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Fungal diversity notes 1611–1716: taxonomic and phylogenetic contributions on fungal genera and species emphasis in south China

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Abstract

This article is the 15th contribution in the Fungal Diversity Notes series, wherein 115 taxa from three phyla, nine classes, 28 orders, 48 families, and 64 genera are treated. Fungal taxa described and illustrated in the present study include a new family, five new genera, 61 new species, five new combinations, one synonym, one new variety and 31 records on new hosts or new geographical distributions. Ageratinicolaceae *fam. nov.* is introduced and accommodated in Pleosporales. The new genera introduced in this study are *Ageratinicola*, *Kevinia*, *Pseudomultiseptospora* (Parabambusicolaceae), *Marasmiellomycena*, and *Vizzinia* (Porotheleaceae). Newly described species are *Abrothallus altoandinus*, *Ageratinicola kunmingensis*, *Allocryptovalsa aceris*, *Allophoma yuccae*, *Apiospora cannae*, *A. elliptica*, *A. pallidesporae*, *Boeremia wisteriae*, *Calycina papaeana*, *Clypeococcum lichenostigmoides*, *Coniochaeta riskali-shoyakubovii*, *Cryphonectria kunmingensis*, *Diaporthe angustiapiculata*, *D. campylandrae*, *D. longipapillata*, *Diatrypella guangdongense*, *Dothiorella franceschinii*, *Endocalyx phoenicis*, *Epicoccum terminosporum*, *Fulvifomes karaiensis*, *F. pannaensis*, *Ganoderma ghatensis*, *Hysterobrevium baoshanense*, *Inocybe avellaneorosea*, *I. lucida*, *Jahnula oblonga*, *Kevinia lignicola*, *Kirschsteiniothelia guangdongensis*, *Laboulbenia caprina*, *L. clavulata*, *L. cobiae*, *L. cosmodisci*, *L. nilotica*, *L. omalii*, *L. robusta*, *L. similis*, *L. stigmatophora*, *Laccaria rubriporus*, *Lasiodiplodia morindae, Lyophyllum agnijum*, *Marasmiellomycena pseudoomphaliiformis*, *Melomastia beihaiensis*, *Nemania guangdongensis*, *Nigrograna thailandica*, *Nigrospora ficuum*, *Oxydothis chinensis*, *O. yunnanensis*, *Petriella thailandica*, *Phaeoacremonium chinensis*, *Phialocephala chinensis*, *Phytophthora debattistii*, *Polyplosphaeria nigrospora*, *Pronectria loweniae*, *Seriascoma acutispora*, *Setoseptoria bambusae*, *Stictis anomianthi*, *Tarzetta tibetensis*, *Tarzetta urceolata*, *Tetraploa obpyriformis*, *Trichoglossum beninense*, and *Tricoderma pyrrosiae*. We provide an emendation for *Urnula ailaoshanensis Agaricus duplocingulatoides* var. *brevisporus* introduced as a new variety based on morphology and phylogeny.

Keywords Agaricomycetes · Ascomycota · Basidiomycota · Dothideomycetes · Eurotiomycetes · Fungal diversity · Geoglossomycetes · Geographical distribution · Host records · *Incertae sedis* · Laboulbeniomycetes · Lecanoromycetes · Leotiomycetes · Novel taxa · New combination · Oomycota · Peronosporea · Pezizomycetes · Phylogeny · Sordariomycetes · South Chinese fungi · Taxonomy

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Subclass Diaporthomycetidae Senan., Maharachch. & K.D. Hyde
Coniochaetales Huhndorf et al.

Coniochaetaceae Malloch & Cain
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Diaporthaceae Höhn. ex Wehm.
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1677. ***Diaporthe longipapillata*** Senan., ***sp. nov.*** (Contributed by I.C. Senanayake)

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Togniniaceae Réblová, et al.
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Microascaceae Luttr. ex Malloch
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Hydnangiaceae Gäum. & C.W. Dodge
1702. ***Laccaria rubriporus*** S. M. Tang, ***sp. nov.*** (Contributed by S. M. Tang)

Inocybaceae Jülich
1703. ***Inocybe avellaneorosea*** Esteve-Rav., E. Larss. & Pancorbo, ***sp. nov.*** (Contributed by F Esteve-Raventós, E. Larsson, F. Pancorbo, G. Moreno, A. Altés, Y. Turégano)
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1705. ***Lyophyllum agnijum*** K. N. A. Raj, K. P. D. Latha & Manim., ***sp. nov.*** (Contributed by K.P.D. Latha, K.N.A Raj, P. Manimohan)

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1708. ***Marasmiellomycena omphaliiformis*** (Kühner) Mateos, Kolařík, De la Peña-Lastra, Ševčíková & Antonín, ***comb. nov.*** (Contributed by S. De la Peña-Lastra, A. Mateos, M. Kolařík, V. Antonín, H. Ševčíková)
1709. ***Vizzinia*** Ševčíková & Kolařík, ***gen. nov.*** (Contributed by H. Ševčíková, M. Kolařík)
1710. ***Vizzinia nigripes*** (Angelini, Vizzini, Consiglio & M. Marchetti) Ševčíková & Kolařík, ***comb. nov.*** (Contributed by H. Ševčíkova, M. Kolařík,S. De la Peña-Lastra, A.Mateos, V. Antonín)
1711. ***Vizzinia domingense*** (Angelini, Vizzini, Consiglio & M. Marchetti) Kolařík & Ševčíková, ***comb. nov.*** (Contributed by H. Ševčíková, M. Kolařík,S. De la Peña-Lastra, A.Mateos, V. Antonín)

Agaricales ***incertae sedis***
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Hymenochaetales Oberw.
Hymenochaetaceae Donk
1713. ***Fulvifomes karaiensis*** M. Kaliyaperumal, S. Gunaseelan & K. Kezo ***sp. nov.*** (Contributed by S. Gunaseelan, K. Kezo, M. Kaliyaperumal)
1714. ***Fulvifomes pannaensis*** S. Gunaseelan, M. Kaliyaperumal & K. Kezo ***sp. nov.*** (Contributed by S. Gunaseelan, K. Kezo, M. Kaliyaperumal)

Polyporales Gäum.
Ganodermataceae Donk
1715. ***Ganoderma ghatensis*** K. Kezo, S. Gunaseelan & M. Kaliyaperumal ***sp. nov.*** (Contributed by S. Gunaseelan, K. Kezo, M. Kaliyaperumal)

Phylum Oomycota Arx
Class Peronosporea
Peronosporales Bek.

Peronosporaceae de Bary

1716. ***Phytophthora debattistii*** C. Bregant, L. Montecchio & B.T. Linaldeddu, ***sp. nov.*** (Contributed by C. Bregant, L. Montecchio and B.T. Linaldeddu)

Introduction

South China contains both tropical and subtropical areas with warm, moist to cold, dry climatic conditions and it encompasses a wide range of biodiversity (Zhao et al. 2015; Naruse et al. 2018; Niu et al. 2019). Moreover, this region has untouched, virgin ecological patches and urbanized, exploited regions (Zhao et al. 2015). There are some studies on the diversity and taxonomy of macro and microfungi in the south China region (Senanayake et al. 2020a, b, c; Jiang et al. 2022; Kularathnage et al. 2022; Liu et al. 2022a; Wang et al. 2022; Zhang et al. 2022). However, the fungal diversity in these areas is still understudied and a high number of novel taxa is expected to be recognized if studied (Hyde et al. 2018; 2020a).

Discovering novel fungal taxa is essential not only in classification or nomenclature-based studies, but also in the pharmaceutical industry, agriculture, ecological and environment management, plant disease control, epidemiology, and environmental conservation (Hyde et al. 2019b). New geographical distributions and host records are also important in taxonomy and ecology-based studies. The new records of plant pathogenic fungi reveal the disease spread or give clues on future pathogenic spreads (Chethana et al. 2021a). Several contemporary webpages and also some studies related to fungal numbers provide data on fungal taxa of different life modes, habitats and regions with descriptions, illustrations, phylogenetic trees, notes and the current number of accepted species (Pem et al. 2019; Bundhun et al. 2020; Chaiwan et al. 2021; Wijesinghe et al. 2021; Calabon et al. 2022; Phukhamsakda et al. 2022; Senanayake et al. 2022). It is therefore, necessary to reveal the host ranges of species and also their life-modes (Hyde et al. 2020d). This information predicts life-mode shifting and adaptations of fungi to new habitats. Further, new combinations can be proposed for species that not fit to the current genus and match other genera by morphology and phylogeny (Turland et al. 2018).

In this study, we revealed some novel fungal taxa mostly collected in south China and also from different geographical regions in the world and publish them in this Fungal Diversity Notes series. The Fungal Diversity Notes series have been contributed a great work on taxonomy, phylogeny and diversity of fungi in the phyla of Ascomycota, Basidiomycota and Oomycota. The series provides an outlet for publishing new species, new combinations, new records of host associations and geographical distributions. From the first to 14th series of the Fungal Diversity Notes, a total of 1610 taxa were included with 11 new families, 115 new genera and 1124 new species (Ariyawansa et al. 2015a; Liu et al. 2015; Li et al. 2016; Hyde et al. 2016, 2017a, b, 2019a, b, 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. 2023).

The aims of this paper are to introduce novel fungal family, genera, species, combinations and records of host and geographical distribution in Ascomycota, Basidiomycota and Oomycota based on polyphasic approaches (Chethana et al. 2021b; Maharachchikumbura et al. 2021) providing descriptions, illustrations, phylogenetic analysis and notes. We introduced several species sole based on morphology in Laboulbeniaceae, because recent studies have introduced species in this family only based on morphology (Kaishian et al. 2020; Kaishian and Weir 2021). Further, five new species combinations have been proposed here following articles in International Code of Nomenclature for Algae, Fungi, and Plants providing relevant information. There are 32 novel geographical and host records illustrated and described here providing notes. We provide descriptions of sexual morph for *Cytospora lumnitzericola* Norph. et al. and *Apiospora gaoyouensis* (C.M. Tian & N. Jiang) Pintos & P. Alvarado,for first time and *Paraphaeosphaeria verruculosa* Verkley, Göker & Stielow is synonymized under *Paraphaeosphaeria parmeliae* Crous & Trakun.

Materials and methods

Fresh specimens were collected mainly from south China and additional specimens were obtained from Africa, America, Asia and Europe (i.e. Australia, Benin, Bolivia, Canada, France, India, Indonesia, Iran, Italy, Mongolia, Norway, Russia, Spain, Sri Lanka, Sweden, Thailand, Uganda, USA, Uruguay and Uzbekistan). Materials and methods discussed in Senanayake et al. (2020d) were followed for isolation and sporulation. Illustrations of macro and microscopic characters and molecular phylogenetic analyses were performed following recent FDN issues (Phookamsak et al. 2019; Boonmee et al. 2021; Jayawardena et al. 2023). New species were introduced based on guidelines in Maharachchikumbura et al. (2021).

Taxonomy

Ascomycota Caval.-Sm.

The latest updated account of Ascomycota followed in Wijayawardene et al. (2020).

Dothideomycetes O.E. Erikss & Winka.

We follow the latest treatments and updated accounts of Dothideomycetes as available in Hongsanan et al. (2020a, b).

Dyfrolomycetales K.L. Pang et al.

Dyfrolomycetales was introduced to accomodate a marine fungal genus *Dyfrolomyces* representing by *D. tiomanensis* from Malaysia (Pang et al. 2013). Only the single family Pleurotremataceae was accepted in this order with three associated genera *Dyfrolomyces*, *Melomastia* and *Pleurotrema* (Pem et al. 2021).

Pleurotremataceae Walt. Watson

Pleurotremataceae was introduced by Watson (1929), with *Pleurotrema* Müll. Arg. as the type genus and *P. polysemum* (Nyl.) Müll. Arg. as the type species. The family is characterized by immersed ascomata, bitunicate or fissitunicate asci, and multi-septate ascospores with or without a sheath (Watson 1929; Barr 1994). Pleurotremataceae was transferred from Sordariomycetes to Dothideomycetes by Maharachchikumbura et al. (2016) based on the bitunicate or non-fissitunicate asci of *Pleurotrema* and morphological similarity to *Melomastia* and *Saccardoella* (Li et al. 2022a, b). Wijayawardene et al. (2022) listed three genera viz., *Dyfrolomyces* K.D. Hyde, *Melomastia* Nitschke ex Sacc and *Pleurotrema* in Pleurotremataceae. Subsequently, based on multigene phylogeny between *Dyfrolomyces* and *Melomastia*, Li et al. (2022a, b) synonymized *Dyfrolomyces* under *Melomastia*, and 11 *Dyfrolomyces* species have been transferred to *Melomastia*. However, some species were incorrectly transferred. Kularathnage et al. (2023a) however proposed that melomastia-like taxa may comprise several genera if we obtain molecular data for most species. Members of Pleurotremataceae are saprobes on decaying wood and are distributed in terrestrial, mangrove, and freshwater habitats (Li et al. 2022a, b).

Melomastia Nitschke ex Sacc., Atti Soc. Veneto-Trent. Sci. Nat., Padova, Sér. 4 4: 90 (1875)

Melomastia was introduced and typified by *M. mastoidea* (=*M. friesii* Nitschke) by Saccardo (1875). Previously, *Melomastia* was classified under Ascomycota genera *incertae sedis* due to the lack of molecular data (Maharachchikumbura et al. 2016). Norphanphoun et al. (2017) placed *Melomastia* in Pleurotremataceae together with *Dyfrolomyces* and *Pleurotrema* based on morphology and phylogeny. However, Li et al. (2022a, b) concluded that *Dyfrolomyces* and *Melomastia* are congeneric. Therefore, *Dyfrolomyces* was synonymized under *Melomastia* based on molecular phylogeny transferring 11 species. However, Kularathnage et al. (2023a) proposed to resurrect the genus *Dyfrolomyces* for *D. tomanensis* and *D. chromolaenae*. Currently, there are 50 accepted species in *Melomastia* are listed in Species Fungorum (2023). However, only 17 species have molecular data.

Melomastia species are saprobic on dead woody branches, twigs and culms in terrestrial, freshwater, and mangrove habitats (Li et al. 2022a, b). This genus is characterized by solitary, coriaceous to carbonaceous ascomata; narrow, conical periphysate papilla; septate pseudoparaphyses; 8-spored, bitunicate, cylindrical asci and overlapping uni-seriate, ellipsoid to fusiform ascospores with 1–10-septate (Li et al. 2022a, b). This study introduces a new *Melomastia* species.

Melomastia beihaiensis T.Y. Du, K.D. Hyde & Tibpromma, ***sp. nov***.

Index Fungorum number: IF 558764; *Facesoffungi number:* FoF 10262; Fig. 1

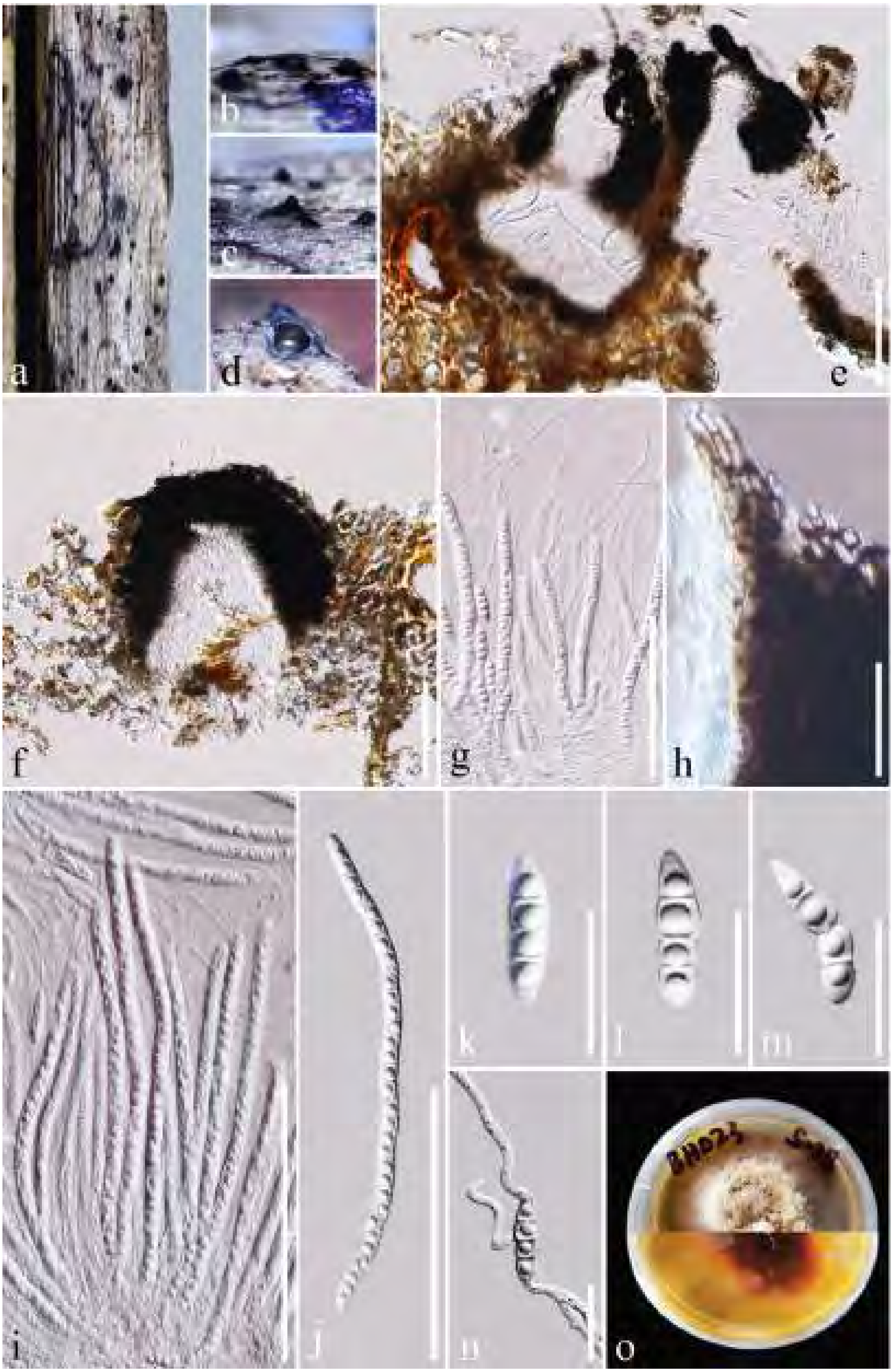
Etymology: based on "Beihai" where the fungus was collected.

Saprobic on dead stems of *Chromolaena odorata* (L.) R.M.King & H.Rob. **Sexual morph**: *Ascomata* (including neck) 250–360 µm high × 200–340 µm diam. ($\bar{x}$ = 302 × 241 µm, n = 10), clearly visible on the host surface as dark, raised spots, solitary or aggregated, semi-immersed to immersed, dark brown to black, uni-loculate, clypeate to wide subglobose, irregular bottom, long ostiolate, black, carbonaceous. *Ostiolar canal* 150–230 µm high × 115–185 µm diam. ($\bar{x}$ = 183 × 158 µm, n = 10), surrounded by a layer of clypeus, thick, dense, black cells, filled with hyaline cells, periphyses absent. *Peridium* 5–25 µm wide ($\bar{x}$ = 13 µm, n = 20), comprising an outer layer of dense, dark brown cells of *textura angularis* to *textura prismatica*, becoming lighter inwardly, fused with host tissues. *Hamathecium* 1.5–2.5 µm wide, comprising numerous, hyaline, aseptate, unbranched pseudoparaphyses, longer than asci, attached at the base and between the asci, embedded in a gelatinous matrix. *Asci* (125–)135–190 × 5–7 µm ($\bar{x}$ = 163 × 5.9 µm, n = 20), 8-spored, bitunicate, cylindrical, extremely short-pedicellate, rounded at the apex. *Ascospores* 16–28 × 5–7 µm ($\bar{x}$ = 22 × 5.8 µm, n = 30), overlapping-uniseriate, hyaline, broadly fusiform, conical at upper part and the lower end is truncate, 3-septate, constricted at the septa, constricted at the central septum where the spore seem likely to separate into two parts, smooth-walled, with a large guttule in each cell when spores are mature, not surrounded by a mucilaginous sheath. **Asexual morph**: Undetermined.

Culture characteristics: Colonies on PDA reaching 5 cm diam., after 20 days at room temperature (20–25 ℃), white to pale orange, irregular in shape, margin filiform, with white aerial mycelia; reverse orange to brown, smooth, producing pigments in culture.

Material examined: China, Guangxi Province, Beihai, Yinhai District, Yintan Middle Road, 20° 54′ 34″ N 108° 50′ 46″ E, on dead stems of *Chromolaena odorata* (Asteraceae), 6 October 2020, Tianye Du, BHD23 (HKAS 121125, **holotype**), ex-type culture, KUMCC 21-0084.

GenBank numbers: ITS: MZ726997, LSU: MZ726990, SSU: MZ727002, *tef*1-α: OK043822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◂**Fig. 1** ***Melomastia beihaiensis*** (HKAS 121125, **holotype**). **a–c** Appearance of ascomata on the substrate. **d, e** Vertical sections through the ascomata. **f** Ostiole. **g** Pseudoparaphyses. **h** Peridium. **i, j** Asci. **k–m** Ascospores. **n** Germinated ascospore. **o** Colonies on PDA surface and reverse view. Scale bars: e–g, i, j = 100 μm, h, k–n = 20 μm

Notes: In the combined LSU, SSU and *tef*1-α gene analysis (Fig. 2), our collection forms a distinct clade which is basal to *Melomastia distoseptata*, *M. fusispora*, *M. oleae*, *M. thamplaensis* and *M. winteri* with ML = 99% and BI = 1.00 bootstrap support. Our collection differs with these genetically close *Melomastia* species viz. *Melomastia distoseptata* has septate pseudoparaphyses and 3-distoseptate ascospores, *M. fusispora* has ascospores with a gelatinous sheath, *M. oleae* has periphyses in the ostiolar canal, *M. thamplaensis* has immersed ascoma and peridium with cells of *textura angularis* and *M. winteri* has septate pseudoparaphyses (Zhang et al. 2017a; Hongsanan et al. 2020a, b; Li et al. 2022a, b). *Melomastia chromolaenae* has also been reported from *Chromolaena odorata*, however, our collection is morphologically different from *M. chromolaenae* having aseptate, unbranched pseudoparaphyses, broadly fusiform ascospores with 3-septa when mature, while *M. chromolaenae* has septate, branched pseudoparaphyses, fusiform ascospores with 9–11-septate when mature (Mapook et al. 2020). Therefore, we introduce our collection as a new species, *Melomastia beihaiensis.*

Hysteriales Lindau

The order Hysteriales was introduced by Lindau (1897) and this order includes only the type family Hysteriaceae that is characterised by hysteriform apothecia. They are mostly saprobic and distributed worldwide in most ecosystems (Jayasiri et al. 2018). Some species have been reported from clinical samples (Valenzuela-Lopez et al. 2019). We follow the latest treatment and updated accounts of Hysteriales in Jayasiri et al. (2018).

Hysteriaceae Munk

Hysteriaceae was introduced by Chevallier (1826). This family is phylogenetically well-supported and characterized by immersed to erumpent, superficial, ellipsoid to elongate ascomata (hysteriothecia) with longitudinal slits, bitunicate asci and hyaline to pigmented, one to multi-septate, or muriform ascospores (Boehm et al. 2009a; Hyde et al. 2013; de Almeida et al. 2014). Members of this family are distributed in tropical and temperate regions as saprobes on decaying wood (Liu et al. 2015; Yacharoen et al. 2015) and as phytopathogens (Alexopoulos et al. 1996). Thirteen genera are currently accepted in this family (Hongsanan et al. 2020a, b).

Hysterobrevium E. Boehm & C.L. Schoch

Hysterobrevium was introduced by Boehm et al. (2009a) with *Hysterobrevium mori* (Schwein.) E. Boehm & C.L. Schoch as the type species. This genus is characterized by navicular hysterothecia and bitunicate, cylindrical to clavate asci with generally ovoid to obovoid, pigmented or hyaline dictyospores (Boehm et al. 2009a). There are seven species listed in Species Fungorum (2023). This study introduces a new *Hysterobrevium* species.

Hysterobrevium baoshanense M. Raza & M. Hussain, ***sp. nov.***

Index Fungorum number: IF900236; *Facesoffungi number*: FoF 14165; Fig. 3

Etymology: Referring to the the region (Baoshan) where sample has been collected.

Saprobic on decaying wood of *Pinus armandii* Franch. **Sexual morph**: *Ascomata* 310–400 μm high, 200–280 μm wide ($\bar{x}$ = 383 × 255 μm, n = 10), hysterothecial, superficial, scattered, solitary to rarely clustered, uni-loculate, black, flexuous, glabrous, rough-walled, with a thick slit-like opening. *Peridium* 35–60 μm wide, thick-walled of unequal thickness, thinner at the base (50–85 μm), thicker at the sides towards its apex, with several layers of dark brown to black cells and brittle, carbonaceous tissues. The inner layer contains simple flattened cells and the outer layers contains several layers of dark and black, thick-walled, polygonal pseudoparenchymatous cells, arranged in a *textura angularis*. *Hamathecium* composed of 1–2 μm wide, dense, filamentous, septate, unbranched, cellular pseudoparaphyses, not constricted at the septa, anastomosing at the apex, embedded in a gelatinous matrix. *Asci* 70–110 × 15–25 μm ($\bar{x}$ = 87.5 × 18.5 μm, n = 25), 8-spored, bitunicate, fissitunicate, cylindric-clavate, short pedicellate, apically rounded, with well-developed ocular chamber. *Ascospores* 20–28 × 8–10 μm ($\bar{x}$ = 24.9 × 9.1 μm, n = 35), overlapping bi-seriate, hyaline, becoming pale brown at maturity, fusiform to ellipsoidal, obvoid or muriform, 3–6-transverse septate, 1–2-longitudinally septate, with several segments, constricted at the septum, smooth-walled, with guttules, surrounded by mucilagenous sheath. **Asexual morph**: Undetermined.

Material examined: China, Yunnan Province, Baoshan City (25° 16′ 21.0″ N, 99° 18′ 00.1″ E), on decaying wood of *Pinus armandii* (Pinaceae), 7 October 2015, M. Raza (MFLU 16-2162, **holotype**).

GenBank numbers: ITS: MZ467049, LSU: KX772765, SSU: KX772767, *tef*1-α: KX772769.

Notes: This collection is morphologically similar to "*Hysterobrevium constrictum*" (KUN-HKAS 102101) which was collected from China (Hyde et al. 2020a). However, except for other morphological characters, the ascospore length of KUN-HKAS 102101 is larger than the type specimen of *H. constrictum* (SMH5211) (27–35 × 10–12 μm

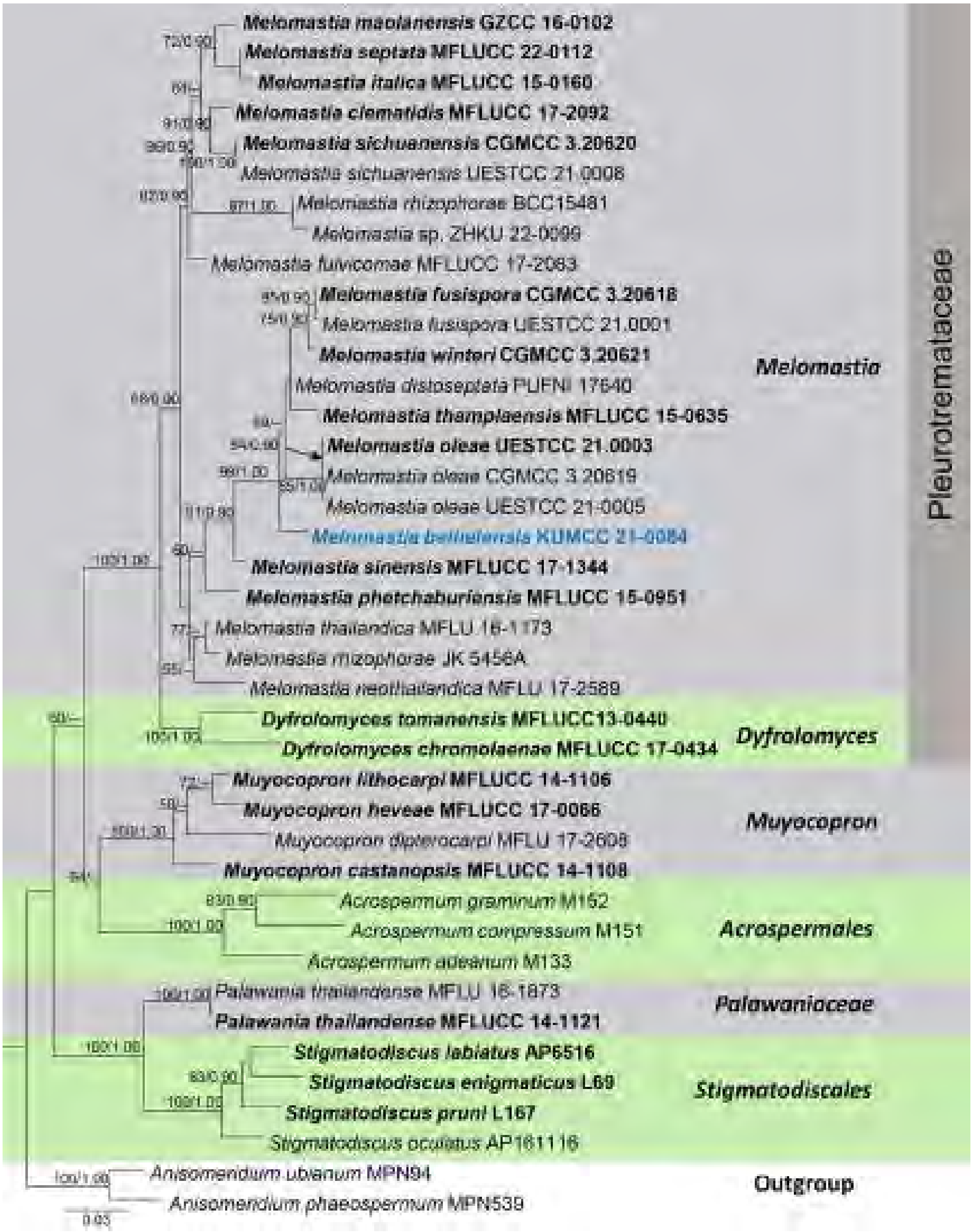


Fig. 2 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and *tef*1-α sequence data which comprised 2857 base pairs of LSU = 927, SSU = 1009, *tef*1-α = 921. The best scoring RAxML tree with a final likelihood value of − 13,807.470835 is presented. The matrix had 1012 distinct alignment patterns, with 25.91% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.241219, C = 0.268619, G = 0.288053, T = 0.202109; substitution rates: AC = 0.779939, AG = 2.032527, AT = 1.173704, CG = 0.889636, CT = 7.202155, GT = 1.0; gamma distribution shape parameter α = 0.220289. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 from Bayesian inference analysis are labelled at each node. Ex-type strains are in bold, while the new isolates are indicated in blue bold. The tree is rooted to *Anisomeridium phaeospermum* (MPN539) and *Anisomeridium ubianum* (MPN94)

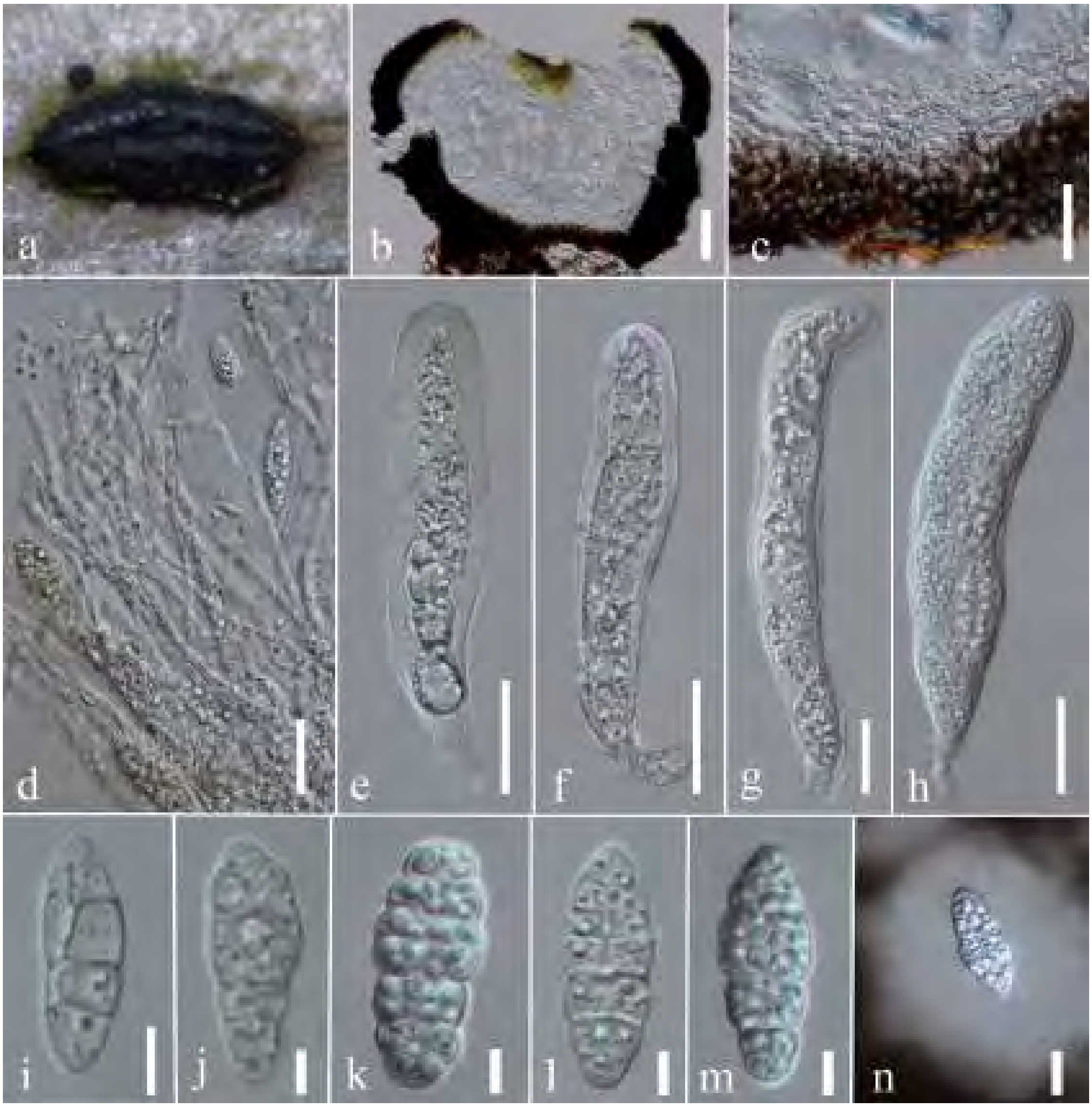
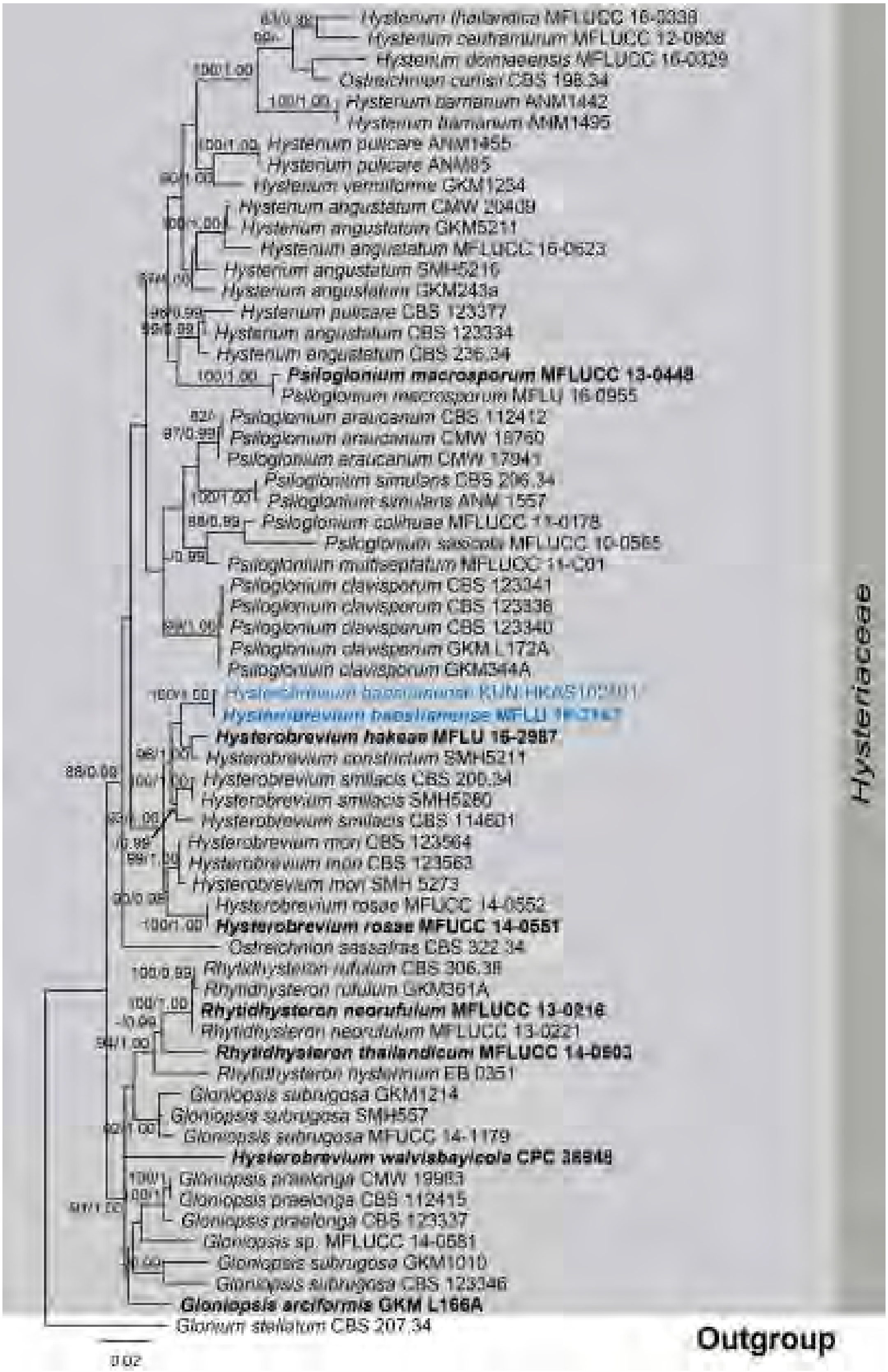


Fig. 3 ***Hysterobrevium baoshanense*** (MFLU 16-2162, **holotype**). **a** Blackish ascomata on substrate. **b** Vertical section of hysterothecia. **c** Peridium. **d** Pseudoparaphyses. **e–h** Asci. **i–m** Ascospores. **n** Ascospore mounted in Indian ink to show mucilaginous sheath. Scale bars: b = 50 µm, c–h = 20 µm, i–n = 5 µm

vs 13–23 × 5–12 µm) (Boehm et al. 2009b). The base-pair difference between ITS locus of our collection and KUN-HKAS 102101 is 2% while these differences for LSU, SSU and *tef*1-α are 9%, 0% and 16% respectively. Therefore, the taxonomy of KUN-HKAS 102101 needs a revision as it is mistakenly identified as *H. constrictum*.

Phylogenetic analysis (Fig. 4) reveals that our collection forms a well-separated, distinct sub-clade in *H. constrictum-H. hakeae-H. smilacis* cluster with bootstrap support ML/BI = 100%/1.00. *Hysterobrevium constrictum* differs from our collection by cylindrical, stipitate asci, uniseriate, ellipsoid, hyaline to brown ascospores, number of septa and mucilagenous sheath around the ascospores, *H. hakeae* by oblong to clavate asci, oblong ascospores and *H. smilacis* by cylindrical to clavate asci, asymmetric, hyaline to pale yellow dictyospores. The collection KUN-HKAS 102101 phylogenetically clusters with our collection and however, our collection morphologically differs from KUN-HKAS 102101. Therefore, further analysis is needed to clarify its taxonomy. These species were collected from various geographical locations viz. *H. constrictum* from Japan, Thailand, and New Zealand (Amano 1983; Boehm et al. 2009a; Farr and Rossman 2023), *H. hakeae* from Australia (Jayasiri et al. 2018), and *H. smilacis* from Kenya, South Africa, Sweden, USA (Boehm et al. 2009b; Table 1). Therefore, based on morphology and phylogeny, we introduce our


83/0.92
99/-
100/1.00
Hysterium thailandica MFLUCC 16-0338
Hysterium cauthamurum MFLUCC 12-0808
Hysterium doimaeensis MFLUCC 16-0329
Ostreichnion curtisii CBS 198.34
100/1.00
Hysterium barrianum ANM1442
Hysterium barrianum ANM1495
100/1.00
Hysterium pulicare ANM1455
Hysterium pulicare ANM85
90/1.00
Hysterium vermiforme GKM1234
Hysterium angustatum CMW 20409
100/1.00
Hysterium angustatum GKM5211
Hysterium angustatum MFLUCC 16-0623
Hysterium angustatum SMH5216
99/1.00
Hysterium angustatum GKM243a
96/0.99
Hysterium pulicare CBS 123377
99/0.99
Hysterium angustatum CBS 123334
Hysterium angustatum CBS 236.34
100/1.00
Psiloglonium macrosporum MFLUCC 13-0448
Psiloglonium macrosporum MFLU 16-0955
82/-
Psiloglonium araucanum CBS 112412
97/0.99
Psiloglonium araucanum CMW 18760
Psiloglonium araucanum CMW 17941
Psiloglonium simulans CBS 206.34
100/1.00
Psiloglonium simulans ANM 1557
88/0.99
Psiloglonium colihuae MFLUCC 11-0178
Psiloglonium sasicola MFLUCC 10-0565
-/0.99
Psiloglonium multiseptatum MFLUCC 11-C01
Psiloglonium clavisporum CBS 123341
Psiloglonium clavisporum CBS 123338
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Psiloglonium clavisporum CBS 123340
Psiloglonium clavisporum GKM L172A
Psiloglonium clavisporum GKM344A
100/1.00
Hysterobrevium baoshanense KUN HKAS102101
Hysterobrevium baoshanense MFLU 18-2167
Hysterobrevium hakeae MFLU 16-2987
98/1.00
Hysterobrevium constrictum SMH5211
88/0.99
100/1.00
Hysterobrevium smilacis CBS 200.34
Hysterobrevium smilacis SMH5280
93/1.00
Hysterobrevium smilacis CBS 114601
-/0.99
Hysterobrevium mori CBS 123564
99/1.00
Hysterobrevium mori CBS 123563
Hysterobrevium mori SMH 5273
90/0.98
Hysterobrevium rosae MFUCC 14-0552
100/1.00
Hysterobrevium rosae MFUCC 14-0551
Ostreichnion sassafras CBS 322.34
100/0.93
Rhytidhysteron rufulum CBS 306.38
Rhytidhysteron rufulum GKM361A
100/1.00
Rhytidhysteron neorufulum MFLUCC 13-0216
-/0.99
Rhytidhysteron neorufulum MFLUCC 13-0221
94/1.00
Rhytidhysteron thailandicum MFLUCC 14-0503
Rhytidhysteron hysterinum EB 0351
Gloniopsis subrugosa GKM1214
Gloniopsis subrugosa SMH557
92/1.00
Gloniopsis subrugosa MFUCC 14-1179
Hysterobrevium walvisbayicola CPC 35949
100/1
Gloniopsis praelonga CMW 19983
100/1
Gloniopsis praelonga CBS 112415
99/1.00
Gloniopsis praelonga CBS 123337
Gloniopsis sp. MFLUCC 14-0581
-/0.99
Gloniopsis subrugosa GKM1010
Gloniopsis subrugosa CBS 123346
Gloniopsis arciformis GKM L166A
Glonium stellatum CBS 207.34
0.02
Hysteriaceae
Outgroup

◂**Fig. 4** Phylogenetic tree generated from Maximum likelihood analysis (RAxML) based on a combined LSU, SSU and *tef*1-α sequence data. The best scoring RAxML tree with a final likelihood value of − 11,201.197321 is presented. The matrix had 726 distinct alignment patterns, with 27.43% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.248438, C = 0.234971, G = 0.281926, T = 0.234665; substitution rates: AC = 1.002659, AG = 2.757938, AT = 1.314755, CG = 0.759494, CT = 10.386178, GT = 1.0; gamma distribution shape parameter α = 0.574084. Maximum likelihood bootstrap support greater than ≥ 75% and Bayesian posterior probabilities ≥ 0.90 are indicated at the branches. Ex-type strains are in bold, while the new isolate is indicated in blue bold. The tree is rooted to *Glonium stellatum* (CBS 207.34)

collection (MFLU 16-2162) as a new species, *Hysterobrevium baoshanense*.

Jahnulales K.L. Pang, Abdel-Wahab, El-Shar., E.B.G. Jones & Sivichai

The order Jahnulales comprises freshwater lignicolous ascomycetes (Pang et al. 2002). Members of the Jahnulales occur on rotting or submerged corticated or decorticated wood (Inderbitzin et al. 2001; Pang et al. 2002; Campbell et al. 2007; Shenoy et al. 2010; Suetrong et al. 2011; Tanaka et al. 2015). Jahnulales is characterized by multilayered, large-celled peridia, stalked or sessile bitunicate asci, and one-septate ascospores with gelatinous sheaths or appendages (Pang et al. 2002; Campbell et al. 2007; Suetrong et al. 2011; Jones et al. 2015). There are two families in this order as Aliquandostipitaceae and Manglicolaceae (Jones et al. 2015).

Aliquandostipitaceae Inderb.

The family by Inderbitzin et al. (2001) to accommodate lignicolous ascomycetes with unusually wide hyphae and dimorphic ascomata. The type genus of this family is *Aliquandostipite* which is typified by *A. khaoyaiensis* Inderbitzin. Species in Aliquandostipitaceae have been mostly reported from tropical rain forests and submerged wood in freshwater streams as saprobes. Currently, there are three genera in this family (Huang et al. 2018a).

Jahnula Kirschst.

Jahnula was introduced by Kirschstein (1936) and is typified by *J. aquatica* (Kirschst.) Kirschst. Species of *Jahnula* are mostly collected from freshwater habitats (Hyde 1993a; Hyde and Wong 1999; Tsui et al. 2000; Ho et al. 2001; Cai et al. 2002; Pang et al. 2002; Pinruan et al. 2002; Raja and Shearer 2006; Raja et al. 2008; Sivichai and Boonyuen 2010; Suetrong et al. 2011; Fournier et al. 2015; Huang et al. 2018a; Bakhit 2022). Several studies have shown the polyphyletic nature of this genus based on combined ITS, LSU, and SSU sequence analysis and *Jahnula aquatica, J. granulosa, J. potamophila,* and *J. rostrata* are accommodated in *Jahnula* sensu stricto (Suetrong et al. 2011; Huang et al. 2018a). There are 12 accepted species listed in *Jahnula* in the Species Fungorum (2023). This study introduces a new *Jahnula* species.

Jahnula oblonga Senan. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900237; *Facesoffungi number*: FoF 14166; Fig. 5

Etymology: based on the oblong-shaped ascospores.

Saprobic on submerged decaying wood. **Sexual morph**: *Ascomata* 350–380 × 310–345 µm ($\bar{x}$ = 360 × 325 µm, n = 5), erumpent to superficial with the immersed base, solitary, scattered, globose to subglobose, dark brown to black, coriaceous, papillate, ostiolate. *Papilla* central, short, lined with hyaline periphyses. *Peridium* 35–75 µm thick, comprising outer, 4–6 layers of large, brown, thick-walled cells of *textura angularis* and inner, 3–5 layers of compressed, hyaline, thick-walled cells of *textura angularis*. *Hamathecium* comprising 2–3 µm wide, septate, branched, filiform pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 110–150 × 30–35 µm ($\bar{x}$ = 125 × 32 µm, n = 20), 8-spored, bitunicate, fissitunicate, oblong fusiform, short or apedicellate, apex rounded, with an indistinct ocular chamber. *Ascospores* 30–33 × 15–18 µm ($\bar{x}$ = 32 × 16 µm, n = 50), biseriate, oblong, 1-septate, slightly constricted at the septum, rough-walled, multi-guttulate, greenish-brown, apiculate. **Asexual morph**: undetermined.

Culture characteristics: Colonies on PDA reaching 2 cm diam., after 10 days in dark at 25 °C, flat, circular, with inner, concentric zonation around the centre with dark brown to greyish brown, woolly aerial mycelia with curled margin, then filamentous hyphae extend out to form paler, thin outer zone with filiform margin, reverse blackish brown, no pigments produced.

Material examined: China, Guangdong Province, Guangzhou City, Baiyun Mountain, on submerged decaying wood, 16 August 2021, Jinzhen Fu, WBHS 12 (MHZU 22-0128, **holotype**), ex-type culture ZHKUCC 22-0223.

GenBank numbers: ITS: OR164944, OR164945, LSU: OR164972, OR164973.

