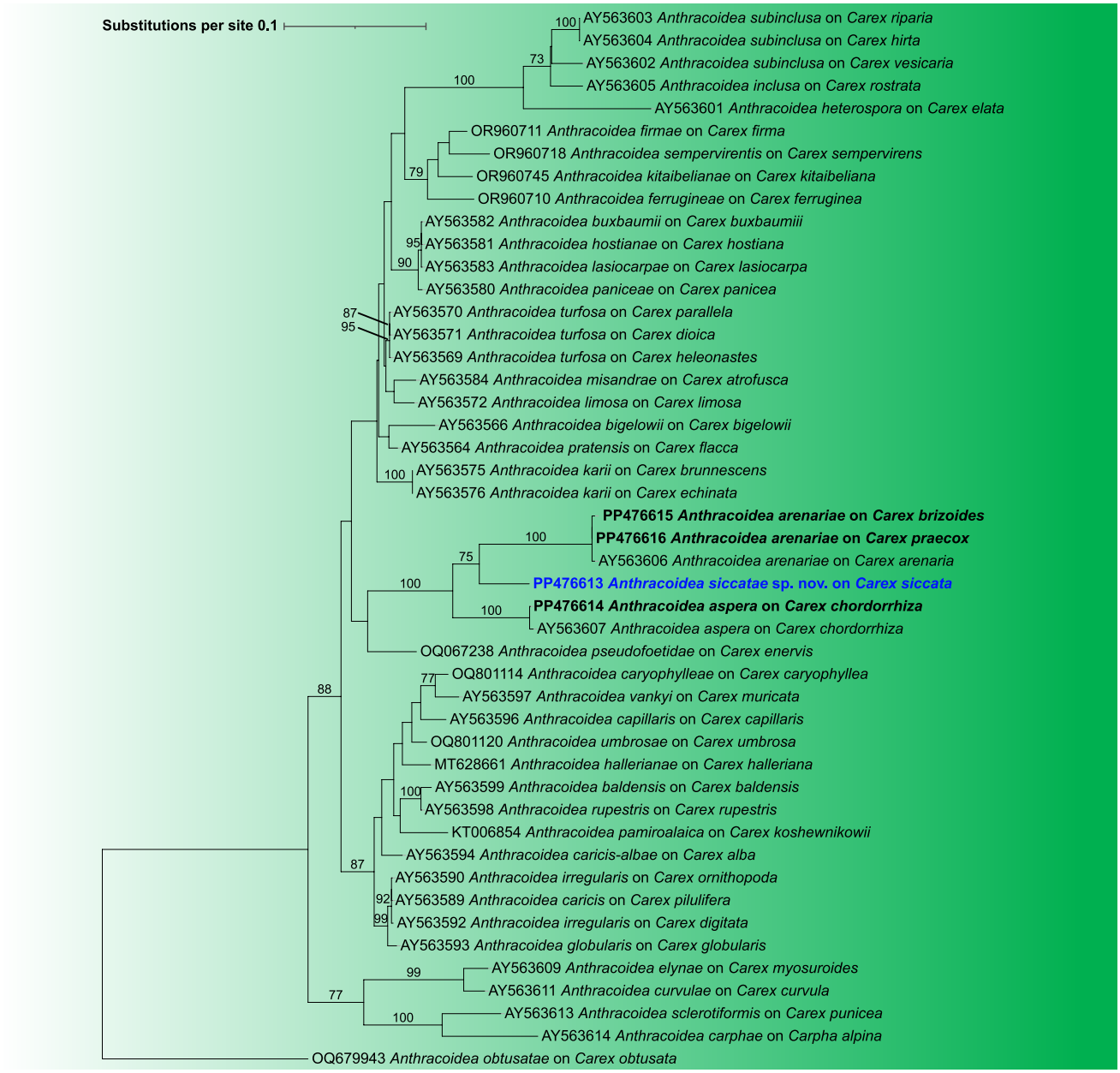


Fig. 169 ML tree generated using RAxML-NG (Kozlov et al. 2019) implemented in raxmlGUI 2.0 (Edler et al. 2021) based on a MAFFT v7.450 (Katoh and Standley 2013) alignment of the LSU dataset. The tree was rooted with *Anthracoidea obtusatae* Denchev et al. (2023a). Values at nodes indicate bootstrap values inferred by 1000 replicates; only values ≥ 70% are shown. Bold names indicate specimens sequenced in this study

on *Phyllostachys nigra* (Lodd.) var. *henonis* (Bean) Stapf., JAPAN, Tottori, Kokoge, 16 March 1976, TSH-R18509 (Epitype); JAPAN, Tottori, Kokoge, 17 March 1976, TSH-R18540.

Host plants and distribution: **Spermogonia and aecia** on *Akebia pentaphylla* Makino (Japan); *A. quinata* (Thunb.) Decaisne (CHINA, JAPAN); *A. trifoliata* (Thunb.) Koidz. (CHINA, JAPAN). **Telia** on *Phyllostachys nigra* var. *henonis* (Bean) Stapf. (JAPAN) (Ito 1950; Hiratsuka 1960; Uchida 1965; Hiratsuka and Kaneko 1977; Tai 1979; Hennings 1900a; Hiratsuka et al. 1992; He et al. 1993).

Notes: *Puccinia cymbiformis* had been reported as *P. nigroconoidea* I. Hino & Katum. by Hiratsuka (1960), Uchida (1965), Hiratsuka and Kaneko (1977) and Hiratsuka et al. (1992). However, *P. nigroconoidea* is morphologically different from this species as reported by He et al. (1993). *Aecidium akebiae* is an anamorph (spermogonial and telial stages) of *P. cymbiformis* because life cycle of this species

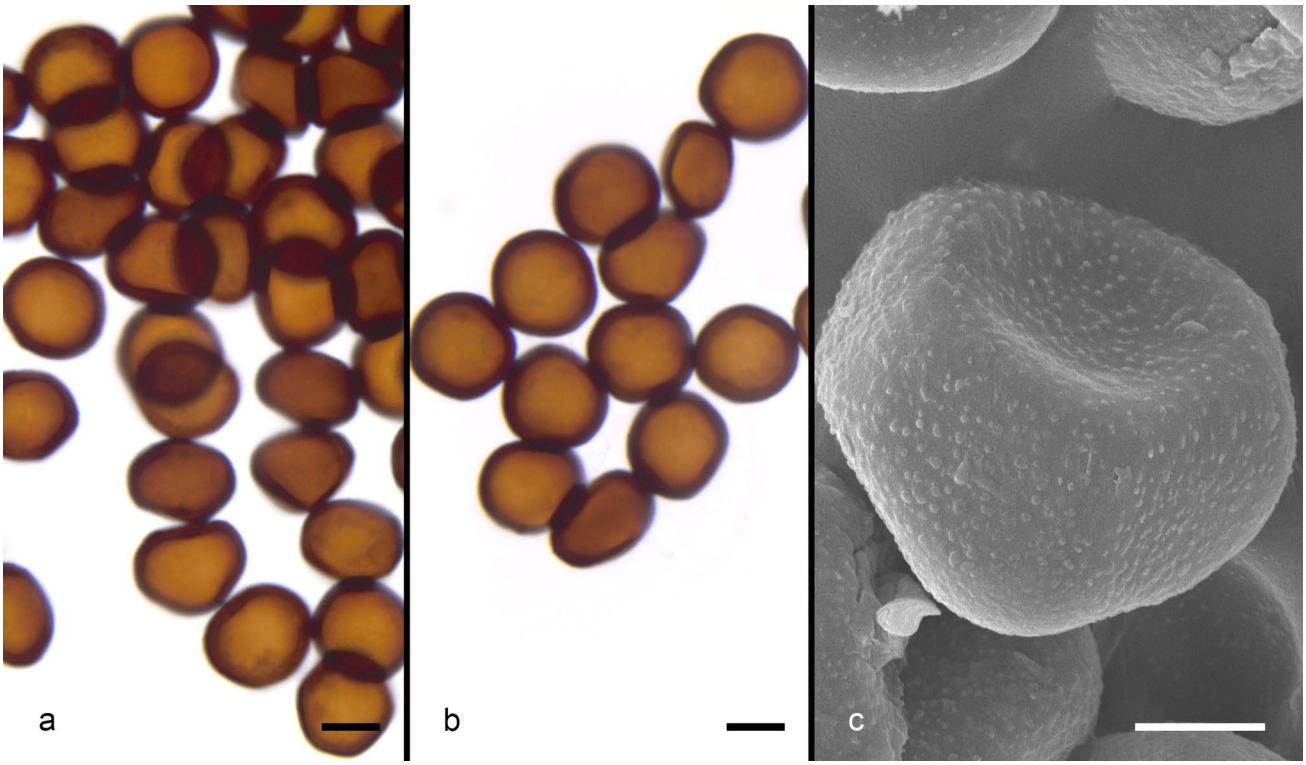


Fig. 170 ***Anthracoidea siccatae***. **a, b** Spores in LM (SOMF 31455, **holotype**). **c** Spores in SEM (E, s.n.). Scale bars: **a, b** = 10 µm, **c** = 5 µm