Notes: In the combined gene analysis of ITS, LSU and SSU showed that our isolate (ZHKUCC 22-0223, MHZU 22-0128) grouped with *Jahnula granulosa* K.D. Hyde & S.W. Wong with ML/BI = 100%/1.00 bootstrap support. The nucleotide differences of ITS, and LSU locus between our isolate and *Jahnula granulosa* revealed that 1.2%, and 0.9% respectively and sequences for SSU couldn't obtained. Morphologically, *Jahnula granulosa* differs from our collection by ascomata attached to the base with a stalk-like strands and a few sparse hair-like projections arise around the base, unbranched pseudoparaphyses, pedicellate asci with an ocular chamber or faint ring, ellipsoid to fusiform ascospores with a germ pore, and surrounded by a thin mucilaginous sheath (Hyde and Wong 1999). *Jahnula granulosa* has been

Table 1 Comparison of the size (µm) of few characters and septation of our collection with closely related *Hysterobrevium* species

Specie name	Ascomata	Peridium	Asci	Ascosopres	Septation
H. baoshanense^{H}	310–400 × 200–280	35–60	70–110 × 15–25	21–28 × 8–10	3–6 T, 1–2 L
"*H. constrictum*" (KUN-HKAS 102101)	350–450 × 700–1000	35–50	115–130 × 25–32	27–35 × 10–12	5–6 T, 1–2 L
H. constrictum ^{H}	200–320 × 240–320	N/A	74–112 × 8–10	13–20 × 5–12	1–4 L, 1 L
H. hakeae ^{H}	235– 345 × 285–395	27–67	65–105 × 10–14	18–22 × 8–12	3–4 T, 1 L
H. smilacis ^{H}	200–250 × 300–400	25–50	70–120 × 15–25	15–26 × 5–9	3–5 T, 1 L
H. mori ^{H}	190–330 × 220–275	30–60	80–110 × 10–18	14–22 × 7–10	5–7 T, 1–2 L
H. rosae ^{H}	180–240 × 150–200	30–60	70–83 × 12–15	18–22 × 5–8	2–4 T, 6–7 L

^{H} = holotype, L = longitudinal septa, T = transverse septa, N/A = not available

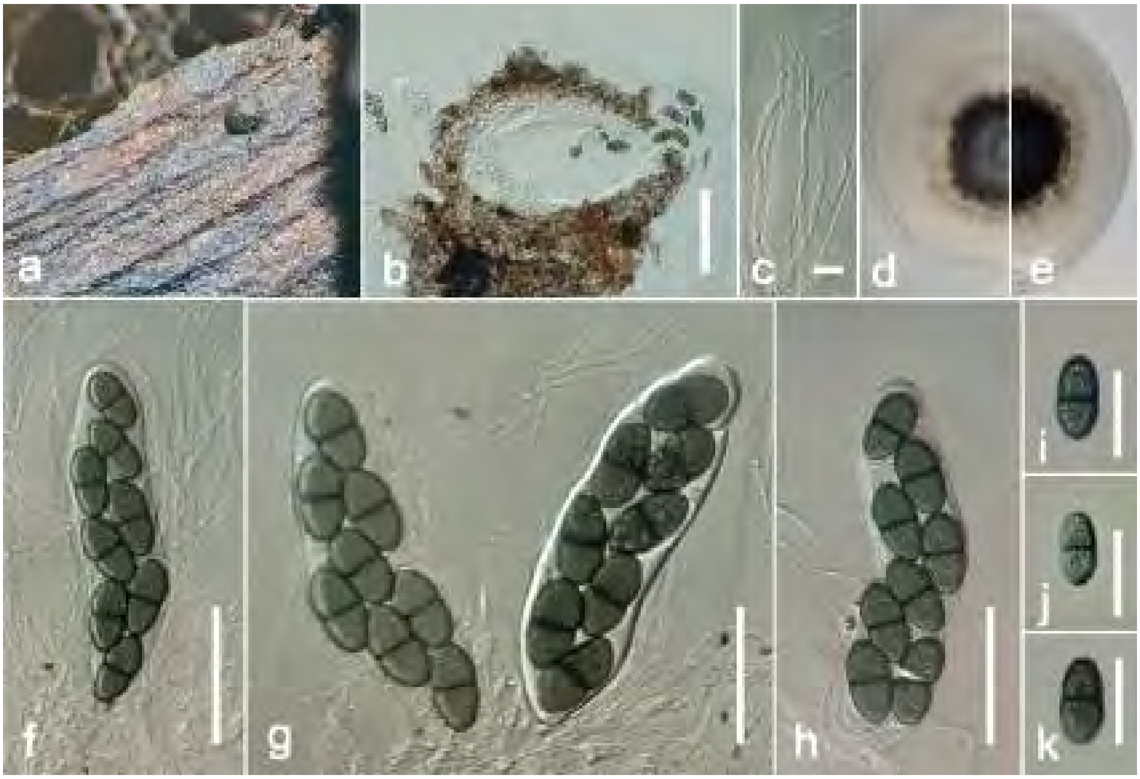


Fig. 5 ***Jahnula oblonga*** (MHZU 22-0128, **holotype**). **a** Ascomata on submerged wood. **b** Vertical section of ascoma. **c** Pseudoparaphyses. **d** Surface view of colony on PDA. **e** Reverse view of colony on PDA. **f–h** Asci. **i–k** Ascospores. Scale bars: b = 200 µm, c = 10 µm, f–h = 60 µm, i–k = 30 µm

reported from China, South Africa and Thailand (Hyde and Wong 1999; Liew et al. 2000; Cai et al. 2002; Suetrong et al. 2011). *Jahnula* species are only found in freshwater mostly in relatively undisturbed streams (Calabon et al. 2022). Therefore, it is highly likely that at present *Jahnula* species will have evolved in isolated stream worldwide (Hyde et al. 2020a). We therefore, introduce a new species and expect many more discoveries (Fig. 6).

Kirschsteiniotheliales Hern.-Restr., R.F. Castañeda, Gené & Crous

The monotypic order Kirschsteiniotheliales was introduced by Hernándes-Restrepo et al. (2017) with Kirschsteiniotheliaceae Boonmee & K.D. Hyde as the type family. This family comprises mostly saprobic taxa.

Kirschsteiniotheliaceae Boonmee & K.D. Hyde

Boonmee et al. (2012) established the family Kirschsteiniotheliaceae to accommodate *Kirschsteiniothelia* sensu stricto in the class Dothideomycetes, based on morphological characters and phylogenetic analysis. This monotypic family is typified by *Kirschsteiniothelia* D. Hawksw.

and members in this family are saprobes on dead wood in tropical habitats or subtropical regions (Su et al. 2016; Bao et al. 2018).

Kirschsteiniothelia D. Hawksw.

Kirschsteiniothelia was introduced with *K. aethiops* (Berk. & M.A. Curtis) D. Hawksw. as the type species (Hawksworth 1985). The asexual morph of *Kirschsteiniothelia* are characterized by macronematous, simple or branched at the apex, brown to dark brown conidiophores with monotretic, integrated, terminal or discrete, determinate or percurrently extending conidiogenous cells that produce solitary, acrogenous, euseptate conidia (Chen et al. 2006; Boonmee et al. 2012; Hyde et al. 2013; Mehrabi et al. 2017; Sun et al. 2021). Species in this genus are saprobes on dead wood and usually obtained from terrestrial, aquatic and marine habitats (Mehrabi et al. 2017). There are 30 species listed in this genus (Species Fungorum 2023). This study introduces a new *Kirschsteiniothelia* species.

Kirschsteiniothelia guangdongensis Senan. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900339; *Facesoffungi number:* FoF 14167; Fig. 7

Etymology: based on the region where sample has been collected.

Saprobic on dead branches of unidentified plant. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate, superficial, hairy, black, scattered, single or in groups, with superficial, dark brown to black hyphae. *Conidiophores* 250–350 µm long, 10–18 µm wide, superficial on host surface, macronematous, mononematous, simple, erect to slightly flexuous, unbranched, septate, not constricted at the septa, dark brown, cylindrical. *Conidiogenous cells* 15–18 × 9–12 µm ($\overline{x}$ = 17 × 10 µm, n = 20), monoblastic, integrated, percurrently proliferating, terminal, cylindrical to ampulliform, determinate, dark brown. *Conidia* 290–300 µm long, 42–50 µm wide at base, 20–22 µm wide at apex, elongated, flask-shaped, straight or slightly curved, rounded at the apex, apical cell paler than others, 13 transverse septa with one longitudinal septum in 5 basal cells, a thin sheath at apex extend up to 3rd cell from the top, blackish brown to black, thin-walled, smooth; secession by schizolysis or rhexolysis.

Culture characters: Colonies on PDA reached 4 cm diam., after 7 days incubated in dark at 25 °C; circular, flat, filiform margin, with moderate aerial mycelia, surface view blackish green with grey aerial mycelia, reserve olivaceous grey.

Material examined: China, Guangdong Province, Guangzhou, Haizhu District, (23° 06′ 28.4″ N 113° 16′ 51.7″ E), on twigs of unidentified plant, 18 June 2021, Kularathnage N.D., NDK 19–2, (MHZU 22-0137, **holotype**), ex-type culture ZHKUCC 22-0233.

GenBank numbers: ITS: OR164946, LSU: OR164974.

Notes: The combined ITS, LSU and SSU gene analysis (Fig. 8) showed that our collection (MHZU 22-0137) is phylogenetically close to *Kirschsteiniothelia tectonae* forming a distinct clade with ML/BI = 98/1.00 bootstrap support. The nucleotide differences in ITS and LSU sequences of our collection and *Kirschsteiniothelia tectonae* revealed 2.96% and 5.82% respectively. Our collection morphologically differs from *Kirschsteiniothelia tectonae* by its flask-shaped, elongated, thin-walled highly pigmented conidia with 13 transverse septa and one longitudinal septum in five basal cells, large conidiophores and conidiogenous cells while *K. tectonae* has small ($\overline{x}$ = 137 × 16 µm), cylindric-obclavate, dark reddish-brown, thick-walled conidia with 9–25 or more transverse septa (Li et al. 2016). It should be noted that, the characters of *Kirschsteiniothelia tectonae* were described from sporulating cultures while the characters of our collection were obtained from the substrate. Therefore, based on morphology, and phylogeny, we describe our collection as *Kirschsteiniothelia guangdongensis*.

Patellariales D. Hawksw. & O.E. Erikss.

Patellariales was introduced by Hawksworth and Eriksson (1986) and this order only comprises its type family Patellariaceae Corda. Members of the Patellariales are saprobes on woody bark of trees while some are lichenized species (Jones et al. 2015; Yacharoen et al. 2015). Species are commonly found in terrestrial habitats and occasionally in aquatic habitats (Kirk et al. 2008; Jones et al. 2015). Morphologically, species in Patellariales are characterized by apothecial ascomata, pseudoparaphyses attached to the base and apex, cylindric-clavate asci and mostly fusoid ascospores (Kutorga and Hawksworth 1997). The asexual morphs are aposphaeria-like and diplodia-like species (Yacharoen et al. 2015).

Patellariaceae Corda

Patellariaceae was introduced by Corda (1838) with *Patellaria* Fr. as the type genus. The family includes 21 genera (Jaklitsch and Voglmayr 2016; Wijayawardene et al. 2017) and members in this family mostly occur on bark or wood as saprobes (Kutorga and Hawksworth 1997; Yacharoen et al. 2015; Jaklitsch and Voglmayr 2016).

Rhytidhysteron Speg.

The genus *Rhytidhysteron* was described by Spegazzini (1881) and this genus is characterized by forming hysterothecia, with lenticular or irregular, striated, or smooth openings, various coloured epithecium, excipulum composed of 1–2 layers of cells of *textura angularis* or *textura globosa*, octosporic, bitunicate, cylindrical asci, reddish-brown to

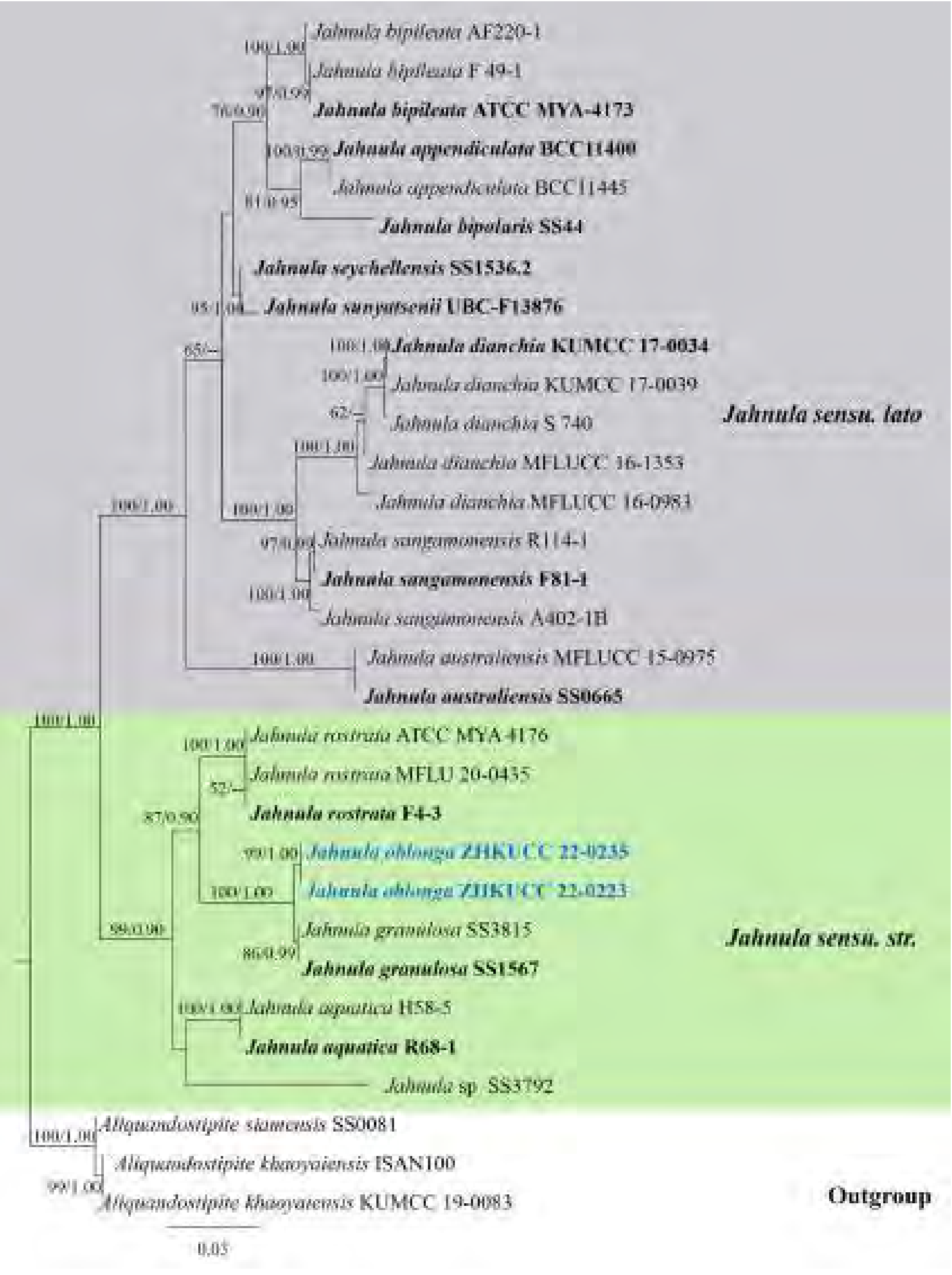


Fig. 6 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data which comprised 2434 characters (ITS = 543, LSU = 866, SSU = 1025). The best scoring RAxML tree with a final likelihood value of − 8034.098510 is presented. The matrix had 576 distinct alignment patterns, with 31.95% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.225508, C = 0.330133, G = 0.230543, T = 0.213816; substitution rates: AC = 1.338925, AG = 2.498969, AT = 1.195768, CG = 0.746582, CT = 5.928346, GT = 1.0; gamma distribution shape parameter α = 0.118818. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (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 blue bold. The tree is rooted to *Aliquandostipite khaoyaiensis* (ISAN100), *A. khaoyaiensis* (KUMCC 19-0083) and *A. siamensis* (SS0081)

brown, 1–3-septate ascospores, constricted at the central septum, (Boehm et al. 2009b; Thambugala et al. 2016). Most species in this genus are saprobes (Cobos-Villagrán et al. 2021) while some species are human pathogens (Chander et al. 2017; Mudhigeti et al. 2018). This study reports a new host record of *Rhytidhysteron hongheense*.

Rhytidhysteron hongheense Wanas., in Wanasinghe et al., Journal of Fungi 7(3, no. 180): 27 (2021)

Index Fungorum number: IF837992; *Facesoffungi number:* FoF 14168; Fig. 9

Saprobic on the dead twigs of *Prunus pseudocerasus* Lindl. **Sexual morph**: *Hystherothecia* 1000–2000 µm long × 300–500 high × 500–1,000 µm diam. ($\overline{x}$ = 1680 × 420 × 740 µm, n = 10), solitary or gregarious, sessile, slightly erumpent. *Receptacle cupulate* black, flat or slightly concave, with a slightly dentate margin. *Excipulum* 60–105 µm ($\overline{x}$ = 75.4, n = 20) wide, with the ecto-excipulum narrow-layered, deep, and thick-walled, with black cells of *textura globulosa* to *textura angularis*. *Hamathecium* 2–5 µm wide ($\overline{x}$ = 4.1 µm, n = 20), numerous, propoloid, pseudoparaphyses, reddish-orange pigmented. *Asci* 180–285 × 9–18 µm ($\overline{x}$ = 212.3 × 12 µm, n = 50), 8-spored, bitunicate, fisitunicate, long cylindrical, short pedicellate, rounded at apex. *Ascospores* 18–40 × 8.7–13.8 µm ($\overline{x}$ = 28.1 × 11.1 µm, n = 30), overlapping uniseriate, hyaline to light brown when young, dark brown at maturity, one-septate, ellipsoid, 3-septate, rarely muriform, guttulate. **Asexual morph**: Undetermined.

Culture characteristics: Colonies on PDA reached 40 mm in diameter after 7 days at 20 °C in the dark. Initially, the colony was white, circular, smooth, with an undulated edge, with floccose. After 4 weeks, it became greenish-grey and slightly raised at the centre and pale brown towards margin, dark brown from the reverse side. The hyphae were septate, branched, hyaline, thin, and smooth-walled.

Material examined: China, Sichuan Province, Jianyang City, Xingfucun, on decaying twigs of *Prunus pseudocerasus* (Rosaceae), N30° 28′ 37, E104° 20′ 58, 18 April 2021, Y. Chen, XFC14 (HUEST 21.0018), living culture UESTCC 21.0018.

Hosts and distribution: On decaying wood of *Dodonaea* Mill in Yunnan, China (Wanasinghe et al. 2021), on decaying twigs of *Prunus pseudocerasus* Lindl in Sichuan, China (This study).

GenBank numbers: ITS: OL741380, LSU: OL741320, SSU: OL741383, *tef1-α*: ON411270

Notes: The combined ITS, LSU, SSU and *tef1-α* sequences analysis (Fig. 10) of our isolate (UESTCC 21.0018) show that our strain clusters with the type strain of *R. hongheense* (KUMCC 20-0222). Our collection is similar to *R. hongheense* (Wanasinghe et al. 2021) and we identified our strain as *Rhytidhysteron hongheense*. This is the first report of *Rhytidhysteron hongheense* on *Prunus pseudocerasus*.

Pleosporales Luttrell ex M.E. Barr

Pleosporales was introduced by Luttrell (1955) to accommodate ascomycetous species having perithecioid ascomata with pseudoparaphyses among the asci (Zhang et al. 2009). The members of this order can be endophytes or epiphytes, parasites, saprobes or lichenicolous in terrestrial or aquatic environments or even occur on animal dung (Zhang et al. 2009). Pleosporales comprises 91 families and we follow the latest updated account of Pleosporales included in Hongsanan et al. (2020a).

Didymellaceae Gruyter, Aveskamp & Verkley

The family Didymellaceae was established by de Gruyter et al. (2009) to accommodate *Phoma* and phoma-like genera. Aveskamp et al. (2010) demarcated the taxonomic boundaries of Didymellaceae and resolved generic delimitations and reveal more natural evolutionary relationships (Ariyawansa et al. 2015a; Chen et al. 2015a; Crous and Groenewald 2016; Wijayawardene et al. 2016; Wanasinghe et al. 2018; Hongsanan et al. 2020a, b; Kularathnage et al. 2023b). Currently, the family comprises more than 44 accepted genera (Kularathnage et al. 2023b). Species of Didymellaceae are cosmopolitan and distributed in wide range of hosts and habitats. Most of them are plant pathogens of a wide range of hosts causing leaf and stem lesions and fruit rots (Aveskamp et al. 2008, 2010; Chen et al. 2015a, b) while some are saprobes that occur in soil and dead plant parts (Tennakoon et al. 2019). Few species have been reported as human and animal pathogens (Gkoutselis et al. 2021).

Allophoma Qian Chen & L. Cai

The genus *Allophoma* was introduced to accommodate the type species, *A. tropica* (Chen et al. 2015a). The genus is characterized by globose to flask-shaped conidiomata, with papillate ostioles, and with variable in shape and size, hyaline, thin-walled, smooth, mostly guttulate, aseptate conidia (Chen et al. 2015b; Kularathnage et al. 2023b). *Allophoma* species are morphologically similar and hard to differentiate from one another. Therefore, molecular data are essential for accurate identification of species within this genus, with ITS, LSU, *β-tubulin* and *rpb2* (Chen et al. 2015a; Hou et al. 2020). No sexual morph of this genus has been observed to date. Presently, this genus comprises 14 species (Index Fungorum 2023) and here, we introduce a novel *Allophoma* species in this study.

Allophoma yuccae A. Ahmadpour, Z. Heidarian, Z. Alavi, F. Alavi & Y. Ghosta, ***sp. nov.***

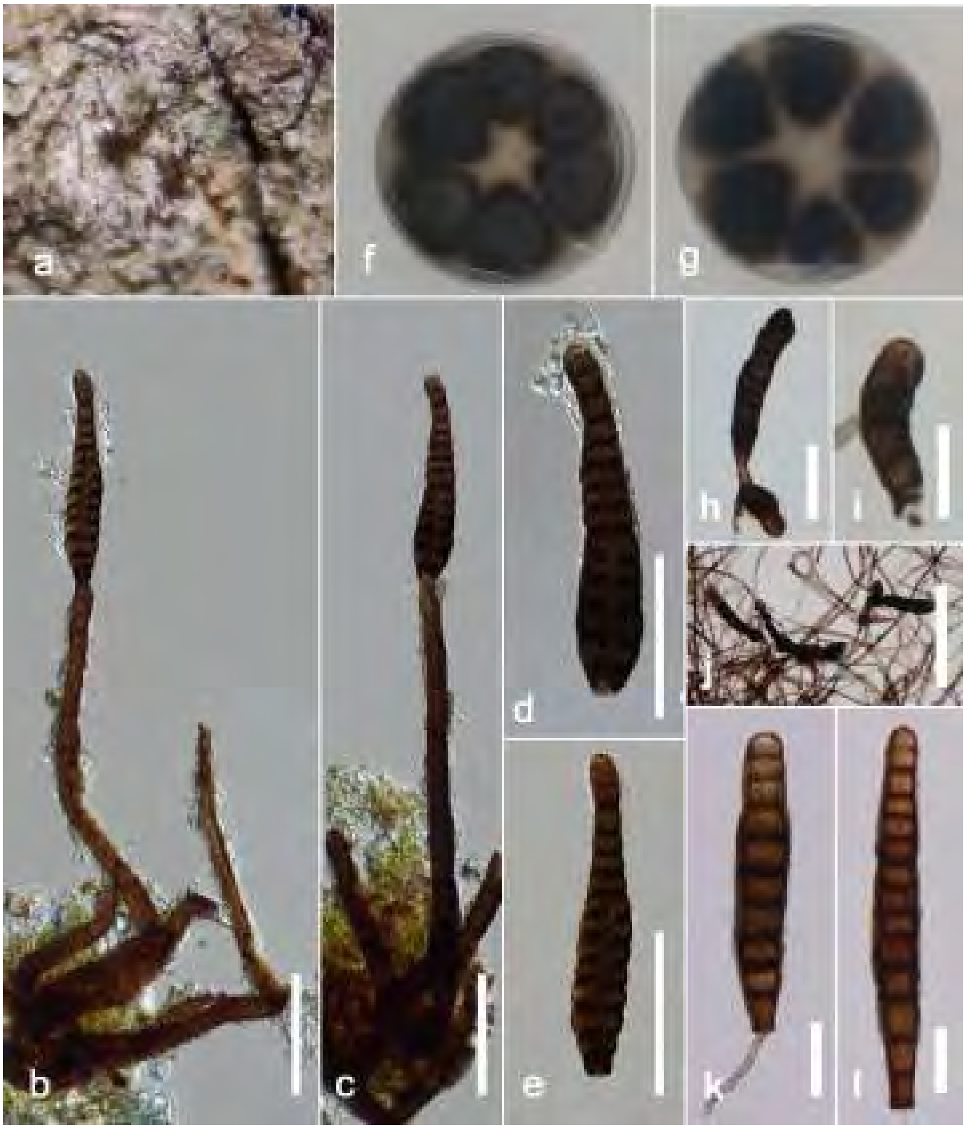


Fig. 7 ***Kirschsteiniothelia guangdongensis*** (MHZU 22-0137, **holotype**). **a** Colonies on natural substrate. **b, c** Conidiophores with conidia. **d, e** Conidia. **f** Surface view of colony. **g** Reserve view of colony. **h**–**l** Conidia of *Kirschsteiniothelia tectonae* (MFLUCC 12-0050). Scale bars: b–e = 150 µm

Index Fungorum number: IF900340; *Facesoffungi number*: FoF 14169; Fig. 11

Etymology: based on the host plant genus, *Yucca.*

Pathogenic on the leaf spots of *Yucca gigantean* Lem. *Lesions* up to 10–15 mm diam., spread on the upper surface, scattered, distinct, irregular, brown to dark brown. **Sexual morph**: Undetermined. **Asexual morph**: Coelomycetous. *Conidiomata* (100–)130–250 × (100–)120–240 µm, pycnidial, semi-immersed to immersed, mostly solitary, rarely aggregated, scattered, globose to subglobose, pale brown to brown, thin-walled, glabrous, ostiolate, papillate. *Papilla* 1(–2), elongate, short, open with wide ostiole. *Pycnidial wall* 10–35 µm thick, pseudoparenchymatous, 3–5 layered, composed of oblong to isodiametric cells, pale brown. *Conidiogenous cells* 4–6(–8) × 4–8 µm, phialidic, hyaline, smooth, globose to ampulliform. *Conidia* 4–7 × 2–3 µm ($\bar{x}$ = 4.5 × 2.5 µm, n = 50), ellipsoidal to oblong, occasionally ovoid, with rounded ends, hyaline, smooth and thin-walled, aseptate, with 1–3-polar guttules.

Culture characteristics: Colonies on PDA reaching 60–67 mm diam. after 7 days at 25 °C, smooth margin, sparse aerial mycelia, floccose, olivaceous green at the center, white at the margin; reverse white to pale brown. Colonies on MEA reaching 55–60 mm diam. after 7 days at 25 °C, filiform margin, sparse aerial mycelia, floccose, surface white to pale brown; reverse white, pale brown at the center. Colonies on OA reaching 55–60 mm diam. after 7 days at 25 °C, smooth margin, surface white to pale olivaceous, floccose aerial mycelia, abundant production of pycnidia, conidial matrix visible; reverse buff, with pale olivaceous near the center. Colonies on CMA reaching 50–56 mm diam. after 7 days, smooth margin, sparse aerial mycelia, white to pale olivaceous; reverse with pale olivaceous near the center. NaOH test negative.

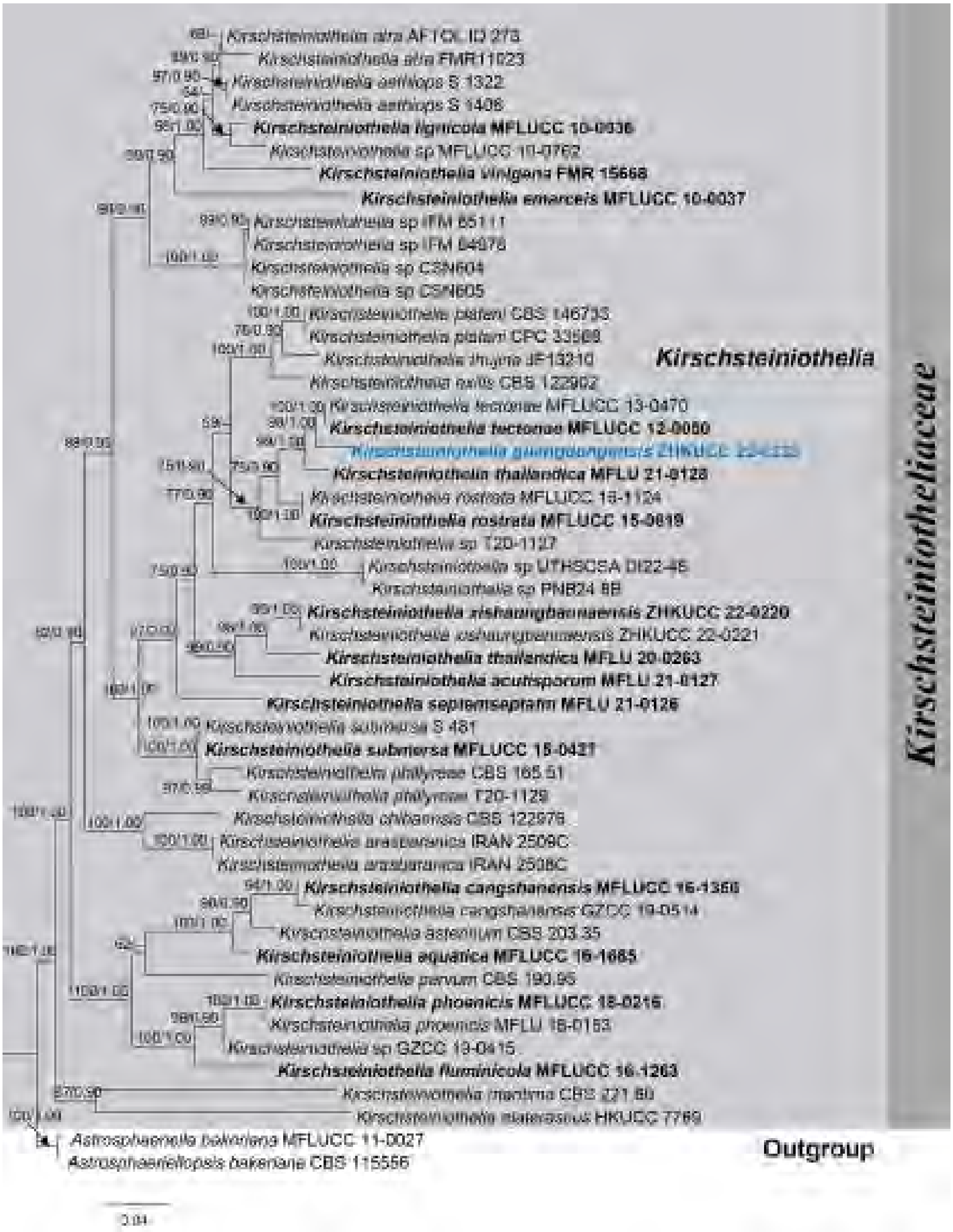


Fig. 8 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data which comprised 1801 characters (ITS = 590, LSU = 876, SSU = 1035). The best scoring RAxML tree with a final likelihood value of − 17,128.646756 is presented. The matrix had 1148 distinct alignment patterns, with 36.37% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.237038, C = 0.247650, G = 0.281313, T = 0.233999; substitution rates: AC = 1.304030, AG = 2.746538, AT = 0.938119, CG = 1.489864, CT = 5.666453, GT = 1.0; gamma distribution shape parameter α = 0.518282. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (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 blue bold. The tree is rooted to *Astrosphaeriella bakeriana* (MFLUCC 11-0027, CBS 115556)

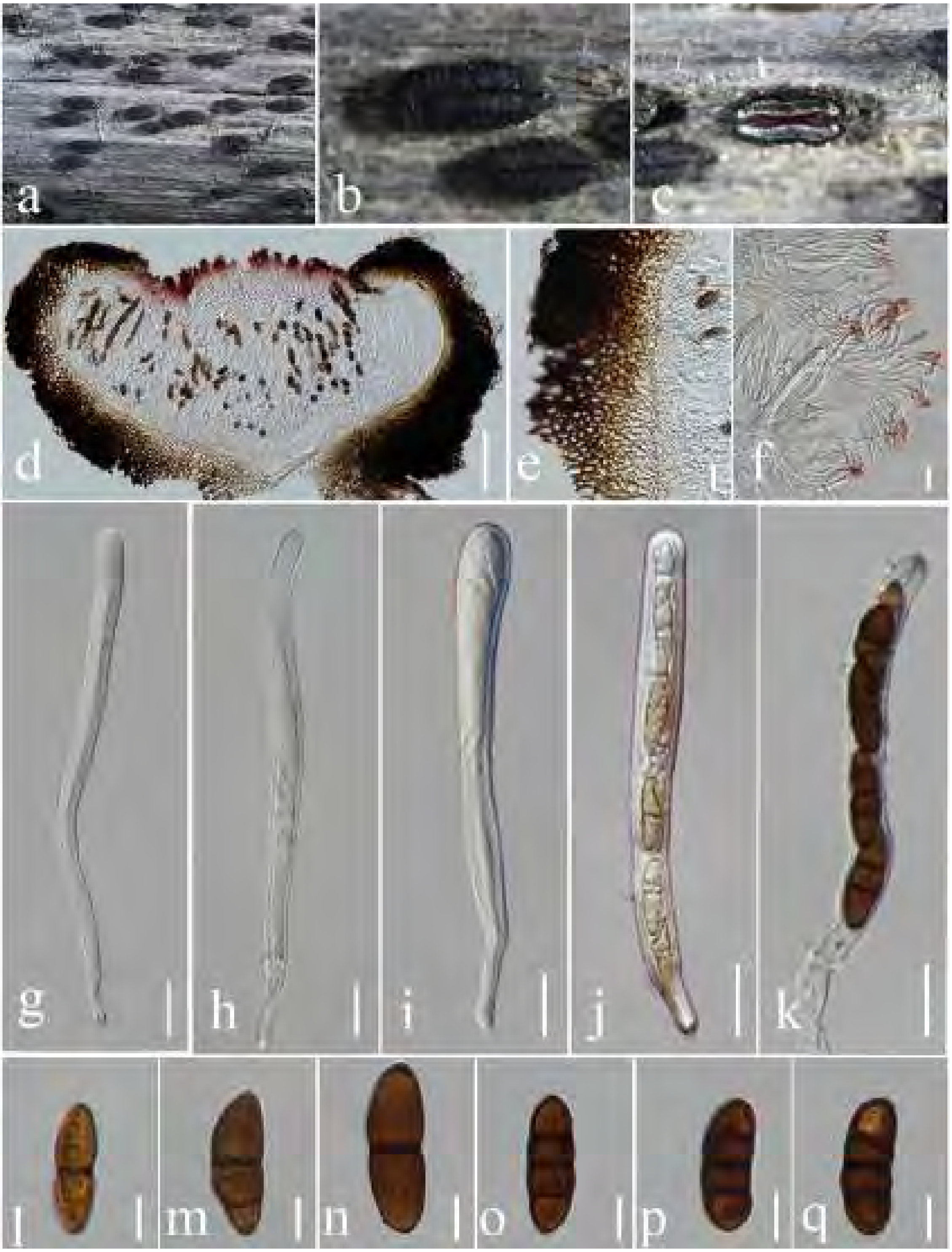


Fig. 9 ***Rhytidhysteron hongheense*** (HUEST 21.0018). **a, b** Hysterothecia on decaying wood. **c** Horizontal section of hysterothecium. **d** Vertical section through hysterothecium. **e** Wall of the hysterothecium. **f** Pseudoparaphyses. **g–k** Asci. **l–q** Ascospores. Scale bars: d = 100 µm, e–f = 20 µm, g–q = 10 µm

Material examined: Iran, West Azarbaijan Province, Miyandoab City, on leaves of *Yucca gigantean* (Asparagaceae), 20 September 2021, A. Ahmadpour, (IRAN 18108F, **holotype**), ex-type culture, IRAN 4238C; *ibid.* East Azarbaijan Province, Maraghe City, on *Y. gigantean*, 30 September 2021, A. Ahmadpour, living culture, FCCUU 1901.

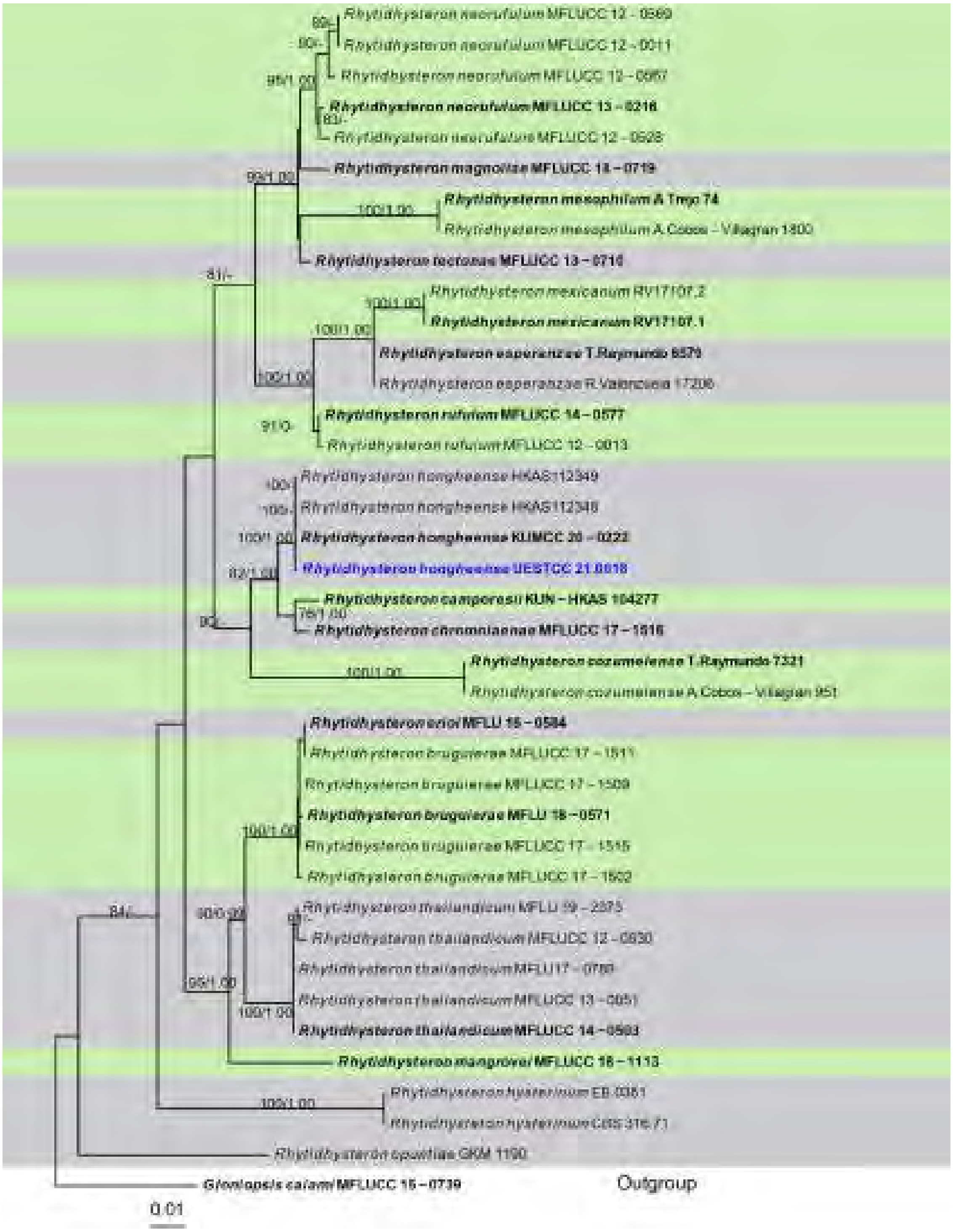


Fig. 10 The best scoring RAxML tree with a combined dataset of ITS, LSU, SSU and *tef*1-α sequence data of species of *Rhytidhysteron*. The topology and clade stability of the combined gene analyses was compared to the single gene analyses and no significant differences. The tree is rooted with *Gloniopsis calami* (MFLUCC 15-0739). The matrix had 850 distinct alignment patterns with 31.32% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.239, C = 0.250, G = 0.276, T = 0.235; substitution rates AC = 1.213710, AG = 2.120204, AT = 1.148572, CG = 1.118178, CT = 5.920120, GT = 1.0; gamma distribution shape parameter α = 0.212865 and final likelihood value of − 13,078. Ex-type strains are in bold and newly generated sequences are in blue bold. Bootstrap support for ML ≥ 75% and BI ≥ 0.95 are given at the nodes. The scale bar presents the expected number of nucleotide substitutions per site

Fig. 11 ***Allophoma yuccae*** (IRAN 4238C, **holotype**). **a** Host plant. **b–d** Symptoms on leaves. **e** Colony on PDA after 7 days (front and revers). **f** Colony on MEA after 7 days (front and revers). **g** Colony on OA after 7 days (front and revers). **h** Colony on CMA after 7 days (front and revers). **i–j** Pycnidia producing on OA. **k–l** Pycnidia producing on PDA. **m–o** Pycnidia. **p–r** Conidiogenous cells. **s** Conidia. Scale bars: m–o = 50 µm, p–s = 10 µm

GenBank numbers: ITS: OP805927, OP805928, *rpb2*: OP838915, OP838916, *β-tubulin*: OP838917, OP838918.

Notes: Our collection is phylogenetically closely related to *Allophoma hayatii* (CBS 142859 and CBS 142860) with statistical support BI = 0.96 and ML = 95% (Fig. 12). A comparison of nucleotide differences in ITS, *rpb2* and *β-tubulin* indicates that our isolate (IRAN 4238C) differs from *A. hayatii* (CBS 142859) by 1.03% in ITS and 1.91% in *rpb2* while *β-tubulin* sequences are identical. Morphologically, our collection differs from *A. hayatii* by pycnidia with single ostiole, aseptate conidia and absence of chlamydospores formation while *A. hayatii* has 1–3-ostiole per pycnidium, 1-septate conidia and chlamydospores formation (Babaahmadi et al. 2018). Furthermore, the shape and size of pycnidia and conidia of our collection are similar to *A. labilis* and however, differs from *A. labilis* by NaOH test (reddish-brown discoloration in *A. labilis* and negative in our collection) (Boerma et al. 2004). A comparison of nucleotide

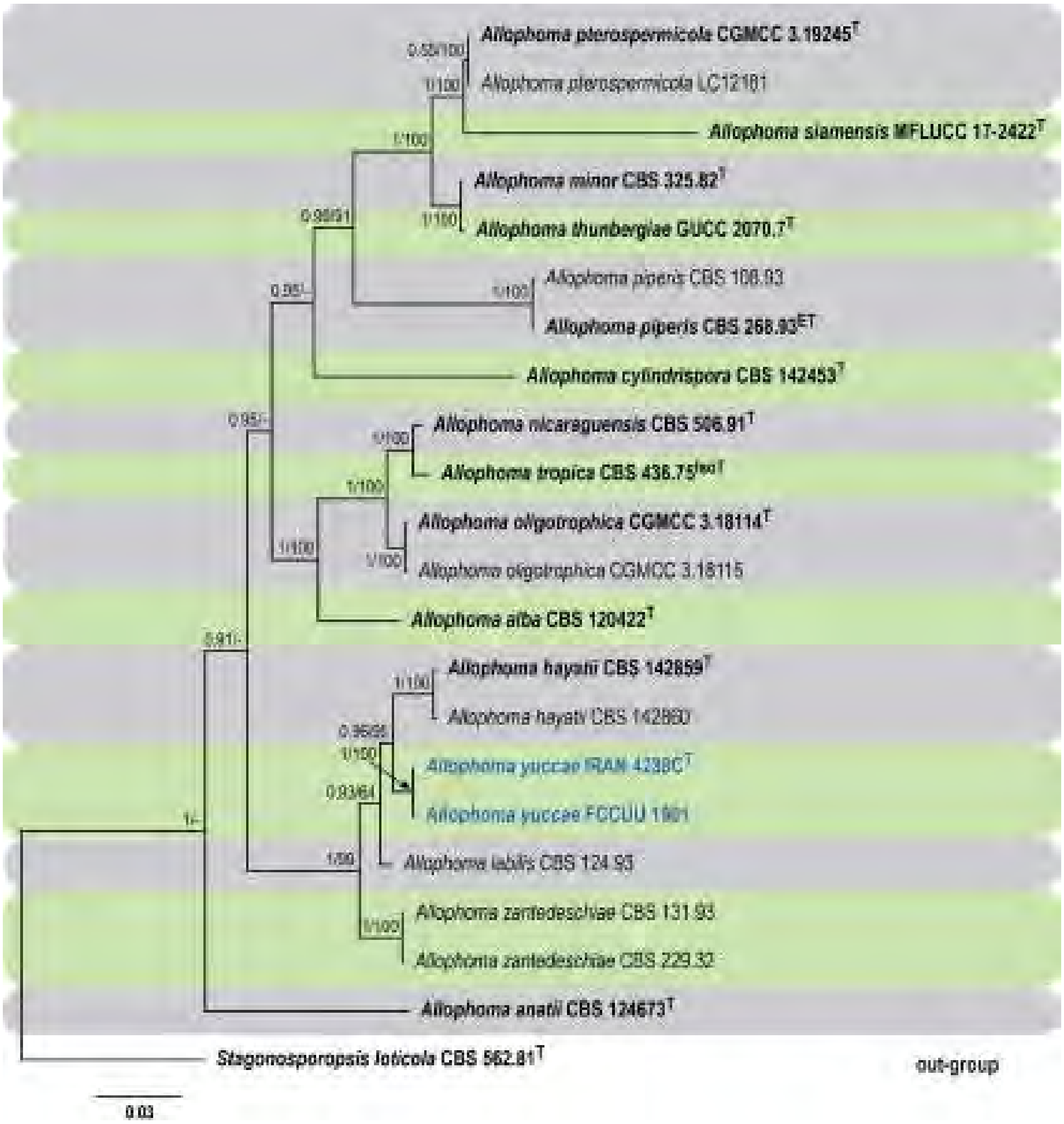


Fig. 12 Phylogenetic tree inferred from Bayesian Inference (BI) of combined dataset of ITS, *rpb2* and *β-tubulin* of *Allophoma* species. Twenty two strains are included in the combined analyses which comprise a total of 1384 characters (ITS = 455 bp, *rpb2* = 596 bp and *β-tubulin* = 333 bp) and inferred substitution models were K80 + I (ITS), SYM + G (*rpb2*), and GTR + G (*β-tubulin*). Bootstrap support obtained in a complementary Maximum Likelihood (ML) analysis with RAxML using 1000 replicates. The Bayesian posterior probabilities (BI) > 0.50 and Maximum Likelihood bootstrap support (ML) values > 50% are given at the nodes (BI/ML). The tree was rooted to *Stagonosporopsis loticola* (CBS 562.81) and newly identified strains are in blue bold and ex-type strains are in bold. The scale bar indicates the number of nucleotide substitutions

difference in ITS, *rpb2* and *β-tubulin* loci of our collection and *A. labilis* shows 0.83% in *rpb2*, 2.8% in *β-tubulin* and no difference in ITS. Therefore, we introduce our collection as *A. yuccae*.

Boeremia Aveskamp, Gruyter & Verkley

The genus *Boeremia* represents species that are most similar to *Phoma exigua* (Aveskamp et al. 2010), but it has been phylogenetically shown that they are two distinct groups (Aveskamp et al. 2010; Chen et al. 2015a, 2017). Identification of *Boeremia* species are mainly based on host association (Berner et al. 2015; Jayasiri et al. 2017). There are no previous records of *Boeremia* from genus *Wisteria*. We herein introduce a new species *Boeremia wisteriae* from a decaying pod of *Wisteria* species.

Boeremia wisteriae Jayasiri & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556935; *Facesoffungi number*: FoF 07391; Fig. 13

Etymology: based on the host genus that specimen was collected.

Saprobic on decaying pod of *Wisteria* sp. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 155–225 high × 186–220 µm diam. ($\bar{x} = 187 \times 196$ µm, n = 20), pycnidial, mostly globose to subglobose, glabrous or with few mycelial outgrowths, superficial on agar surface or immersed, solitary or confluent. *Ostioles* indistinct papillate, internal wall covered with hyaline filiform cells when mature. *Pycnidial wall* 32–53 µm wide, pseudoparenchymatous, Ellipsoid, globose, oblong to allantoid. *Conidiogenous cells* 3–7.5 × 3–6.5 µm. ($\bar{x} = 5.5 \times 4.5$ µm, n = 20), ampulliform to doliiform, phialidic, hyaline, simple, smooth. *Conidia* 6–8 × 2–4 µm ($\bar{x} = 6.8 \times 3.5$ µm, n = 20), ellipsoid, globose, oblong to allantoid, hyaline, thin-walled, smooth, aseptate, polar biguttulate.

Culture characteristics: Conidia germinating on MEA within 24 h. Germ tubes produced from ends of conidia. Colonies circular, flat, filiform margin, cottony, pinkish white, light brown to grey, lower surface off white to pale brown, reaching 40–50 mm diam. in 14 days at 18 °C. Mycelia are superficial, effuse and radially striate with regular edge. Sporulation observed after 30 days under 18 °C.

Material examined: China, Yunnan Province, Kunming City, garden of Kunming Institute of Botany, decaying pod of *Wisteria* sp., (Fabaceae), 25 May 2018, Jayasiri S.C., C 455 (MFLU 18-2209, **holotype**; KUN-HKAS 102439, **isotype**), ex-type culture, MFLUCC 18-1562.

GenBank numbers: ITS: MK347804, LSU: MK348023, *tef*1-α: OQ304686, *β-tubulin*: OQ304687, *rpb2*: OQ304685, SSU: MK347912

Notes: Our isolate (MFLUCC 18-1562) groups with *Boeremia pseudolilacis* (CBS 101207, CBS 462.67 and CBS 423.67) and *B. rhapontica* (CBS 113651) with week bootstrap support in our multigene phylogenetic analysis (Fig. 14). The pycnidial and conidial characters of our new strain fits with the *Boeremia* species (Aveskamp et al. 2010). The nucleotide differences of *β-tubulin* and *rpb2* of our strain with *B. rhapontica* gives 0.84% and 1.34% and the

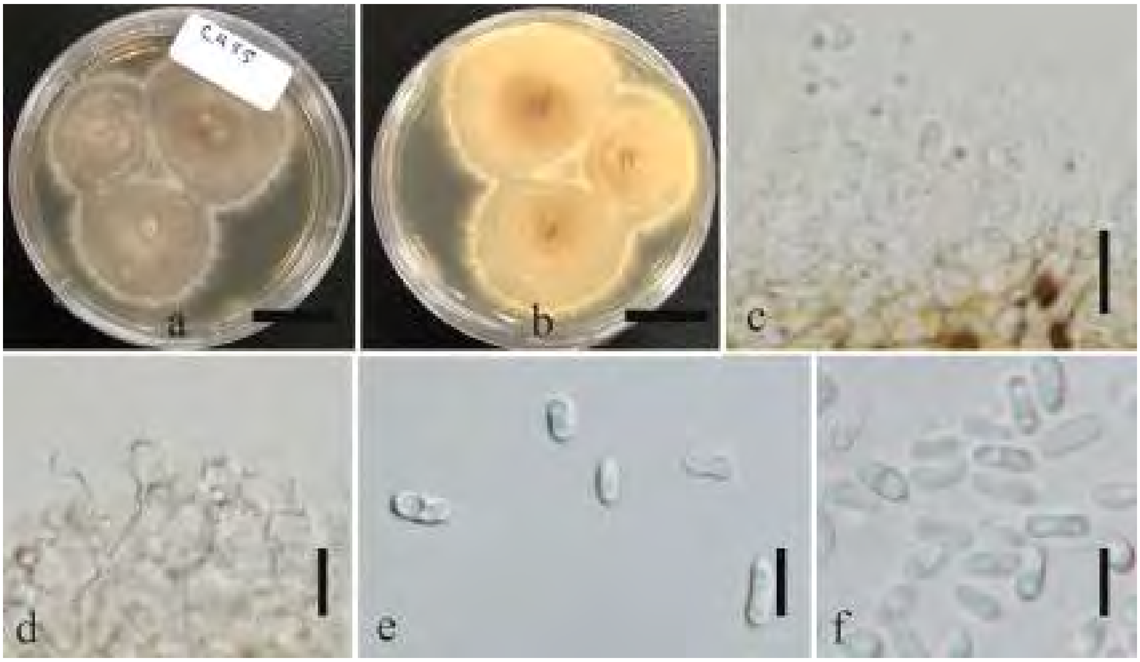


Fig. 13 ***Boeremia wisteriae*** (MFLUCC 18-1562, **ex-type**). **a** Frontal view of the culture on MEA. **b** Reverse view of the culture on MEA. **c, d** Formation of conidiogenous cells. **e, f** Conidia. Scale bars: a, b = 1 cm, c = 10 µm, d–f = 5 µm

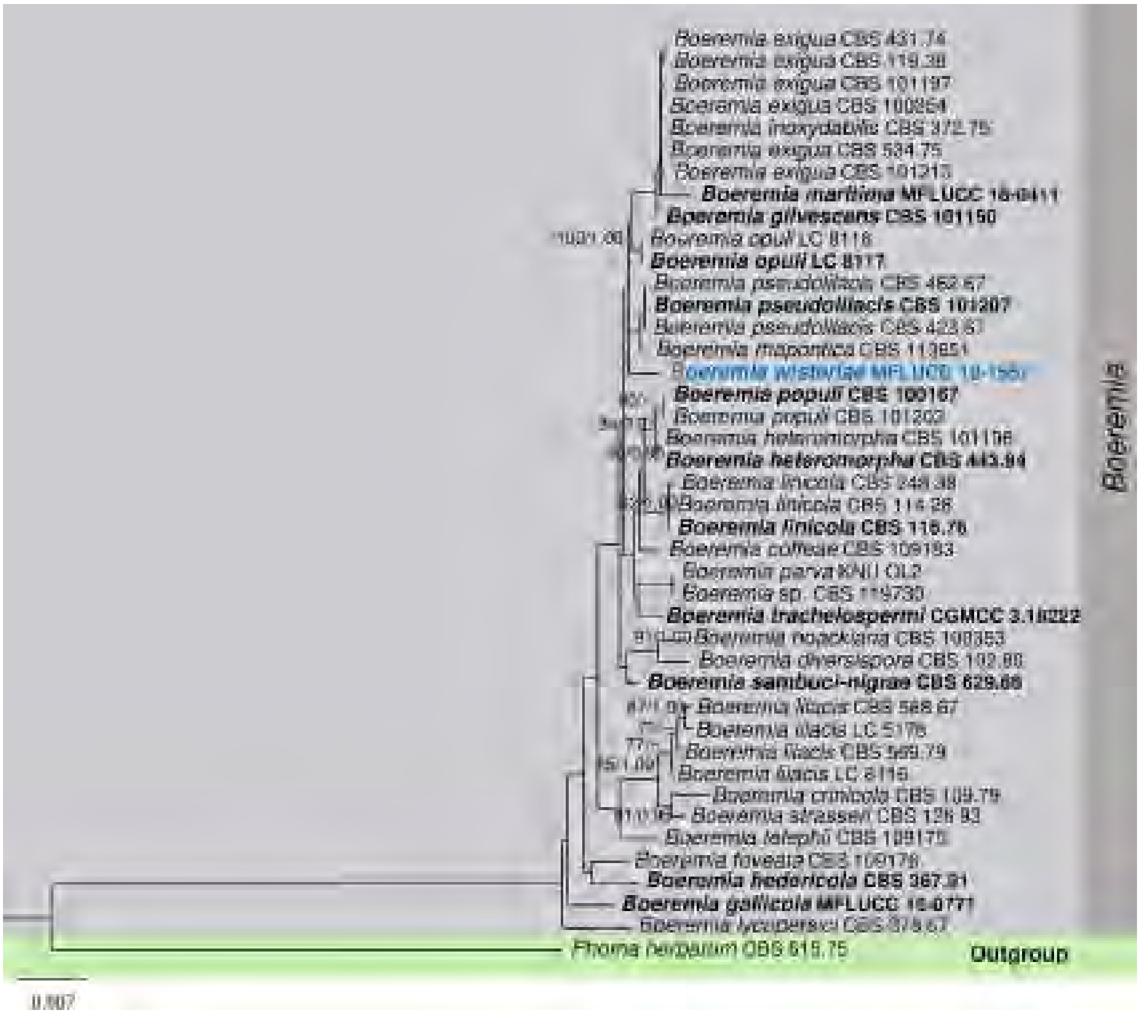


Fig. 14 Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined multi-gene (ITS, LSU, *rpb2*, and *β-tubulin*). The matrix comprises 2745 characters with gaps. The tree is rooted with *Phoma herbarum* (CBS 615.75). The best scoring RAxML tree with a final likelihood value of − 8211.587479 is presented. The matrix had 406 distinct alignment patterns, with 18.95% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.238114, C = 0.240500, G = 0.268943, T = 0.252444; substitution rates AC = 1.468423, AG = 3.444817, AT = 1.827506, CG = 1.210667, CT = 10.782158, GT = 1.0. ML bootstrap support (first set) equal or greater than 70% and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue bold. The ex-type strains are in bold

nucleotide differences of *β-tubulin* and *rpb2* of our strain with *B. pseudolilacis* (CBS 101207, CBS 423.67) gives 1.29% and 1.34% respectively. Morphologically, these three species are similar, but *Boeremia pseudolilacis* does not have clear morphological description with the measurements. Our new strain can be distinguished from *B. rhapontica* by the measurements of conidiomata and conidia (186–220 µm vs 50.3–199.1 µm diam. and 6–8 × 2–4 µm *vs* 3.6–7.1 × 1.7–3.9 µm) (Berner et al. 2015). *Boeremia pseudolilacis* identified from *Syringa vulgaris*, and *Boeremia rhapontica* as a pathogen on *Rhaponticum repens*, but our new strain has collected from decaying pod of *Wisteria* sp. Therefore, we introduce this collection as *Boeremia wisteriae* sp. nov.

Epicoccum Link

Epicoccum was introduced by Link (1816) with *Epicoccum nigrum* Link as type species. *Epicoccum* species are ubiquitous (de Gruyter et al. 2009) and found in the air, in soil, on human toe nails, in various plant parts as saprobes, endophytes or pathogens (Beasley et al. 2001; Araújo et al. 2012; Taguiam et al. 2020) and in water (Melgarejo et al. 1985; Domsch and Gams 1993; Arenal et al. 1999; Chen et al. 2017). Some *Epicoccum* species are insect and fish parasites (Wright et al. 2003; Vannini et al. 2017) while some are fungicolous that grow on mushrooms (Arenal et al. 1999). Some endophytic *Epicoccum* species have biological control ability against various plant pathogens (Bagy et al. 2019) and some species produce mycotoxins (Oliveira et al.

2018). This study introduces two new *Epicoccum* species and a record of new host association.

Epicoccum terminosporum Kular. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900414; *Facesoffungi number*: FoF 14170; Fig. 15

Etymology: Based on the terminal or acropleurogenous conidiogenous cells.

Saprobic on leaves of *Livistona chinensis* (Jacq.) R.Br. ex Mart. Appears as black, scattered spots. **Asexual morph**: *Conidiomata* 180–200 × 230–260 µm ($\overline{x}$ = 190 × 243 µm, n = 10), pycnidial, solitary, scattered, immersed to erumpent, compressed-globose, black, coriaceous, ostiolate, apapillate. *Conidiomata wall* 20–30 µm ($\overline{x}$ = 23 µm, n = 10), pseudoparenchymatous, 3–6 cell layered, composed of thick-walled, long, compressed, brown cells of *textura angularis*. *Conidiogenous cells* 15–20 × 5–10 µm ($\overline{x}$ = 18 × 8 µm, n = 20), terminal or acropleurogenous, enteroblastic, phialidic, doliiform to ampulliform, hyaline, thin-walled. *Conidia* 4–5 × 3–4 µm ($\overline{x}$ = 4.5 × 3.3 µm, n = 20), oblong to oval, rounded at ends, hyaline, aseptate, guttules absent. **Sexual morph**: Not observed.

Culture characters: Colonies on PDA reaching 3 cm diam. after 10 days in dark at 25 °C, floccose, flat, circular, smooth margin, white, woolly aerial mycelia concentrate at the centre, reverse off-white, no pigments produced.

Material examined: China, Guangdong Province, Guangzhou City, South China Botanical Garden (23° 11′ 12″ N 113° 21′ 51″ E), on leaves of *Livistona chinensis* (Arecaceae), 8 June 2021, N.D. Kularathnage, NDK 22N (MHZU 22-0129, **holotype**), ex-type cultures ZHKUCC 22-0224, ZHKUCC 22-0229.

GenBank numbers: LSU: OR164967, OR164968, ITS: OR164939, OR164940, *β-tubulin*: OR166315, OR166316, *rpb2*: OR166290, OR166291.

Notes: This phoma-like collection (MHZU 22-0129) is phylogenetically affiliated with *Epicoccum bambusae* (ML/BI = 89/0.90, Fig. 17). The nucleotides in ITS, LSU and *β-tubulin* genes differ between these two isolates as 1.26%, 0.53%, 5.7% respectively. Our collection (MHZU

Fig. 15 ***Epicoccum terminosporum*** (MHZU 22-0129, **holotype**). **a, b** Host plant and name board. **c, d** Conidiomata appear on host substrate. **e** Vertical section of a conidioma. **f–h** Conidiogenous cells attached to conidia. **i** Conidia. **j** Surface view of colony on PDA. **k** Reverse view of colony on PDA. Scale bars: e = 100 µm, f–h = 25 µm, i = 10 µm

22-0129) morphologically differs from *E. bambusae* by having immersed to erumpent, compressed-globose conidiomata, terminal or acropleurogenous, enteroblastic conidiogenous cells and oblong to oval, hyaline, aguttulate conidia. Our collection (MHZU 22-0129) is a foliar saprobe while *Epicoccum bambusae* was collected from bamboo culms. Therefore, we introduce this collection as *Epicoccum terminosporum*.

Epicoccum layuense Qian Chen, Crous & L. Cai, in Chen et al., Stud. Mycol. 87: 145 (2017)

Index Fungorum number: IF818963; *Facesoffungi number*: FoF 09381; Fig. 16

Holotype: HMAS 247165

Saprobic on dead stem of *Heteropanax fragrans* (Roxb.) Seem. **Sexual morph:** Undetermined. **Asexual morph**: *Conidiomata* 140–280 × 95–180 µm ($\overline{x}$ = 180 × 140 µm, n = 20), sporodochia, scattered or aggregated, subglobose to globose, brownish to black. *Conidigenous cells* 2–6 × 2–4 µm ($\overline{x}$ = 4 × 3 µm, n = 10), short cylindrical, pale brown to blackish brown, smooth walled. *Conidia* 9–23 × 9–24 µm ($\overline{x}$ = 18 × 20 µm, n = 30), initially light-brown, becoming black-brown, multicellular-phragmosporous ellipsoid, subglobose to globose, verrucose.

Culture characteristics: Colonies on PDA reaching 5–6 cm diameter after 10 days at 25 ± 2 °C, circular, margin entire, flat, with velvety, orange to umber, with aerial mycelia; reverse orange to reddish orange, pigment produced with age.

Material examined: China, Yunnan Province, Kunming City, from dead steam of *Heteropanax fragrans* (Araliaceae), 15 August 2020, C.F. Liao, (KUN–HKAS 112882, **new host record**), living culture KUMCC 21-0017.

Hosts and distribution: *Perilla* sp., *Camellia sinensis*, *Oxalis corymbosa* from China (Chen et al. 2020; Xie et al. 2022a), *Vitis vinifera* from Portugal (Del Frari et al. 2019), Weigela florida from China (Tian et al. 2021), *Avena sativa* from Northwestern China (Chen et al. 2020), *Oxalis corymbosa* from China (Niu et al. 2022), Oat from China (Chen et al. 2020).

GenBank numbers: ITS: OP575932, LSU: OP565037

Notes: Our isolate (KUMCC 21-0017) clustered with the type strain of *E. layuense* (CGMCC 3.18362) with ML/BI = 100/1.00 bootstrap support in the multigene

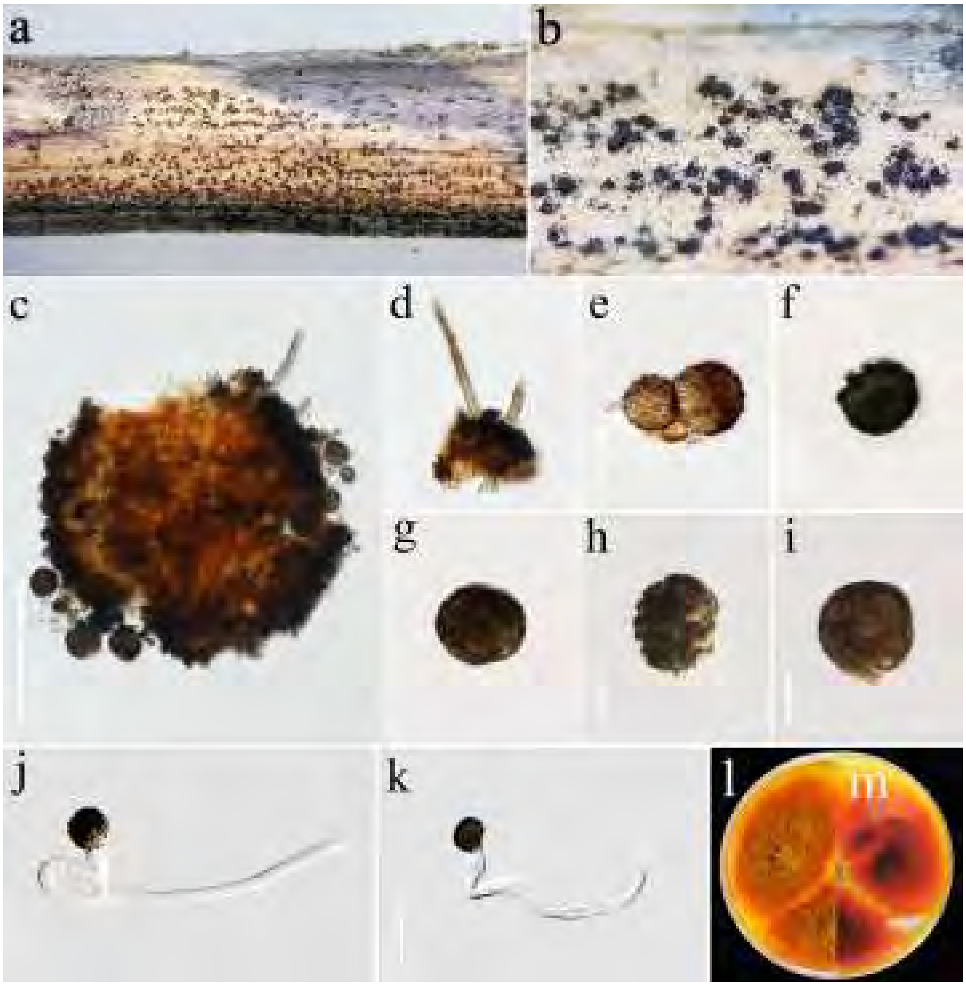


Fig. 16 ***Epicoccum layuense*** (KUN-HKAS 112882). **a, b** Sporodochia on host substrate. **c** Sporodochium. **d** State. **e–i** Conidia. **j, k** Germinating conidia. **l** Surface view of colony on PDA. **m** Reverse view of colony on PDA. Scale bars: c = 20 µm, d–i = 10 µm

phylogenetic analyses (Fig. 17). *Epicoccum layuense* was introduced by Chen et al. (2017) based on morphology and multigene phylogeny of ITS, LSU and *β-tubulin* sequences. The LSU sequence of our collection is identical to the LSU sequence of ex-type strain of *Epicoccum layuense* while ITS locus comprises one base pair difference. Morphological characters of our collection are very similar to the holotype (Chen et al. 2017). Therefore, considering morphology, phylogeny and similarity in sequences, we identified our collection as *Epicoccum layuense.*

The holotype was collected from the leaves of *Perilla* sp. (Lamiaceae) in China (Chen et al. 2017) and this species has been collected from various host plants. However, *Epicoccum layuense* has not collected from *Heteropanax fragrans* before and this is the first report of *E. layuense* on *H. fragrans.*

Didymosphaeriaceae Munk

Didymosphaeriaceae was established by Munk (1953) with type genus *Didymosphaeria* Fuckel. The members of Didymosphaeriaceae can be found as saprobes, endophytes and pathogens in various habitats (Mapook et al. 2020; Samarakoon et al. 2020a, b). Morphologically, species in Didymosphaeriaceae have immersed to semi-immersed, globose or subglobose ascomata and brown to dark brown ascospores with one or multiple septa (Aptroot 1995; Hyde et al. 2013; Hongsanan et al. 2020a, b; Du et al. 2021). The family contains 33 genera (Wijayawardene et al. 2022).

Montagnula Berl.

Montagnula was introduced by Berlese (1896) and is typified by *M. infernalis* (Niessl). There are 38 species listed under *Montagnula* in Species Fungorum (2023). Most species in this genus are saprobes on dead wood and leaves in terrestrial habitat (Ariyawansa et al. 2014a). *Montagnula* species are characterize by immersed, globose or subglobose ascomata, with central ostioles, clavate asci with long pedicels encasing septate, brown to dark brown ascospores (Barr 1990; Ariyawansa et al. 2014b; Tennakoon et al. 2016; Hongsanan et al. 2020a, b; Du et al. 2021).

Montagnula chromolaenicola Mapook & K.D. Hyde, in Mapook, et al., Fungal Diversity 101: 35 (2020)

Index Fungorum number: IF557298; *Facesoffungi number*: FoF 07791; Fig. 18

Saprobic on dead stems of *Citrus maxima* Merr. **Sexual morph**: *Ascomata* 230–340 µm high × 180–300 µm diam. ($\overline{x}$ = 300 × 250 µm, n = 10), semi-immersed, conspicuous protruding through host surface, solitary, scattered, elliptical or subglobose, most uniloculate, few multiloculate, brown to black, smooth-walled, papillate, with a central ostiole. *Ostiole* 60–240 µm diam. ($\overline{x}$ = 100 µm, n = 20), central, closed, filled with periphyses or empty, consisting of light brown to brown stromatal tissue cells. *Peridium* 20–50 µm wide, thin-walled, containing of 5–7-layers of transparent to dark brown cells of *textura angularis* from inner to outside, outermost layer fuses with host tissues. *Hamathecium* 1.5–3 µm wide ($\overline{x}$ = 2.5 µm, n = 50), dense, cylindrical, filamentous, branched, with indistinct septate, gelatinous matrix wraps the trabeculate pseudoparaphyses and clearly match between asci. *Asci* 30–50 × 3–5 µm ($\overline{x}$ = 40 × 5 µm, n = 15), 8-spored, bitunicate, thin-walled, clavate, blunt apically, with long slightly curved furcated pedicel. *Ascospores* 5–10 × 3–5 µm ($\overline{x}$ = 6 × 4 µm, n = 30), biseriate, ellipsoidal, 1-septate, significant contraction at the septa, tapering from the center to the ends, cells at the upper are slightly wider than lower cells, hyaline when immature, dark brown to brown at maturity, without appendages and mucilaginous sheath. **Asexual morph**: not observed.

Culture characteristics: Ascospore germinating on PDA within 24 h at room temperature. Colonies on PDA reaching 50 mm diam. after 1 week at 25 °C, circular, flat, smooth, dense and soft, surface view white to light gray from center to edge; reverse with olive-green to light brown center, white edge.

Material examined: China, Guangdong Province, Shaoguan City, Renhua County, Dongtang town, 25° 3′ 50″ N, 113° 39′ 17″ E, on the bark of *Citrus maxima* (Rutaceae), 25 August 2021, Y.H. Yang (MHZU 22-0065); living cultures ZHKUCC 22-0118, ZHKUCC 22-0119, ZHKUCC 22-0120.

Hosts and distribution: Thailand, on dead stems of *Chromolaena odorata* (Mapook et al. 2020); China, on the bark of *Citrus maxima* (this study).

GenBank numbers: ITS: OQ976005, OQ976006, OQ976007; LSU: OQ976015, OQ976016, OQ976017; SSU: OQ976021, OQ976022; *tef*1-α: OQ980478.

Notes: In the phylogenetic analysis of combined ITS, LSU, SSU and *tef*1-α sequences of (Fig. 19) our isolates (ZHKUCC 22-0118, ZHKUCC 22-0119, ZHKUCC 22-0120) grouped with ex-type strain of *Montagnula chromolaenicola* (MFLUCC 17-1469) with ML/BI = 78%/1.00 bootstrap support. Morphologically, our collection is similar to type collection of *M. chromolaenicola* by its central ostiole, asci with long, slightly curved, furcate pedicels, having ellipsoid, 1-septate ascospores, with significant contraction at the upper cell slightly wider and ends tapering to and septa without terminal appendages. We identify our collection as *Montagnula chromolaenicola* which is the first record on *Citrus maxima* in China.

Paraphaeosphaeria O.E. Erikss.

Eriksson (1967) introduced *Paraphaeosphaeria* to accommodate the type species, *Paraph. michotii*, and other three species, namely *Paraph. castagnei*, *Paraph. obtusispora*, *Paraph. rusci*, with oblong-cylindrical ascospores. The sexual morph of *Paraphaeosphaeria* is characterized

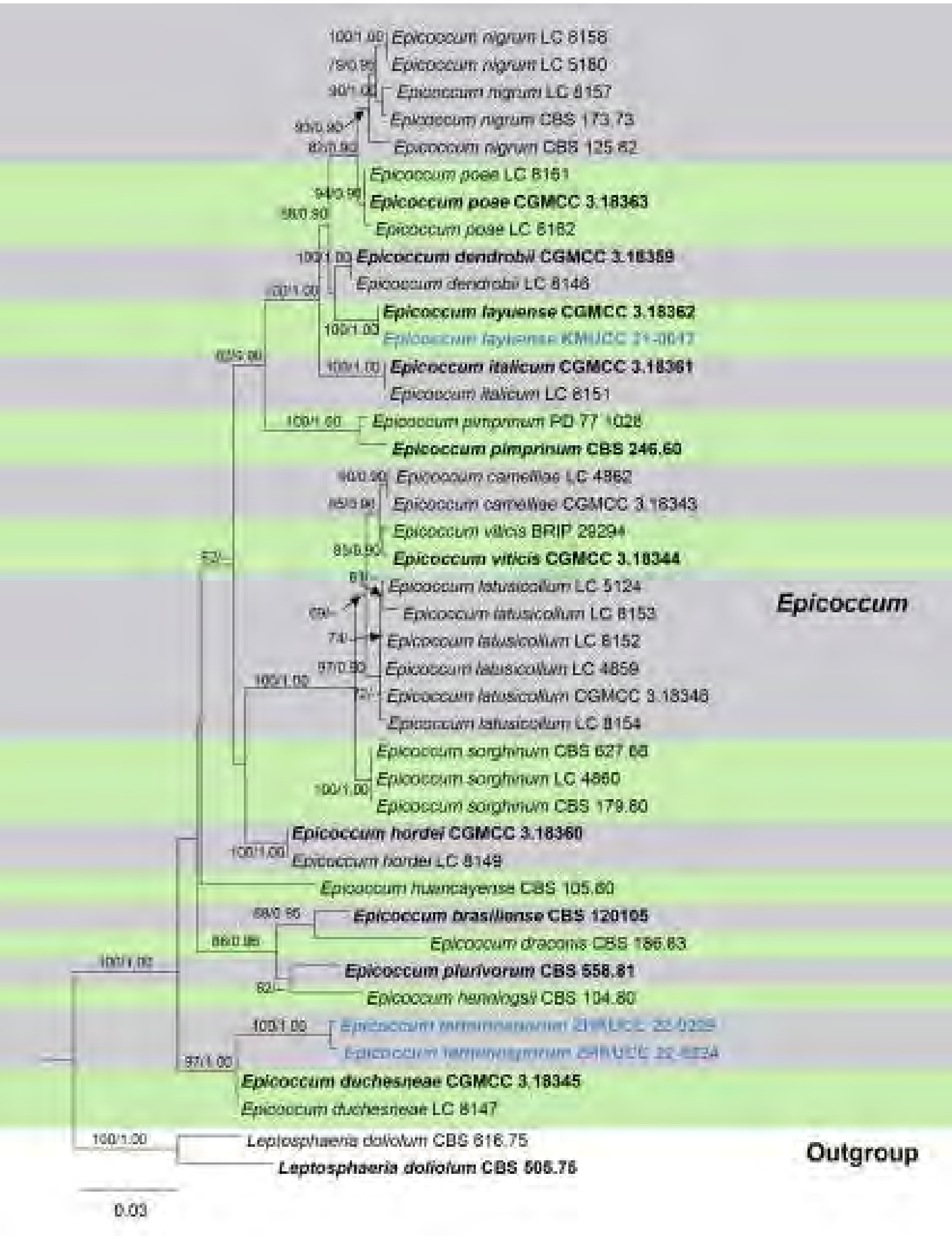


Fig. 17 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *β-tubulin* and *rpb2* sequence data which comprised 2321 characters (ITS = 476, LSU = 941, *β-tubulin* = 333, *rpb2* = 571). The best scoring RAxML tree with a final likelihood value of − 8757.729573 is presented. The matrix had 422 distinct alignment patterns, with 7.29% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.245371, C = 0.247182, G = 0.273997, T = 0.233450; substitution rates: AC = 1.183550, AG = 3.903447, AT = 1.6002, CG = 0.898268, CT = 11.877761, GT = 1.0; gamma distribution shape parameter α = 0.150149. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (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 blue bold. The tree is rooted to *Leptosphaeria doliolum* (CBS 616.75, CBS 505.75)

Fig. 18 ***Montagnula chromolaenicola*** (MHZU 22-0065). **a, b** Ascomata on the host surface. **c** Vertical cross section of ascomata. **d** Cross section through the ostiole. **e** Peridium. **f** Pseudoparaphyses. **g** Asci. **h–j** Ascospores. **k** Germinating ascospore. **l** Surface view of colony on PDA. **m** Reverse view of colony on PDA. Scale bars: c, d = 100 µm, e, f, h–j = 20 µm, g, k = 30 µm

by immersed to semi-immersed ascomata, short-pedicellate bitunicate asci without a pedicel, and 1–10-septate, cylindrical to elliptical, yellowish to reddish-brown ascospores (Ariyawansa et al. 2014a; Hongsanan et al. 2020a, b). The asexual morphs are coniothyrium-like and characterized by eustromatic or pycnidial conidiomata, phialidic, or annelidic conidiogenous cells, 0–1-septate, and smooth to verrucose conidia (Verkley et al. 2014). *Paraphaeosphaeria* comprises 31 epithets in Species Fungorum (2023) wherein 21 species are supported with molecular data. Three *Paraphaeosphaeria* species are known from their holomorphs viz., *Paraph. michotii*, *Paraph. barriae*, and *Paraph. pilleata* (Kohlmeyer et al. 1996; Caâmara et al. 2001; Checa et al. 2002; Wanasinghe et al. 2018). Ten species (*Paraph. concentrica*, *Paraph. cylindrospora*, *Paraph. hongkongensis*, *Paraph. maximiliani*, *Paraph. microspora*, *Paraph. rubrotincta*, *Paraph. schoenoplecti*, and *Paraph. trimerioides*) are known only from their sexual morphs (Ahmad 1978; Shoemaker and Babcock 1985; Barr 1992; Huhndorf 1992; Shearer et al. 1993; Barr et al. 1996; Kohlmeyer et al. 1999; Fröhlich and Hyde 2000; Wong et al. 2000) while 18 species have only asexual morphs (Lee et al. 2005; Verkley et al. 2014; Liu et al. 2015; Crous et al. 2017; Thambugala et al.

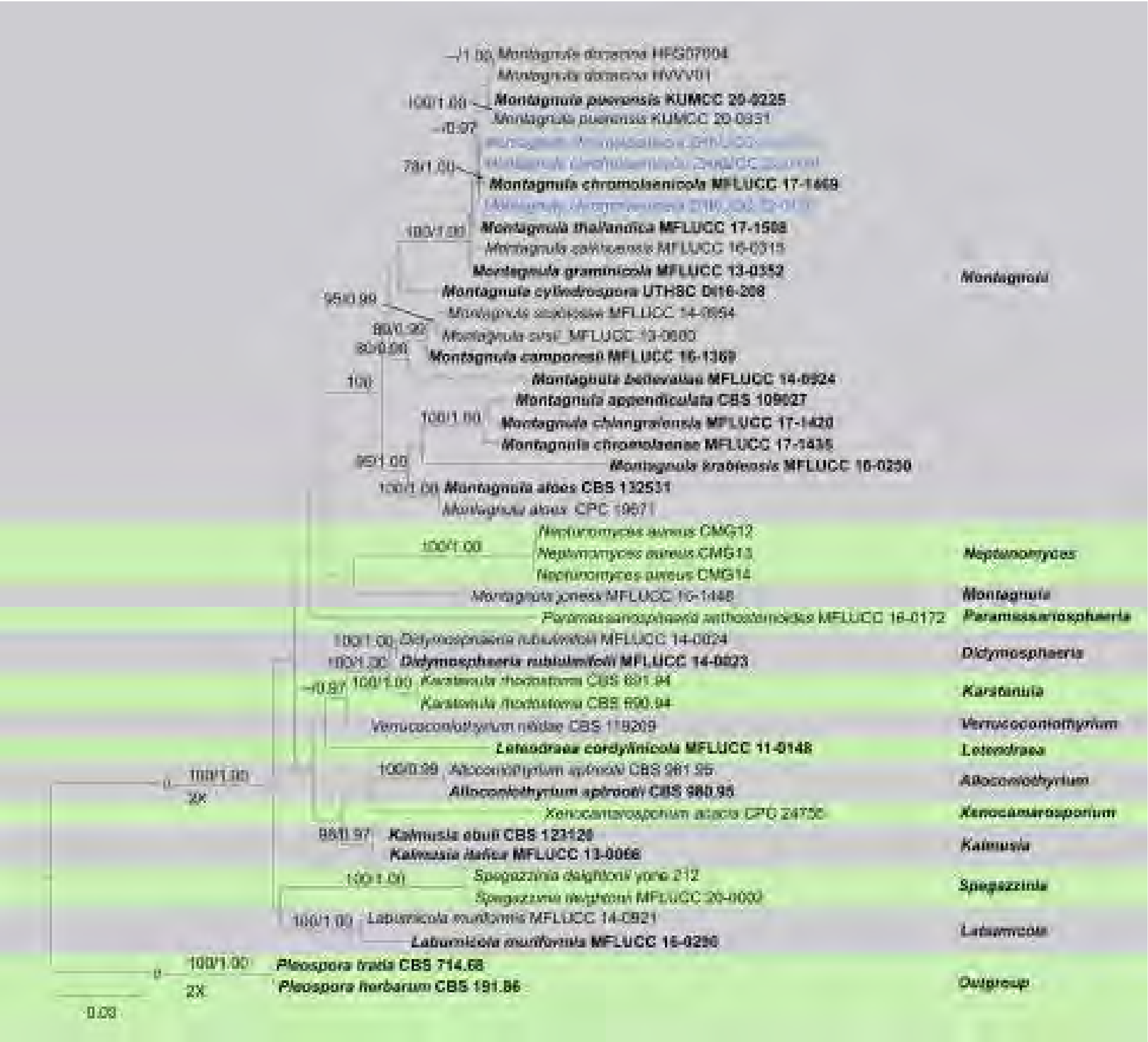


Fig. 19 The best scoring RAxML tree for combined ITS, LSU, SSU and *tef*1-α sequence data of species in Didymosphaeriaceae. The tree is rooted with *Pleospora herbarum* (CBS 191.86) and *P. trada* (CBS 714.68). The matrix had 871 distinct alignment patterns with 31.98% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.242601, C = 0.248012, G = 0.271675, T = 0.237711; substitution rates AC = 1.679480, AG = 2.352353, AT = 1.661334, CG = 1.143072, CT = 6.754494, GT = 1.0; gamma distribution shape parameter α = 0.187527 with a final likelihood value of − 13,247.100866. Ex-type strains are in bold and newly generated sequences are in blue bold. Bootstrap support for ML equal to or greater than 75% and BI equal to or greater than 0.95 are given above the nodes

2017; Tibpromma et al. 2017; Wanasinghe et al. 2018; Ariyawansa et al. 2020; Zhang et al. 2021).

Paraphaeosphaeria sporulosa (W. Gams & Domsch) Verkley, Göker & Stielow, Persoonia 32: 47 (2014)

Index Fungorum number: IF800768; *Facesoffungi number*: FoF12739; Fig. 20

Saprobic on driftwood in the intertidal zone. **Sexual morph**: Undetermined. **Asexual morph**: Coelomycetous. *Mycelium* mostly immersed, composed of septate, branched, hyphae. *Conidiomata* 110–170 × 140–220 µm ($\bar{x}$ = 139 × 175 µm, n = 10) diam., pycnidial, solitary, globose, superficial or semi-immersed, glabrous, dark brown to black, thin-walled, unilocular, ostiolate. *Ostiole* up to 45 µm long, circular, papillate, laterally or centrically located. *Conidiomatal wall* 10–30 µm, composed of thick-walled, dark brown to hyaline cells of *textura angularis*, lined by a thin layer of globose hyaline cells. *Conidiophores* reduced to

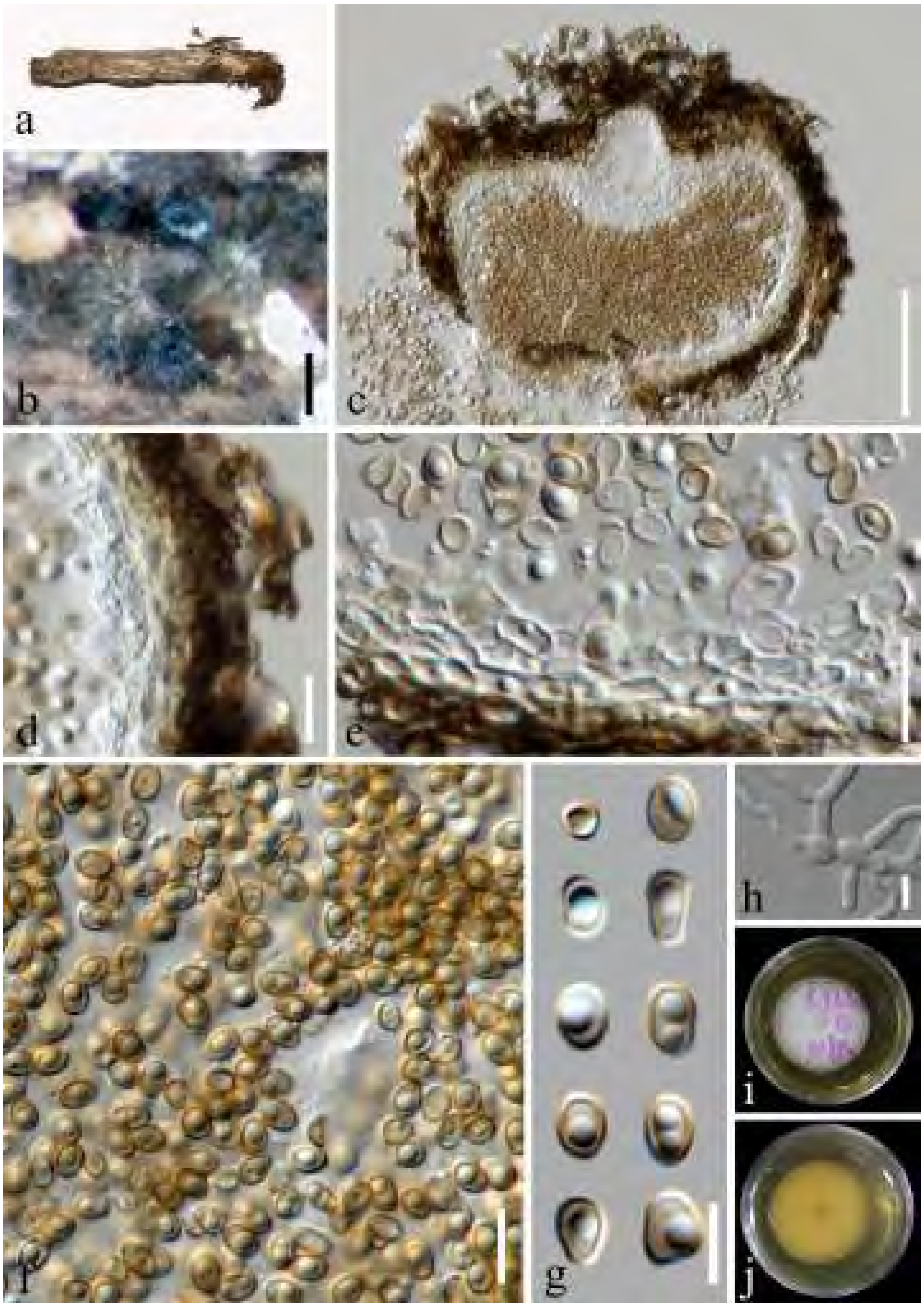


Fig. 20 ***Paraphaeosphaeria sporulosa*** (MFLU 22-0118). **a** Examined material. **b** Conidiomata on the substrate. **c** Vertical section of conidioma. **d** Conidioma wall. **e** Conidiogenous cells and developing conidia. **f**, **g** Conidia. **h** Germinated conidium. **i** Surface view of colony on MEA. **j** Reverse view of culture on MEA. Scale bars: b = 200 µm, c = 50 µm, d–f = 10 µm, g, h = 5 µm

conidiogenous cells. *Conidiogenous cells* 5.5–10 × 2–4 µm ($\bar{x}$ = 7.7 × 3.1 µm, n = 20) subglobose to ampulliform, swollen at the base, hyaline, enteroblastic, phialidic, with periclinal thickening or percurrent proliferation at apex, smooth, thin-walled. *Conidia* 3–5.5 × 2–3.5 µm ($\bar{x}$ = 4.1 × 2.7 µm, n = 50), highly variable in shape, subglobose, ellipsoid, obovoid-pyriform, initially hyaline, after secession olivaceous-brown, aseptate, smooth, thin-walled, with one large (1.4–2.5 µm diam.) and often also 1–2 additional smaller oil-droplets (1–1.5 µm).

Culture characteristics: Conidia germinating on malt extract agar (MEA) within 24 h. Germ tubes produced around conidium. Colonies growing on MEA, reaching 30–35 mm in 2 weeks at 25 °C, colony circular, flat, entire to filiform edge, dry, surface rough, white in top view, reverse white.

Material examined: Sweden, Sudersand, on driftwood in a sandy beach, 7 March 2019, E.B. Gareth Jones, GJ660B (MFLU 22-0118, **new geographical record**).

Hosts and geographical distribution: France, Germany, Netherlands (Verkley et al. (2014); China (Wu et al. 2013); Sweden (This study)

GenBank numbers: ITS: OP216407, LSU: OP216402, *rpb2*: OP251196, *tef*1-*α*: OP251192

Notes: BLASTn results of the LSU, ITS, and *rpb2* sequence data of our isolate (MFLU 22-0118) showed a high similarity with *Paraph. sporulosa* and *Curreya pityophila*. Hence, *Curreya pityophila* strains were included in the phylogenetic analysis. Multi-locus phylogenetic analyses revealed that our isolate grouped with *Paraph. sporulosa* and *Curreya pityophila* (CBS 149.32, CBS 986.69, UTHSC: DI16–357) with ML = 99%, BI = 1.00 statistical support (Fig. 21). Morphological data of *Curreya pityophila* strains CBS 149.32, CBS 986.69, UTHSC: DI16-357 are not available and hence, morphological comparison between our collection and *Paraph. sporulosa* is not possible. Eventhough, *Curreya pityophila* clustered with *Paraph. sporulosa*, its sexual morph does not conform with the generic description of *Paraphaeosphaeria* wherein ascospores are cylindrical to elliptical, 1–10-septate with broadly rounded apex and tapering to a more narrowly rounded base. *Curreya pityophila* has an oblong ascospores with 3–5-transverse septa constricted at the middle septum (von Arx and Muller 1975; Ariyawansa et al. 2014b). With morphological differences, we will retain *Curreya pityophila* as a distinct species. The relationship between these two taxa warrants further morphological observations of *C. pityophila* with molecular information and obtaining the sequence data of the type specimen of *C. pityophila*.

The pairwise nucleotide comparisons of our collection (MFLU 22-0118) with the type strain *Paraph. sporulosa* (CBS 218.68) revealed no nucleotide difference in the ITS region and four nucleotide differences in LSU. The only difference in the morphology between MFLU 22-0118 and CBS 218.68 is the conidiomatal size as CBS 218.68 has wider conidiomata (300–450(–600) µm). Our collection is the second report of *Paraph. sporulosa* in marine habitats and this species previously reported from sea mud in China (strains YK-03 and PYL05-10) (Wu et al. 2013; Zhang et al. 2017a, b; Zhao et al. 2018).

The identification of strains YK-03 and PYL05-10 were only based on the ITS sequences. Therefore, phylogeny of the ITS sequence data was done to determine the placements of these strains and showed that only strain PYL05-10 clustered with the type species CBS 218.68 (data not shown). Strain YK-03 is placed basal to *Paraph. rosicola* (MFLU 18-0108) (Zhang et al. 2017b; Pei et al. 2022). Since strain YK-03 was identified based only on molecular data, this study provides the morphological data of marine *Paraph. sporulosa* for the first time.

Paraphaeosphaeria michotii and *Paraph. neglecta* were earlier recorded in marine environments (Jones et al. 2019). Furthermore, this is the first report of *Paraph. sporulosa* in Sweden. Based on molecular data, *Paraph. sporulosa* was previously reported in France, Germany, Netherlands (Verkley et al. (2014) and China (Wu et al. 2013).

Paraphaeosphaeria verruculosa Verkley, Göker & Stielow, in Verkley, Dukik, Renfurm, Göker & Stielow, Persoonia 32: 48 (2014)

Index Fungorum number: IF800770; *Facesoffungi number*: FoF 12740

= *Paraphaeosphaeria parmeliae* Crous & Trakun., IMA Fungus 5(2): 401 (2014)

Holotype: Germany, Bayerischer Wald, from needle of *Picea abies*, Mar. 1985, H. Butin, CBS H-21041.

Prologue and illustrations: in IMA Fungus 5(2): 401, Nov. 2014 and Fig. 8, 403, Nov. 2014)

Hosts and geographical distribution: Belgium, from thallus of *Parmelia sulcata* Taylor; Chile, from wood logs of *Pinus radiata* D.Don; Colombia, from burned soil; Germany, from needle of *Picea abies* (L.) H. Karst.

Notes: Multi-locus phylogenetic analysis showed that *Paraph. parmeliae* CBS 131728 clustered with two strains of *Paraph. verrucolosa* (CBS 263.85; CBS 682.84) with ML = 100%, BI = 1.00 bootstrap support. Pairwise nucleotides comparison between the LSU (845 bp), ITS (560 bp), and *β-tubulin* (427 bp) sequence data of the type strains of two species showed no nucleotide differences. *Paraphaeosphaeria verrucolosa* and *Paraph. parmeliae* share similar morphology also (Trakunyingcharoen et al. 2014; Verkley et al. 2014). Therefore, we proposed that *Paraph. parmeliae* is a synonym of *Paraph. verrucolosa*.

Ageratinicolaceae Lu L., K.D. Hyde & Tibpromma, *fam. nov.*

Index Fungorum number: IF900619, *Facesoffungi number*: FoF 14374

Saprobic on dead or dying plant litter, wood, stems, and branches in terrestrial habitat. **Sexual morph**: Undetermined. **Asexual morph**: Coelomycetous. *Conidiomata* eustromatic, immersed, globose to subglobose, uni- to multi-loculate with ostioles. *Pycnidial walls* comprising cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, globose to cylindrical, with periclinal thickening or percurrent proliferation at the apex, hyaline. *Conidia* oval to ellipsoid, muriform, septate, hyaline to brown.

Type genus: *Ageratinicola* Lu L., K.D. Hyde & Tibpromma

Notes: Ageratinicolaceae is introduced to accommodate *Foliophoma* and *Ageratinicola gen. nov*. In the phylogenetic analyses, Ageratinicolaceae formed an independent branch between Libertasomycetaceae and Coniothyriaceae. Ageratinicolaceae can be distinguished from Coniothyriaceae and


Paraphaeosphaeria sporulosa CBS 340.85
Curreya pityophila CBS 149.32
Paraphaeosphaeria sporulosa CBS 132.26
Paraphaeosphaeria sporulosa CBS 688.70A
Paraphaeosphaeria sporulosa LG1401_GL5A
Paraphaeosphaeria sporulosa CBS 824.68
Paraphaeosphaeria sporulosa CBS 680.70
Paraphaeosphaeria sporulosa CBS 688.70B
Paraphaeosphaeria sporulosa CBS 162.69
Paraphaeosphaeria sporulosa CBS 165.76
Curreya pityophila UTHSC DI16-357
Curreya pityophila CBS 986.69
Paraphaeosphaeria sporulosa CBS 218.68
Paraphaeosphaeria sporulosa MFLU 22-0118
Paraph. sporulosa
38/1.00
70/0.92
Paraphaeosphaeria sardoa CBS 501.71
Paraph. sardoa
98/1.00
96/1.00
Paraphaeosphaeria michotii MFLUCC 130349
Paraphaeosphaeria michotii CBS 652.86
Paraph. michotii
94/1.00
Paraphaeosphaeria pilleata CBS 102207
Paraph. pilleata
Paraphaeosphaeria angularis CBS 167.70
Paraph. angularis
Paraphaeosphaeria viciae MFLU 15-1231
Paraph. viciae
100/1.00
Paraphaeosphaeria minitans CBS 111750
Paraphaeosphaeria minitans CBS 111752
Paraph. minitans
100/-
100/1.00
Paraphaeosphaeria verruculosa CBS 283.85
Paraphaeosphaeria verruculosa CBS 131728
Paraphaeosphaeria verruculosa CBS 682.84
Paraph. verruculosa
Paraphaeosphaeria viridescens CBS 854.73
Paraph. viridescens
Paraphaeosphaeria xanthorrhoeae CBS 142164
Paraph. xanthorrhoeae
100/1.00
Paraphaeosphaeria neglecta CBS 119637
100/1.00
Paraphaeosphaeria neglecta CBS 124078
Paraph. neglecta
Paraphaeosphaeria camelliae NTUCC 18-095-2
100/1.00
Paraphaeosphaeria camelliae NTUCC 18-095-1
Paraph. camelliae
-/0.80
-/0.92
Paraphaeosphaeria rosae MFLUCC 17-2547
Paraph. rosae
Paraphaeosphaeria spartii MFLU 14-0810
Paraph. spartii
Paraphaeosphaeria rosicola MFLU 15-0186
Paraph. rosicola
100/1.00
Paraphaeosphaeria arecacearum CBS 158.75
Paraph. arecacearum
Paraphaeosphaeria graminicola MFLUCC 15-0466
Paraph. graminicola
100/1.00
Paraphaeosphaeria hydei CGMCC 3-19317
Paraphaeosphaeria hydei LC12585
Paraph. hydei
Paraphaeosphaeria sporulosa YK-03
Paraphaeosphaeria
98/1.00
Paraconiothyrium cyclothyrioides CBS 972.95
Paraconiothyrium estuarinum CBS 109850
Paraconiothyrium
-/0.97
100/1.00
Chromolaenicola lampangensis MFLUCC 17-1462
Chromolaenicola chiangraiensis MFLUCC 17-1493
Chromolaenicola
96/1.00
Paramassariosphaeria clematidicola MFLU 16-0172
Paramassariosphaeria anthostomoides CBS 615.86
Paramassariosphaeria
79/-
76/-
Letendraea padouk CBS 485.70
Letendraea eurotioides CBS 212.31
Letendraea magnoliae MFLUCC 19-0062
100/1.00
Letendraea helminthicola MFLUCC 19-0055
Letendraea helminthicola CBS 884.85
-/0.99
Letendraea cordylinicola MFLUCC 11-0150
95/1.00
Letendraea cordylinicola MFLUCC 11-0148
Letendraea
98/1.00
92/1.00
Neokalmusia brevispora KT 2313
Neokalmusia brevispora KT 1466
Neokalmusia
-/0.96
Montagnula aloes CPC 19671
Montagnula saikhuensis MFLUCC 16-0315
Montagnula
73/0.94
Trematosphaeria arundicola MFLU 16-1275
Trematela
100/1.00
Xenocamarosporium acacia CPC 24755
-/0.98
Xenocamarosporium acacia C354
Xenocamarosporium
100/1.00
Neptunomyces aureus CMG11
Neptunomyces aureus CMG10A
Neptunomyces
-/0.99
Alloconiothyrium aptrootii CBS 980.95
Alloconiothyrium camelliae NTUCC 17-032-1
Alloconiothyrium
92/1.00
100/1.00
Kalmusia italica MFLUCC 13-0066
Kalmusia ebuli CBS 123120
Kalmusia
Kalmusibambusa triseptata MFLUCC 13-0232
Kalmusibambusa
100/1.00
98/1.00
Spegazzinia camelliae WNA03
Spegazzinia tessarthra SH 287
Spegazzinia
97/1.00
100/1.00
Laburnicola dactylidis MFLUCC 16-0286
Laburnicola hawksworthii MFLUCC 13-0602
Laburnicola
Paraphaeosphaeria barriae CBS 109841
Paraph. barriae
Didymosphaeriaceae
100/1.00
Periconia pseudobyssoides H 4151
Periconia byssoides H 4432
Periconiaceae (outgroup)
0.04

◂**Fig. 21** Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS, *rpb2, tef*1-α, and *β-tubulin* sequence data representing the species of Didymosphaeriaceae. *Periconia byssoides* (H 4432) and *P. pseudobyssoides* (H 4151) were used as the outgroup taxa. Seventy-three taxa are included in the combined analyses which comprised 4907 characters (LSU = 1339, ITS = 412, SSU = 900, *tef1-α* = 687, *rpb2* = 1,100, *β-tubulin* = 450) after alignment. The best scoring RAxML tree with a final likelihood value of − 25,918.844688 is presented. The matrix had 1440 distinct alignment patterns, with 56.15% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.239744, C = 0.250490, G = 0.271816, T = 0.237951; substitution rates: AC = 1.420690, AG = 2.626732, AT = 1.570948, CG = 0.994736, CT = 5.458583, GT = 1.0; gamma distribution shape parameter α = 0.332015. Bootstrap support for ML equal to or greater than 70% and BI equal to or greater than 0.90 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue bold

Libertasomycetaceae by their muriform, non-constricted conidia at the septa. However, conidia of Coniothyriaceae are phoma-like, camarosporium-like, coniothyrium-like, or cladosporium-like, and Libertasomycetaceae has conidia which constricted at the median septum with longitudinal striations (Crous and Groenewald 2017; Wijesinghe et al. 2023).