was clarified with inoculations by Hiratsuka and Kaneko (1977). Therefore, both species are identical and should be treated as a same species. *Aecidium akebiae* is the legitimate earliest name of this species. Although *Aecidium* Pers. 1796 is a sanctioned former anamorphic genus name of rust fungi, *Puccinia* Pers. 1794 similarly sanctioned has its priority (Aime et al. 2018b). Therefore, a new name, *Puccinia shojiana* Jing X. Ji & Kakish. is proposed in *Puccinia* for this species under the ICNafp Shenzhen Code (Turland et al. 2018) to avoid taxonomic confusion because *Puccinia akebiae* Y.Z. Wang & S.X. Wei is preoccupied available name. Specimens deposited in Mycological Herbarium of Faculty of Life and Environmental Sciences, University of Tsukuba, Japan (TSH) were examined and photographed.

Ustilaginomycetes Warm.
Ustilaginales Bek.

Notes: The order is divided into seven families: *Anthracoideaceae, Clintamraceae, Ustilaginaceae, Websdaneaceae, Geminaginaceae, Pericladiaceae,* and *Melanotaeniaceae* (He et al. 2024a).

Anthracoideaceae Denchev.

Notes: The family *Anthracoideaceae* was introduced by Denchev (1997). Nineteen genera are currently recognized in this family (He et al. 2024a). The species are parasites on *Cyperaceae* and *Juncaceae*.

Anthracoidea Bref.

Notes: *Anthracoidea* comprises 117 species (Denchev et al. 2023a; Kemler et al. 2024). During a collection trip held in Quebec, and an examination of *Carex* specimens from the herbaria of the New York Botanic Garden (NY) and the Royal Botanic Garden Edinburgh (E), a smut fungus belonging to the genus *Anthracoidea* was found on specimens of *Carex siccata* from Canada and USA. Based on phylogenetic evidence (Fig. 169), morphology, and host specialization, this fungus is introduced here as a novel species.

Anthracoidea siccatae T. Denchev, Denchev, Lév.-Bourret & Kemler, **sp. nov.**

Index Fungorum: IF 901732; *Facesoffungi*: FoF 15566; Figs. 169, 170

Etymology: The specific epithet is derived from the host plant, *Carex siccata*.

Holotype: SOMF 31455.

Parasitic on *Carex siccata*. *Infection* local. **Sori** in some female flowers, around aborted nuts as subglobose, ovoid or broadly ellipsoidal hard bodies, 1.2–2.0 mm long, initially covered by a thin, grayish peridium that later flakes away exposing a black, powdery on the surface spore mass.

Spores small to medium-sized, flattened, in plane view irregularly rounded, broadly elliptical, suborbicular, subpolygonal or ovate in outline, in plane view (15–)16–21(–22.5) × (14–)15–18.5(–19.5) (18.8 ± 1.1 × 16.9 ± 1.0) µm ($n/_4 = 500$), in side view 10.5–13(–14) µm thick, medium to dark reddish brown; spore wall unevenly to almost evenly thickened, 1.0–2.5(–2.8) µm thick, thickest at the angles, sometimes with 1(–2) internal swellings, light refractive areas sometimes present, protuberances absent; minutely verruculose, spore profile not affected or very slightly affected. In SEM punctate to minutely verruculose; warts up to 0.2 µm high, usually isolated, sometimes 2–3 warts partly confluent, forming small groups. **Spore germination** unknown.

Material examined: CANADA, Quebec, near Pontiac Station, 45.4714°N 76.3247°W, on *Carex siccata* Dewey (*Cyperaceae*), 4 July 2015, *É. Léveillé-Bourret*, *768* (SOMF 31455, **holotype;** DAOM 744257, isotype). USA, Montana, Flathead Lake and vicinity mainland opposite Wild Horse Island, on *Carex siccata*, 15 August 1908, *J. Clemens* (E, s.n., paratype); Colorado, Lake Eldora, on *C. siccata*, 12 September 1915, *E. Bethel*, s.n., as '*Cintractia caricis*' (NY, s.n., paratype); Vermont, Burlington, lake shore, on *C. siccata*, 16 July 1898, *T.E. Hazen*, s.n., as '*Ustilago caricis*' (NY, s.n., paratype).

Additional specimens examined: *Anthracoidea arenariae* (Syd.) Nannf.: FRANCE, Grand Est, Haut-Rhin, Colmar, grassy slopes near a pond, 48.044582°N 7.372248°E, on *Carex praecox* Schreb, 10 June 2019, *E. Piselli*, det. Jac. Koopman (SOMF 31454); AUSTRIA, Styria, Koralpe, 11.4 km WNW of Stainz, 1.5 km WSW of the inn "Gasthof Klugveitl", NE below the summit of the Reinischkogel, 46°55′40″N 15°07′10″E, alt. 1420 m, on *Carex brizoides* L., 1 August 2009, *P. Zwetko*, *Mycoth. Graec.*, *441* (SOMF 31457). —*Anthracoidea aspera* (Liro) Kukkonen: CANADA, Quebec, at the end of Akpik Road, about 26 km N of Kuujjuaq, 58.3506°N 68.3479°W, on *Carex chordorrhiza* L.f., 6 August 2015, *É. Léveillé-Bourret*, no. *822* (SOMF 31456).

Hosts: Disticha Clade of *Carex* (*Carex* subg. *Vignea*, *Cyperaceae*): *Carex siccata*.

Distribution: North America (Canada and USA).

GenBank: PP476613 (LSU).

Notes: *Anthracoidea* are considered to be restricted to host plants belonging to the same or closely related sections of *Carex* (Vánky 1979). *Carex siccata* is a North American sedge, distributed in Canada and USA, that has been traditionally included in *C.* sect. *Ammoglochin* Dumort. (Reznicek 2002). A recently proposed classification of *Carex* places this sedge within the Disticha Clade of Carex subg. *Vignea* (Roalson et al. 2021). The Disticha Clade is an informal group of species that includes 27 carices. Five *Anthracoidea* species have been previously reported on carices in the Disticha Clade: *A. variabilis* (S. Ito) Kakish. on *Carex arenicola* F. Schmidt, *A. verrucosa* on *Carex hoodii* Boott, *A. fischeri* (P. Karst.) Kukkonen on *Carex disticha* Huds., *A. pseudofoetidae* L. Guo on *Carex pseudofoetida* Kük., *C. maritima* Gunnerus, and *C. enervis* C.A. Mey., and *A. vankyi* Nannf. on *Carex occidentalis* L.H. Bailey (Vánky 2011; Denchev et al. 2020, 2023b). *Anthracoidea siccatae* differs from *A. variabilis* by having smaller spores (15–24 µm long for *A. variabilis*, Denchev et al. 2013) and the presence of spore walls with internal swellings; from *A. verrucosa* by having a thicker spore wall 1.0–2.5(–2.8) µm thick versus ca. 1 µm thick, uniform wall of *A. verrucosa*; Vánky 2011), and from *A. fischeri* by having minutely verruculose spore ornamentation with warts up to 0.2 µm high versus echinate ornamentation with spines up to 1.0 µm high for *A. fischeri* (Vánky 2011). For the distinctness of *A. siccatae* from *A. pseudofoetidae* and *A. vankyi*, there is molecular phylogenetic evidence (Fig. 169). In addition, there are morphological differences that distinguish *A. siccatae* from these two species very well, viz. *A. pseudofoetidae* possesses sori, covered by a thick, dark brown peridium, and very small-sized spores (8.5–12.5) µm long (Denchev et al. 2020, 2023b), while *A. vankyi* has more irregular spores in outline and a spore wall without internal swellings (Vánky 2011).

The overall topology of the phylogenetic tree of the genus *Anthracoidea* was similar to previous studies. *Anthracoidea siccatae* was inferred as a sister clade to *A. arenariae* on the three different host species *Carex arenaria*, *C. brizoides*, and *C. praecox*. Both groups together formed a sister group to *A. aspera* on *C. chordorrhiza*. Although *A. siccatae* is morphologically similar to *A. arenariae*, they are distinguished well on the bases of molecular phylogeny and host specialization – *Carex arenaria* is a member of Arenaria Clade (Roalson et al. 2021). *Anthracoidea siccatae* differed from *A. arenariae* by –110 bp.

A record of *Carex siccata* infected with *Anthracoidea* (as '*Ustilago urceolorum*', q.e. *A. caricis*) has been previously reported from Ontario, Lake Nipigon (Ellis and Everhart 1885). Thus, *Anthracoidea siccatae* is considered to be distributed in Canada (Ontario and Quebec) and USA (Montana, Colorado, and Vermont).

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Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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