Foliophoma was introduced based on *Phoma fallens* (= *Foliophoma fallens*) accommodating in Coniothyriaceae and it is characterized by distinct eustromatic, uni—to multiloculate conidiomata with 1–3 ostioles, hyaline and ellipsoidal conidia (Crous and Groenewald 2017). Multi-gene phylogenetic trees in Hyde et al. (2020a) and Wijesinghe et al. (2023) are shown that *Foliophoma* is clustered basal to Coniothyriaceae. In our phylogenetic tree (Fig. 23), *Foliophoma* grouped with the new genus *Ageratinicola* forming a sister clade to Coniothyriaceae with ML = 89%, BI = 0.97 statistical support (Fig. 23). However, *Foliophoma* shares similar characters with Coniothyriaceae such as globose to short, cylindrical conidiogenous cells and also similar to the Ageratinicolaceae fam. nov. by having oval to ellipsoid and brown conidia (Crous and Groenewald 2017; Hyde et al. 2020a). Therefore, based on morphology and phylogeny, we introduced Ageratinicolaceae as a distinct family in Pleosporales for *Foliophoma* and *Ageratinicola gen. nov*.

Ageratinicola Lu L., K.D. Hyde & Tibpromma, ***gen. nov.***

Index Fungorum number: IF559942; *Facesoffungi number*: FoF 10844

Etymology: Name refers to the host genus it was isolated from "*Ageratina*".

Saprobic on dead or dying stems and branches. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* pycnidial, globose to subglobose, or irregular, solitary or aggregated, immersed with a short neck. *Pycnidial walls* multi-layered, cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, doliiform or cylindrical, hyaline. *Conidia* oval to ellipsoid, or ovoid, muriform, hyaline when young, becoming brown when mature, multi-septate with or without mucilaginous sheath, smooth-walled.

Notes: ITS and LSU sequences of our collection (HKAS 122688) are highly similar to *Foliophoma* species. The phylogenetic analyses based on ITS, LSU and SSU showed that our collection and *Foliophoma* species formed a distinct clade with ML/BI = 100%/1.00 statistical support (Fig. 23). However, morphologically, our collection is distinct from *Foliophoma* species by having brown, muriform conidia, while *Foliophoma* has hyaline, aseptate and broadly ellipsoidal conidia (Crous and Groenewald 2017). In addition, our collection is also distinct from other genera in Coniothyriaceae by having initially hyaline, oval to ellipsoid, or ovoid conidia becoming brown, multi-septate and muriform at maturity (Sutton 1971; Taylor and Crous 2001; Crous et al. 2007; Crous and Groenewald 2017). Therefore, our collection represents a new monotypic genus and it is introduced here as *Ageratinicola gen. nov*. and we accommodated *Ageratinicola* and *Foliophoma* in new family Ageratinicolaceae.

Ageratinicola kunmingensis Lu L., K.D. Hyde & Tibpromma, ***sp. nov.***

Index Fungorum number: IF559943; *Facesoffungi number*: FoF 10845; Fig. 22

Etymology: based on the location where fungus was collected.

Saprobic on dead stem of *Ageratina adenophora* (Spreng.) King & H. Rob. **Sexual morph**: Undetermined. **Asexual morph**: Coelomycetous. *Conidiomata* 100–240 × 90–180 µm ($\overline{x}$ = 180 × 140 µm, n = 10), pycnidial, globose to subglobose, or irregular, immersed, ostiolate, with a short neck, black. *Pycnidial walls* 10–16 µm thick, comprised 2–4-layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.7–5 × 3–3.7 µm ($\overline{x}$ = 4 × 3 µm, n = 10), enteroblastic, cylindrical, hyaline. *Conidia* 8–17 × 6–14 µm ($\overline{x}$ = 12 × 10 µm, n = 20), oval to ellipsoid, or ovoid, muriform, hyaline when young, becoming pale yellow to brown when maturity, multi-septate at maturity.

Culture characteristics: Colonies on PDA reaching 15 mm diam. after 4 weeks in room temperature at 20 °C, flat, slightly raised, circular, smooth, dense, front gray with white aerial mycelia at the margin; reverse sunken, from the inside to the outside, dark gray, dark brown to white, not produced pigments in culture.

Material examined: China, Yunnan Province, Kunming City, Chang Chong Mountain, on dead stem of *Ageratina adenophora* (Asteraceae), 20 June 2021, Li Lu, CCS 18, (HKAS 122688, **holotype**); ex-type culture KUMCC 21-0217.

Fig. 22 ***Ageratinicola kunmingensis*** (HKAS 122688, **holotype**). **a** Examined material. **b–c** Close view of conidiomata. **d–e** Cross sections of conidioma. **f** Pycnidial wall. **g–h** Conidia attached to conidiogenous cells. **i–k** Conidia. **l** Germinated conidium. **m–n** Culture on PDA from surface and reverse. Scale bars: d = 100 µm, e = 80 µm, f–i, l = 20 µm, j–k = 5 µm

GenBank numbers: ITS: ON359920, ON359921; LSU: ON340721, ON340722; SSU: ON359915, ON359916.

Notes: The combined ITS, LSU, and SSU gene analyses (Fig. 23) showed that our collection (HKAS 122688) forms a distinct sister clade with *Foliophoma* with ML/BI = 100%/1.00 bootstrap support. The nucleotide differences of ITS and LSU sequences among our collections and the type species of *Foliophoma*, *F. fallens* (CBS 161.78) revealed 5.22% and 0.7% respectively. Besides, morphological characteristics of our collection are also very different from *Foliophoma* by larger and multi-septate conidia (Hyde et al. 2020a). Therefore, we introduce our collection as *Ageratinicola kunmingensis*.

Lentitheciaceae Y. Zhang, C.L. Schoch, J. Fourn., Crous & K.D. Hyde

Lentitheciaceae was introduced by Zhang et al. (2009) and typified by *Lentithecium* K.D. Hyde, J. Fourn. & Ying Zhang. The members of this family are characterized by lenticular to globose ascomata with brown setae or glabrous, cylindrical to clavate asci with short pedicels, and morphologically diverse ascospores, mostly narrow to broad fusiform, hyaline to brown, aseptate or 1–3-septate (muriform in some species), sometimes filiform, fasciculate, surrounded by an entire mucilaginous sheath or fusiform gelatinous sheath (Liu et al. 2022b) with stagonospora-like or dendrophoma-like asexual

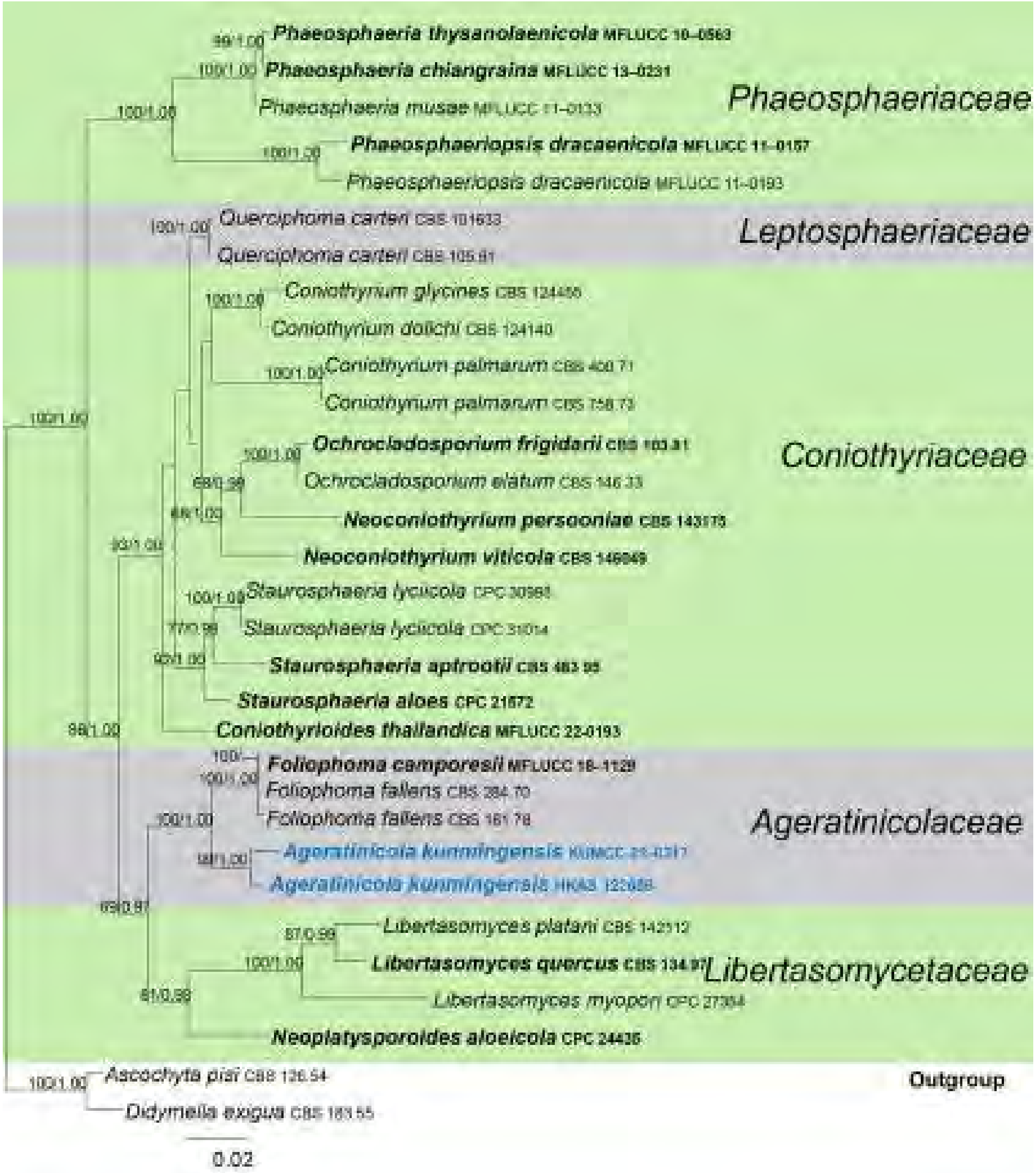


Fig. 23 Phylogram generated from maximum likelihood analyses based on combined ITS, LSU and SSU sequence data. Thirty taxa were included in the combined analyses, which comprised 2538 characters (ITS = 594, LSU = 905, SSU = 1039). The matrix had 506 distinct alignment patterns, with 24.52% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.251501, C = 0.216231, G = 0.272433, T = 0.259835; substitution rates: AC = 1.610597, AG = 3.537196, AT = 2.613191, CG = 0.671725, CT = 6.148363, GT = 1.0; gamma distribution shape parameter α = 0.084053 with a final likelihood value of − 8485.427171. Bootstrap support for maximum likelihood (ML) ≥ 50% and clade credibility values ≥ 0.90 from Bayesian inference analyses are labelled at each node. Ex-type strains are in bold, while the new isolate is indicated in blue bold. The tree is rooted to *Ascochyta pisi* (CBS 126.54) and *Didymella exigua* (CBS 183.55)

morphs (Hongsanan et al. 2020a, b). Most genera in this family have sexual morphs and only two genera, namely *Phragmocamarosporium* and *Towyspora* are only reported from the coelomycetous asexual morphs (Wijayawardene et al. 2015; Li et al. 2016). Species of Lentitheciaceae are generally saprobic on stems and twigs of herbaceous and woody plants in freshwater, terrestrial and marine environments (Hyde et al. 2018). Additionally, some endophytic species in this family have been isolated from semiarid habitat (Knapp et al. 2015).

Setoseptoria Quaedvlieg, Verkley & Crous

Setoseptoria was introduced to accommodate saprobic septoria-like coelomycetes having setose conidiomata (Quaedvlieg et al. 2013) and is typified by *S. phragmitis*. There are seven accepted species in this genus (Species Fungorum 2023). This study is introduced a new *Setoseptoria* species.

Setoseptoria bambusae Senan., J.Z. Fu & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900416; *Facesoffungi number*: FoF 12786; Fig. 24

Etymology: based on the host genus *Bambusa*.

Saprobic on dead stem of *Bambusa* sp. **Sexual morph***: Clypeus* spread over ascomata, lenticular, comprise of small, highly melanized, black, compressed cells. *Ascomata* 180–210 µm high, 150–190 µm diam. ($\bar{x}$ = 200 × 160 µm, n = 10), superficial to erumpent, solitary to rarely gregarious, scattered, globose, uni to multiloculate, black, short papillate, ostiolate. *Ostiole* canal comprises filiform, hyaline pseudoparaphyses. *Peridium* 8–10 µm wide at the base, 15–20 µm wide at the sides, thick, comprised of heavily pigmented, thick-walled, dark brown, tightly packed cells of *textura angularis*. *Hamathecium* comprising numerous, 1.5–2.5 µm wide ($\bar{x}$ = 2 µm), filamentous, branched, septate, pseudoparaphyses. *Asci* 85–100 × 12–15 µm ($\bar{x}$ = 96 × 13 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, pedicellate, apex rounded with a minute ocular chamber. *Ascospores* 20–25 × 3–4.5 µm ($\bar{x}$ = 23 × 4 µm, n = 20), overlapping uniseriate to biseriate, narrowly fusiform, 1–3-septate, deeply constricted at the middle septum, slightly constricted at the other septa, hyaline, asymmetric, narrowly rounded at the ends, one large guttule in each cell or multi-guttulate, surrounded by a thin (1.5–3 µm wide) mucilaginous sheath. **Asexual morph**: Undetermined.

Culture characteristics: Colonies on PDA reaching 5 cm diam. after 14 days in dark at 25 °C, flat, circular, filamentous margin, zonate, greenish grey, wooly aerial mycelial clots crowed on surface, margin with white filamentous

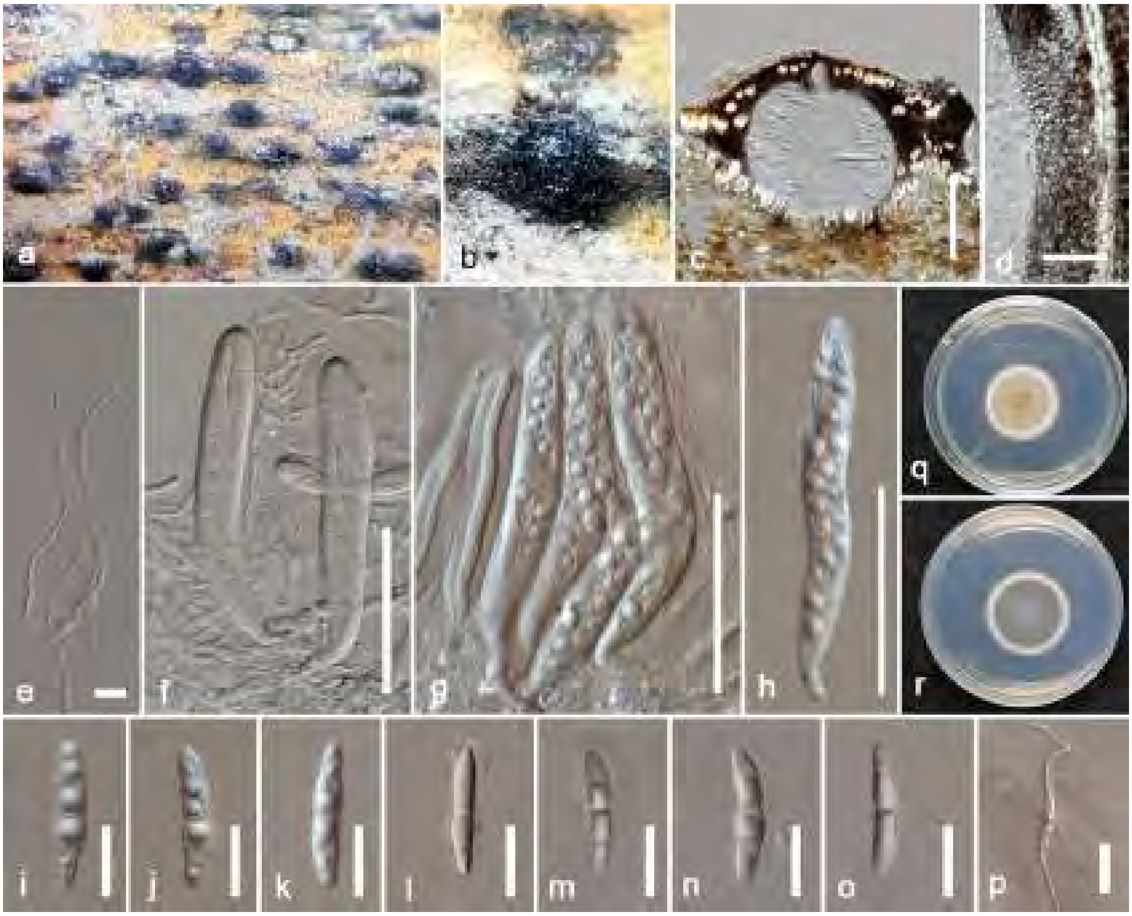


Fig. 24 ***Setoseptoria bambusae*** (MHZU 22-0133, **holotype**). **a** Ascomata on substrate. **b** Close-up view of ascoma. **c** Vertical cross section of ascoma. **d** Peridium. **e** Pseudoparaphyses. **f–h** Asci. **i–o** Ascospores. **p** Germinating ascospores. **q** Surface view of colony on PDA. **r** Reverse view of colony on PDA. Scale bars: c = 100 µm, f–h = 50 µm, i–o = 12.5 µm, d, p = 25 µm

hyphae, reverse dark grey with white margin, no sporulate, no pigments produced.

Material examined: China, Guangdong Province, Guangzhou City, a freshwater stream near Baiyun Mountain (23° 09′ 35″ N 113° 17′ 40″ E), stem of *Bambusa* sp., 23 September 2021, Jizhen Fu, SHB 1 (MHZU 22-0133, **holotype**), ex-type culture ZHKUCC 22-0228.

GenBank numbers: ITS: OR164941, LSU: OR164969, SSU: OR150418.

Notes: The combined gene analysis of ITS, LSU, SSU and *tef*1-*α* sequences (Fig. 25) showed that our isolate (ZHKUCC 22-0228) grouped with *Setoseptoria* species and they formed a distinct sub-clade between *S. phragmitis* and *S. magniarundinacea* with ML/BI = 81%/0.95 support. The base pair differences of ITS, LSU, and SSU loci of our isolate with *S. phragmitis* were 3.32%, 1.4%, 0.29% while these differences for *S. magniarundinacea* are 9.98%, 1.63%, 0.19% respectively.

Morphologically, our collection differs from *S. magniarundinacea* by subglobose to hemispherical ascomata with a flattened base, tetra-seriate, fusiform asci and large ($\bar{x}$ = 74.0 × 7.7 µm) ascospores with a submedian primary septum and minute, multi-guttules spread in it spores, except the thickened basal end (Tanaka et al. 2015). However, *S. phragmitis* has only been obtained from its asexual morph and therefore we are unable to compare its morphology (Quaedvlieg et al. 2013). *Setoseptoria phragmitis* was collected from leaves of *Phragmites australis* (Poaceae) from the Mai Po Mangrove forest in Hong Kong, while *S. magniarundinacea* was collected from a submerged stems of herbaceous plant in a small freshwater stream in Japan. All these species share similar habitat conditions. Therefore, we introduce our collection as *Setoseptoria bambusae* sp. nov.

Nigrogranaceae Jaklitsch & Voglmayr

Jaklitsch and Voglmayr (2016) treated Nigrogranaceae for *Nigrograna* and discontinued the family Biatriosporaceae until fresh material of *B. marina* became available for sequencing. However, Tibpromma et al. (2017) continued the family Biatriosporaceae based on distinguishing morphology by introducing a new species, *Nigrograna cangshanensis*, into the family Nigrogranaceae. Wijayawardene et al. (2018) accepted both Biatriosporaceae and Nigrogranaceae in Pleosporales. At present, Nigrogranaceae comprises 17 *Nigrograna* species (Boonmee et al. 2021).

Nigrograna thailandica Samarak. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556462; *Facesoffungi number*: FoF06105; Fig. 26.

Etymology: The specific epithet reflects the name of Thailand, where the species was collected

Saprobic on dead branches of an unidentified plant. **Sexual morph**: *Ascomata* 250–380 µm high × 390–440 µm diam., perithecioid, single or gregarious, immersed in bark, sometimes erumpent, subglobose or ellipsoidal, black, with an ostiole, cylindrical neck. *Ostiole* mostly central, brittle. *Peridium* 3–4-layered, composed of *textura angularis* cells, outer layer, dark brown, thick-walled, large cells, often surrounded by an olivaceous to dark brown subiculum of 1.5–2.4 µm wide brown hyphae, middle and inner layers, pale brown, thin-walled small cells. *Hamathecium* composed of 1.4–2 µm ($\bar{x}$ = 1.7 µm, n = 25) wide, numerous, distally tapering, rarely trabeculate pseudoparaphyses. *Asci* 50–95 µm × 8.5–11 µm ($\bar{x}$ = 80 × 10 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, short pedicellate, apically rounded, sometimes with an ocular chamber. *Ascospores* 13.8–16 × 4.2–5.6 µm ($\bar{x}$ = 14.8 × 4.9 µm, n = 30), biseriate, fusoid to clavate, yellowish-brown to dark brown, 3-septate, apical cell often acute, second cell usually slightly widened, constricted at the medium, only slightly at other septa, straight or curved, terminal cells often slightly longer than mid cells. **Asexual morph**: Undetermined.

Culture characteristics: Ascospore germinating within 12 h on PDA at 25 °C, germ tube from four cells. Colonies on PDA reaching 23.5 mm diam. after 16 days at 25 °C, dull, white to light brown, circular, flat, slightly woolly, smooth margin; reverse dark brown centre and light brown marginal area.

Material examined: Thailand, Lampang Province, Wang Nuea, on dead branches of an unidentified plant, 18 August 2017, M.C. Samarakoon, SAMC009 (MFLU 18-0851, **holotype**; HKAS 102335, **isotype**), ex-type culture, MFLUCC 17-2663.

GenBank numbers: ITS: MK762709, LSU: MK762716, SSU: MK762704

Notes: Our collection (MFLU 18-0851) is morphologically similar to other taxa in *Nigrograna* in having globose to subglobose ascomata, periphysate ostioles, pseudoparenchymatous peridium, clavate asci, and asymmetric, fusoid to narrowly ellipsoid ascospores. Our collection is in a cluster with *N. yasuniana* with ML = 100%, BI = 1.00 statistical support. The base pair comparison of ITS shows 98% similarity (452/461, 3/461 gaps) of *N. thailandica* to *N. jinghongensis* (HKAS 115776). However, *N. yasuniana* was described as an endophyte from South and Central America. Since there is an incomplete morphological comparison, our combined phylogeny (LSU-SSU-*tef1-α-rpb2*) reveals that our strain forms a distinct clade in *Nigrograna* (Ahmed et al. 2018; Kolařík 2018), as we introduce this collection as *Nigrograna thailandica* (Fig. 27).

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

Occultibambusaceae was introduced by Dai et al. (2017) with *Occultibambusa* D.Q. Dai & K.D. Hyde as the type genus. The family comprises the genera *Brunneofusispora*,

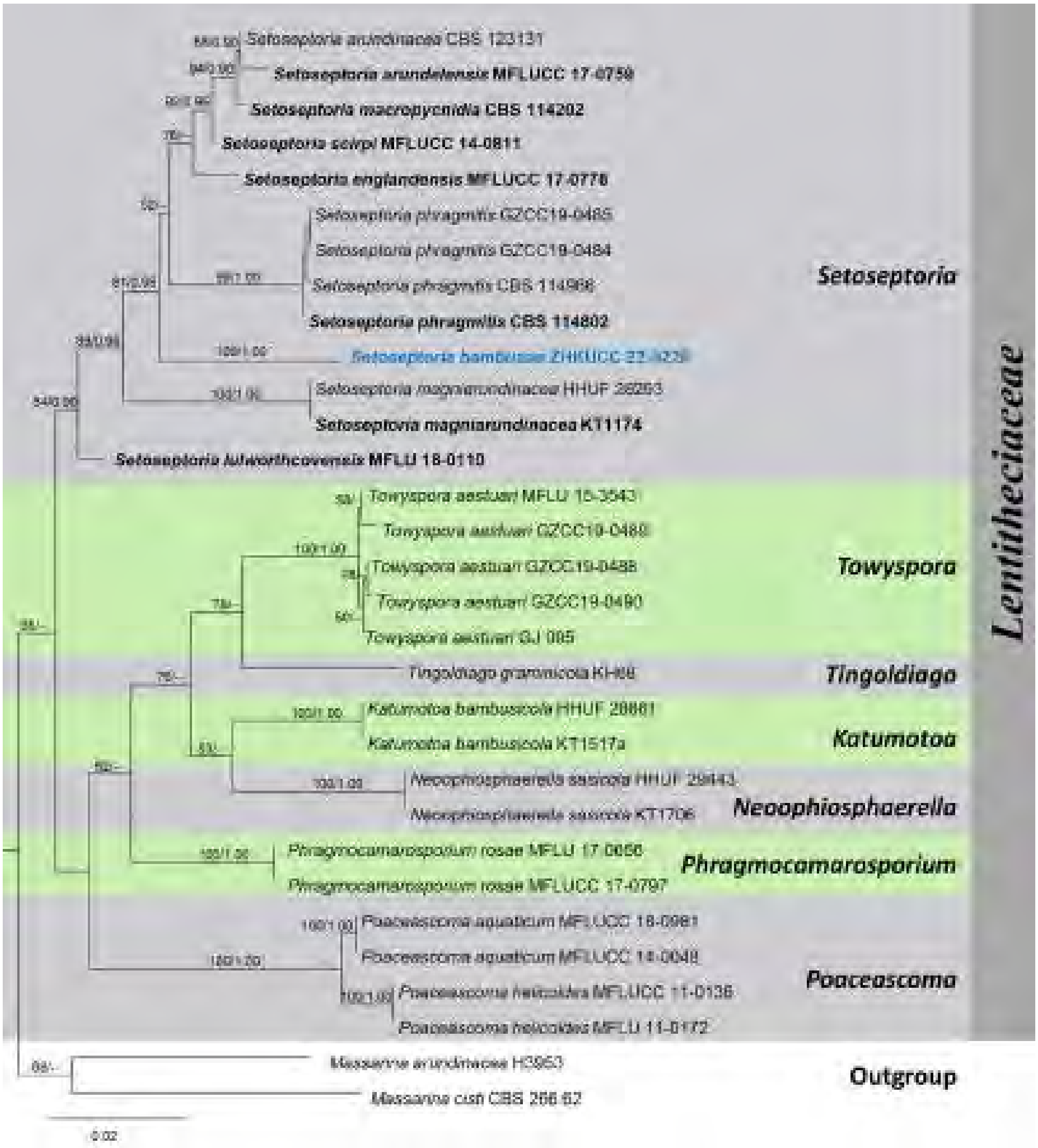


Fig. 25 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef*1-*α* sequence data which comprised 3408 characters (ITS = 601, LSU = 856, SSU = 1,022, *tef*1-*α* = 929). The best scoring RAxML tree with a final likelihood value of − 10,069.029510 is presented. The matrix had 646 distinct alignment patterns, with 28.8% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.237780, C = 0.274787, G = 0.244558, T = 0.242875; substitution rates: AC = 1.519491, AG = 2.922803, AT = 1.750316, CG = 1.738507, CT = 9.995833, GT = 1.0; gamma distribution shape parameter α = 0.334816. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (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 blue bold. The tree is rooted to *Massarina arundiaaceae* (H3953) and *M. cisti* (CBS 266.62)

Neooccultibambusa, *Occultibambusa*, *Seriascoma* and *Versicolorisporium* (Hatakeyama et al. 2008; Doilom et al. 2017; Wijayawardene et al. 2018; Phookamsak et al. 2019). Members of this family are usually collected from the monocotyledon plants and especially bamboo (Dai et al. 2017) and they are morphologically distinguished by immersed, solitary to gregarious ascomata with black ostioles, bitunicate, broadly cylindrical to clavate asci, cellular pseudoparaphyses and broad-fusiform, hyaline to dark brown, 1–3-septate ascospores (Dai et al. 2017). Asexual morphs

Fig. 26 ***Nigrograna thailandica*** (MFLU 18-0851, **holotype**). **a–d** Ascomata on the substrate. **e, i** Cross sections of ascomata. **f** Section of the peridium. **g** Subicular hyphae. **h** Pseudoaraphyses. **j–m** Asci. **n–r** Ascospores. **s** Germinating ascospore. **t** Upper view of the colony. **u** Reverse view of the colony. Scale bars: a, b = 1 cm, d = 500 µm, c, e = 200 µm, i = 100 µm, f, j–m = 20 µm, g, n–s = 10 µm, h = 5 µm

of Occultibambusaceae comprise eustromatic conidiomata with phialidic conidiogenous cells and enteroblastic conidiogenesis (Dai et al. 2017; Boonmee et al. 2021).

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

The genus *Seriascoma* was introduced by Dai et al. (2017) with *S. didymospora* Phookamsak, D.Q. Dai & K.D. Hyde as the type species from bamboo. *Seriascoma* species are characterized by elongated, gregarious, ostiolate ascostromata, immersed beneath the clypeus, a thick-walled peridium composed of dark brown cells of *textura angularis* and clavate to fusiform, hyaline, didymospores arranged in bitunicate asci (Dai et al. 2017; Rathnayaka et al. 2019). The asexual morphs of *Seriascoma* comprise solitary to

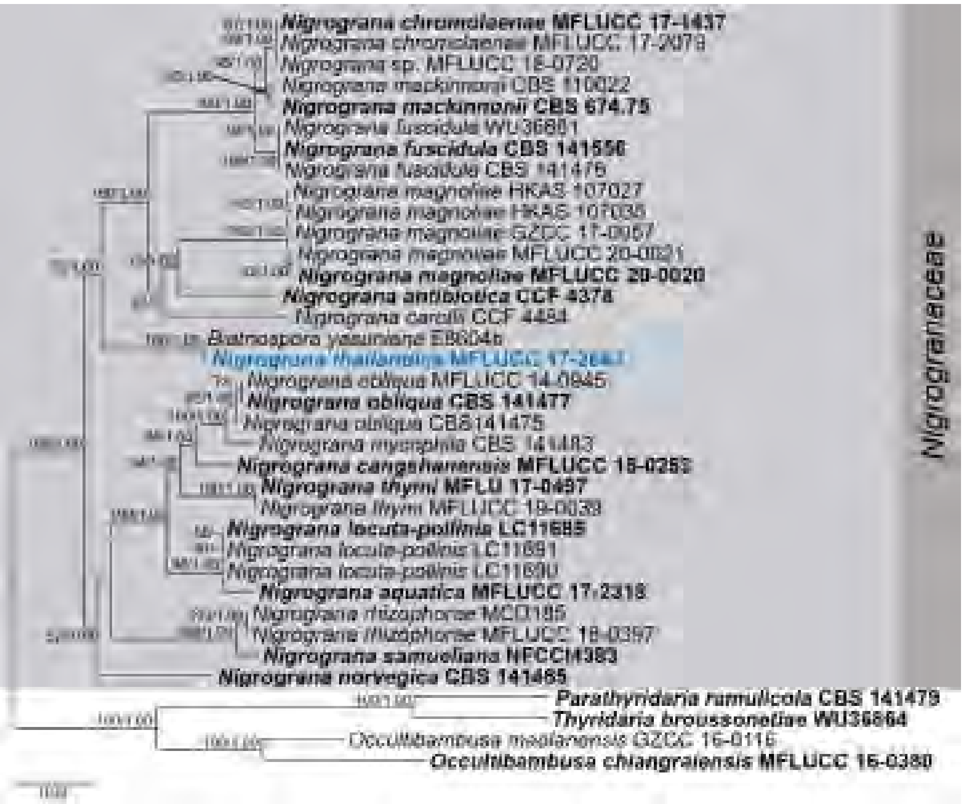


Fig. 27 Phylogram generated from ML analysis based on combined LSU-SSU-*tef1-α*-*rpb2* sequence data of the genus *Nigrograna*. Thirty-six strains are included in the combined analyses which comprised 3799 characters (833 characters for LSU, 1023 characters for SSU, 933 characters for *tef1-α*, 1010 characters for *rpb2*). The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of − 14,937.288660 is presented. The matrix had 951 distinct alignment patterns, with 25.69% of undetermined characters or gaps. Evolutionary models applied for all genes are GTR + G + I, respectively. Bootstrap support for ML greater than 50% and Bayesian posterior probabilities greater than 0.95 are given at nodes, respectively. The tree was rooted with *Occultibambusa chiangraiensis* (MFLUCC 16-0380), *O. maolanensis* (GZCC 16-0116), *Parathyridaria ramulicola* (CBS 141479) and *Thyridaria broussonetiae* (WU36864). Ex-type strains are in bold. The newly generated sequences are indicated in blue bold

gregarious, conical, uniloculate, black, eustromatic conidiomata (Dai et al. 2017; Boonmee et al. 2021). The conidiomatal wall consists of pseudoparenchymatous cells, arranged in a *textura angularis* and produce oblong, aseptate, hyaline conidia (Dai et al. 2017). This study introduces a new *Seriascoma* species.

Seriascoma acutispora Senan., B. Xu & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF900417; *Facesoffungi number*: FoF 14171; Fig. 28

Etymology: based on the acute ends of ascospores.

Saprobic on dead branches of an unidentified plant. **Sexual morph**: *Clypeus* spread over the ascostromata, comprised of highly pigmented, tightly-packed cells. *Ascostromata* 300–330 µm high, 475–550 µm diam., solitary, scattered, uniloculate, erumpent in host, immersed beneath the clypeus, conical to pyriform, coriaceous, with a central ostiole, dark brown to black, apapillate. *Peridium* 10–15 µm, thin, thinner at the base, composed of several layers of very small, brown to dark brown cells of *textura angularis*, combined with plant epidermis cells. *Hamathecium* 1.4–2.8 µm wide, comprising numerous, branched, filiform, septate pseudoparaphyses and longer than asci. *Asci* 100–110 × 20–30 µm ($\bar{x} = 102 \times 24$ µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, long pedicellate, apically rounded, with well-developed ocular chamber. *Ascospores* 33–40 × 7–9 µm ($\bar{x} = 35 \times 8$ µm, n = 20), biseriate, didymosporous, slightly narrow, elongated fusiform, with acute ends, hyaline, slightly constricted at the septum, straight to curved, upper cell slightly wider than lower cell, smooth-walled, surrounded by a gelatinous sheath, 4 or more guttulate. **Asexual morph**: Undetermined.

Culture characters: Colonies on PDA reaching 1 cm diam. after 10 days in dark at 25 °C, circular, umbonate, filiform margin, with greenish black mycelia, centre crowed with grey aerial, mycelial clots; reverse black.

Material examined: Thailand, Chiang Mai Province, Saluang Mae Rim District, on dead twigs of *Bambusa* sp., 17

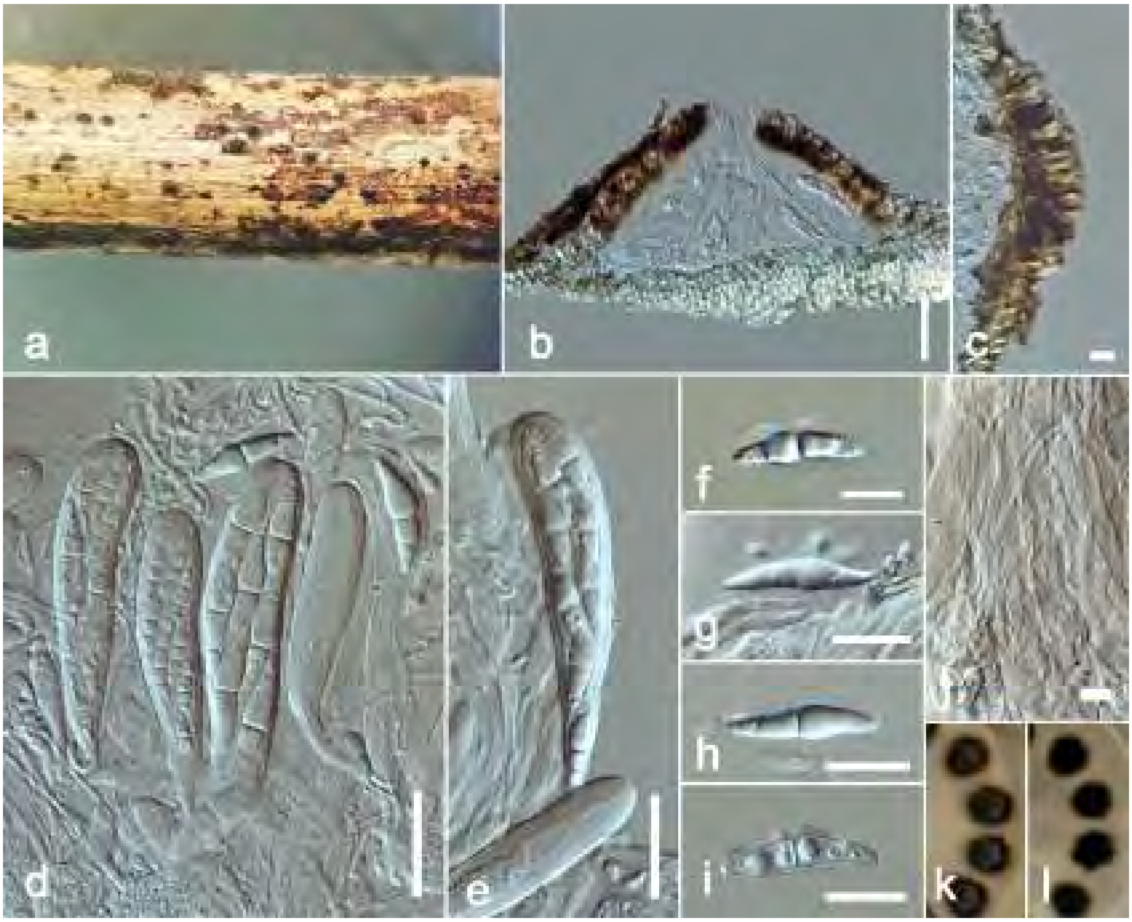


Fig. 28 ***Seriascoma acutispora*** (MHZU 22-0143, **holotype**). **a** Appearance of ascomata on the dead woody twigs of *Bambusa* sp. **b** Vertical cross section of ascoma. **c** Peridium. **d, e** Asci. **f–i** Ascospores. **j** Pseudoparaphyses. **k** Surface view of colony on PDA. **l** Reserve view of colony on PDA. Scale bars: b = 100 µm, d, e = 25 µm, c, f–i = 15 µm

February 2019, I.C. Senanayake, S3 23–2 (MHZU 22-0143, **holotype**), ex-type cultures ZHKUCC 22-0273, ZHKUCC 22-0274.

GenBank numbers: LSU: OR164965, OR164966, ITS: OR164937, OR164938, *rpb2*: OR166288, OR166289, *tef1-α*: OR166279.

Notes: The combined gene analysis of ITS, LSU, *rpb2* and *tef*1-α (Fig. 29) showed that our new strains clustered with the type strain of *Seriascoma yunnanense* forming a distinct clade with ML/BI = 94%/0.90 statistical support. There are 11.62%, 2.64%, 12.26% and 6.2% base pair differences in ITS, LSU, *rpb2* and *tef*1-α sequences between our isolate and *Seriascoma yunnanense* respectively.

Our collection is morphologically similar to *Seriascoma yunnanense*, but distinct from *S. yunnanense* in having solitary, scattered, conical to pyriform, apapillate ascomata with wide ostioles, septate, pseudoparaphyses longer than the asci, and biseriately arranged, narrow ascospores with acute ends, while *S. yunnanense* has aggregated, globose to sub-globose, papillate ascomata, pseudoparaphyses not longer than asci, and overlapping uni to tri-seriately arranged, wide ascospores with obtuse ends (Rathnayaka et al. 2019). Therefore, we introduce this collection as *Seriascoma acutispora*.

Parabambusicolaceae Kaz. Tanaka & K. Hiray.

Parabambusicolaceae typified by *Parabambusicola* Kaz. Tanaka & K. Hiray., was introduced by Tanaka et al. (2015) to accommodate massarina-like species from grasses along with the six additional genera and two undescribed *Monodictys* species. Currently, *Parabambusicolaceae* comprises 12 genera viz. *Aquastroma*, *Lonicericola*, *Multilocularia*, *Multiseptospora*, *Neoaquastroma*, *Neomultiseptospora*, *Parabambusicola*, *Paramonodictys*, *Paramultiseptospora*, *Paratrimmatostroma*, *Pseudomonodictys*, and *Scolecohyalosporium* (Tanaka et al. 2015; Li et al. 2016; Wanasinghe et al. 2017; Phukhamsakda et al. 2018; Phookamsak et al. 2019, 2022; Hongsanan et al. 2020a, b; Hyde et al. 2020a; Wijayawardene et al. 2020; Xie et al. 2022b). Remarkably, this family has been restricted to Asia and more taxon

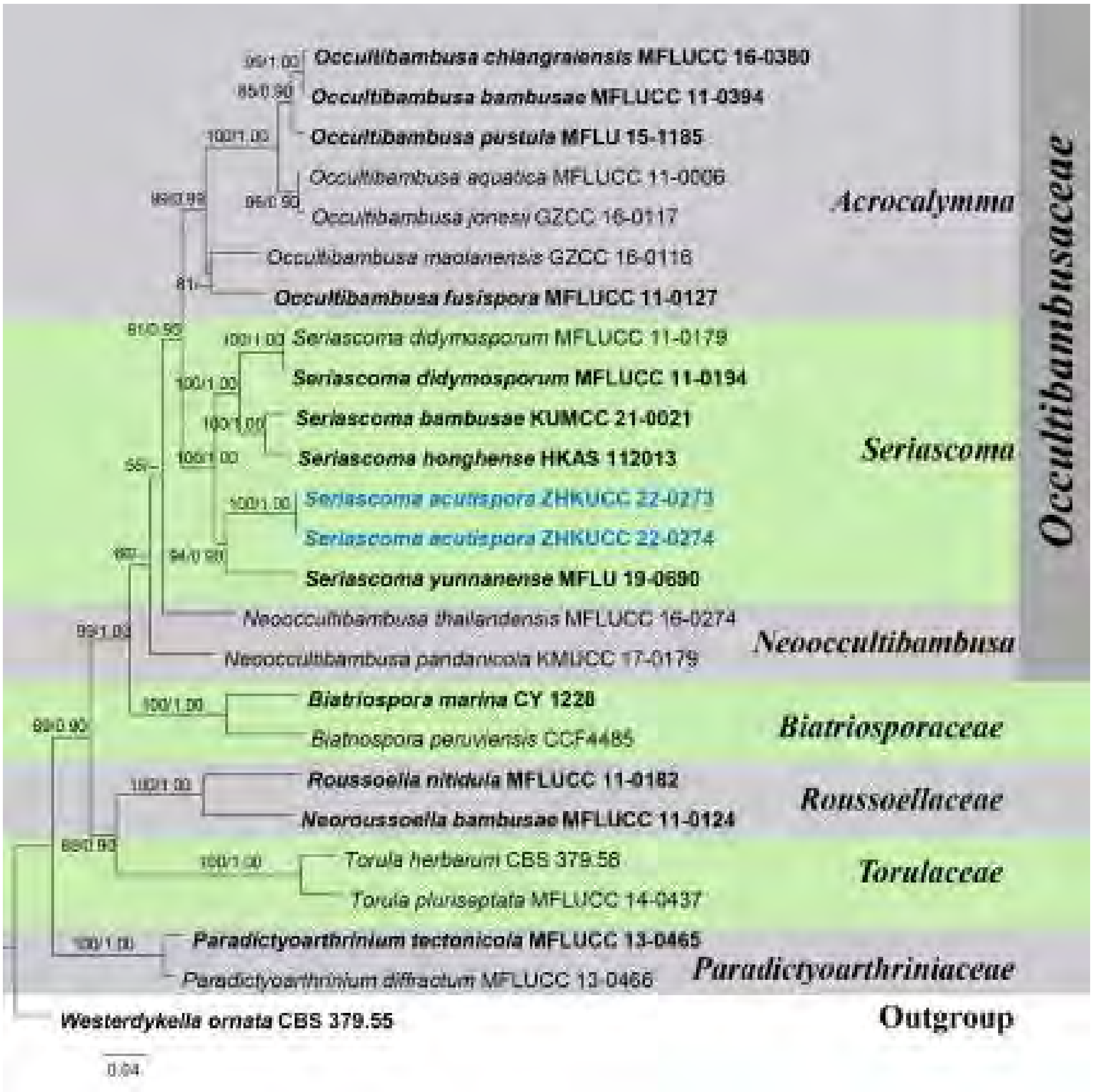


Fig. 29 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2* and *tef1-α* sequence data which comprised 3137 characters (ITS = 516, LSU = 870, *rpb2* = 1,076, *tef*1-α = 516). The best scoring RAxML tree with a final likelihood value of − 19,614.282564 is presented. The matrix had 1299 distinct alignment patterns, with 17.87% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.234151, C = 0.279510, G = 0.258584, T = 0.227755; substitution rates: AC = 1.581558, AG = 4.062963, AT = 1.691894, CG = 1.106792, CT = 8.475079, GT = 1.0; gamma distribution shape parameter α = 0.191641. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (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 blue bold. The tree is rooted to *Westerdykella ornata* (CBS 379.55)

sampling may enlighten its specific geographical distribution (Yasanthika et al. 2020). Species in Parabambusicolaceae are saprobic, bambusicola-like species in both freshwater and terrestrial environments that mostly occur on bamboos and grasses but are also found on different hosts and substrates.

Aquastroma Kaz. Tanaka & K. Hiray.

The monotypic genus *Aquastroma* was introduced by Tanaka et al. (2015) based on a single collection of the type species *A. magniostiolatum* from pond water in Japan. The genus was reported from freshwater (Dong et al. 2020) and terrestrial environments (Chethana et al. 2021a) in Thailand. In this study, a new host record of *Aquastroma magniostiolatum* was documented from submerged decaying twigs of riverine *Sonneratia caseolaris* and we provide an updated phylogenetic tree for *Aquastroma*.

Aquastroma magniostiolatum Kaz. Tanaka & K. Hiray. [as 'magniostiolata'], in Tanaka et al., Stud. Mycol. 82: 115 (2015)

Index Fungorum number: IF828557; *Facesoffungi number*: FoF08694, Fig. 30

Saprobic on submerged decaying *Sonneratia caseolaris* (L.) Engl. stem in a freshwater habitat. **Sexual morph**: *Ascomata* 220–260 × 190–250 µm (x̅ = 232 × 228 µm, n = 10), black domes visible on host cortex, solitary to gregarious, immersed to erumpent, subglobose, black, coriaceous, ostiolate, 77–82 µm wide. *Peridium* 15–27.5 µm (x̅ = 21 µm, n = 15), thick-walled, thinner at the base, becoming thick at the apex, composed of two layers: outer layer composed of one or two layers of brown thick-walled cells of *textura angularis*, inner layer composed of hyaline thin-walled cells of *textura angularis*. *Pseudoparaphyses* 1.5–3 µm, numerous, cellular, broad, septate, hyaline, smooth-walled, branched and anastomosing above the asci. *Asci* 60–105 × 15.5–27 µm (x̅ = 76.6 × 22.1 µm, n = 25), bitunicate, 8-spored, clavate, fissitunicate, apically rounded

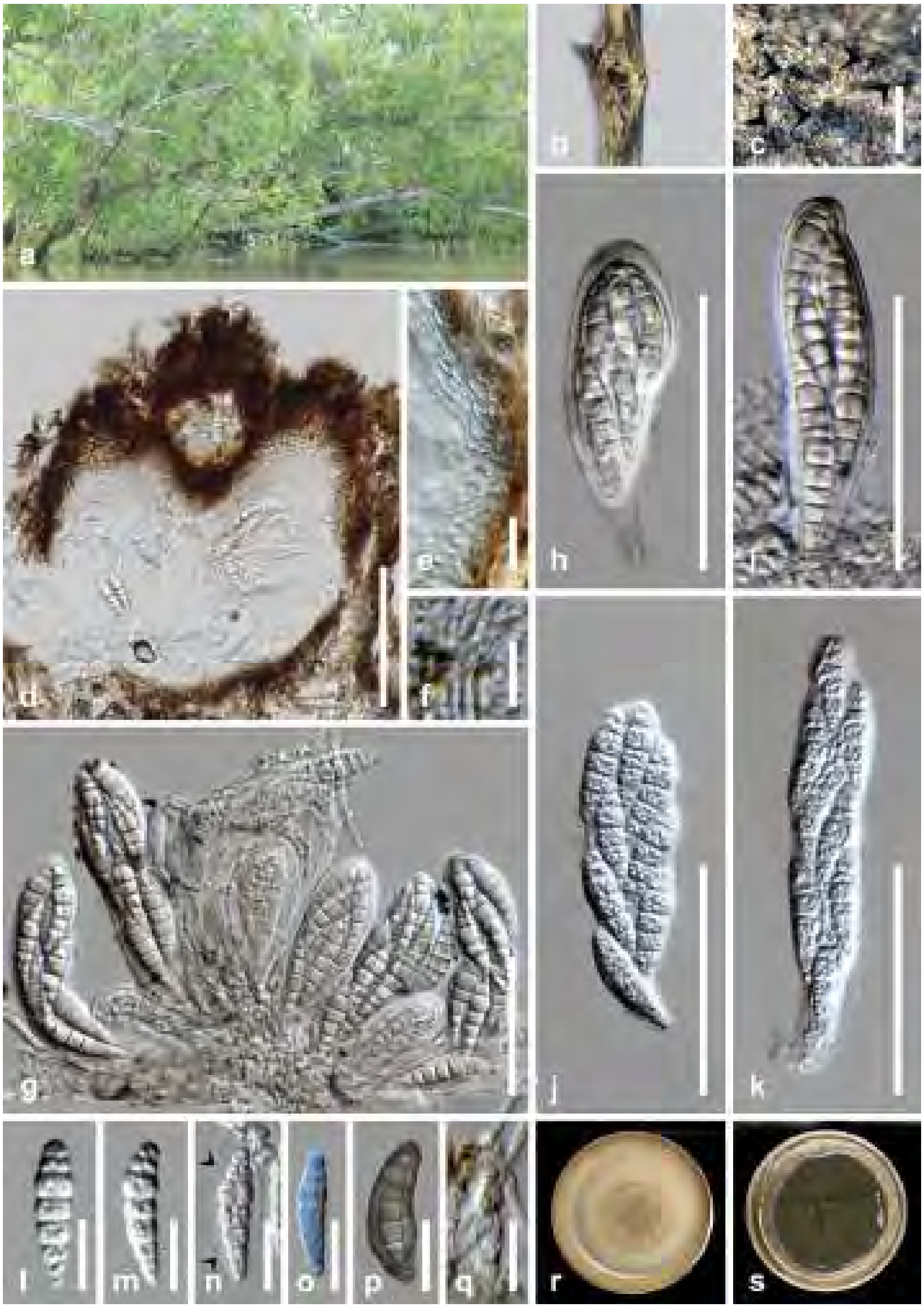


Fig. 30 ***Aquastroma magniostiolatum*** (MFLU 22-0121). **a** Riverine mangrove *Sonneratia caseolaris*. **b** Examined material. **c** Appearance of ascomata in host substrate. **d** Vertical section of ascoma. **e** Peridium. **f** Pseudoparaphyses. **g–k** Asci. **l–p** Ascospores. [Ascospores stained with Lactophenol Cotton Blue (**o**) and Indian Ink (**p**)]. **q** Germinated ascospore. **r** Surface view of culture on MEA. **s** Reverse view of culture on MEA. Scale bars: c = 500 µm, d = 100 µm, e = 20 µm, f = 10 µm, g–k = 50 µm, l–q = 20 µm

with invisible apical chamber, sessile or short pedicellate. *Ascospores* 30–45 × 4–12 µm ($\bar{x}$ = 38.83 × 8.53 µm, n = 30), bi- to tri-seriate, clavate to fusiform, guttulate to granular, straight, mostly curved, 6–7-septate, constricted at septa, hyaline, smooth-walled, surrounded with mucilaginous sheath. **Asexual morph**: Undetermined.

Culture characteristics: Conidia germinating on malt extract agar (MEA) within 24 h. Colonies growing on MEA, reaching 25–30 mm in 2 weeks at 25 °C, colony circular, flat, entire, dry, surface rough, smooth hyphae, light brown in surface view, reverse dark gray.

Material examined: Thailand, Samut Songkhram Province, Mueang Samut Songkhram District, on submerged decaying wood of *Sonneratia caseolaris* (Lythraceae) in a river, 8 September 2020, M. Calabon, SS04 (MFLU 22-0121), living culture, MFLUCC 22-0081.

Hosts and geographical distribution: Dead wood culms of unidentified plant in Japan (Tanaka et al. 2015), and Thailand (Dong et al. 2020), twigs of *Sonneratia caseolaris* in Thailand.

GenBank numbers: LSU: OP216403, ITS: OP216408, *tef*1-*α*: OP251193

Notes: Multi-locus phylogenetic analysis showed that our collection MFLUCC 22-0081 clustered with strains of *Aquastroma magniostiolatum* with ML/BI = 100%/1.00 bootstrap support. The pairwise nucleotide comparisons of our isolate (MFLUCC 22-0081) with the type strain (CBS 139680) showed 0.12%, 1.09% and 0.76% nucleotide differences in the ITS, LSU, and *tef*1-*α* regions, respectively. *Aquastroma magniostiolatum* was isolated in freshwater pond and stream (Tanaka et al. 2015; Dong et al. 2020) and terrestrial habitats (Chethana et al. 2021a). The fungus was reported twice in Thailand from unidentified wood (Dong et al. 2020; Chethana et al. 2021a). Morphological comparisons of our collection (MFLUCC 22-0081) with the freshwater strains CBS 139680 and MFLUCC 18-0976 revealed their similarity. However, our isolate differs from CBS 139680 with a narrower conidiomata (220–260 × 190–250 µm *vs*. 180–250 × 260–340 µm) and shorter asci (60–105 × 15.5–27 µm *vs*. 112.5–137.5 × 25–29.5 µm). We identified our collection as *A. magniostiolatum* and this is the first record in decaying twigs of *Sonneratia caseolaris* (Fig. 31).

Kevinia Rajeshk., Verma R., Wijayaw., Karun. & Tibpromma, ***gen. nov.***

Index Fungorum number: IF559647; *Facesoffungi number*: FoF 10829

Etymology: Named after Prof. Kevin D. Hyde for his contributions to the fungal diversity of Asia.

Saprobic on the surface of decaying branches. **Sexual morph**: Undetermined. **Asexual morph**: hyphomyceteous. *Conidiophores* reduced to conidiogeneous cells. *Conidiogenous cells* macronematous, mononematous, erect, ampulliform, wider base, smooth, unbranched or rarely branched. *Conidia* holoblastic, monoblastic, digitate or irregular, dictyosporous, brown to dark-brown, smooth to slightly roughened, euseptate, base truncate.

Notes: The nucleotide BLAST results of ITS, LSU and *tef*1-*α* sequences of our collection (AMH 10455) revealed the closest matches as species in *Neomultiseptospora*, *Neoaquastroma*, *Monodictys*, *Parabambusicola* and *Pseudomonodictys*. In the phylogenetic analyses (Fig. 35), our collection (AMH 10455) clustered with species in *Neoaquastroma* with ML/BI = 72/0.88 statistical support. *Neoaquastroma* is characterized by immersed, globose to subglobose or irregular-shaped ascomata, short papillate ostioles, a thin peridium, clavate asci with short pedicels, and multi-septate, hyaline ascospores with guttules in each cell.

However, the sexual morph of our collection is undetermined and the asexual morph of *Neoaquastroma* is also not known. Therefore, our collection cannot morphologically be compare with species in *Neoaquastroma*. The asexual morph of Parabambusicolaceae is phoma-like species and our collection (AMH 10455) is distinct from them. Further, our collection (AMH 10455) has been obtained from decaying litter from Thane, India, while *Neoaquastroma* species have been collected from dead twigs of *Bauhinia variegate* (L.) Benth. and *Barringtonia acutangula* (L.) Gaertn. in Thailand and on dead twigs of unidentified plant in Thailand and Guizhou Province (China). Thus, geographical distribution of these two genera is significant. Therefore, we propose a new anamorphic genus *Kevinia* for this lineage.

Type species: *Kevinia lignicola* Rajeshk., Verma R., Wijayaw., Karun. & Tibpromma

Kevinia lignicola Rajeshk., Verma R., Wijayaw., Karun. & Tibpromma, ***sp. nov.***

Index Fungorum number: IF559657; *Facesoffungi number*: FoF 10830; Figs. 32, 33, and 34

Etymology: based on the lignicolous nature of the fungus.

Saprobic. **Sexual morph**: Undetermined. **Asexual morph**: hyphomyceteous. *Conidiophores* reduce to conidiogenous cells. *Conidiogenous cells* (–38) 50–99 × (–15.5) 21–30.5 µm, macronematous, mononematous, ampulliform, wider base, smooth, erect, unbranched or rarely branched. *Conidia* 46–74 (–93) × 20–48 µm, holoblastic, monoblastic, dictyosporous, dark at base, digitate and branched towards paler apex, smooth base, brown to dark-brown, smooth to slightly roughened, euseptate, base truncate.

Culture characteristics: Colonies on MEA, reaching 30 to 40 mm diam. after 20 days at 25 °C, initially aerial mycelium greyish to brownish grey (4D2), velutinous, in old cultures brownish grey (4D2) to dark brownish grey, colonies reverse dark grey (4F1). Soluble pigments and exudates are absent.

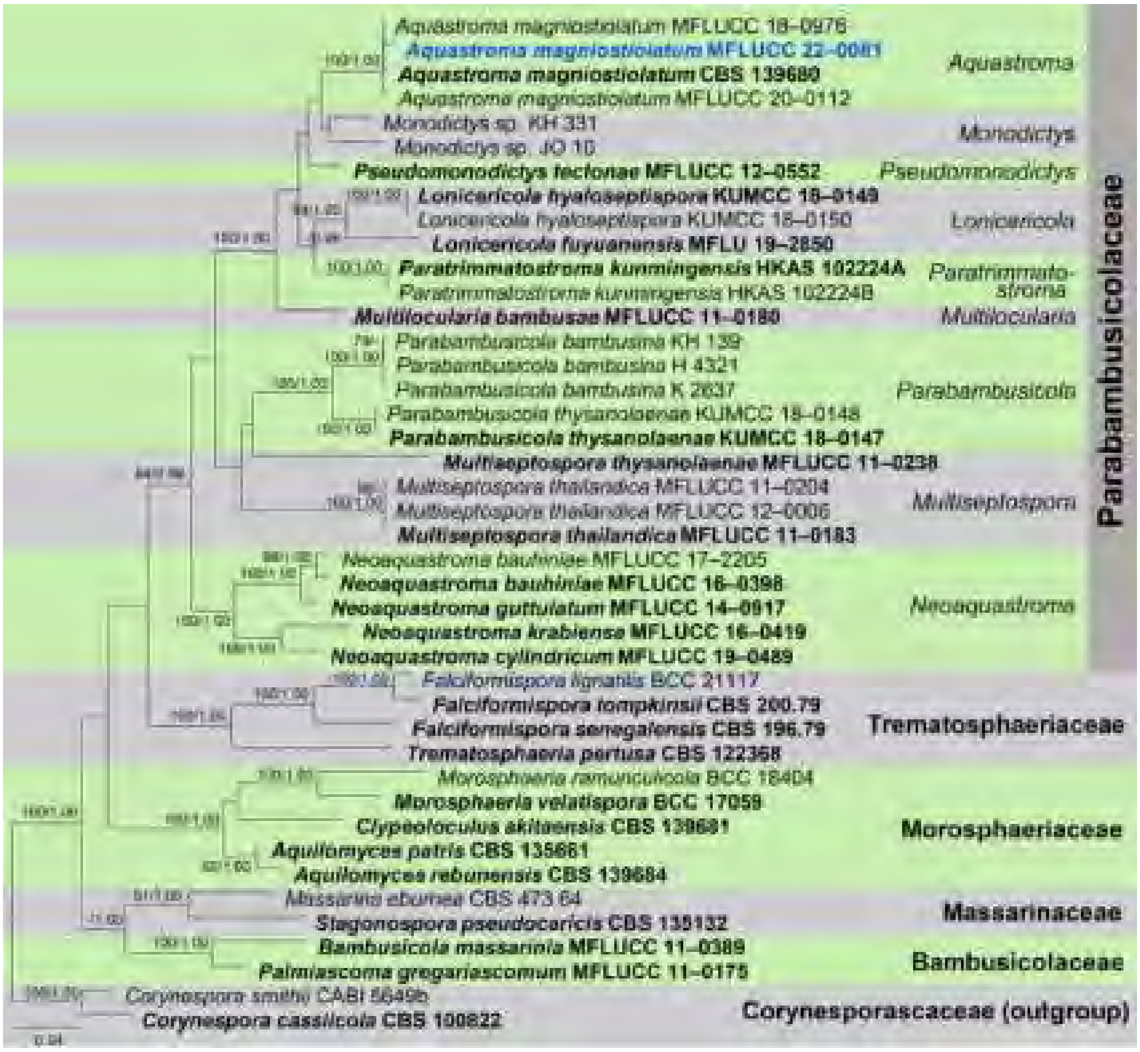


Fig. 31 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, and *tef*1-*α* sequence data representing the species of Parabambusicolaceae and related families. *Corynespora cassiicola* (CBS 100822) and *C. smithii* (CABI 5649b) were used as the outgroup taxa. Forty-two taxa are included in the combined analyses which comprised 3552 characters (2178 characters for LSU, 474 characters for ITS, 900 characters for *tef*1-*α*) after alignment. The best scoring RAxML tree with a final likelihood value of – 14,144.062065 is presented here. The matrix had 758 distinct alignment patterns, with 17.47% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.222957, C = 0.274911, G = 0.283984, T = 0.218148; substitution rates: AC = 1.015664, AG = 2.212569, AT = 1.355468, CG = 1.027432, CT = 5.589665, GT = 1.0; gamma distribution shape parameter α = 0.210099. Bootstrap support for ML equal to or greater than 75% and BI equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue bold

Material examined: India, Maharashtra, Thane, (19° 13′ 13″ N 72° 57′ 17″ E), decaying branches of unidentified plant, July 2020, K. C. Rajeshkumar, (AMH 10455, **holotype**), ex-type cultures NFCCI 5058, NFCCI 5059.

GenBank numbers: ITS: OK255497, OK255498; LSU: OK255501, OK255500; *tef*1*α*: OK236374, OK236375.

Notes: The proposed new genus *Kevinia* does not have any morphological resemblance to any of the known genera and species of Parabambusicolaceae. The morphological characteristics of our collection such as apically branched, digitate, dictyosporous conidia and mononematous conidiogenous cells distinguish this taxon as unique and different from all the species in this family. An indefinite morphological comparison is probable with the allied genera *Paratrimmatostroma* Jayasiri, Phookamsak, D.J. Bhat & K.D. Hyde. However, the sporodochial conidiomata, black powdery, superficial mass on host substrates, helicoid, sigmoid, or reniform conidia that are tapering near apex and base are absent in our collection. The combined ITS, LSU and *tef*1-*α* sequence analysis showed that our collection is allied to *Neoaquastroma* species well within Parabambusicolaceae. Morphological comparison between our

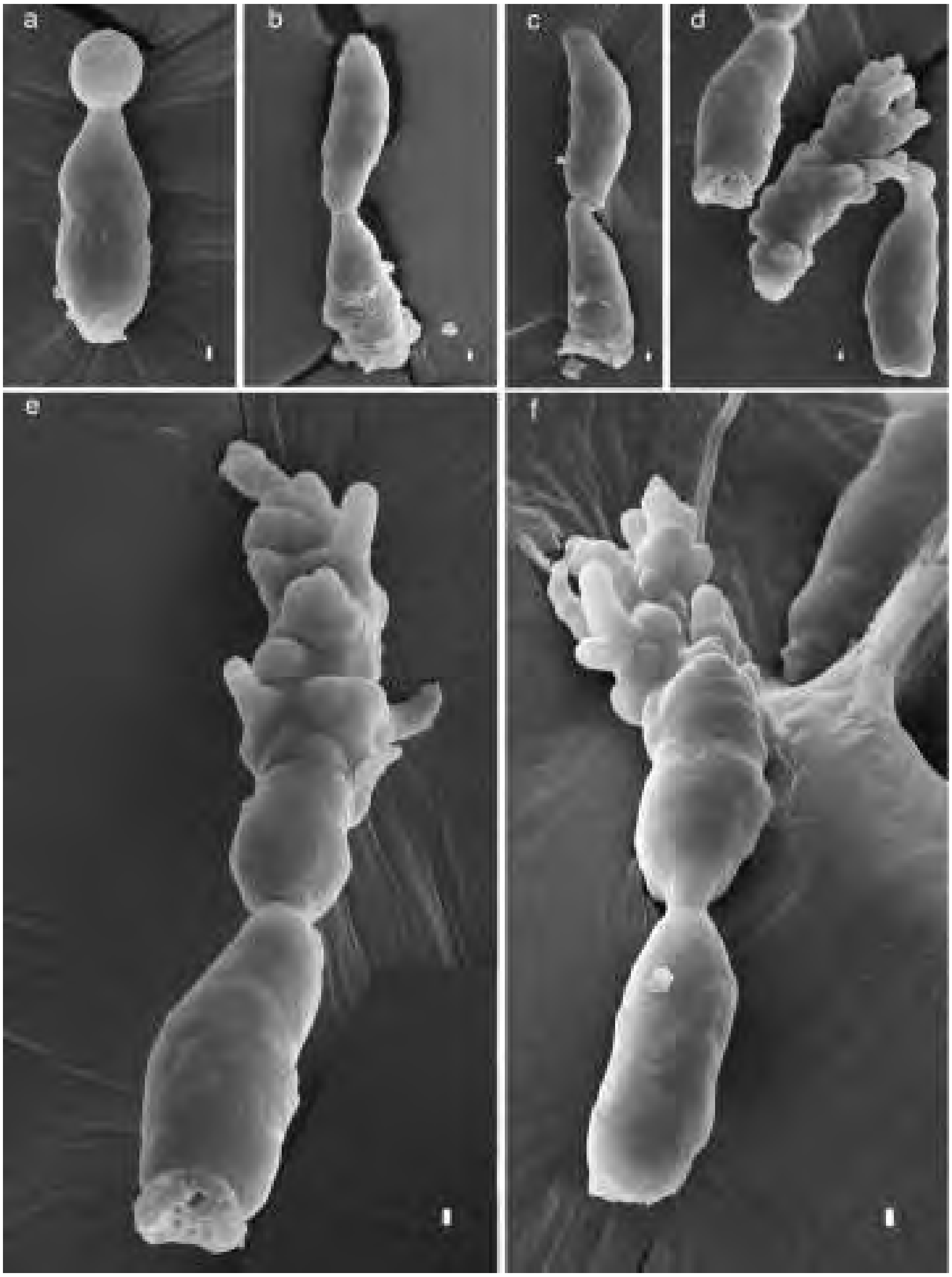


Fig. 32 ***Kevinia lignicola*** (AMH 10455, **holotype**). **a–c** SEM of conidiophores and developing conidia. **d** Conidiophore and mature conidia. **e, f** Conidiophore with apical conidia. Scale bars: a–f = 2 μm

collection, *Neoaquastroma* and *Pseudomultiseptospora* is improbable due to the absence of anamorph in these genera. Hence, we introduce our collection as *Kevinia lignicola* sp. Nov (Fig. 35).

Parabambusicola Kaz. Tanaka & K. Hiray

Parabambusicola was introduced by Tanaka et al. (2015) based on morphology and molecular analyses. Only four species are arranged in this genus, of which three were isolated from Poaceae plants in terrestrial habitats and one from decaying wood in freshwater (Tanaka et al. 2015; Phookamsak et al. 2019; Dong et al. 2020; Xie et al. 2022b).

Parabambusicola yunnanensis L.S. Han & D.Q. Dai, in Han, Dai, Du, Wijayawardene, Promputtha, Bhat & Gao, Phytotaxa 589(3): 250 (2023)

Index Fungorum number: IF559989; *Facesoffungi number*: FoF 12952, Fig. 36

Saprobic on submerged decayed stems of bamboo in freshwater habitats, appearing as raised, dome-shaped areas on the host surface. **Sexual morph**: *Ascomata* 175–260 µm high, 375–675 µm wide, immersed, subglobose, mostly clustered together, sometimes solitary. *Peridium* 25–60 µm wide, thick, 2-layered; outer layer consisting of thick-walled, multi-rows of brown, polyhedral cells of *textura*

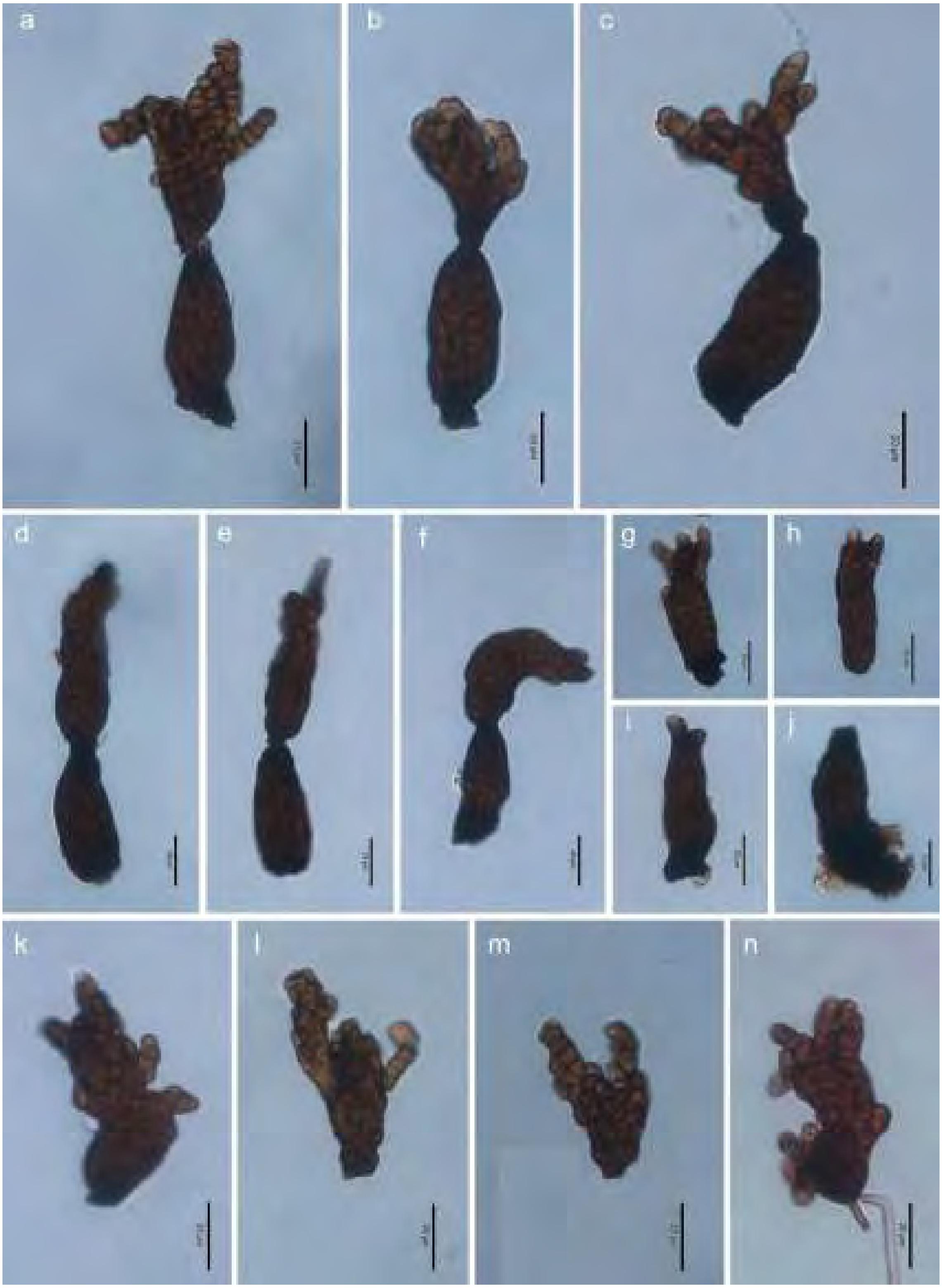


Fig. 33 ***Kevinia lignicola*** (AMH 10455, **holotype**). **a–c** Conidiophores with apical branched dictyosporous digitate conidia (front view). **d–f** Conidiophore with conidia (side view). **g, h** Developing conidia. **i, j** Conidiophores. **k–n** Mature conidia. Scale bars: a–n = 10μm

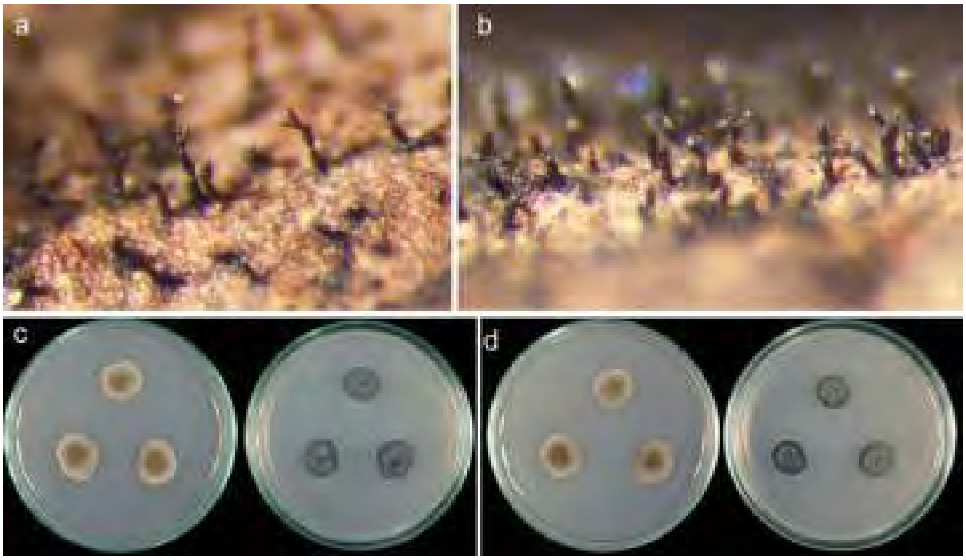


Fig. 34 *Kevinia lignicola* (AMH 10455, **holotype**) **a, b** Colonies on the decaying wood. **c** Colonies of NFCCI 5058 (ex-type) on MEA obverse and reverse view. **d** Colonies of NFCCI 5059 obverse and reverse view

angularis, inner layer comprising multi-rows of pale brown to hyaline, elongated cells of *textura angularis* or *taxtura prismatica*. *Hamathecium* composed of numerous, filamentous, 1–2.5 µm wide, septate pseudoparaphyses. *Asci* 85–130 × 18–24 µm ($\overline{x}$ = 108 × 21 µm, n = 25), broadly cylindrical to cylindric-clavate, 8-spored, hyaline, bitunicate, subsessile, rounded at the apex, with clearly visible inconspicuous ocular chamber when young. *Ascospores* 45.5–57 × 6–8.5 µm ($\overline{x}$ = 51 × 7.5 µm, n = 25), overlapping 2–3-seriate, hyaline, fusiform to vermiform, slightly curved, narrower towards the lower cell, 3–(4)-septate, primary septum mostly median, smooth-walled, with sheath. **Asexual morph**: Undetermined.

Culture characteristics: Colonies on PDA reaching 35 mm diam. after 4 weeks at 25 °C. Colony dense, circular, flattened, surface smooth, with entire edge, velvety to floccose; from above greenish grey to dark green, paler at the edge; from below, black; produced dark brown pigmentation around colony on agar medium.

Material examined: China, Guizhou Province, Guiyang City, Changpoling Forest Park, on submerged decayed stems of bamboo in fresh water stream, 20 August 2021, Y.R. Sun, CL19 (HGUP 22-0810), living culture, GUCC 22-0821.

GenBank numbers: ITS: OR004597, LSU: OP942442, SSU: OP938586, *tef1-α*: OQ995148.

Notes: *Parabambusicola yunnanensis* was introduced by Han et al. (2023) from dead culm of bamboo in terrestrial habitats. Phylogenetically, our isolate GUCC 22-0821 clusters together with *P. yunnanensis* ZHKUCC 22-0290 by 100% ML and 1.00 BI support (Fig. 37). Morphologically, GUCC 22-0821 shares similar ascomata and ascospore characters with ZHKUCC 22-0290, but shorter asci (85–130 µm vs 130–180 µm). This may be caused by the different habitats. In addition, the nucleotide pairwise comparison of LSU and SSU sequences showed no base pair difference and the ITS sequence showed only two base pair differences. However, our collection was obtained from aquatic habitat. We identified our collection as *Parabambusicola yunnanensis* and described and illustrated here.

Pseudomultiseptospora Phookamsak, Rajeshk., Karun. & Wijayaw., ***gen. nov.***

Index Fungorum number: IF559658, *Facesoffungi number*: FoF 10840

Etymology: based on the morphological similarity with *Multiseptospora.*

Saprobic on grass. **Sexual morph**: *Ascomata* solitary to gregarious, scattered, immersed, visible as raised, black dots on host surface, uni-loculate, globose to subglobose, glabrous, ostiole, with minute papilla. *Peridium* inner layers comprise compressed, hyaline, cells of *textura prismatica*, outer layers comprising brown to dark brown cells of *textura angularis*. *Hamathecium* composed of dense, cellular pseudoparaphyses, septate, slightly constricted at the septa, anastomosing among the asci, embedded in a hyaline gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, broadly cylindric-clavate to clavate, subsessile to short pedicellate, apically rounded, with an indistinct ocular chamber. *Ascospores* overlapping 3–4-seriate, initially hyaline, becoming brown to dark brown at maturity, fusiform, with slightly rounded ends, slightly curved, septate, not constricted at the septa, smooth-walled, surrounded by thin, mucilaginous sheath, with small appendages at both ends.

Notes: The genus *Multiseptospora* Phookamsak & K.D. Hyde was introduced in Liu et al. (2015) to accommodate a single species *M. thailandica* Phookamsak & K.D. Hyde which was collected on *Thysanolaena maxima* Kuntze. The genus was accommodated in the Pleosporales genera *incertae sedis* (Liu et al. 2015). However, Tanaka et al. (2015) placed the genus *Multiseptospora* in Parabambusicolaceae based on its phylogenetic relationships. Li et al. (2016) introduced the second species *M. thysanolaenae*. Our multi-locus sequence analyses (Fig. 35) delineated that *M. thysanolaenae* distantly related to *Multiseptospora* sensu stricto. The morphological comparison of *M. thysanolaenae* with *M. thailandica* also supported their distant affinity. Therefore, we propose a new genus *Pseudomultiseptospora*, for *M. thysanolaenae* as *Pseudomultiseptospora thysanolaenae*.

Type species: *Pseudomultiseptospora thysanolaenae* (Phookamsak, Ariyawansa & K.D. Hyde) Phookamsak, Rajeshk., Karun. & Wijayaw.

Pseudomultiseptospora thysanolaenae (Phookamsak, Ariyawansa & K.D. Hyde) Phookamsak, Rajeshk., Karun. & Wijayaw., ***comb. nov.***

Basionym: *Multiseptospora thysanolaenae* Phookamsak, Ariyawansa & K.D. Hyde, in Li et al., Fungal Diversity 78: 1–237 [46] (2016)

Index Fungorum number: IF559659; *Facesoffungi number*: FoF 01660; Fig. 38

Prologue and illustration: in Fungal Diversity 78: 1–237, 46 pp, 2016; Fig. 27, 47pp

Holotype: MFLU 11-0238

Saprobic on *Thysanolaena maxima* Kuntze. **Sexual morph**: *Ascomata* 190–270 µm high, 300–350 µm diam., gregarious, scattered, immersed, visible as raised, black dots on host surface, uni-loculate, globose to subglobose, glabrous, ostiole central, with minute papilla. *Peridium* 12–40 µm wide, thin- to thick-walled, slightly thick at the sides towards apex, composed of several layers of flattened, pseudoparenchymatous cells, inner layers comprising flattened, hyaline cells, arranged in a *textura prismatica*, outer layers comprising brown to dark brown cells, arranged in a *textura angularis*. *Hamathecium* composed of dense, 1.8–4 µm wide, cellular pseudoparaphyses, slightly constricted at the septum, anastomosing among the asci, embedded in a hyaline gelatinous matrix. *Asci* (93–)100–120(–143) × (26–)28–32(–35) µm ($\bar{x} = 114.3 \times 30.4$ µm, n = 30), 8-spored, bitunicate, fissitunicate, broadly cylindric-clavate to clavate, subsessile to short pedicellate, apically rounded, with an indistinct ocular chamber. *Ascospores* (55–)60–65(–73) × (8–)9–11(–13) µm ($\bar{x} = 64.6 \times 10.5$ µm, n = 30), overlapping 3–4-seriate, initially hyaline, becoming brown to dark brown at maturity, fusiform, with slightly rounded ends, slightly curved, (6–)7-septate, not constricted at the septa, smooth-walled, surrounded by thin, mucilaginous sheath, with small appendages at both ends. **Asexual morph**: Undetermined.

Material examined: Thailand, Chiang Mai Province, Doi Suthep-Pui, on dead leaf sheath of *Thysanolaena maxima* (Poaceae), 5 June 2011, R. Phookamsak, RP0118 (MFLU 11-0238, **holotype**), ex-type culture MFLUCC 11-0202.

GenBank numbers: LSU: NG_059655; SSU: NG_063600; *tef*1-*α*: KU705658

Notes: Both *Multiseptospora thysanolaenae* and *M. thalandica* comprise multi-septate ascospores and host association with *Thysanolaena maxima*. However, *M. thysanolaenae* significantly differs from *M. thailandica* by its glabrous ascostromata with brown ascospores. *Pseudomultiseptospora thysanolaenae* has larger ascomata, asci and ascospores than *Multiseptospora thailandica*, but has less ascospore septation (10–11-septate in *M. thailandica*, 6–7-septate in *P. thysanolaenae*). A concatenate analysis of LSU and *tef*1-α formed a paraphyletic lineage of *M. thysanolaenae* (distant from its type *M. thailandica*) that endorse the recombination of new genus as *Pseudomultiseptospora* that typified by *P. thysanolaenae* comb. nov.

Pleosporaceae Nitschke

Pleosporaceae is a specious family distributed worldwide, especially in tropical regions (Ariyawansa et al. 2015b). The species in this family are saprobes, pathogens and endophytes on various plants as well as opportunistic human pathogens (Kodsueb et al. 2006; Hongsanan et al. 2020a, b). *Alternaria*, *Bipolaris*, phoma-like, and *Stemphylium* are more common asexual morphs in Pleosporaceae Currently there are 23 accepted genera in Pleosporaceae.

Alternaria Nees

Alternaria species are ubiquitous and often isolated from plants, soil, air, dust, and wet surfaces (Rotem 1994; Woudenberg et al. 2013). Many *Alternaria* species can infect commercial crop plants and cause diseases leading to economic losses (Chaerani and Voorrips 2006; Logrieco et al. 2009). This genus is characterized by dark brown, multicelled conidia with transverse and longitudinal septa. Conidia commonly occur in chains or sometimes remain solitary and usually contain an apical beak or tapering apical cells (Elliott 1917). *Alternaria* species produce a variety of secondary metabolites that act as phytotoxins or mycotoxins (Thomma 2003; Lawrence et al. 2016; Li et al. 2023).

Alternaria alternata (Fr.) Keissl., Beih. bot. Zbl., Abt. 2 29: 434 (1912)

Index Fungorum number: IF119834; *Facesoffungi number*: FoF 03825; Fig. 39

Basionym: *Torula alternata* Fr., Syst. mycol. (Lundae) 3(2): 500 (1832)

Neotype: L 910.262-129 (Designated by Simmons 1967); *Epitype*: CBS 916.96 (Designated by de Hoog and Horré 2002).

Pathogenic caused leaf spot of *Impatiens balsamina* L. **Sexual morph**: The detailed characterization offered

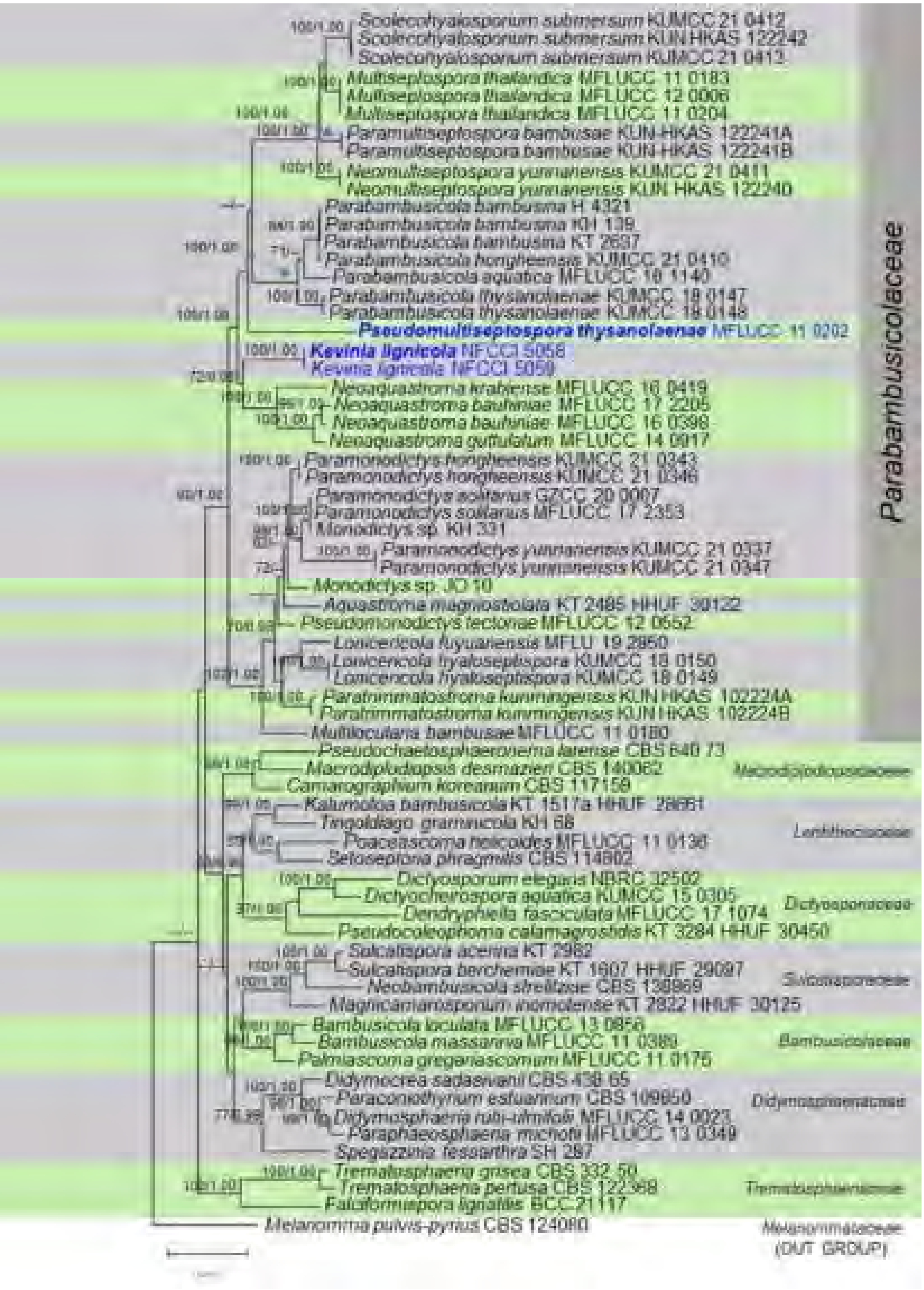


Fig. 35 The best scoring RAxML tree for the combined ITS, LSU and *tef*1-α sequence data of Parabambusicolaceae and allied families is shown. The topology and clade stability of the combined gene analyses were not significantly different from the single gene analyses. The matrix had 1036 distinct alignment patterns with 19.45% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.211898, C = 0.289868, G = 0.265372, T = 0.232861; substitution rates AC = 1.185503, AG = 2.613342, AT = 1.743890, CG = 0.861391, CT = 5.838493, GT = 1.0; gamma distribution shape parameter α = 0.648723. Bootstrap support for ML equal to or greater than 70%, Bayesian posterior probabilities (PP) equal to or greater than 0.88 are shown as ML/PP at the nodes. The tree is rooted to *Melanomma pulivis-pyrius* CBS 124080. The newly generated sequences are indicated in blue bold

by Ariyawansa et al. (2015b). **Asexual morph**: *Hyphae* 3.3–6.7 µm ($\bar{x}$ = 5.0 µm, n = 20), superficial or submerged, pale brown, branched, smooth to verruculose, septate. *Conidiophores* 3.4–67.7 × 3.1–5.6 µm ($\bar{x}$ = 38.6 × 4.7 µm, n = 20), solitary, simple or branched, brown, multi-septate, with a single terminal conidiogenous loci. *Conidia* 7.3–26.7 × 6.8–14 µm ($\bar{x}$ = 17.1 × 10.7 µm, n = 50), solitary or in branched chains of 20 or more, first 1–2 conidia in each chain longer than others, straight, ellipsoidal or ovoid, pale to dark brown to olivaceous green, with smooth outer wall, some muriform, usually with 1–6-transverse septa and 0–3-longitudinal septa, rounded apex, conidial beaks pale brown to subhyaline, not branched, 9.1–27.2 × 3.4–4.5 µm ($\bar{x}$ = 16.2 × 4.1 µm, n = 20).

Culture characteristics: Colonies on PDA reached a 40 mm diameter in the dark after 2 weeks at 25 °C. Initially, the colony was grey, dense, circular, with an entire edge, becoming creamy white, slightly raised at the center and greenish grey towards margin after 2 weeks, and reverse light brown. Two months old cultures on the WA sporulated with grey to dark, chained conidia and greyish green, septate and branched hyphae.

Material examined: China, Sichuan Province, Pengzhou City, Huilonggou, on fresh leaves of *Impatiens balsamina* (Balsaminaceae), N31° 17′ 34, E103° 4′ 64, 28 July 2021, Y. Chen, HLG661 (HUEST 21.0017), living culture, UESTCC 21.0017.

Host and distribution: Causing leaf spot on *Fagopyrum tataricum* (L.). Gaertn. (Li et al. 2021), *Rumex vesicarius* L. (Sankar et al. 2012), as well as various hosts worldwide (Mirkova and Konstantinova 2003; Bajwa et al. 2010; Noelting et al. 2011).

GenBank numbers: ITS: OL741379, *tef1-α*: ON411269, *rpb2*: OL742706, *gapdh*: ON411271.

Notes: *gapdh*, ITS, *rpb2*, and *tef*1-α sequences of our collection (HUEST 21.0017) give *Alternaria* species as the closest matches with NCBI. Our isolate clusters with the epitype strain of *A. alternata* (CBS 916.96). Our collection is morphologically similar to the holotype of *A. alternata* by its chained conidia, hypha, and colony characteristics on PDA (Woudenberg et al. 2013). Therefore, we identified our isolate as *A. alternata* and this is the first record of *A. alternata* from *Impatiens balsamina* (Fig. 40).

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray.

Tetraplosphaeriaceae was introduced with *Tetraploa* Berk. & Broome as the type genus (Tanaka et al. 2009). Members of Tetraplosphaeriaceae are characterized by massarina-like sexual morphs with hyaline, 1(–3)-septate ascospores and/or tetraploa**-**like asexual morphs with several setose appendages (Tanaka et al. 2009). There are seven genera accepted in this family as *Ernakulamia*, *Polyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Shrungabeeja*, *Tetraploa* (≡*Tetraplosphaeria*) and *Triplosphaeria* (Tanaka et al. 2009; Tibpromma et al. 2018; Dong et al. 2020). Tetraploa-like species have existed since Miocene to the Late Devonian (–5.33 to 358.9 Million years) (Nuñez Otaño et al. 2022).

Polyplosphaeria Kaz. Tanaka & K. Hiray.

Polyplosphaeria is typified by *P. fusca* Kaz., Tanaka & K. Hirayama and species in this genus are saprobes which are characterized by globose ascomata surrounded by numerous, brown hyphae and piricauda-like conidia (Tanaka et al. 2009). *Polyplosphaeria xishuangbannaensis* was transferred to *Ernakulamia* Subram. by Dong et al. (2020). Currently, there are four species listed in this genus (Species Fungorum 2023). We introduce a new *Polyplosphaeria* species in this study.

Polyplosphaeria nigrospora Kular., & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900418; *Facesoffungi number*: FoF 14173; Fig. 41

Etymology: based on the black conidia.

Saprobic on dead stem of unidentified plant. **Sexual morph**: Undetermined. **Asexual morph**: Hyphomycetous. *Colonies on natural substrate* solitary, scattered, as black spots. *Hyphae* superficially spreading over the substrate, dark brown. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* micronematous, monoblastic, forming directly on creeping hyphae, holoblastic, integrated, terminal, determinate, connected to base of conidia, with guttules, hyaline. *Conidia* 60–70 × 45–65 µm ($\bar{x}$ = 68 × 57 µm, n = 20), globose to subglobose, pyriform or irregular, solitary, black, verrucose at base, with unbranched, brown setose appendages at base and almost hyaline at apex, setose appendages on surface in two forms; long appendages 40–65 × 3–4 µm ($\bar{x}$ = 55 × 3.6 µm, n = 10), thick-walled, 4-septate, arising from apical part of conidia; short appendages 30–50 × 3.5–5 µm ($\bar{x}$ = 40 × 4 µm, n = 10), aseptate, thin-walled, arising eccentrically from conidial base.

Culture characteristics: Colonies on PDA reaching 4 cm diam. after 14 days in dark at 25 °C, irregular, flat, wavy margin and zonation with bluish brown, inner zone comprises white aerial, mycelial clots; outer zone comprises pale brown, filiform hyphae forming wings-like pattern; reverse black with brown margin, sporulate after 14 days.

Material examined: China, Guangdong Province, Guangzhou City, Nansha District, Huangshan Lu Forest Park (22° 78′ 74.2″ N 113° 58.4′ 21″ E), dead stem of unidentified plant, 18 July 2021, N.D. Kularathnage, NDK 13–2 (MHZU 22-0136, **holotype**), ex-type cultures ZHKUCC 22-0132, ZHKUCC 22-0134.

GenBank numbers: ITS: OR164935, OR164936; LSU: OR164963, OR164964.

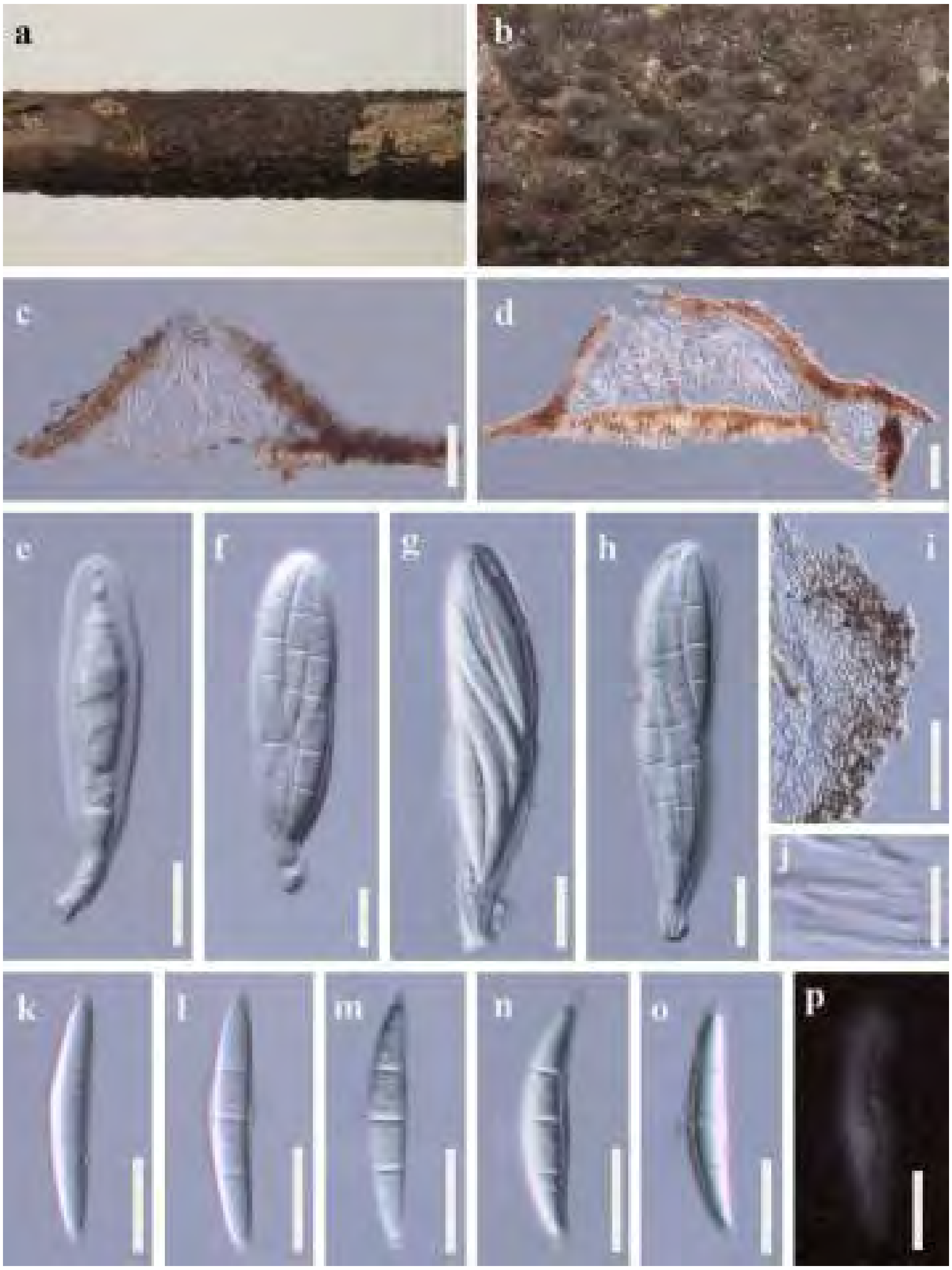


Fig. 36 ***Parabambusicola yunnanensis*** (HGUP 22-0810). **a, b** Appearance of ascomata on host substrate. **c**, **d** Section through ascoma. **e**–**h** Asci. **i** Peridium. **j** Pseudoparaphyses. **k**–**o** Ascospores. **p** Ascospores stained in Indian ink. Scale bars: c, d = 100 µm, e–h, k–p = 20 µm, i = 50 µm, j = 10 µm

Notes: The combined gene analyses of ITS, LSU, SSU, *tef1-α* and *β-tubulin* (Fig. 42) show that our isolates clustered with the type strain of *Polyplosphaeria pandanicola* forming a clade with ML/BI = 100%/1.00 support. There are 4.08%, and 0.56% base pair differences in ITS and LSU. Our collection differs from *P. pandanicola* by its solitary, black, highly-melanized, setose conidia with thick-walled, 4-septate, long appendages (40–65 µm) and aseptate, thin-walled, short appendages (35–50 µm), while *P. pandanicola* has gregarious, brown to dark brown, less-melanized, setose conidia with 4–6-septate, long (60–105 µm) appendages and 0–2-septate, short (20–35 µm) appendages. Setae of our collection are equal in width, while long setae of *P. pandanicola* are wider at the apex and the short setae are wider at the base. Therefore, we introduce this collection as *Polyplosphaeria nigrospora.*

Tetraploa Berk. & Broome

Tetraploa was introduced by Berkeley and Broome (1850) to accommodate *T. aristata* as the type species. *Tetraploa* species are characterized by globose to subglobose, glabrous, papillate ascomata, fissitunicate, cylindrical to clavate, short-stalked, 8-spored asci, and fusiform, hyaline, 1-septate ascospores with mucilaginous appendage-like sheaths (Tanaka et al. 2009). The asexual morphs have micronematous conidiophores, monoblastic conidiogenous

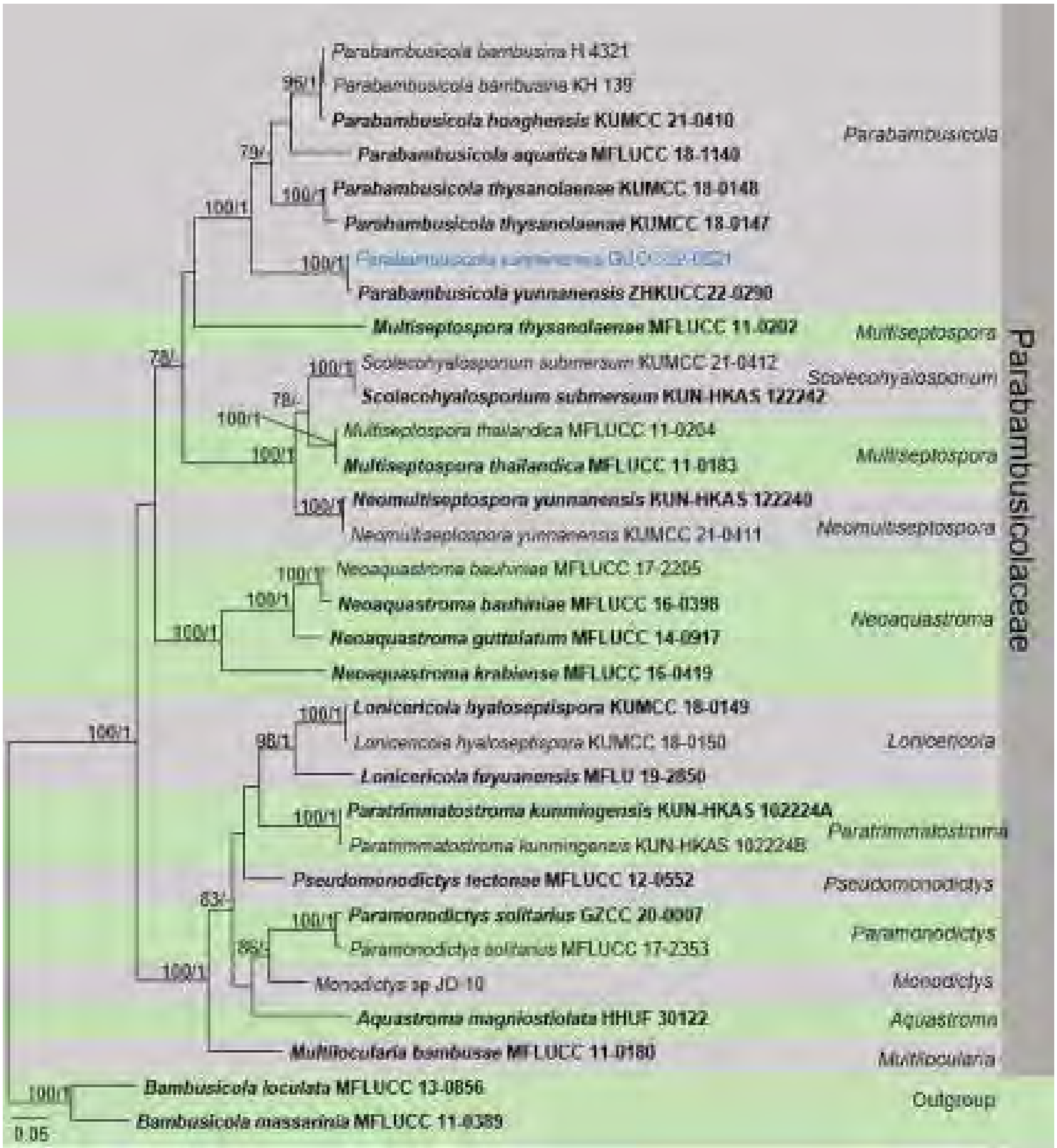


Fig. 37 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *tef1-α* sequence data. Thirty one taxa were included in the combined gene analyses, which comprised 3409 characters (LSU = 838 bp, SSU = 1,002 bp, ITS = 699 bp, *tef*1-α = 870 bp). The best scoring RAxML tree with a final likelihood value of − 24,627.042646 is presented. Bootstrap support for ML equal to or greater than 75% and BI equal to or greater than 0.95 are given above the nodes. *Bambusicola loculate* (MFLUCC 13-0856) and *B. massarinia* (MFLUCC 11-0389) were used as the outgroup taxa. The newly generated sequence is indicated in blue. The ex-type strains are indicated in bold

cells, and short cylindrical, brown conidia with four setose appendages at the apex and conidia composed of four columns (Tanaka et al. 2009; Hyde et al. 2013; Hongsanan et al. 2020a, b; Li et al. 2020). Currently, 17 *Tetraploa* species are listed in Species Fungorum (2023). We introduce a new *Tetraploa* species and record a new host association of *T. nagasakiensis*.

Tetraploa obpyriformis C.F. Liao, K.D. Hyde & Doilom, ***sp. nov.***

Index Fungorum number: IF559272; *Facesoffungi number*: FoF10586; Fig. 43

Etymology: referring to the obpyriform conidia character of this fungus.

Saprobic on dead stem of *Tripidium arundinaceum* (Retz.) Welker, Voronts. & E.A. Kellogg. **Sexual morph**:

Fig. 38 ***Pseudomultiseptospora thysanolaenae*** (MFLU 11-0238, **holotype**). **a** Appearance of ascomata on host substrate. **b** Vertical cross-section of ascoma. **c** Section of peridium. **d**–**f** Asci. **g**–**j** Ascospores. Scale bars: b = 50 μm, c = 20 μm, d = 5 μm, e–f = 20 μm, g–j = 10 μm

Undetermined. **Asexual morph**: *Colonies* pale brown to black, effuse, superficial on the host substrate. *Mycelium* pale brown, branched, aseptate. *Conidiophores* absent. *Conidigenous cells* monotretic, intercalary, clavate, aseptate, verrucose. *Conidia* 30–47 × 17–39 μm ($\bar{x} = 36 \times 26$ μm, n = 30), obpyriform, dark green to light brown, verrucose at base, composed of four columns, 2–4-septate in each columns, 1–5 appendages, mostly 4 appendages. *Appendages*

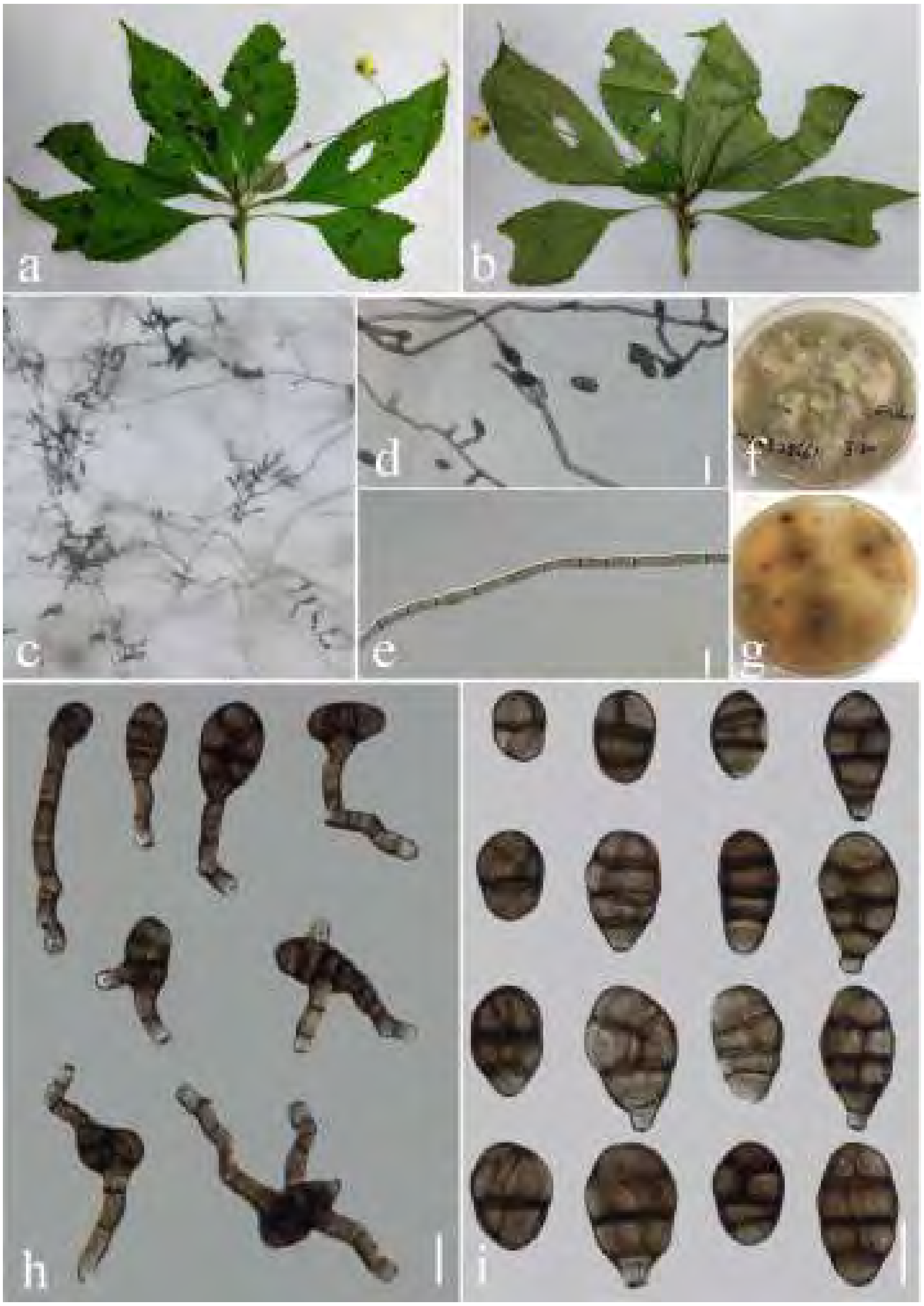


Fig. 39 ***Alternaria alternata*** (HUEST 21.0017). **a, b** Diseased leaves infected by *A. alternata* front and reverse view. **c** Sporulation on the water agar. **d** Conidia and conidiophores attached to hyphae. **e** Hyphae. **f** Reverse view of colony on PDA. **g** Surface view of colony on PDA. **h** Conidia, conidiophores and conidiogenous cells. **i** Conidia. Scale bars: d = 20 µm; e, h, i = 10 µm

50–160 µm long ($\overline{x}$ = 98 µm, n = 30), 6–10 µm wide at the base, 2–4 µm wide at the apex, divergent, straight or slightly flexuous, smooth-walled, unbranched, gradually tapering to the tip, brown to dark brown, subhyaline at the apex, 4–12-septate, smooth-walled.

Culture characteristics: Colonies on PDA at 25 ± 2 ℃, after 17 days reaching to 40–45 mm, floccose, convex or dome-shaped, mucoid or oil droplets at the center, light gray to dark green and almost glabrous towards the periphery, with a fimbriate margin; reverse blackish green to light brown; no pigment production.

Material examined: China, Yunnan Province, Kunming City, from dead stem of *Tripidium arundinaceum* (Poaceae), 4 July 2020, C.F. Liao, (KUN–HKAS 107637, holotype), ex-type culture KUMCC 21-0011.

GenBank numbers: ITS: OL473558, LSU: OL473554, SSU: OL473557, *β tubulin*: OL473558, *tef*1-*α*: OL505598.

Notes: In the multigene phylogenetic analyses of ITS, LSU, SSU, *β tubulin*, and *tef1-α* our collection (KUMCC 21-0011) grouped with *Tetraploa bambusae* (KUMCC 21-0844) and an undescribed *Tetraploa* species (KT 1684) with ML = 92% and BI = 0.99 statistical support (Fig. 45).

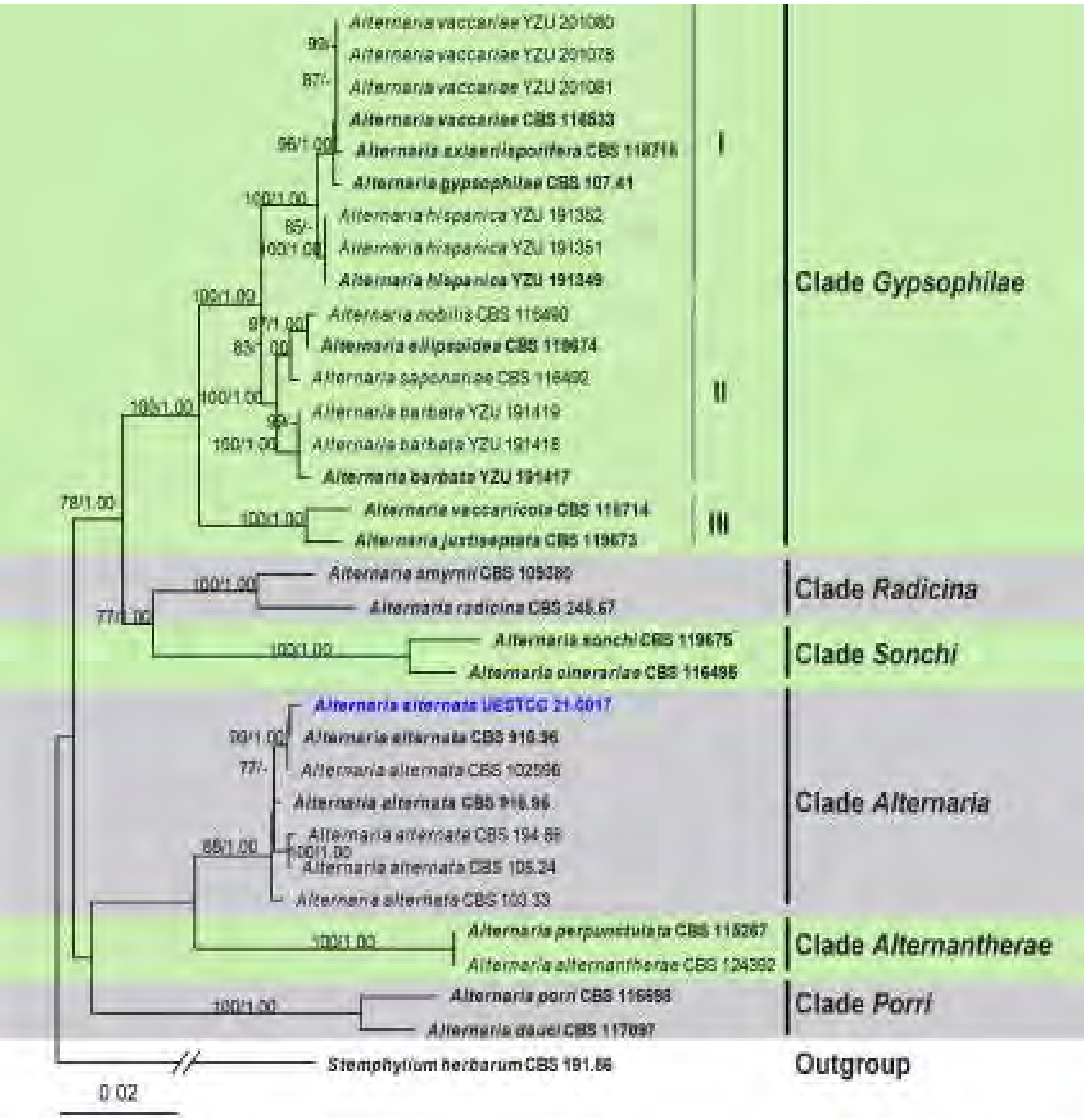


Fig. 40 The best scoring RAxML tree with a combined dataset of *gapdh*, ITS, *rpb2*, and *tef1-α* sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses and no significant differences. The tree is rooted with *Stemphylium herbarum* (CBS 191.86). The matrix had 476 distinct alignment patterns with 1.86% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.245, C = 0.282, G = 0.241, T = 0.233; substitution rates AC = 1.201041, AG = 3.391612, AT = 1.290665, CG = 0.667892, CT = 7.923937, GT = 1.0; gamma distribution shape parameter α = 0.263849 and final likelihood value of − 8057. Ex-type strains are in bold and newly generated sequences are in blue bold. Bootstrap support for ML ≥ 75% and BI ≥ 0.95 are given at the nodes. The scale bar presents the expected number of nucleotide substitutions per site

A comparison of LSU, ITS, SSU and *β tubulin* sequences of our isolate showed 0.36%, 5.15%, 0.6% and 5.67% nucleotide differences with *T. bambusae* and the nucleotide differences between our isolate and *Tetraploa* sp. (KT 1684) are 0.48%, and 0.7% for LSU and SSU.

Our collection differs from *T. bambusae* in having larger conidia (30–47 × 17–39 µm *vs* 21–33 × 17–26 µm) and longer appendages (50–160 µm *vs* 15–40 µm). Additionally, our collection has obpyriform, dark green to pale brown conidia, while *T. bambusae* has obovoid to turbinate, brown to dark brown conidia (Phookamsak et al. 2022). *Tetraploa* sp. (KT 1684) has not been described (Tanaka et al. 2009). Thus, we could not compare the morphology of our collection with *Tetraploa* sp. (KT 1684). We introduced our collection as *T. obpyriformis.*

Tetraploa nagasakiensis (Kaz. Tanaka & K. Hiray.) Kaz. Tanaka & K. Hiray., Fungal Divers 63: 253 (2013)

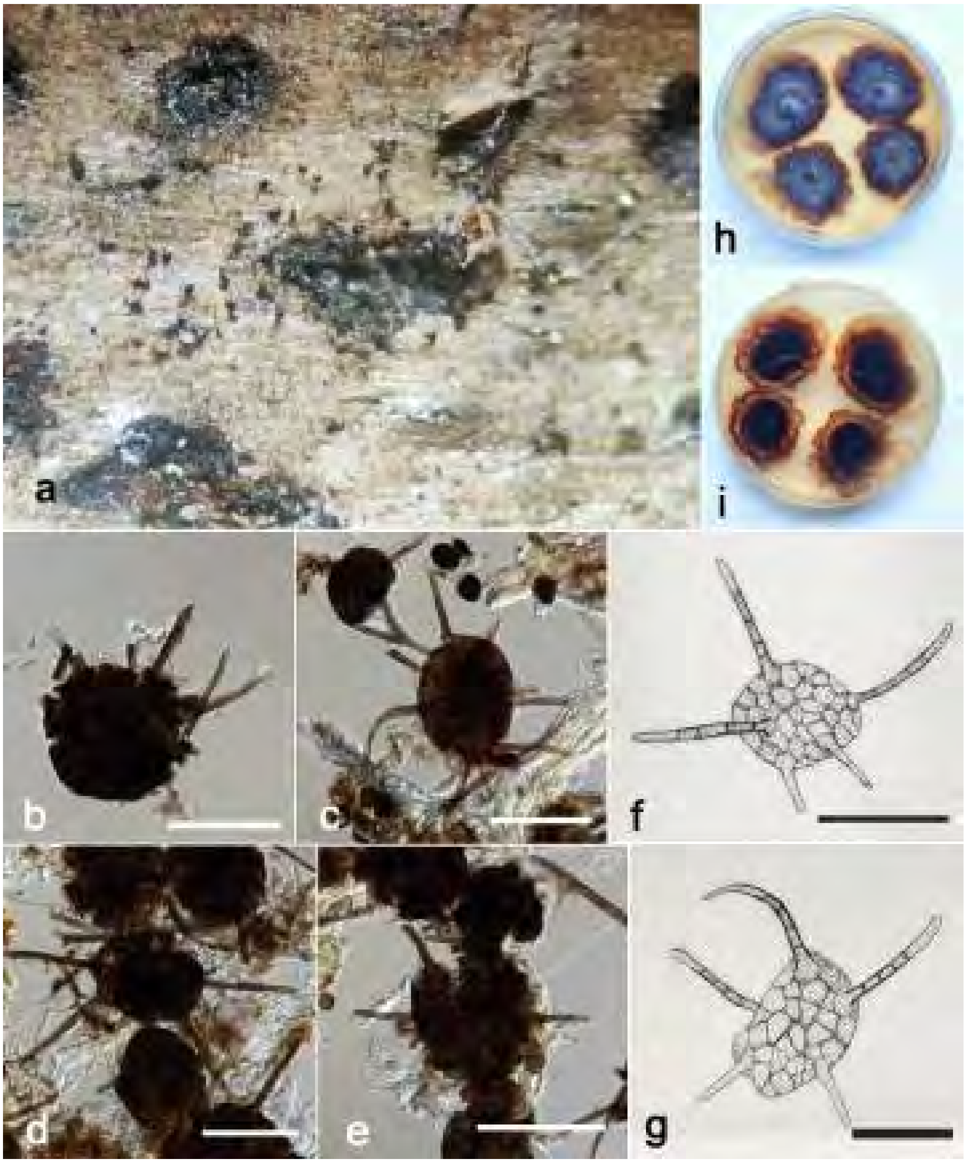


Fig. 41 ***Polyplosphaeria nigrospora*** (MHZU 22-0136, **holotype**). **a** Colonies on substrate. **b**–**g** Conidia. **h** Surface view of colony on PDA. **i** Reverse view of colony on PDA. Scale bars: b–e = 50 µm

Basionym: *Tetraplosphaeria nagasakiensis* Kaz. Tanaka & K. Hiray., in Tanaka et al., Stud Mycol 64: 180 (2009)

Index Fungorum number: IF801978; *Facesoffungi number*: FoF05080; Fig. 44

Saprobic on dead stem of *Hedychium coronarium* J. Koenig. **Sexual morph**: *Ascomata* 150–210 µm high × 140–250 µm diam. ($\bar{x}$ = 180 × 205 µm, n = 10), solitary or scattered, coriaceous, immersed to erumpent, visible as black dots on the host surface, unilocular, globose to subglobose, brown to dark brown, ostiolate, with minute papilla, filled with short, hyaline periphyses. *Peridium* 16–25 µm wide, comprising light brown cells of *textura angularis*, fusing at the outside indistinguishable from the host tissues. *Hamathecium* comprising 1.2–1.8 µm wide, cylindrical to filiform, septate, branched, pseudoparaphyses. *Asci* 100–115 × 14–17 µm ($\bar{x}$ = 108 × 15 µm, n = 20), 8-spored, bitunicate, clavate to cylindrical, short pedicellate, with ocular chamber. *Ascospores* 28–34 × 4–5 µm ($\bar{x}$ = 30 × 4.2 µm, n = 30), overlapping 1–2-seriate, hyaline, narrowly fusiform with acute ends, slightly curved, 1-septate, constricted at the septum, smooth-walled. **Asexual morph**: Undetermined.

Culture characteristics: *Colonies* on PDA, 16–20 mm diam. after three weeks, colonies from above: medium dense, circular, flat, slightly raised, surface smooth with crenate edge, with smooth aspects, grey to dark brown at the margin, light brown in the center; reverse: dark brown to black at the margin, brown to grey in the center.

Material examined: China, Yunnan Province, Baoshan, dead stem of *Hedychium coronarium* (Zingiberaceae), 22 August 2017, D.S. Tennakoon, DS009 (MFLU 18-0089); living culture, MFLUCC 17-2647.

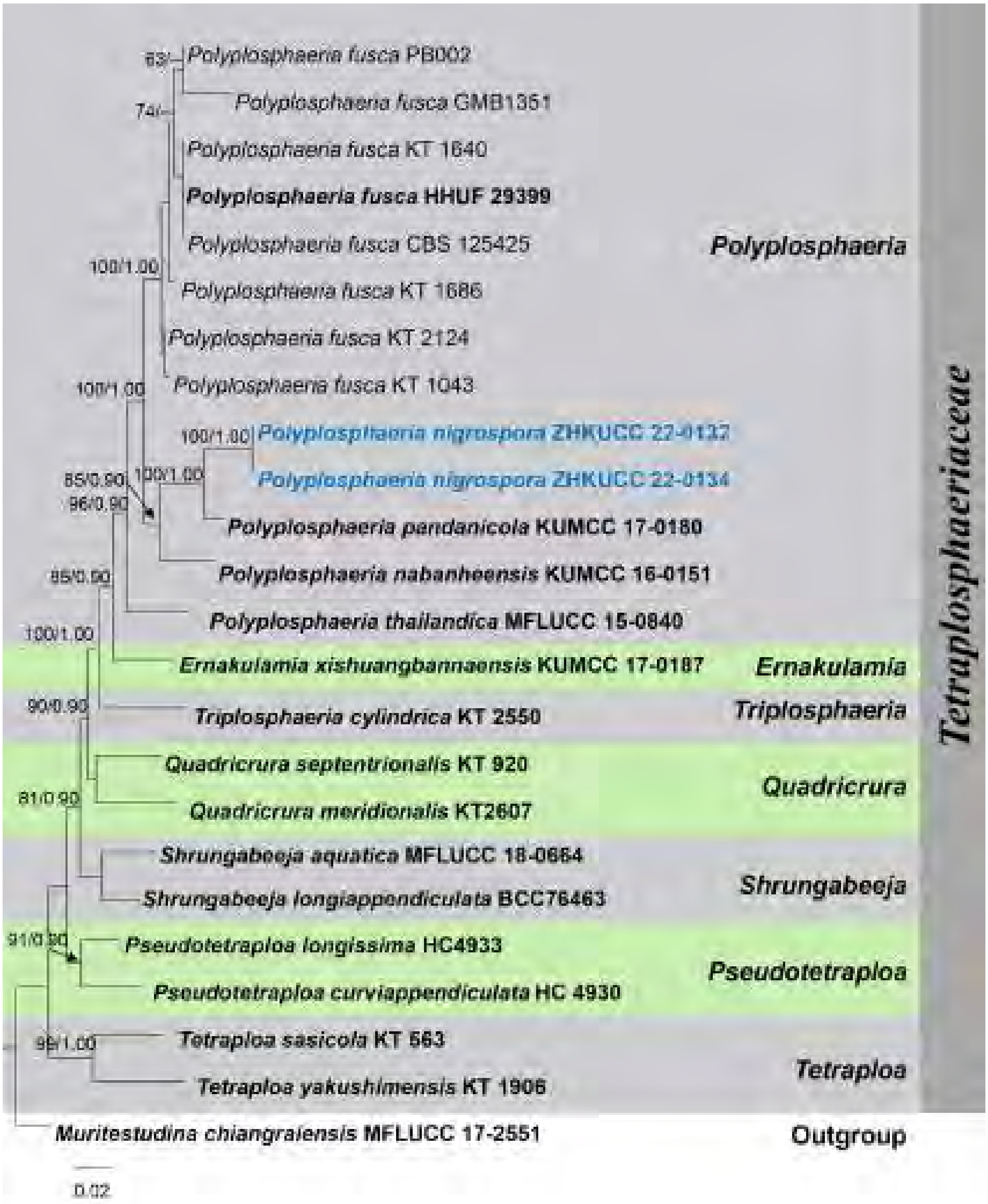


Fig. 42 Phylogram generated from maximum likelihood analyses based on combined ITS, LSU, SSU and *tef1-α* sequence data which comprised 3137 characters (ITS = 539, LSU = 879, SSU = 764, *tef1-α* = 306, *β-tubulin* = 635). The best scoring RAxML tree with a final likelihood value of − 11,531.618251 is presented. The matrix had 782 distinct alignment patterns, with 22.63% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.229550, C = 0.267919, G = 0.242735, T = 0.259795; substitution rates: AC = 2.192656, AG = 3.421541, AT = 1.919197, CG = 1.287792, CT = 8.523851, GT = 1.0; gamma distribution shape parameter α = 0.154399. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (the rounding of values to 2 decimal proportions) from Bayesian inference analyses are labelled at each node. Ex-type strains are in bold, while the new isolate is indicated in blue bold. The tree is rooted to *Muritestudina chiangraiensis* (MFLUCC 17-2551)

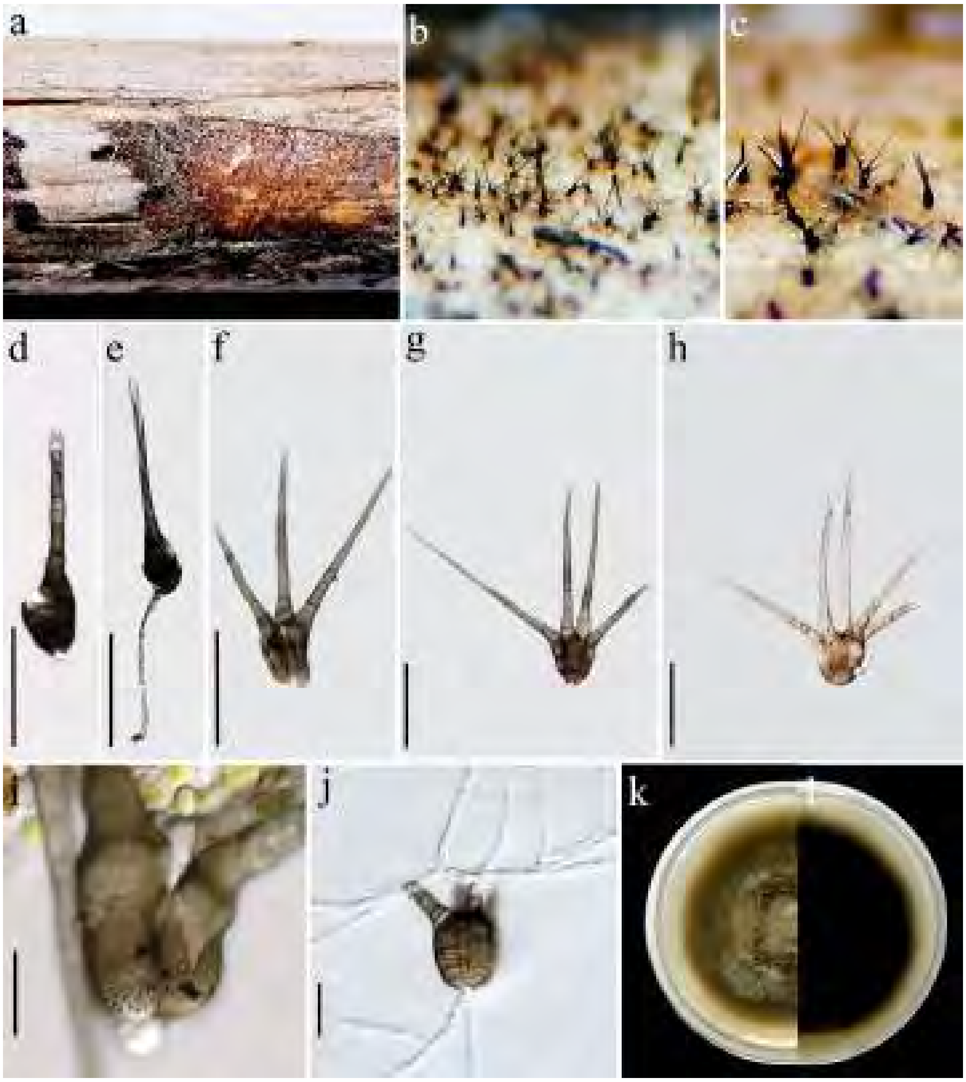


Fig. 43 ***Tetraploa obpyriformis*** (KUN-HKAS 107637, **holotype**). **a–c** Conidia on host substrate. **d–h** Conidia. **i** Conidia with conidiogenous cell. **j** Germinating conidium. **k** Surface view of colony on PDA. **l** Reverse view of colony on PDA. Scale bars: d, i, j = 20 μm, e–h = 50 μm

Hosts and distribution: Bamboo (Poaceae) in China, Japan; *Hedychium coronarium* (Zingiberaceae) in China (Tanaka et al. 2009; Hyde et al. 2019a; this study).

GenBank numbers: ITS: OQ970538, LSU: OQ970466; SSU: OQ970468

Notes: *Tetraplosphaeria nagasakiensis* was introduced by Tanaka et al. (2009) from culms of bamboo in Japan. Subsequently, this species was synonymized by Hyde et al. (2013) as *Tetraploa nagasakiensis*. This has been recorded from dead bamboo branches in China as well (Hyde et al. 2019a). The morphological characteristics of our collection (MFLU 18-0089) fit well with the *Tetraploa nagasakiensis* in having immersed to erumpent, unilocular, globose to subglobose, coriaceous ascomata, clavate to cylindrical, short pedicellate asci and hyaline, narrowly fusiform, 1-septate ascospores (Tanaka et al. 2009; Hyde et al. 2019a). Multigene phylogeny (Fig. 45) also indicate that our collection (MFLU 18-0089) clusters with *Tetraploa nagasakiensis* in 93% ML, 91% MP, 0.99 BI support. Therefore, based on both morphology and phylogeny evidence, we introduce our collection as a new host record of *Tetraploa nagasakiensis* from *Hedychium coronarium* (Zingiberaceae).

Thyridariaceae Q. Tian & K.D. Hyde

The family Thyridariaceae was introduced to accommodate the genus *Thyridaria* Sacc., with type species *T. broussonetiae*. This family is characterized by stromatic, pigmented, prosenchymatous tissues, ostioles with a disclike ostiolar tubes, and solitary or gregarious, immersed to erumpent, globose, coriaceous ascomata, in valsoid configurations. Five genera were accepted in this genus as *Neoroussoella*, *Thyridaria*, *Roussoella*, *Roussoellopsis*, and *Parathyridaria*. Thyridariaceae described to date are associated with terrestrial plants, especially bamboo and palm species (Taylor et al. 1999; Jaklitsch and Voglmayr 2016; Tibpromma et al. 2017).

Thyridaria Sacc.

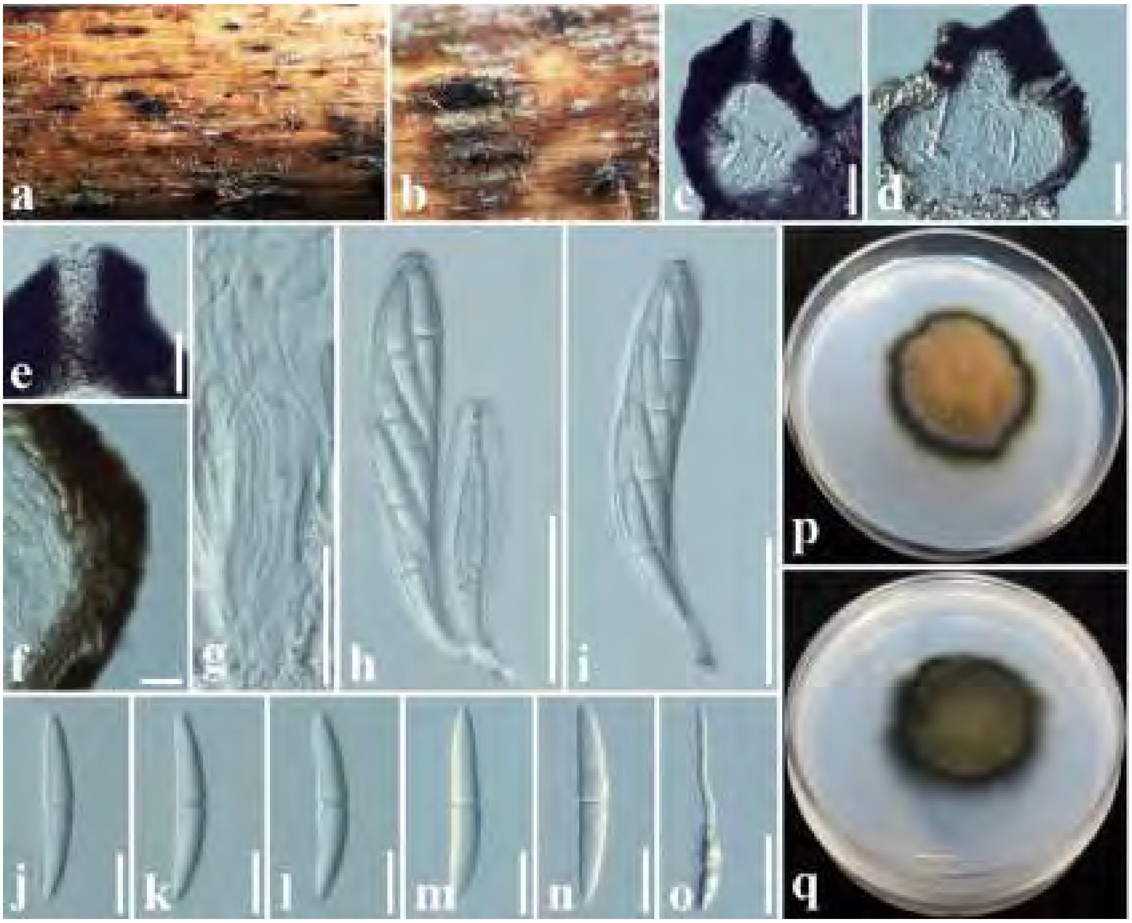


Fig. 44 ***Tetraploa nagasakiensis*** (MFLU 18-0089). **a, b** Appearance of ascomata on substrate. **c, d** Vertical cross-sections through ascomata. **e** Vertical cross-sections through neck region. **f** Peridium. **g** Pseudoparaphyses. **h, i** Asci. **j–n** Ascospores. **o** A germinating ascospore. **p** Colony on PDA from above. **q** Colony on PDA from below. Scale bars: c, d = 80 µm, e = 20 µm, f, j–o = 10 µm, g–i = 50 µm

Thyridaria was introduced by (Saccardo 1875) and *T. broussonetiae* was adopted as the type species (Barr 1990). There are 59 species listed in the Index Fungorum (2023). This genus is characterized by immersed to erumpent, solitary or gregarious ascomata in valsoid arrangement, a well-developed ostiolar neck, cylindrical asci and yellowish to dark-brown, ellipsoid or fusoid, verruculose ascospores with transversal, eu- and distosepta. The asexual morphs reported as coelomycetous taxa that form solitary or clustered pycnidia (Boonmee et al. 2021).

Thyridaria broussonetiae (Sacc.) Traverso, Fl. ital. crypt., Pyrenomycetae (Florence) 1(2): 301 (1906)

Index Fungorum number: IF569945; *Facesoffungi number*: FoF 08376; Fig. 46

Holotype: not indicated. W 2009-01175 (Lectotype designated by Jaklitsch and Voglmayr 2016).

Saprobic on the bark of *Citrus maxima* Merr. **Sexual morph**: *Stromata* 0.5–1.0 mm diam., flaky, solitary or aggregated, yellow or pale brown, lose or dense fluff on the surface, flat circular to convex disc or poolville. *Ascomata* 300–660 µm high, 420–550 µm diam. ($\overline{x}$ = 480 × 500 µm, n = 10), immersed, solitary, part aggregated, subglobose, dark brown to black, central ostiole, with minute papilla. *Ostiole* 20–100 µm filled with black keratinous substance. *Peridium* 20 × 50 µm wide, consists of 5–7-layers of hyaline to brown, cells of *textura angularis* from the inside to the outside. *Hamathecium* of 2–3 µm wide, cylindrical, filamentous, unbranched, hyaline pseudoparaphyses. *Asci* 100–150 × 10–20 µm ($\overline{x}$ = 130 × 15 µm, n = 23), 4–8-spored, cylindric to clavate, slightly curved, with bulbous short pedicels, apically rounded, endotunica thick, wall thin. *Ascospores* 20–30 × 7–11 µm ($\overline{x}$ = 20 × 7 µm, n = 30), uniseriate, ellipsoid to fusiform, ends blunt, straight or slightly curved, pale or light brown when young, blackish-brown at maturity, 3-septate, constricted at the septate, some have obvious guttulate, smooth-walled. **Asexual morph**: Undetermined.

Culture characteristics: Ascospore germinating on PDA within 24 h at room temperature, Colonies on PDA reaching 35 mm diam. after 1 month at 25 °C, circular, white grey at the edge, dull brown to olivaceous brown from the center to edge, mycelium dense and soft. Reverse with dark brown center, light grey edge.

Material examined: China, Guangdong Province, Shaoguan City, Renhua County, Dongtang Town, 25° 3′ 50″ N, 113° 39′ 17″ E, alt. 100 m, on the bark of *Citrus maxima* (Rutaceae), 25 August 2021, Y.H. Yang, (MHZU 22-0064); living culture, ZHKUCC 22-0116, ZHKUCC 22-0117.

Hosts and distribution: Southern Europe: Italy on *Broussonetia papyrifera,* Hungary on *Amorpha fruticose* (Epitype), Croatia on *Hippocrepis emerus* (Jaklitsch and Voglmayr 2016); China on *Citrus maxima* (this study); as *Cucurbitaria broussonetiae* on *Albizzia* sp., *Calycanthus, Chimonanthus*, *Colutea* sp., *Fagus sylvatica*, *Juglans regia*, *Morus* sp., *Prunus padus*, *Rhus* sp. and *Robinia* (Saccardo 1875).

GenBank numbers: ITS: OQ976012, OQ976013; LSU: OQ976019, OQ976020.

Notes: In the multi-gene analysis of ITS, LSU and *tef*1-α gene sequences of *Thyridaria* species indicates that our isolates (ZHKUCC 22-0116, ZHKUCC 22-0116) grouped with the *Thyridaria aureobrunnea* including ex-type strains (CBS 141481) with ML/BI = 100%/1.00 bootstrap support (Fig. 47). Our collection is morphologically similar to the epitype collection of *T. aureobrunnea.* We identified our collection as *T. aureobrunnea* and this is the first record of *T. aureobrunnea* on honey pomelo (*Citrus maxima*).

Versicolorisporium Sat. Hatak., Kaz. Tanaka & Y. Harada

The monotypic genus *Versicolorisporium* was established for a coelomycetous taxon collected in Japan on dead culms of the bamboos (Hatakeyama et al. 2008). The type species of the genus, *V. triseptatum* is characterized by the production of holoblastic, 3-septate, obovoid, versicolored conidia and *Versicolorisporium* is morphologically distinct from other similar taxa in Pleosporales in having the uniloculate pycnidial conidiomata with a periphysate ostiole, lacking paraphyses, and the versicolored conidia without black-banded septa. This study describes a new geographical record of *Versicolorisporium triseptatum.*

Versicolorisporium triseptatum Sat. Hatak., Kaz. Tanaka & Y. Harada, in Sat. Hatak., et al. Mycoscience 49(3):211 (2008).

Index Fungorum number: IF559943; *Facesoffungi number*: FoF 10845; Fig. 48

Saprobic on decaying culms of bamboo. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 150–210 × 240–260 µm ($\bar{x}$ = 173 × 251 µm, n = 10), pycnidial, subepidermal, solitary or gregarious, black, coriaceous, slightly papillate, ostiolate. *Periphyses* short, hyaline. *Conidiomatal wall* 19–43 µm ($\bar{x}$ = 28.4 µm, n = 10) wide, comprise of brown, cells of *textura angularis*. *Conidiophores* reduce to conidiogenous cells. *Conidiogenous cells* formed from the inner layer of the conidiomatal wall, ampulliform to cylindrical, holoblastic, bearing a single terminal conidium. *Conidia* 22–35 × 13–18 µm ($\bar{x}$ = 27.7 × 15.2 µm, n = 22), obovoid, rounded at the apex, truncate at the base, 3–4-septate, with a submedian primary septum, smooth; apical cell 3.5–6.5 µm ($\bar{x}$ = 4.4 µm, n = 20) long, pale brown; second cell from the apex 12–15 µm ($\bar{x}$ = 13.2 µm, n = 20) long, dark brown; third cell 4.5–7.6 µm ($\bar{x}$ = 5.3 µm, n = 20), long, pale brown; basal cell 2.8–4.6 µm ($\bar{x}$ = 3.70 µm, n = 20) long, hyaline.

Culture characteristics: Colonies on PDA at 25 °C in the dark reached 40 mm in diam. after 3 weeks, circular, flat, entire, filamentous, cottony, surface view grey green; reverse dark olive green.

Material examined: China, Sichuan Province, Qionglai City, Nanmuxi (N 30° 19′ 15, E 103° 7′ 39), on decaying culms of *Bambusa* sp. (Poaceae), 24 August 2021, Y. Chen, NMX1222 (HUEST 21.0016), living culture UESTCC 21.0016.

Hosts and distribution: On decaying culms of *Pleioblastus chino* (Franch. & Sav.) Makino and *Sasamorpha borealis* (Hackel.)Nakai. (Poaceae) in Japan (Hatakeyama et al. 2008),on decaying culms of bamboo in Sichuan, China (This study).

GenBank numbers: ITS: OL741378, LSU: OL741318, SSU: OL741381

Notes: *Versicolorisporium triseptatum* is characterized by versicolored conidia formed from holoblastic conidiogenous cells (Hatakeyama et al. 2008). Our collection (HUEST 21.0016) is similar to the holotype of *V. triseptatum* (JCM 14775 = HHUF 28815). The multilocus phylogeny shows that our isolate clustered with the ex-type strain of *V. triseptatum* with MP/BI = 100%/1.00 bootstrap support. Therefore, we identified our isolate (HUEST 21.0016) as *V. triseptatum*, and this is the first report of *V. triseptatum* in China (Fig. 49).

Abrothallales Pérez-Ort. & Suija

The order includes exclusively lichenicolous fungi and was established by Pérez-Ortega et al. (2014). It contains a single family with two genera (Diederich et al. 2018; Wijayawardene et al. 2022).

Lichenoconiaceae Diederich & Lawrey

The family was previously introduced to accommodate a single conidial genus *Lichenoconium* (Lawrey et al. 2011; Hyde et al. 2013). Subsequent phylogenetic analyses revealed that *Abrothallus* and *Lichenoconium* are closely

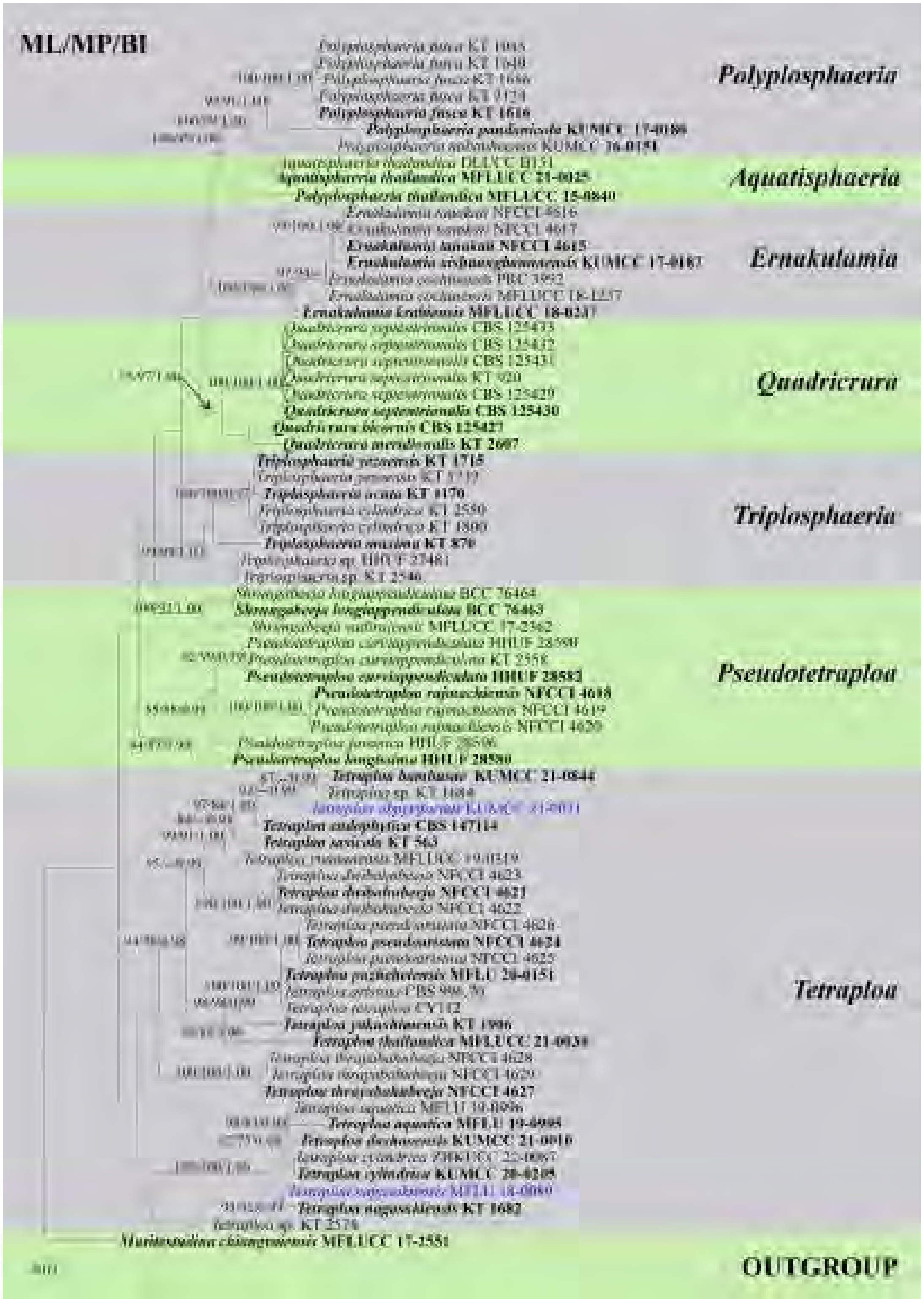


Fig. 45 Phylogram generated from maximum likelihood analyses based on combined LSU, ITS, SSU, *β tubulin* and *tef1-α* sequence data which comprised 3716 characters (LSU = 852, ITS = 571, SSU = 1,336, *β tubulin* = 639, *tef1-α* = 318). The best scoring RAxML tree with a final likelihood value of f − 20,590.306011 is presented. The matrix had 1192 distinct alignment patterns, with 32.10% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.239693, C = 0.252943, G = 0.275644, T = 0.231720; substitution rates AC = 2.413323, AG = 3.943519, AT = 1.709808, CG = 1.421703, CT = 8.021695, GT = 1.0; gamma distribution shape parameter α = 0.164747. Bootstrap support for ML and MP equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled at each node. Ex-type strains are in bold, while the new isolates are indicated in blue bold. The tree is rooted to *Muritestudina chiangraiensis* (MFLUCC 17-2551)

related and the previously monotypic family Abrothallaceae is currently considered to be a synonym of Lichenoconiaceae (Pérez-Ortega et al. 2014; Wijayawardene et al. 2022). However, still further studies including a larger sampling are necessary to finally establish the relationship between both genera.

Abrothallus De Not.

The genus is characterized by having black rounded apothecioid ascomata, frequently covered by greenish or yellowish pruina, bitunicate asci with 2- to 4-celled brown, ornamented ascospores, anastomosed interascal filaments, epiphymenium with granulose pigments and pycnidial anamorph of vouauxiomyces-type (Diederich 2004; Pérez-Ortega et al. 2014). At this moment there are more than 40 accepted species of *Abrothallus* (Diederich et al. 2018). However, as the genus still needs a modern revision and more active sampling in poorly studied regions we may expect much higher diversity. In this study, we introduce a new *Abrothallus* species and a new combination proposed for *Abrothallus usneae* var. *tetraspora* Etayo & Osorio. based on morphology and phylogeny.

Abrothallus altoandinus Flakus, Etayo & Rodr. Flakus, ***sp. nov.***

Index Fungorum number: IF900419; *Facesoffungi number*: FoF 14174; Fig. 50.

Etymology: The epithet refers to the habitat of the new species connected to the higher elevations of the Andes.

Diagnosis: The new species differs from *Abrothallus usneae* in having smaller ascomata (0.1–0.35 mm in diam.) and larger, slightly curved ascospores, composed of unequal cells, with the lower ascospore cell much thinner than the upper one.

Lichenicolous. **Sexual morph**: *Mycelium* immersed, indistinct, I–, K/I–. *Ascomata* apothecioid, superficial, developing directly on the host thallus, black, epruinose, strongly convex, sometimes tuberculate (when mature), strongly constricted at the base, 0.1–0.35 mm in diam., up to 250 µm tall. *Epihymenium* 5–10 µm, dark brown with additional violet pigment, K + emerald greenish, N + greyish. *Exciple* strongly reduced, of few layers of isodiametric to elongated cells, hyaline to pale brown. *Hymenium* 40–65 µm high, hyaline to violet in the upper part, K + emerald green. *Interascal filaments* irregularly branched and sometimes anastomosed, 1–2(–3) µm wide, apical cells slightly widened (up to 5–6 µm wide), brown pigmented. *Hypothecium* 60–80 µm high, pale to dark brown composed of large isodiametric cells forming a paraplectenchymatic tissue. *Asci* 30–60 × 7–22 µm, bitunicate, (4)8-spored, I–, K/I–, broadly clavate, apically widened with evident apical dome. *Ascospores* 1-septated, medium to dark brown, distinctly verrucose, covered by gelatinous cover (especially when younger), narrowly ellipsoid, usually slightly curved, 11–($\bar{x} = 15.1 \pm 1.5$)–19 × 4–($\bar{x} = 5.2 \pm 0.7$)–7 µm, l/b ratio 2–($\bar{x} = 3 \pm 0.5$)–4.2 µm (n = 102), not braking in semi-spores, composed of unequal cells, the lower cell much thinner [(2–)2.5–4(–4.5) µm] than the upper one, slightly constricted near the septum. **Asexual morph**: Undetermined.

Material examined: Bolivia, Department Cochabamba, Tiraque Province, Parque Nacional Carrasco, the crossroad below Cerro Juno, 17° 19′ 50″ S, 65° 43′ 50″ W, 4126 m, open high Andean vegetation, on saxicolous *Usnea durietzii*, 29 November 2014, A. Flakus 25,948 (KRAM-L 73246, **holotype**; LPB **isotype**).

Hosts and distribution: The species occur in Bolivia in the high Andean vegetation where is parasitizing an endemic lichen-forming fungus *Usnea duriezii* growing on siliceous rocks. Ascomata are developed on the main branches and laciniae of *Usnea* and not change the colour of the host thallus.

GenBank numbers: ITS: OR116440

Notes: Our phylogenetic analyses of combined LSU, ITS, SSU and *tef1*-α loci (Fig. 52) revealed that our collection (KRAM-L 73246) is not related to *Abrothallus usneae* s. str., described from Europe and the Portugal specimen described by Pérez-Ortega et al. (2014) has been included into the phylogenetic analyses. Our collection is a parasite on *Usnea durietzii* (Parmeliaceae, Lecanorales). The phylogenetic position of our collection is highly supported within the clade represented by species of *Abrothallus* growing on lichens of the order Peltigerales such as *Erioderma*, *Lobaria*, *Nephroma*, *Pseudocyphellaria* and *Sticta* (Suija et al. 2015).

Our collection is characterized by medium sized, slightly curved ascospores with unequal cells (the lower cell is much larger and thinner than the upper one), 8-spored asci, the presence of violet pigment in ascomata (K + emerald greenish, N + greyish). Diederich (2003) was illustrated the similar shaped ascospores to our collection for *A. pezizicola* which is described from North America on *Cladonia peziziformis*. However, *A. pezizicola* can be easily distinguished by its different host preferences, yellowish pruinose apothecia, olivaceous-green to almost black epihymenium (K + olivaceous, N + brown), and much smaller ascospores (6.5–9 × 2–3 µm) (Diederich 2003).

There were only three taxa of *Abrothallus* known from lichen-forming genus *Usnea* viz. *A. chrysanthus*, *A. usneae* v. *usneae*, and *A. usneae* v. *tetraspora* (Etayo and Osorio 2004; Etayo and van den Boom 2006; Pérez-Ortega et al. 2014; Etayo 2017). Morphologically, our collection is more similar to *Abrothallus usneae* v. *usneae* by presence of 8-spored asci and violet pigment in epihymenium. However, type specimen of *A. usneae* v. *usneae* (Rabenhorst, Lich. europ. 551, W) has much larger ascomata (250–500 µm in diam.), smaller ascospores (11–)12–13(–14) × 4.5–6 µm, and grows mainly on galls of basidiomycete (*Biatoropsis*

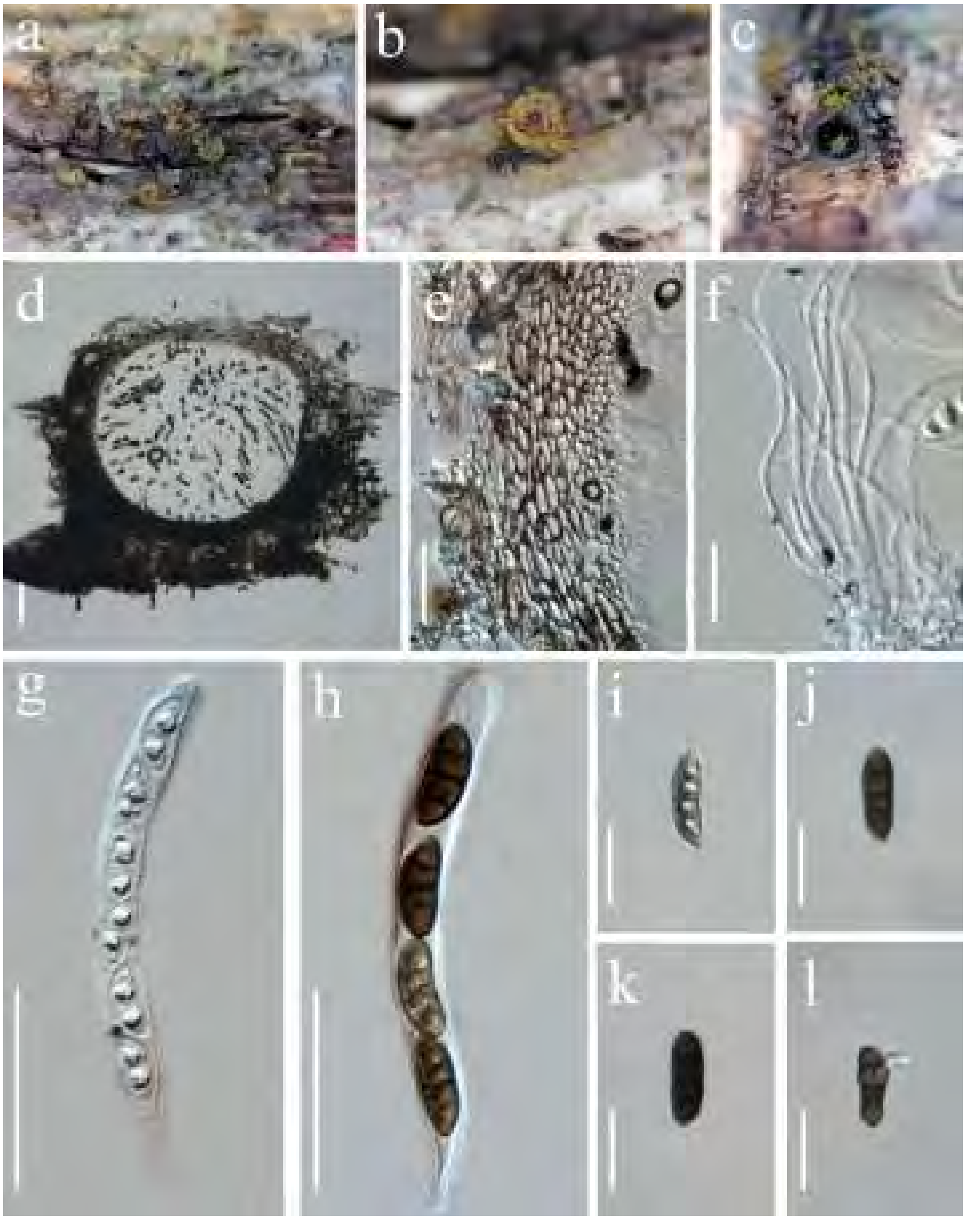


Fig. 46 ***Thyridaria broussonetiae*** (MHZU 22-0064). **a, b** Ostiolar discs and stroma surface on the host substrate. **c, d** Vertical cross section of ascoma **e** Peridium. **f** Pseudoparaphyses. **g, h** Asci. **i–k** Ascospores. **l** Germinating ascospore. Scale bars: d = 200 µm, e, f, i–l = 20 µm, g, h = 50 µm

usnearum s. lat.) parasiting on *Usnea* (Etayo and Osorio 2004). *Abrothallus usneae* v. *usneae* is significantly differs from our collection by having strait ascospores with thicker and shorter lower cell (Etayo and Osorio 2004). *Abrothallus chrysanthus* can be distinguished from our collection by paler, much smaller (8–10 × 3–4.5 µm) ascospores and lack of violet pigment in the epihymenium while *A. usneae* v. *tetraspora* morphologically differs from our collection by bigger ascomata and constantly 4-spored asci (Etayo and Osorio 2004; Etayo and van den Boom 2006). Therefore, we introduce our collection as *Abrothallus altoandinus.*

Abrothallus tetrasporus (Etayo & Osorio) Etayo, Flakus & Rodr. Flakus, ***comb. et stat. nov.***

Index Fungorum number: IF900420; *facesoffungi number*: FoF 14175; Fig. 51.

Basionym: *Abrothallus usneae* var. *tetrasporus* Etayo & Osorio, Comunicaciones Botanicas del Museo Nacional de Historia Natural y Antropologia Montevideo 129(6): 4 (2004).

Holotype: H. S. Osorio 9638a

Lichenicolous. *Parasite* of various saxicolous and corticolous species of *Usnea* growing on main branches and laciniae (more rarely also apothecial disc) of *Usnea* (not changing color of the host thallus) and on galls of *Biatoropsis usnearum* s. lat. **Sexual morph**: *Mycelium* immersed, indistinct, I–, K/I–. *Ascomata* apothecioid, superficial, producing directly on thallus of *Usnea* or on galls of *Biatoropsis usnearum* s. lat., black, epruinose or rarely slightly

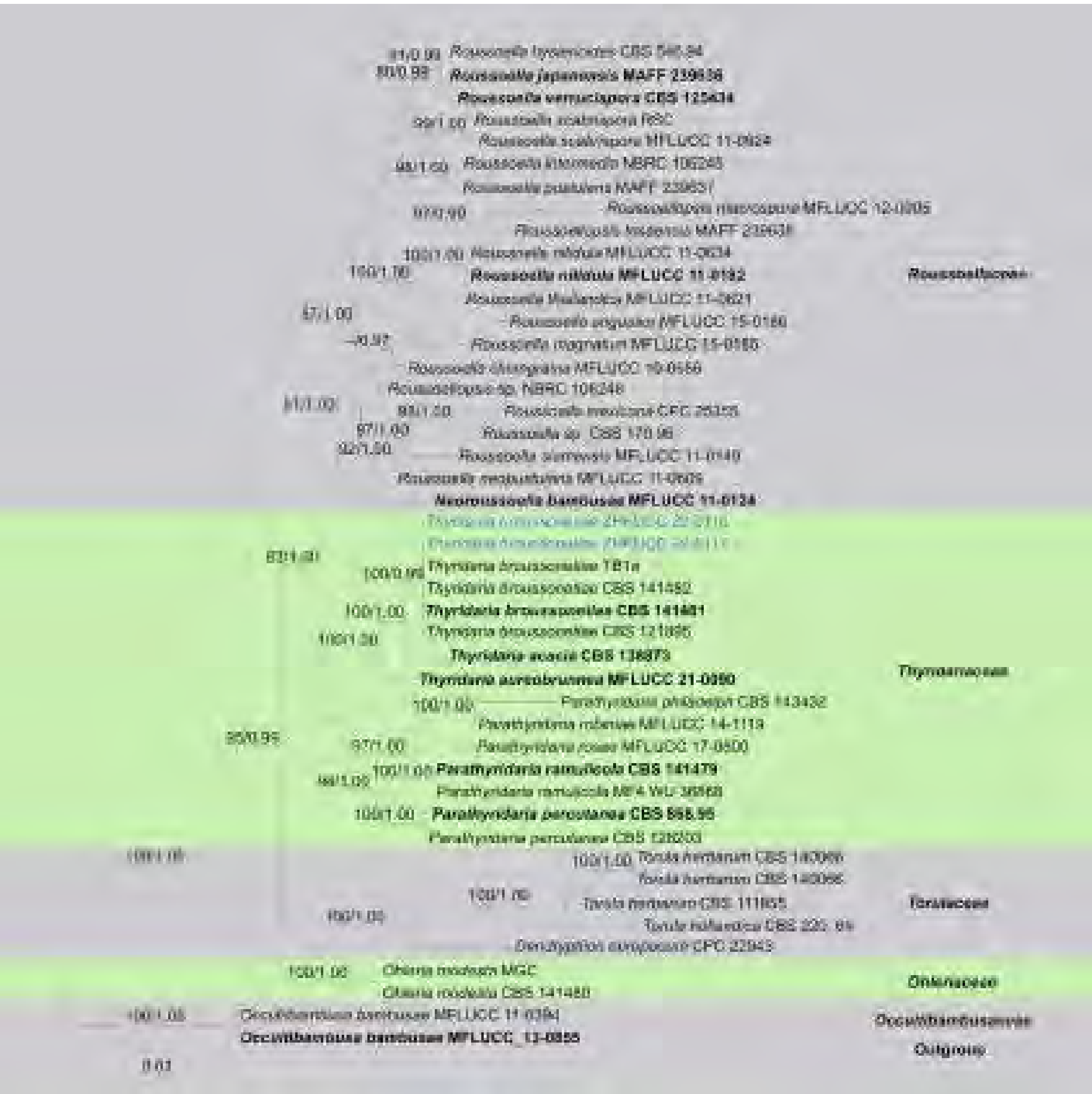


Fig. 47 The best scoring RAxML tree of combined dataset of ITS, LSU and *tef*1-α for sequence data of taxa in Thyridariaceae. The topology and clade stability of the combined gene analyses was compared to the single gene analyses and there is no significant difference between them. The tree is rooted with *Occultibambusa bambusae* (MFLUCC 11-0394 and MFLUCC 13-0855). The matrix had 564 distinct alignment patterns with 23.32% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.238335, C = 0.264925, G = 0.281630, T = 0.215110; substitution rates AC = 1.514255, AG = 3.124473, AT = 2.468484, CG = 1.311510, CT = 8.752761, GT = 1.0; gamma distribution shape parameter α = 0.169591 with a final likelihood value of—9484.250024. Ex-type strains are in bold and newly generated sequences are in blue bold. Bootstrap support for ML equal to or greater than 70% and BI equal to or greater than 0.95 are given above the nodes

yellowish pruinose, strongly convex, emarginate, single or aggregated, constricted at the base, 250–550 µm in diam. *Epihymenium* 5–10 µm, dark brownish violet, K + emerald greenish, N + violet (shortly). *Exciple* strongly reduced, hyaline to dark-brown or violet-brown to black in external part. *Hymenium* 40–90 µm high, hyaline to violet in upper part, K + emerald green,. *Interascal filaments* irregularly branched and sometimes anastomosed (especially in the upper part), 1–2 µm wide, apical cells slightly widened (up to 2–2.5 µm), brown pigmented. *Hypothecium* olive brown to dark brown in the upper part, 90–250 µm high. *Asci* bitunicate, I–, K/I–, narrowly clavate, apically widened with evident apical dome, 40–70 × 8–12 µm, consistently 4-spored. *Ascospores* 1-septated, medium to dark brown, distinctly verrucose, covered by gelatine coat when younger, broadly ellipsoid, 8.5–($\overline{x}$ = 12.6 ± 1.4)–15 × 4–($\overline{x}$ = 5.2 ± 0.5)–6.5 µm, l/b ratio 1.9–($\overline{x}$ = 2.4 ± 0.3)–3 (n = 77), not braking easily in semi-spores, composed of almost equal cells, strongly constricted near septum. **Asexual morph**: *Conidiomata* pycnidial, immersed in the host thallus (sometimes

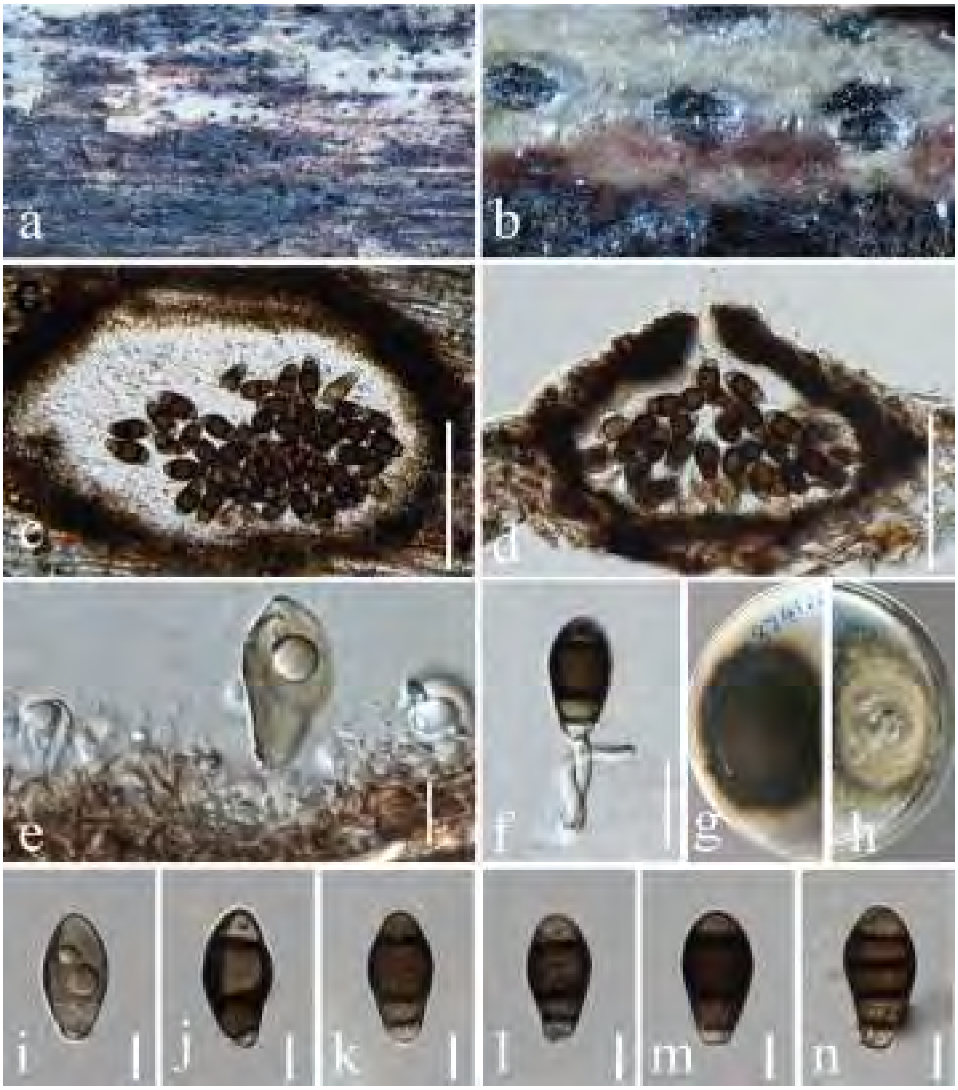


Fig. 48 ***Versicolorisporium triseptatum*** (HUEST 21.0016). **a, b** Appearance of conidiomata on decaying culms of bamboo. **c** Horizontal section through conidioma. **d** Vertical section through conidioma. **e** Condia attached to conidiogenous cells. **f** Germinated conidium. **g** Surface view of culture. **h** Reverse view of culture. **i**–**n** Conidia. Scale bars: c, d = 100 µm, f = 20 µm, e, i–j = 10 µm

below ascomata), 80–160 µm in diam. *Pycnidial wall* pale to dark brown-violet (darker at the upper part), K + emerald greenish, N + violet (shortly), 10–20 µm wide. *Conidiogenous cells* holoblastic, 8–10 × 3–5 µm. *Conidia* simple, hyaline, obpyriform with truncated end, 4.5–($\bar{x}$ = 7.4 ± 0.9)–9 × 4–($\bar{x}$ = 4.6 ± 0.4)–5.5 µm, l/b ratio 1–($\bar{x}$ = 1.6 ± 0.3)–2.3 (n = 45) (Etayo and Osorio 2004).

Material examined: Uruguay, Rocha, Cerro Lechiguana, on *Usnea densirostra* on rocks, 34° 06′ S 53° 50′ W, 24 April 2003, H. S. Osorio 9638a & G. Geymonat (**holotype**); Bolivia, Department Cochabamba, Province Carrasco, Parque Nacional Carrasco, between Meruvia and Monte Punku, 17° 34′ 43″ S, 65° 15′ 25″ W, 3082 m, forest with *Podocarpus* sp., on corticolous *Usnea* sp., 26 November 2014, A. Flakus, (25621 KRAM, LPB); *ibid.* Wayra Mayu close to Monte Punku, 17° 33′ 30″ S, 65° 16′ 08″ W, 2750 m, lower montane Yungas cloud forest, on corticolous *Usnea* sp., 28 November 2014, A. Flakus (25854KRAM, LPB); Department La Paz, Province Nor Yungas, way from La Paz to Coroico towards Unduavi in the way to Chulumani 16º18′ 27″ S, 67º53′ 48″ W, 3210 m, on *Usnea* sp. on bushes in the cloud forest, 31 May 2011, J. Etayo (26948LPB, herb. Etayo); Department Santa Cruz, Province Caballero, near Siberia, 17° 49′ 38″ S, 64° 44′ 45″ W, 3950 m, On *Usnea* sp. on mossy branches, open Yungas cloud forest, 16 August 2012, J. Etayo 29613, 28616 (LPB, herb. Etayo); *ibid*, on dead *Usnea* gr. *florida* on branches, J. Etayo 29417, 29613 (LPB, herb. Etayo); Department Tarija, Province O'Connor, 90 km from Tarija on the way to Entre Ríos, 21° 25′ 32″ S, 64° 19′ 05″ W, 2250 m, Tucumano-Boliviano altimontano forest, with *Alnus acuminata* and *Podocarpus* sp., on *Usnea* with *Biatoropsis* on twigs, 9 August 2012, J. Etayo 29392 (LPB); 28 km from Entre Ríos, near Soledad, 21° 41′ 00″ S, 64° 07′ 29″ W, 1500 m, Tucumano-Boliviano montano forest, 11 Aug. 2012, J. Etayo 55–13 (LPB); Province Aniceto Arce, close to La Mamora between Tarija and Bermejo, 22°

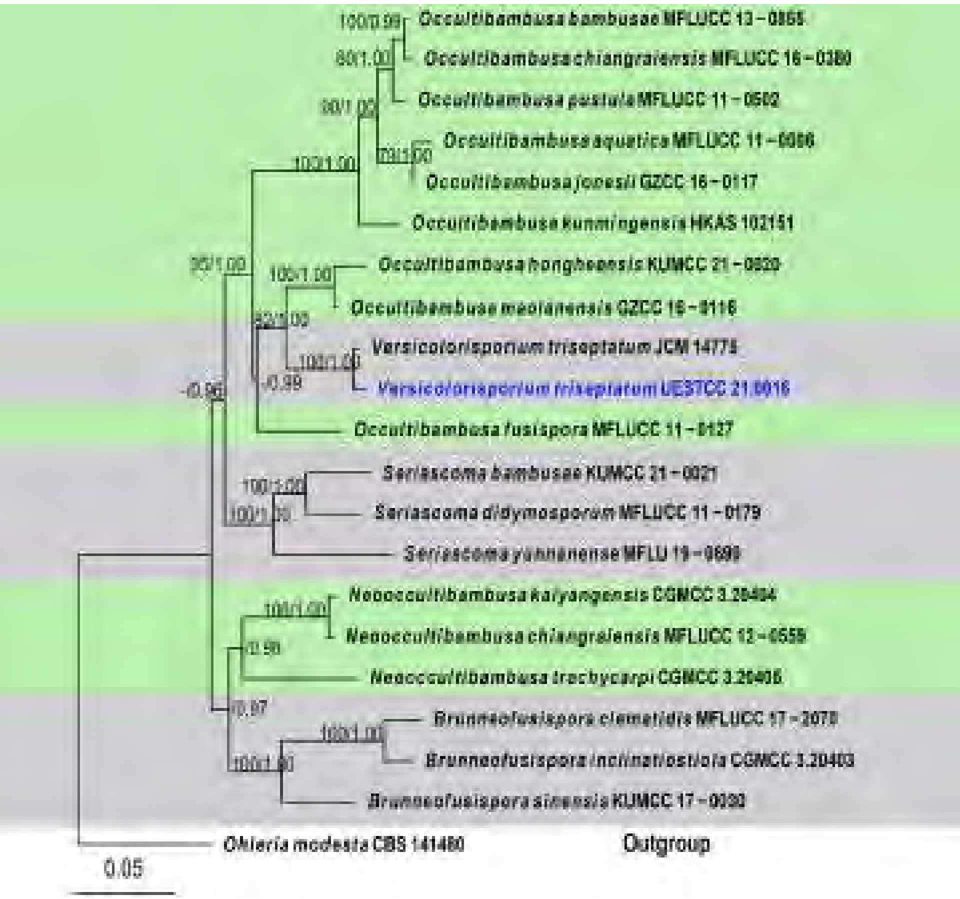


Fig. 49 The best scoring RAxML tree based on a combined dataset of ITS, LSU, SSU, *rpb2*, and *tef*1-*α* sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses and no significant differences. The tree is rooted with *Ohleria modesta* (CBS 141480). The matrix had 1160 distinct alignment patterns with 22.68% undetermined characters and gaps. Estimated base frequencies were as follows; $A = 0.248$, $C = 0.265$, $G = 0.258$, $T = 0.229$; substitution rates $AC = 1.811179$, $AG = 4.286074$, $AT = 1.611330$, $CG = 1.379457$, $CT = 8.862589$, $GT = 1.0$; gamma distribution shape parameter $\alpha = 0.148827$ and final likelihood value of − 16,694. Ex-type strains are in bold and newly generated sequences are in blue bold. Bootstrap support for $ML \geq 75\%$ and $BI \geq 0.95$ are given at the nodes

09′ 51″ S, 64° 40′ 03″ W, 1320 m, disturbed Tucumano-Boliviano forest with Tillandsia, Subandino (Basimontano), on disk of *Usnea* sp. on branches, 27 July 2015, J. Etayo 30407 (LPB, herb. Etayo).

GenBank numbers: LSU: OR133230, ITS: OR116441, OR116442, SSU: OR116445, OR116446, OR116447.

Notes: The species is known from several localities in Bolivia, Uruguay (Etayo and Osorio 2004) and Terceira Island in Azores (Etayo 2018). We included in our phylogenetic analyses (Fig. 52) three Bolivian sample of *A. usneae* v. *tetraspora* forming a strongly supported monophyletic clade, which is phylogenetically different from *A. altoandinus*, and only distantly related to *A. usneae* var. *usneae* (represented on the tree by Portugal sample determined as *A. usneae* s. str. by Pérez-Ortega et al. 2014). The significant phylogenetic distances between those three taxa growing on *Usnea* species, together with the evident anatomical differences, suggest that they represent three distinct species. Therefore, we proposed here to elevate *A. usneae* v. *tetraspora* (the morph producing 4-spored asci) to species level. *A. tetrasporus* can be easily distinguished form *A. usneae* s str. by its constantly 8-spored asci (Etayo and Osorio 2004).

Botryosphaeriales C.L. Schoch, Crous & Shoemaker

Botryosphaeriales was introduced for the type family Botryosphaeriaceae (Schoch et al. 2006). Currently, this order is recognized with six families viz. Aplosporellaceae, Botryosphaeriaceae, Melanopsaceae, Phyllostictaceae, Planistromellaceae and Saccharataceae (Phillips et al. 2019; Hongsanan et al. 2020b).

Botryosphaeriaceae Theiss. & Syd.

Botryosphaeriaceae was introduced by Theissen and Sydow (1918) to accommodate *Botryosphaeria*, *Dibotryon* and *Phaeobotryon* (Phillips et al. 2019). Members of this family are endophytes, saprobes and pathogens (Slippers and Wingfield 2007; Huang et al. 2009; Ghimire et al. 2010; Pérez et al. 2010; González and Tello 2011; Laurent et al. 2020). Species in this family occur on woody branches, leaves, stems and culms of a wide range of monocotyledonous and dicotyledonous hosts and in the thalli of lichens (Barr 1987; Denman et al. 2000; Mohali et al. 2007; Lazzizera et al. 2008; Marincowitz et al. 2008). Members of this family are characterized by ovoid to oblong ascospores which initially aseptate and hyaline, becoming pigmented and septate with age (Phillips et al. 2019). Asexual morphs are characterized by hyaline or pigmented, aseptate, one or multi-septate, sometimes muriform, smooth or striate

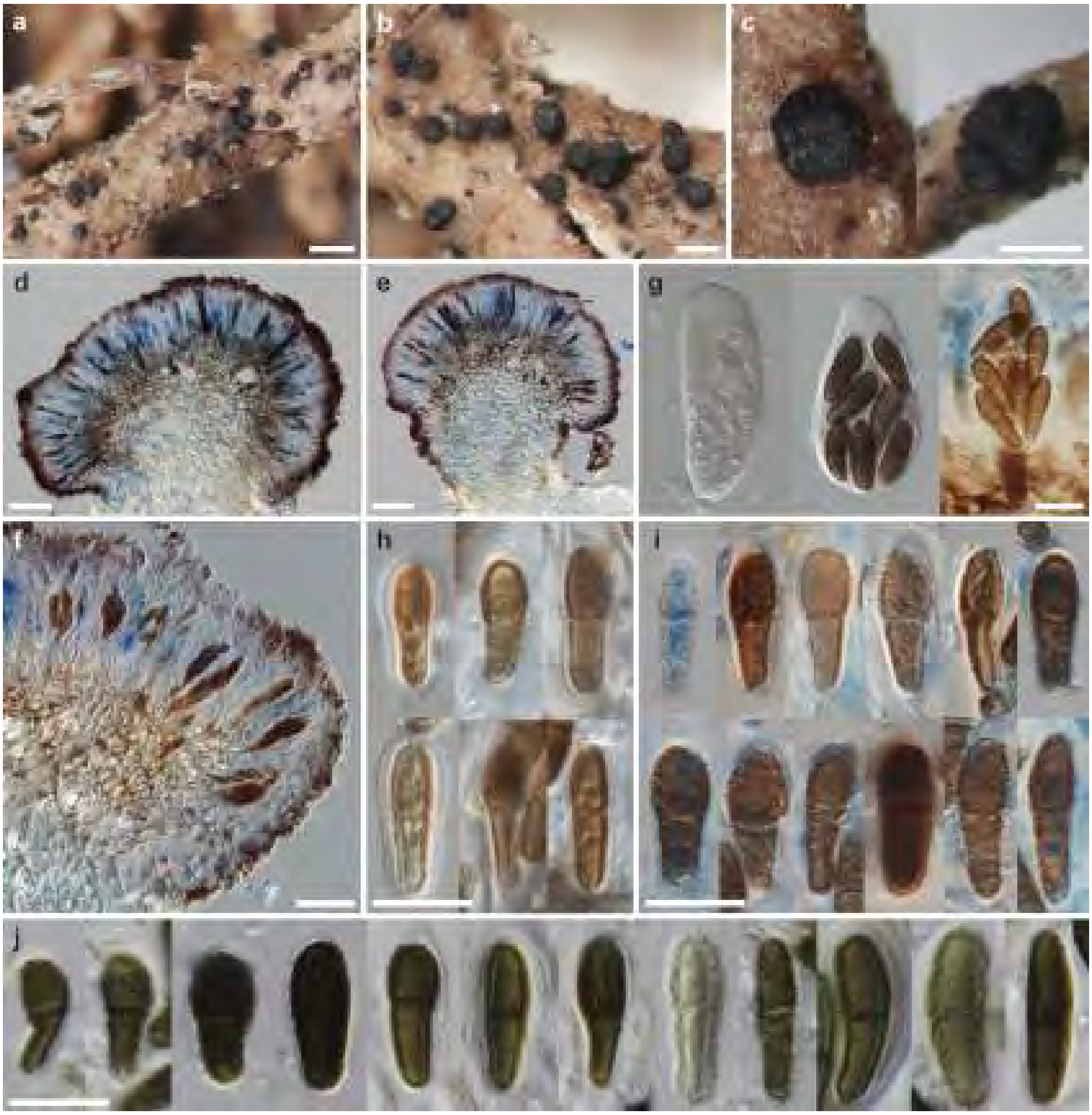


Fig. 50 ***Abrothallus altoandinus*** (KRAM-L 73246, **holotype**). **a–c** Habit of ascomata growing on *Usnea durietzii*. **d–e** Transversal section of ascoma (mounted in LPCB). **f** Strongly reduced exciple (mounted in LPCB). **g** Asci mounted in Lugol's solution pretreated by 10% KOH (two left) and mounted in LPCB (right one). **h** Ascospores mounted in distilled water. **i** Ascospores mounted in LPCB. **j** Ascospores mounted in 10% KOH. Scale bars: a–b = 250 µm, c = 500 µm, d–e = 50 µm, f = 25 µm, g–j = 10 µm

conidia (Phillips et al. 2019). Currently, 22 genera are accepted in Botryosphaeriaceae, and considered as largest family in Botryosphaeriales (Wijayawardene et al. 2020; Zhang et al. 2021).

Botryosphaeria Ces. & De Not.

Botryosphaeria was introduced by Cesati and de Notaris (1863) with *B. dothidea* as the type species. *Botryosphaeria* species have a worldwide distribution and occurr on wide range of hosts including monocotyledonous and dicotyledonous plants (Darge and Woldemariam 2021). *Botryosphaeria* species are characterized by hyaline and aseptate ascospores, becoming pale brown and septate with age (Phillips et al. 2005, 2013). The asexual morph has hyaline and aseptate conidia and sometimes they become pigmented at maturity. Conidia also become one or two septate with age or before germination (Phillips et al. 2013). Currently, 30 species are accepted under this genus (Wu et al. 2021). We described a new host association of *B. dothidea* from China.

Botryosphaeria dothidea (Moug.) Ces. & De Not., Comm. Soc. crittog. Ital. 1(fasc. 4): 212 (1863)

Fig. 51 ***Abrothallus tetrasporus*** (Flakus 25621). **a**–**c** Habit of ascomata growing on *Usnea* sp. **d** Transversal section of ascoma (mounted in LPCB). **e** Strongly reduced exciple (mounted in LPCB). **f** Asci mounted in Lugol's solution pretreated by 10% KOH. **g** Ascospores mounted in distilled water (upper row) and mounted in 10% KOH (lower row). **h** Habit of pycnidial conidiomata immersed in host thallus. **i** Transversal section of conidiomata (mounted in LPCB). **j** Conidia mounted in distilled water. Scale bars: a–c, h = 250 µm, d = 100 µm, e, i = 25 µm, f, g, j = 10 µm

Index Fungorum number: IF83247; *Facesoffungi number*: FoF 03512; Fig. 53.

Epitype: PREM 57372 (Slippers et al. 2004)

Saprobic on dead twig of *Coffea arabica* L. **Sexual morph**: *Ascomata* 230–255 µm high × 235–275 µm diam. ($\overline{x}$ = 255 × 240 µm, n = 10), solitary, semi-immersed, erumpent at maturity, coriaceous, uniloculate, globose, black. *Peridium* 20–30 µm wide, two-layered, outer layer composed of thick-walled, brown to dark brown cells of *textura angularis*, inner layer composed of thin-walled, hyaline cells of *textura angularis*. *Hamathecium* 4–8 µm wide, composed of septate, unbranched, cellular

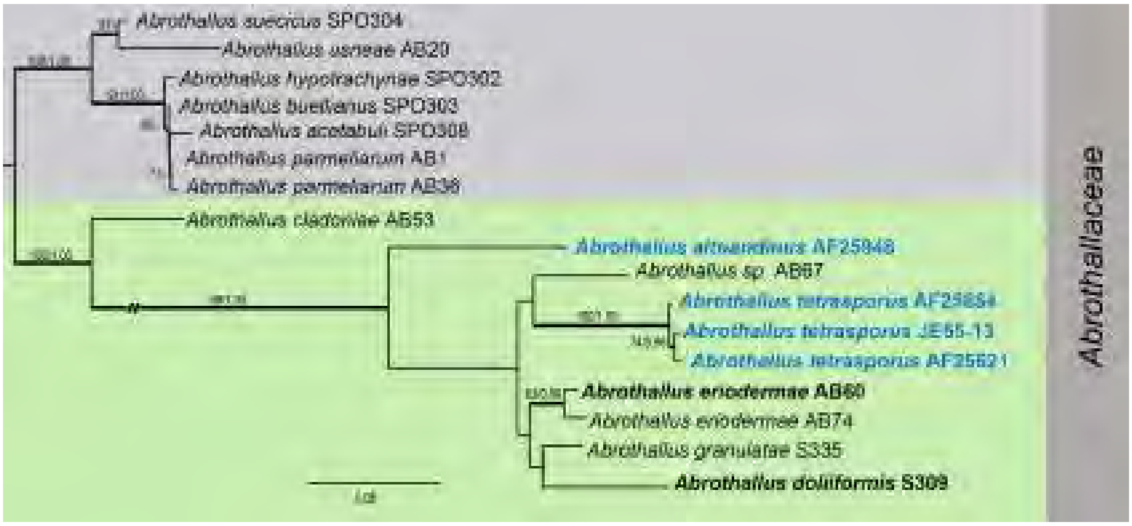


Fig. 52 Phylogenetic reconstruction of the systematic position of *Abrothallus altoandinus* and *A. tetrasporus* inferred from BI analyses of combined dataset of LSU, ITS, SSU and *tef*-α dataset. Bold branches represent either bootstrap values ≥ than 70 and/or Bayesian posterior probabilities ≥ than 0.95

pseudoparaphyses, slightly constricted at the septum. *Asci* 55–110 × 20–27 µm ($\overline{x}$ = 80 × 22 µm, n = 15), 8-spored, bitunicate, fissitunicate, clavate, short-pedicellate, apically rounded, with distinct ocular chamber. *Ascospores* 22–34 × 10–14 µm ($\overline{x}$ = 26 × 12 µm, n = 30), uniseriate at the base, overlapping 2–3-seriate at the apex, hyaline, aseptate, ellipsoid to fusiform, broad at the middle, thick and rough-walled. **Asexual morph**: Not observed in this study; see Rathnayaka et al. (2021).

Culture characteristics: Ascospores germinating on PDA within 6 h and germ tubes produced from both ends of the ascospores, fast growing, reaching 5–6 cm diam. after 3 days at 25 °C, circular, flattened, fluffy, fairly dense, aerial, grey in upper side and black in lower side.

Material examined: China, Taiwan region, Fenghuang Mountain, Lugu Township, Nantou County, on dead twigs of *Coffea arabica* (Rubiaceae), 30 October 2019, A. Rathnayaka (MFLU 22-0230).

Hosts and distribution: on wide range of hosts in worldwide (Jayawardena et al. 2019)

GenBank numbers: ITS: OP800118; *tef*1-α: OP807348; *β-tubulin*: OP807349

Notes: *Botryosphaeria dothidea* was introduced and described by Fires (1823) without designating the type specimen. Therefore, Slippers et al. (2004) designed a neotype from the Fries's collection and however, it was in immaturity stage without ascospores. Thus, an epitype for *B. dothidea* was designated from *Prunus* sp. that collected from Switzerland (Slippers et al. 2004).

Based on the phylogenetic analyses (Fig. 54), our collection (MFLU 22-0230) clustered with the ex-epitype and other isolates of *B. dothidea*. According to previous studies, *B. dothidea* has been recorded on several host species in China (Taiwan region); i.e., *Araucaria cunninghamii* (Huang and Wang 2011), *Camellia sinensis* (Rathnayaka et al. 2021), *Mangifera indica* (Ni et al. 2010), *Prunus mume*, *P. persica* and *P. communis* (Ko et al. 2011) and *Vitis* sp. (Kuo et al. 1989). This is the first record of *B. dothidea* on *Coffea arabica* in China (Taiwan region).

Diplodia Fr.

Diplodia was introduced by Montagne (1834) and typified by *D. mutila* (Fr.) Mont., which has hyaline, aseptate conidia that can become brown and septate with age. *Diplodia* species are considered as endophytes, pathogens and saprobes on a wide range of woody hosts (Crous et al. 2006; Slippers and Wingfield 2007; Phillips et al. 2008, 2013; Dissanayake et al. 2016). According to Phillips et al. (2013), there are two types of distinct conidial morphologies in *Diplodia* species. The first type of conidia is initially hyaline, aseptate and later become pale to dark brown with 1-septum. Pigmentation is often delayed, and some species does not possess dark conidia. In the second type, the conidia become pigmented at an early stage of development, even when they are enclosed within the pycnidia, and these conidia only rarely become septate. These two morphological groups are supported by two distinct phylogenetic lineages (Phillips et al. 2013). This study reports and describes a new host association of *D. seriata* from Italy.

Diplodia seriata De Not., Micr. Ital. Dec. 4: 6. 1942.

≡*Botryosphaeria obtusa* (Schwein.) Shoemaker, Canad. J. Bot. 42: 1298. 1964.

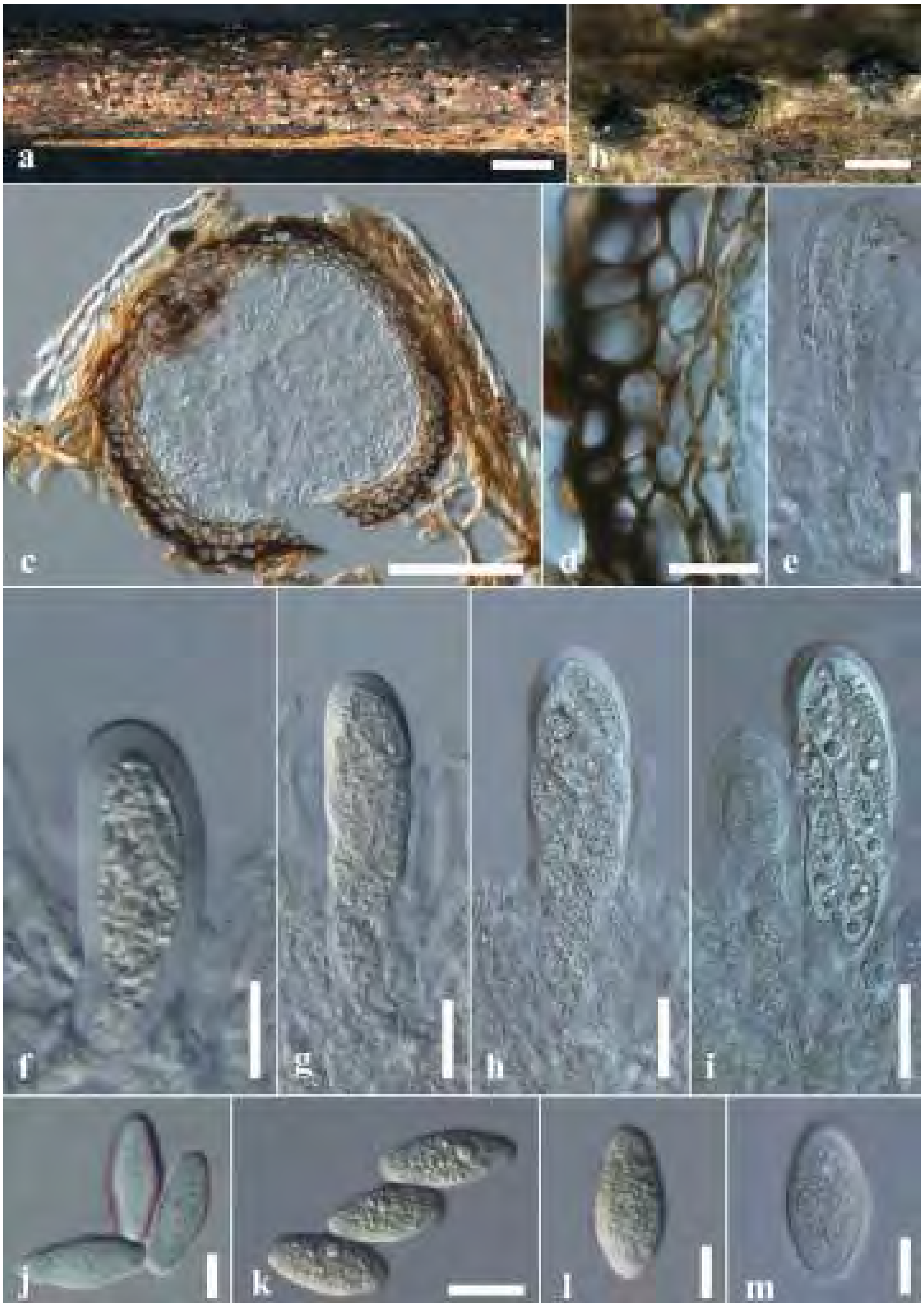


Fig. 53 ***Botryosphaeria dothidea*** (MFLU 22-0230). **a** Examined material. **b** Appearance of ascostromata on host surface. **c** Vertical section through ascostroma. **d** Peridium. **e** Pseudoparaphyses. **f–i** Asci. **j–l** Ascospores. **m** Surface view of colony on PDA. **n** Reverse view of colony on PDA. Scale bars: a = 2 mm, b = 200 µm, c = 100 µm, d–j = 20 µm, k, l = 10 µm

Index Fungorum number: IF180468; *Facesoffungi number*: FoF 03596; Fig. 55.

Saprobic on *Tilla* sp. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 240–380 µm high × 235–275 µm diam. ($\bar{x}$ = 285 × 245 µm, n = 10), solitary or aggregated, immersed in the host, partially emergent at maturity, dark brown to black, ostiolate, apapillate, thick-walled, outer layers composed of dark brown *textura angularis*, inner layers of thin-walled hyaline *textura angularis*. *Conidiogenous cells* 8–15 × 3–6 µm, lining the pycnidial cavity, hyaline, thin-walled, smooth, cylindrical, swollen at the base, discrete, producing a single conidium at the tip, indeterminate, proliferating internally giving rise to periclinal thickenings or proliferating percurrently forming 2–3 annellations. *Conidia* 18–21(–22) × 15–18(–20), initially hyaline, becoming dark brown, moderately thick-walled (ca. 0.5 µm thick), wall externally smooth, roughened on the inner surface, aseptate, globose to ovoid, widest in the middle, apex rounded, base truncate or rounded.

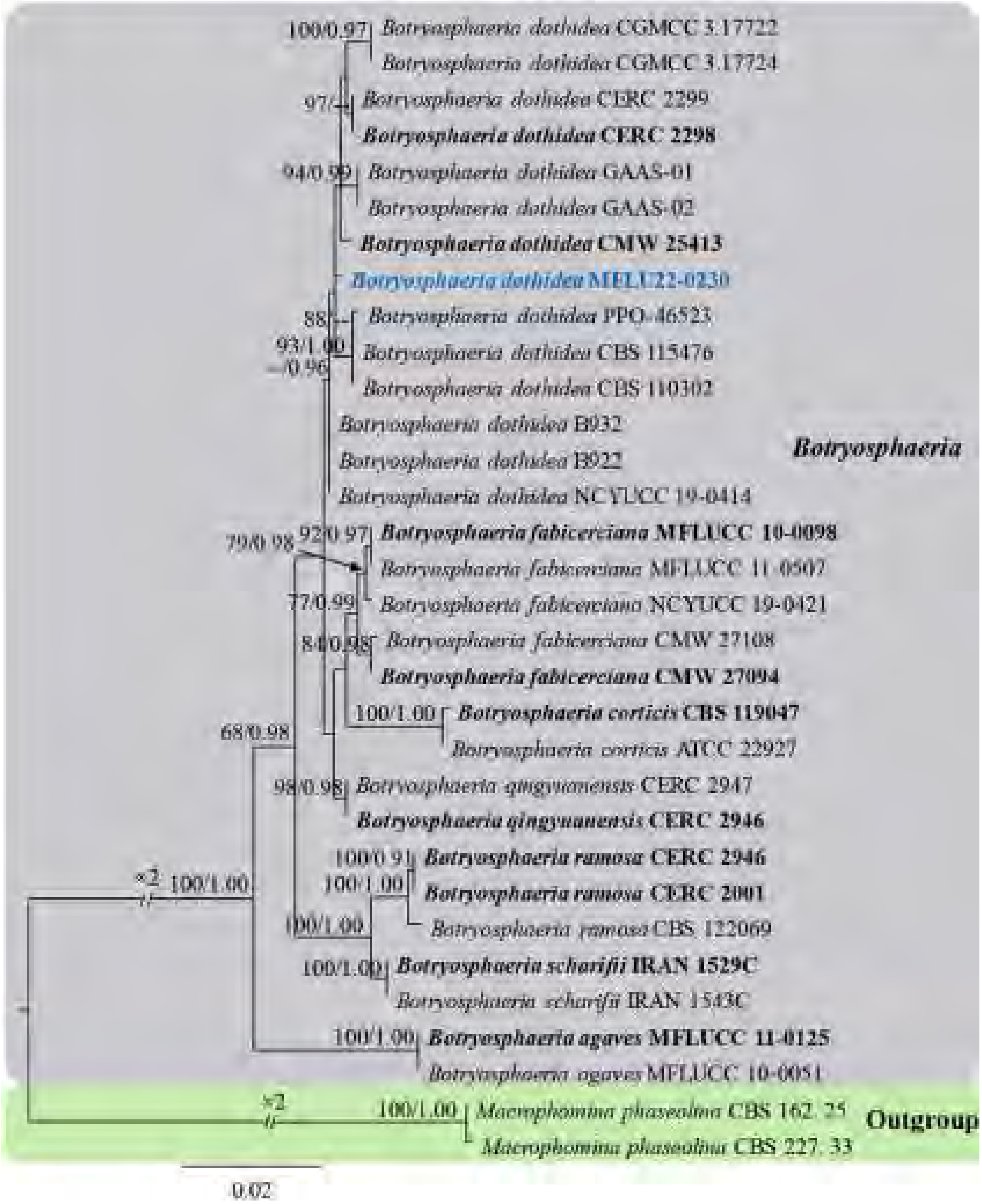


Fig. 54 The best scoring RAxML tree for combined dataset of ITS, *β-tubulin* and *tef*1-*α* sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses and there was no significant difference between them. The tree is rooted to *Macrophomina phaseolina* (CBS 227.33 and CBS 162.25). The matrix had 213 distinct alignment patterns with 14.23% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.209302, C = 0.309977, G = 0.254177, T = 0.226543; substitution rates AC = 0.431175, AG = 2.694467, AT = 0.959678, CG = 0.634099, CT = 4.74039, GT = 1.0; gamma distribution shape parameter α = 0.123912 with a final likelihood value of − 2925.315814. Ex-type strains are in bold and newly generated sequences are in blue bold. Bootstrap support for ML equal to or greater than 65% and BI equal to or greater than 0.90 are given above the nodes

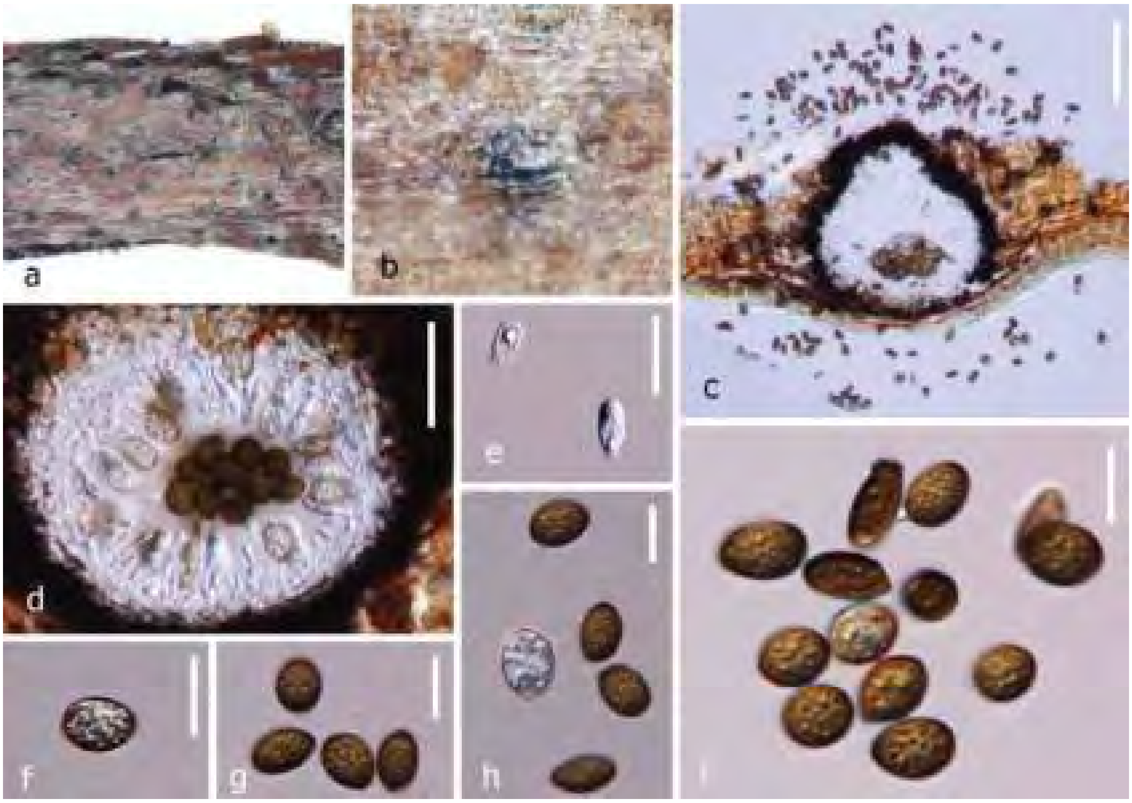


Fig. 55 ***Diplodia seriata*** (MFLU 15-2952). **a** Examined material. **b** Appearance of conidioma on host surface. **c** Vertical section through conidioma. **d** Close-up view of conidiogenous cells and conidia in conidioma. **e–i** Immature, hyaline conidia and mature, brown conidia. Scale bars: c = 100 µm, d = 50 µm, e–i = 20 µm

Culture characteristics: Colonies on PDA, reaching 5–6 cm after 12 days in the dark at 25 °C; circular, initially white, after 7 days becoming greyish brown to black; reverse grey to dark grayish green.

Material examined: Italy, Forlì-Cesena Province, on dead twigs of *Tilla* sp. (Malvaceae), 30 September 2014, E. Camporesi (MFLU 15-2952); living culture MFLUCC 17-0942.

Hosts and distribution: Plurivorous and cosmopolitan (Dissanayake et al. 2016).

Notes: In the combined gene analyses of ITS and *tef*1-α (Fig. 56) showed that, our isolate is phylogenetically closely related to the ex-type isolate of *Diplodia seriata*. The conidia of our isolate are shorter than 25 µm in length than conidia of ex-type isolate of *D. seriata* that are longer than 25 µm (Phillips et al. 2013). *Diplodia seriata* has been recorded on various hosts worldwide (Phillips et al. 2013; Dissanayake et al. 2016) and this is the first record of *D. seriata* on *Tilla* sp.

Dothiorella Sacc.

The genus *Dothiorella* was established by Saccardo (1880) and later reduced to synonymy under *Diplodia* by Crous and Palm (1999). Phillips et al. (2005) resurrected the genus *Dothiorella* to accommodate the species with septate conidia that darken at an early stage of development and sexual morphs with brown 1-septate ascospores. We introduce a new species of *Dothiorella* isolated from *Rhamnus alaternus*.

Dothiorella franceschinii Linaldeddu, A. Alves & A.J.L. Phillips, ***sp. nov.***

Index Fungorum number: IF900190; *Facesoffungi number*: FoF 13942; Fig. 57

Etymology: in honour of Professor Antonio Franceschini for his outstanding work on Mediterranean maquis diseases.

Saprobic or *weak pathogen* on *Rhamnus alaternus* L. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* pycnidial, produced on *R. alaternus* twigs on ½ PDA within 2–3 weeks, solitary or aggregated, dark-brown to black, globose, unilocular or multilocular. *Conidiomatal wall* thick, inner layer comprises thin-walled, hyaline cells of *textura angularis*, and outer layer comprises dark brown, thin-walled cells of *textura angularis*. *Conidiophores* reduce to conidiogenous cells. *Conidiogenous cells* 6–13 × 3–7 µm, holoblastic, discrete, cylindrical, hyaline, smooth, indeterminate, proliferating percurrently to form annellides.

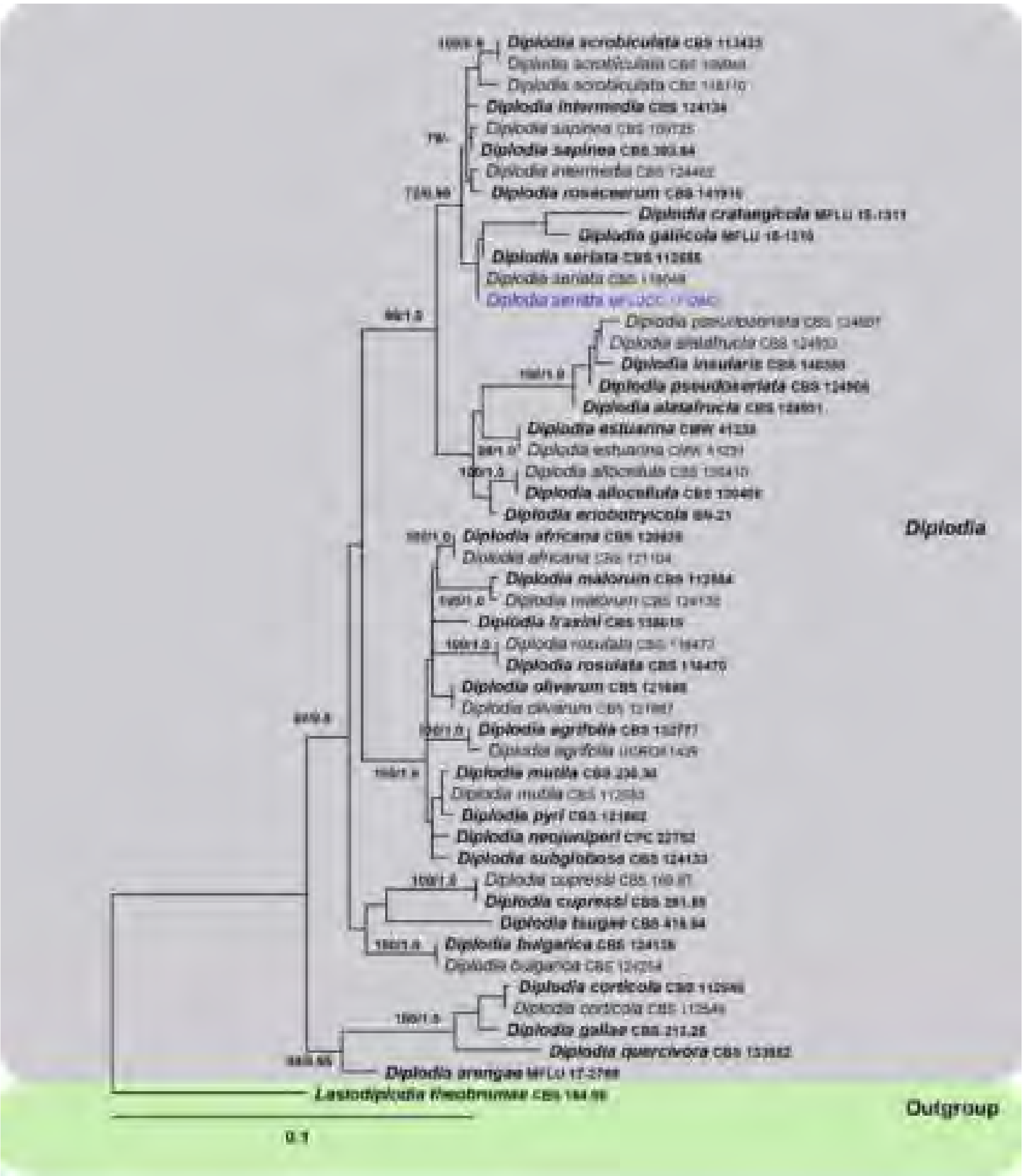


Fig. 56 The best scoring RAxML tree for combined dataset of ITS and *tef*1-*α* sequence data. The tree is rooted to *Lasiodiplodia theobromae* (CBS 164.96). The matrix had 283 distinct alignment patterns with 10.52% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.207698, C = 0.297682, G = 0.261769, T = 0.232852; substitution rates AC = 0.990412, AG = 3.569134, AT = 0.786115, CG = 1.635193, CT = 4.459105, GT = 1.0; gamma distribution shape parameter α = 0.169845 with a final likelihood value of − 3366.787048. Ex-type strains are in bold and newly generated sequences are in blue. Bootstrap support for ML equal to or greater than 60% and BI equal to or greater than 0.80 are given near the nodes

Conidia 18–27 × 7–10 µm ($\bar{x}$ = 22.8 ± 2.4 × 8.8 ± 0.8 µm, l/w ratio = 2.6 ± 0.2, n = 50) ellipsoid to ovoid, moderately thick-walled, smooth to finely verruculose inner surface, ends rounded, sometimes with a truncate base, occasionally constricted at septum, initially hyaline and aseptate, becoming pale brown and 1-septate while attached to the conidiogenous cells, with 2 equal or sometimes asymmetric cells, finally dark brown. *Microconidia* not observed.

Culture characteristics: Colonies on PDA reached 90 mm diam. in 7 days at 22 °C in the dark. Irregular, flat, wavy margin, zonation with maturity, less areal mycelia,

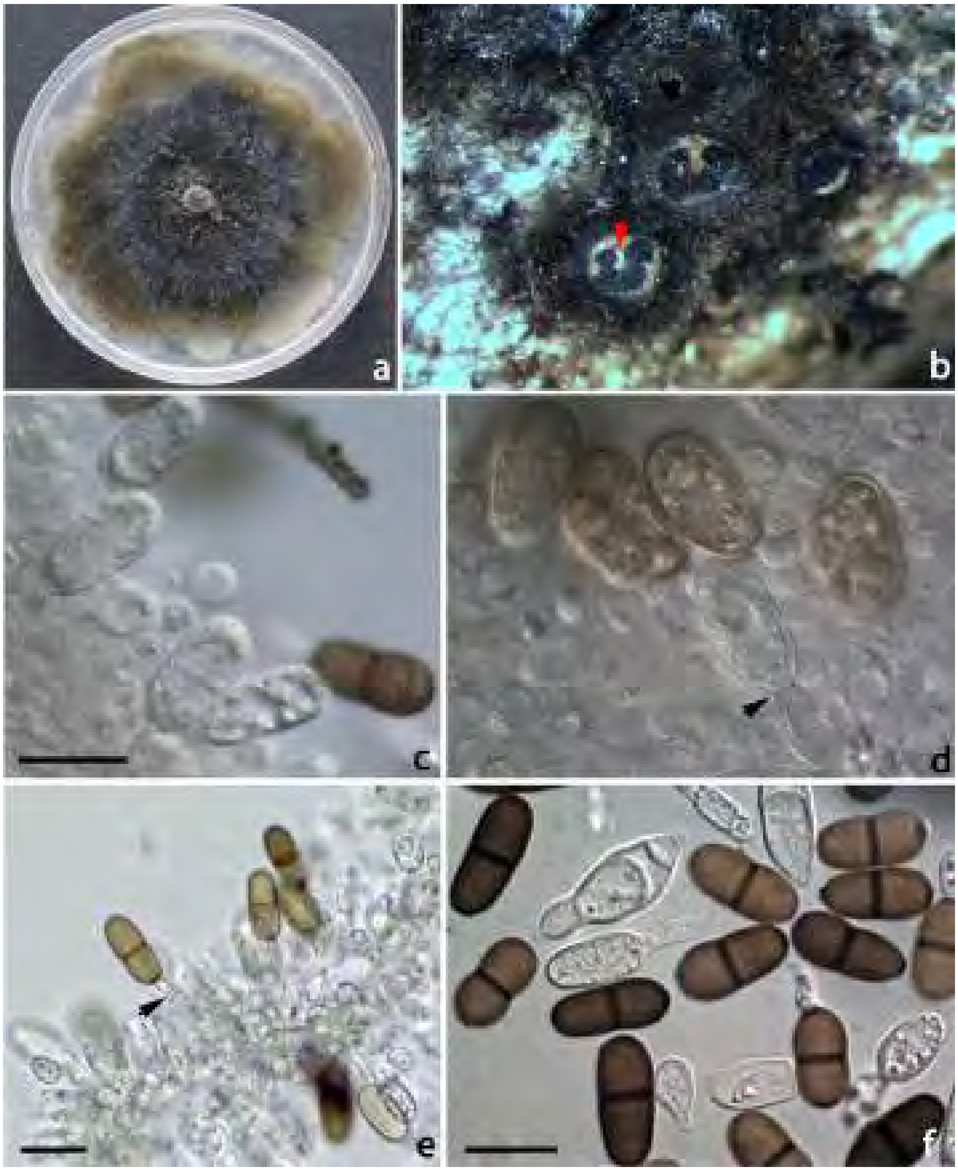


Fig. 57 ***Dothiorella franceschinii*** (CBS 147722, **ex-holotype**). **a** Surface view of colony on PDA. **b** Horizontal cross section of pycnidia formed on *Rhamnus alaternus* twigs. **c**–**d** Immature conidia developing on conidiogenous cells. **e** Mature conidia attached to the percurrently proliferating conidiogenous cell (arrowed). **f** Mature conidia constricted at the septum with asymmetric cells. Scale bars: c–f = 20 µm

initially surface white, turned pale green to dark olivaceous; reserve colony black in middle and dark grey at the edge.

Cardinal temperature for growth: minimum < 5 °C, maximum 33 °C and optimum 22 °C. Isolates failed to grow at 35 °C but mycelium resumed growth when plates were moved to 22 °C.

Material examined: Italy, Caprera Island, from sunken canker on stems of *Rhamnus alaternus* (Rhamnaceae), 3 May 2012, B.T. Linaldeddu, (CBS H-24771, **holotype**, a dried culture sporulating on *Rhamnus alaternus* twigs), ex-holotype culture BL151 = CBS 147722.

GenBank numbers: ITS: OP999677, *tef1-α:* OQ067247.

Notes: Our collection (CBS-H 24771) phylogenetically closed to *Dothiorella eriobotryae* and *D. prunicola*, however form a distinct sister clade to *Dothiorella eriobotryae* with ML = 100% statistical values (Fig. 58). Our collection shows 0.21% and 4.39% base-pair differences in the ITS and *tef1-α* loci of *D. eriobotryae* respectively. The base-pair differences in the ITS and *tef*1-*α* loci of *D. prunicola* with our strain revealed 1.89% and 13.18% respectively. Furthermore, our collection differs from *D. eriobotryae* (average size of conidia 19.7 × 10.3 µm, l/w ratio = 1.9) on account of its longer and narrower conidia and from *D. prunicola* (average conidia size 24.5 × 12.8 µm, l/w ratio = 1.9) on account of its shorter and narrower conidia. Therefore, we introduce our collection as *Dothiorella franceschinii* sp. nov.

Lasiodiplodia Ellis & Everh.

Lasiodiplodia is typified by *L. theobromae* (Pat.) Griffon & Maubl. (Ellis and Everhart 1894). *Lasiodiplodia* species differ from other closely related genera in the

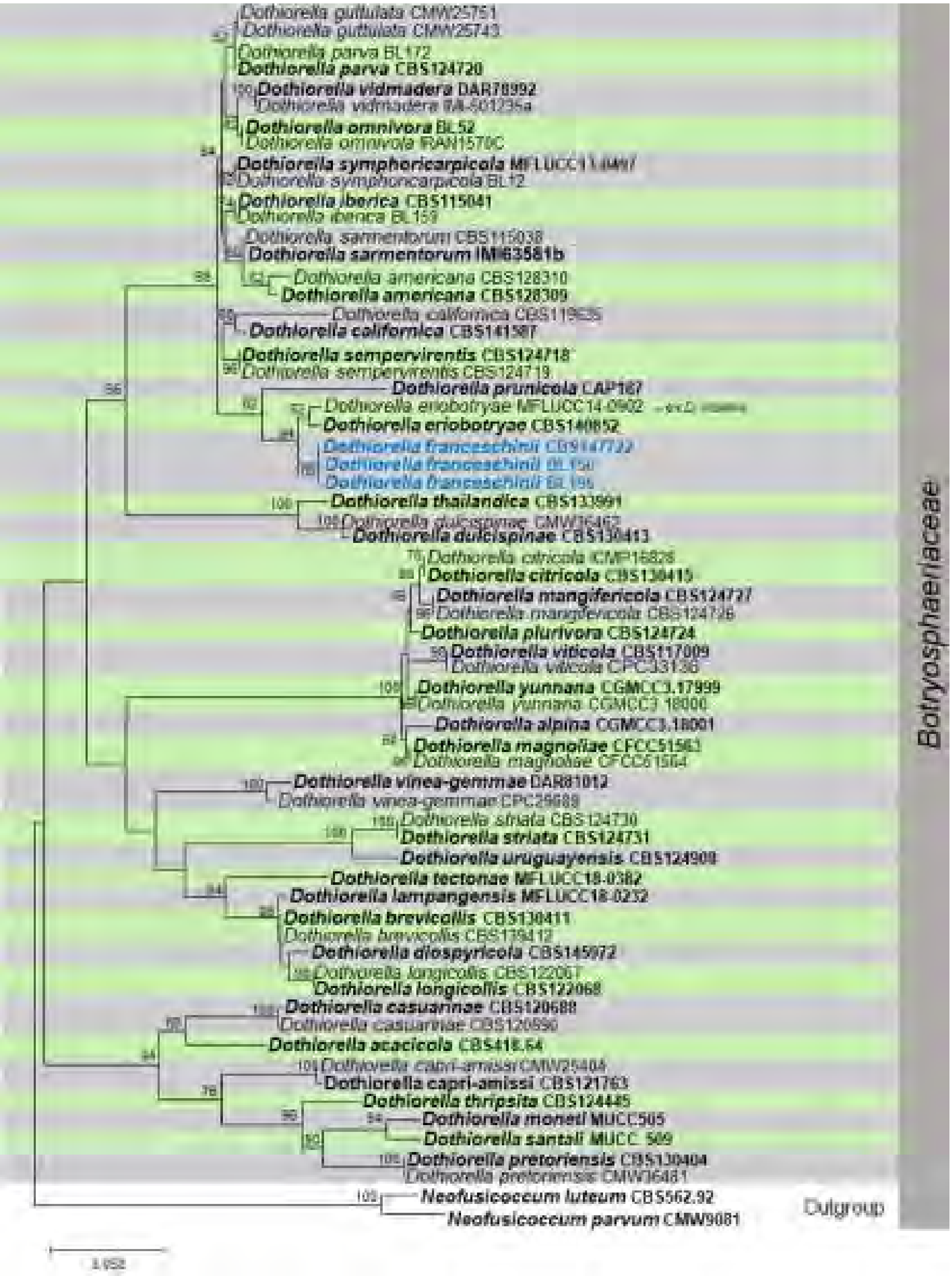


Fig. 58 Phylogram generated from maximum likelihood analysis based on combined ITS and *tef1-α* sequence dataset. Sixty-three *Dothiorella* strains were included in the combined sequence analysis, which comprise 732 characters. *Neofusicoccum luteum* (CBS 562.92) and *N. parvum* (CMW9081) were used as the outgroup taxa. The tree with the highest log likelihood (− 4506.99) is shown. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.2070)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap support equal or greater than 50% are given at the nodes. Ex-type strains are in bold and newly generated sequences are indicated in blue bold

Botryosphaeriaceae by the presence of pycnidial paraphyses and longitudinal striations on mature conidia (Phillips et al. 2013). However, morphology alone is not reliable for distinguishing the different species in *Lasiodiplodia*. The protein coding genes such as *tef*1-α and *β-tubulin* together with ITS and LSU provide best separation of species in this genus (Phillips et al. 2019). Species of *Lasiodiplodia* are cosmopolitan and occur on a wide range of monocotyledonous, dicotyledonous and gymnosperm hosts as endophytes, pathogens and saprobes (Slippers and Wingfeld 2007; Abdollahzadeh et al. 2010; Chen et al. 2015c). Currently, 69 epithets are accepted under this genus in Species Fungorum (2023). This study introduces a new *Lasiodiplodia* species and a new host association of *L. theobromae.*

Lasiodiplodia theobromae (Pat.) Griffon & Maubl., Bull. Soc. mycol. Fr. 25: 57 (1909)

Index Fungorum number: IF188476; *Facesoffungi number*: FoF00167; Fig. 59.

Holotype: Not designated. (CBS H-21411 designated as the neotype with CBS 164.96 as ex-neotype culture in Phillips et al. 2013)

Endophytic on *Morinda officinalis* How. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 200–400 × 100–400 µm diam. ($\bar{x}$ = 348 × 368 µm, n = 10), pycnidial, semi-immersed, unilocular, solitary, scattered, globose or subglobose, dark brown. *Conidiomata wall* 20–50 µm wide, outer layers dark brown to black, thick walled, inner layers thin-walled, pale brown to hyaline, comprising 2–3 layers of dark brown cells of *textura angularis*. *Paraphyses* up to 35 µm long, 2–3 µm wide, hyaline, septate, cylindrical, occasionally branched. *Conidiogenous cells* holoblastic, hyaline, thin-walled, smooth, cylindrical. *Conidia* 20–30 × 10–15 µm ($\bar{x}$ = 24 × 13 µm, n = 50), initially hyaline, aseptate, becoming median, 1-septate, dark brown when mature, thick-walled, ellipsoid to obovoid, base truncate or rounded, with longitudinal striations from apex to base.

Culture characteristics: Colonies growing on PDA reaching 80 mm diam. after 2 days at 25 °C in the dark, initially white, circular, raised, fluffy, dense, filamentous, becoming grey and then dark grey from the center after 4 days. Reverse initially white and turning to dark gray when old.

Material examined: China, Guangdong Province, Zhaoqing City, healthy stem of *Morinda officinalis* (Rubiaceae), June 2020, W. Guo, (MHZU 22-0051), living cultures (ZHKUCC 22-0085, ZHKUCC 22-0086).

Hosts and distribution: wide range of hosts and substrate in worldwide (Farr and Rossman 2023).

GenBank numbers: ITS: ON603982, ON603983, *β-tubulin*: OP893937, OP893935, *tef*1-α: OP893934, OP893936

Notes: The blast results of ITS, *β-tubulin* and *tef1-α* loci of our isolates (ZHKUCC 22-0085, ZHKUCC 22-0086) revealed *Lasiodiplodia theobromae* strains as the closest matches. The phylogenetic analyses of combined loci of ITS, *β-tubulin* and *tef1-α* sequences (Fig. 61) showed that our isolates clustered with the ex-type strain of *L. theobromae* (CBS 164.96) with ML = 78% and BI = 0.90 bootstrap support. Further, our collection is morphologically similar to *L. theobromae* (Alves et al. 2008). Based on the morphology and phylogeny, we identified our isolates as *L. theobromae. Lasiodiplodia theobromae* also reported as a pathogen in several hosts (Kamil et al. 2018; Huda-Shakirah et al.

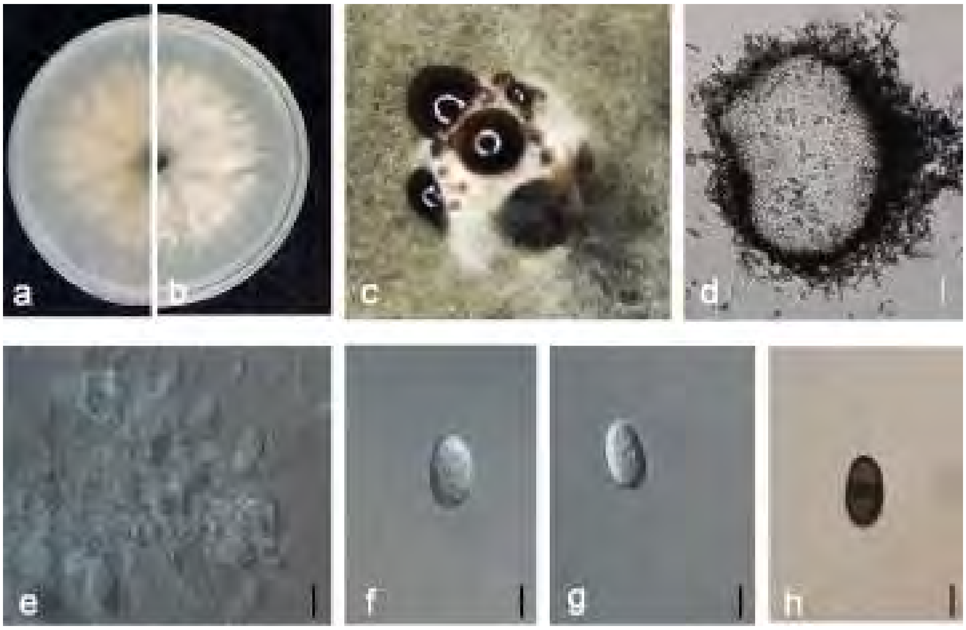


Fig. 59 ***Lasiodiplodia theobromae*** (ZHKUCC 22-0085). **a** Surface view of colony on PDA. **b** Reverse view of colony on PDA. **c** Pycnidia on PDA. **d** Longitudinal section of pycnidium, **e** Conidiogenous cells with developing conidia. **f, g** Immature conidia. **h** Mature conidium. Scale bars: d–h = 10 µm

2022). However, this is the first report of *L. theobromae* on *Morinda officinalis*.

Lasiodiplodia morindae M. Luo & M.P. Zhao, ***sp. nov.***

Index Fungorum number: IF900421; *Facesoffungi number*: FoF 14176; Fig. 60

Etymology: based on its host *Morinda officinalis*.

Endophytic on *Morinda officinalis* How. **Sexual morph**: Undetermined. **Asexual morph**: *Paraphyses* up to 30 µm long, 2–3 µm wide, filiform, hyaline, septate, cylindrical, arising from the inner layer of conidiomatal wall, ends rounded. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, hyaline, thin-walled, smooth, cylindrical. *Conidia* 20–30 × 10–20 µm ($\bar{x} = 24 \pm 2 \times 14 \pm 1$ µm, n = 50), initially hyaline, aseptate, becoming median, 1-septate, dark brown when mature, thick-walled, ellipsoid to obovoid with a round and slightly tapered apex, turning brown with one median septum when mature.

Culture characteristics: Colonies growing on PDA reached to 60 mm diam. after 2 days at 25 °C in the dark, initially white, fast growing, circular, raised, fluffy, filamentous, becoming grey after 5 days. Reverse white first and then turn to grey and dark grey.

Material examined: China, Guangdong Province, Zhaoqing City, healthy stem of *Morinda officinalis* (Rubiaceae), June 2020, W. Guo, (MHZU 22-0050, **holotype**); ex-type cultures, ZHKUCC 22-0084, ZHKUCC 22-0083.

GenBank numbers: ITS: ON603984, ON603985, β-*tubulin*: OP893932, OP893933.

Notes: The combined gene analyses of ITS, β-*tubulin* and *tef*1-α sequences (Fig. 61) showed that our isolates clustered with ex-type strain of *Lasiodiplodia tropica* (CGMCC 3.18477) with ML = 78%, BI = 0.90 bootstrap values. Morphologically, our strain has ellipsoid, thin-walled, larger conidia ($\bar{x} = 24 \times 15$ µm) with one median septum while *L. tropica* has ellipso-ovoid to globose, small conidia ($\bar{x} = 21 \times 12$ µm) with one supra-median septum or two septa (Wang et al. 2019a). The conidia of our strains take five weeks to become fully pigmented while *L. tropica* takes only about two weeks. The pigmentation schedule of conidia has been considered a significant feature for species identification in *Lasiodiplodia* (Dou et al. 2017). Therefore, we introduced this collection as *Lasiodiplodia morindae* sp. nov.

Trypetheliales Lücking, Aptroot & Sipman

The order was introduced by Aptroot et al. (2008) to separate a group of pyrenocarpous lichen-forming fungi previously considered to be a part of Pyrenulales (Eurothiomycetes). The reason for this was a discovery by Del Prado et al. (2006) that members of the order form a separate lineage within Dothideomycetes instead of being a part of Eurothiomycetes. It contains two families with 21 genera, including Trypetheliaceae, one of the most diverse families of pyrenocarpous lichen-forming fungi (Aptroot and Lücking 2016; Wijayawardene et al. 2022).

Polycoccaceae Ertz, Hafellner & Diederich

The family was recently established by Ertz et al. (2015) to place lichenicolous fungi from the genera *Clypeococcum* D. Hawksw. and *Polycoccum* Saut. ex Körb. which were revealed as a well-supported lineage sister to Trypetheliaceae.

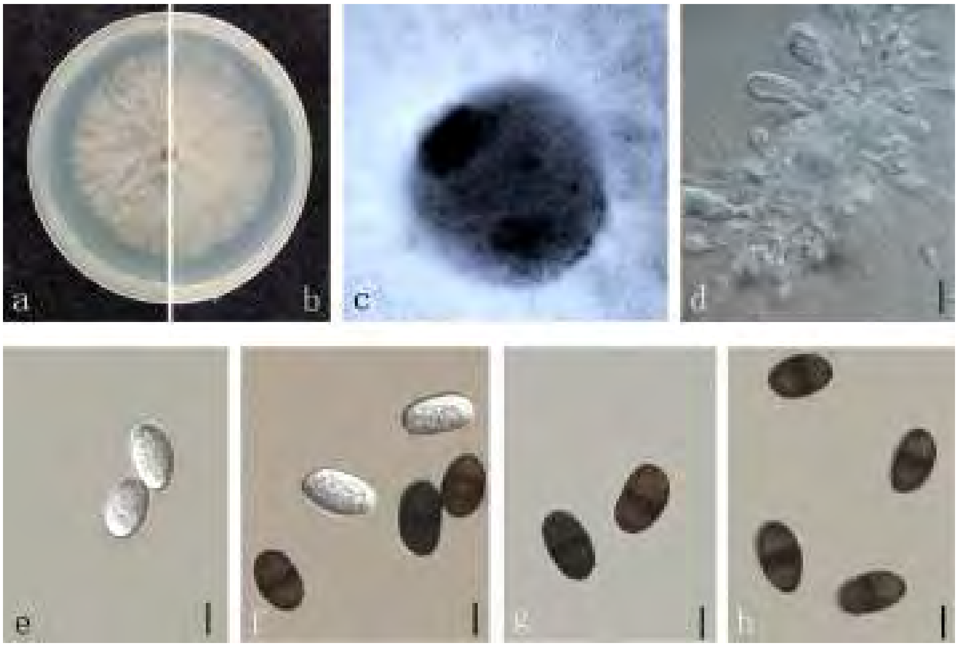


Fig. 60 ***Lasiodiplodia morindae*** (ZHKUCC 22-0084, **ex-holotype**). **a** Upper view of colony on PDA. **b** Reverse view of colony on PDA. **c** Pycnidium on PDA. **d** Conidiogenous cells with developing conidia. **e–h** Conidia (hyaline immature conidia, brown mature conidia). Scale bars: d–h = 10 µm

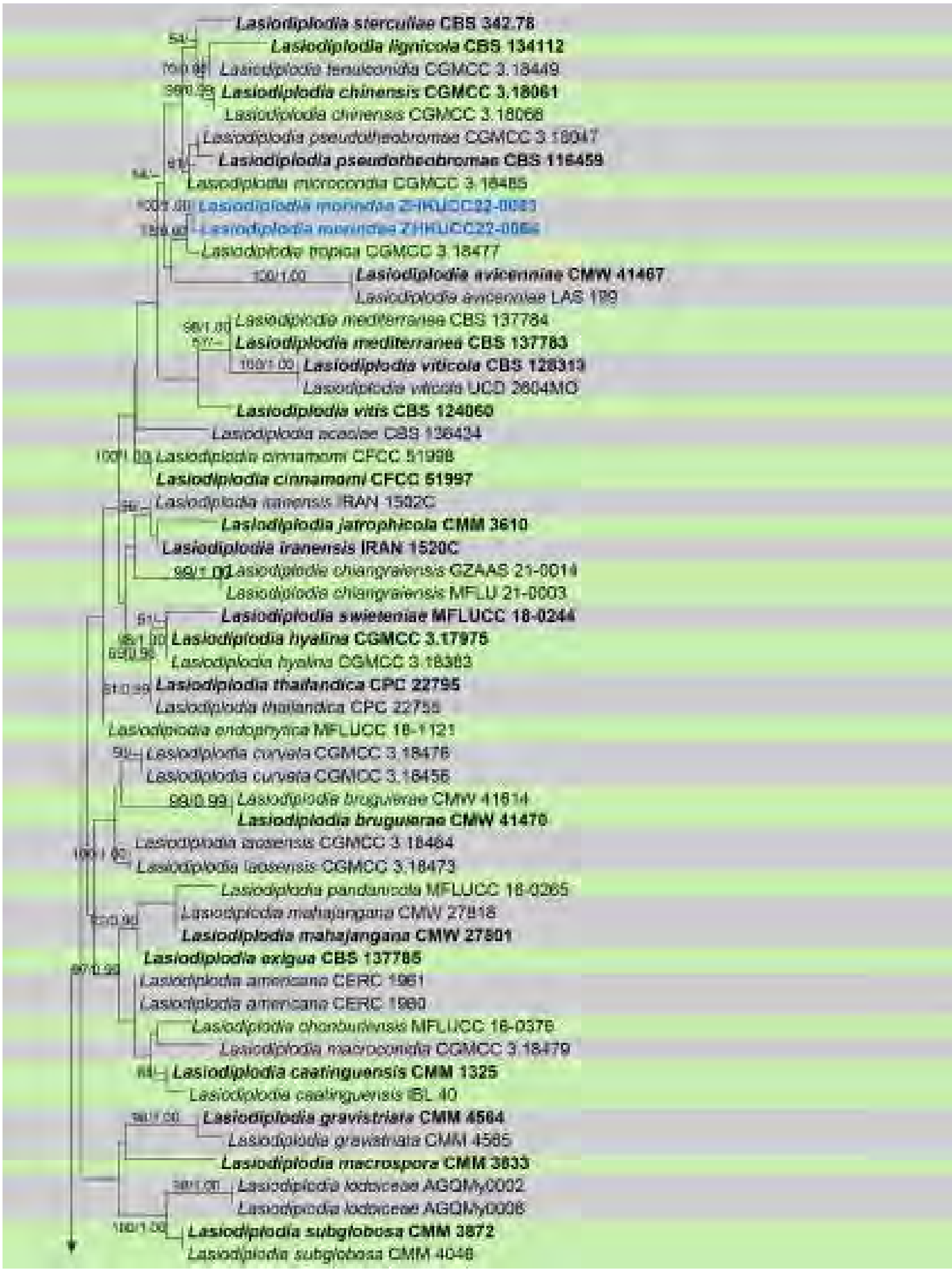


Fig. 61 The best scoring RAxML tree for combined dataset of ITS, *β-tubulin* and *tef*1-*α* sequence data of *Lasiodiplodia*. The topology and clade stability of the combined gene analyses was compared to the single gene analyses and there was no significant difference between them. The tree is rooted to *Diplodia mutila* (CMW 7060). The matrix had 306 distinct alignment patterns with 13.19% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.209302, C = 0.309977, G = 0.254177, T = 0.226543; substitution rates AC = 0.878409, AG = 3.555855, AT = 0.948385, CG = 0.796113, CT = 5.584748, GT = 1.0; gamma distribution shape parameter α = 0.132147 with a final likelihood value of − 3623.854076. Ex-type strains are in bold and newly generated sequences are in blue bold. Bootstrap support for ML equal to or greater than 50% and BI equal to or greater than 0.90 are given at the nodes

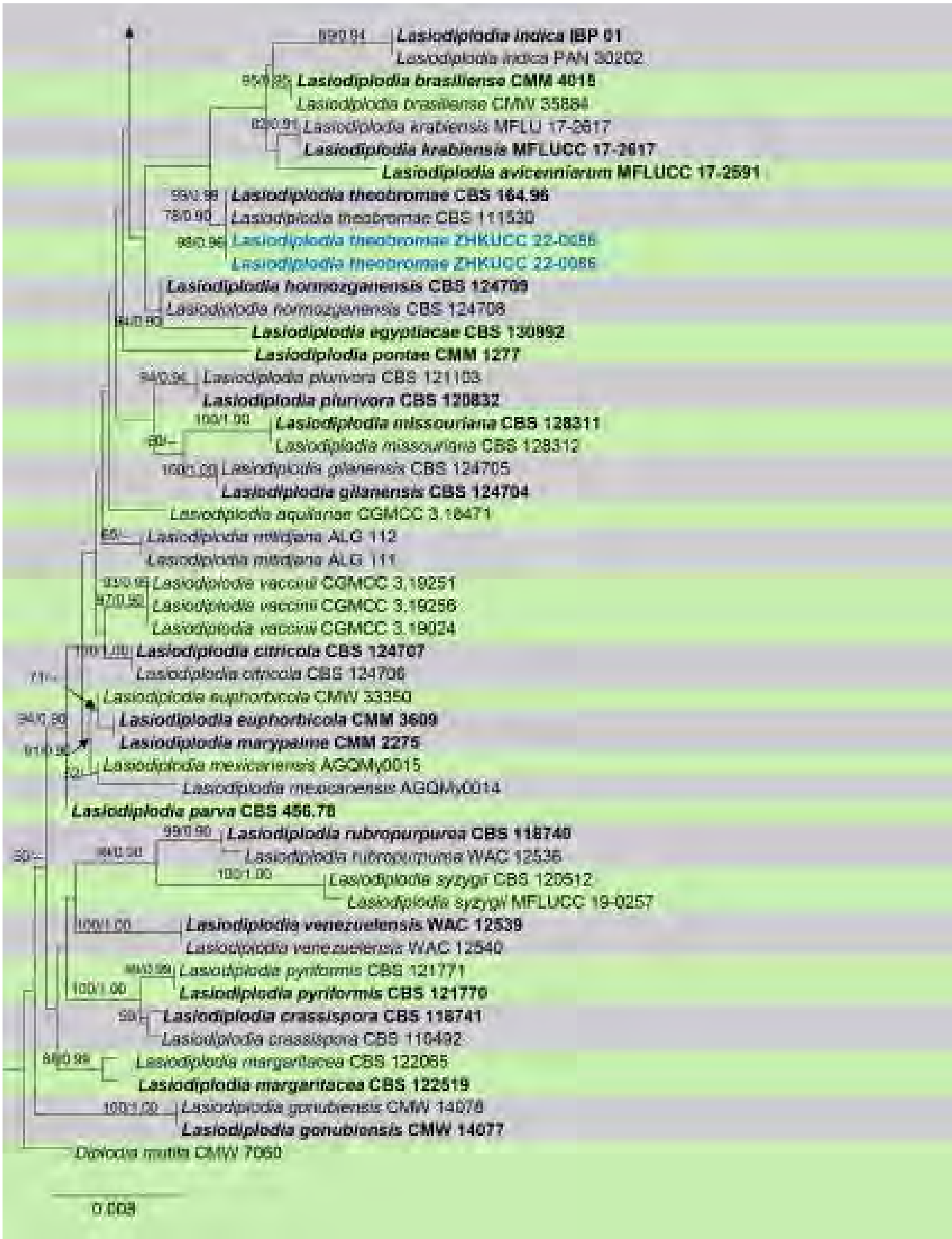


Fig. 61 (continued)

Clypeococcum D. Hawksw.

The genus is very similar to *Polycoccum* and mainly differs by elongated cells in ascomatal walls and by developing ascomata in groups under a common clypeus (Hawksworth 1977). There are more than 10 accepted species of *Clypeococcum* (Diederich et al. 2018). As shown by Ertz et al. (2015), *Clypeococcum* nests within *Polycoccum* and it is not clear whether it should be considered its later synonym or if *Polycoccum* has to be split into several genera. In this study, we introduce a new *Clypeococcum* species.

Clypeococcum lichenostigmoides Flakus, Etayo & Rodr. Flakus, ***sp. nov.***

Index Fungorum number: IF900422; *facesoffungi number*: FoF 14177; Fig. 62

Etymology: The epithet refers to the strongly developed vegetative hyphae of the species, radially spreading over the host thallus, giving the appearance of a member of the genus *Lichenostigma*.

Diagnosis: The new species differs from other species of *Clypeococcum* by having strongly developed vegetative hyphae radially spreading over the host thallus, 4–8-spored asci, dark greenish-grey to brown, 1-septate, strongly verrucose ascospores of size 10–($\bar{x}$ = 18.6 ± 2.1)–24 × 8–($\bar{x}$ = 9.8 ± 0.6)–11 µm, and its host selection (*Lecanora rupicola* group).

Lichenicolous. Growing on saxicolous lichen of *Lecanora rupicola* species complex (thallus C + yellow) in humidity high, Andean vegetation and break the host thallus detaching from the substrate. **Sexual morph**: *Mycelium* well-developed, composed of pale to dark brown, usually verrucose, vegetative hyphae, immersed and radially spreading over the host thallus, (1.5–)3–4 µm wide, often developing 1–5 × 0–2 septate, dark brown conidia (7–35 × 4–10 µm). *Pseudothecia* globose to subglobose, black, matt, ostiolate, 150–250 µm diam., 150–200 µm high, immersed, arising singly or aggregated in groups, covered by black, common clypeus. *Clypeus* forming a rounded, convex, black patch, in section dark brown, 40–50 µm high. *Pseudothecial wall* proso- to paraplectenchymatous in transversal section, 15–30 µm wide, composed of several layers of narrowly elongated to almost isodiametric, dark-brown, pigmented cells, K + greyish brown, N + slightly reddish-brown. *Hymenium* hyaline, I–, K/I–. *Pseudoparaphyses* persistent, hyaline, filiform, scarcely branched and anastomosing, 1.5–2.5 µm thick, slightly constricted at the septum. *Asci* bitunicate, subcylindrical, short-stalked, with evident tholus, I–, K/I– (endoascus K/I + orange), 60–110 × 15–23 µm, 4–8-spored. *Ascospores* broadly ellipsoid, 1–septate, with almost equal cells or with larger upper cell, constricted at the septum, with torus-like structure (stronger pigmented at the septum), walls 0.5–2.0 µm wide, dark greenish grey to brown, guttulate, strongly verrucose, with thin gelatinous coat, 10–($\bar{x}$ = 18.6 ± 2.1)–24 × 8–($\bar{x}$ = 9.8 ± 0.6)–11 µm, l/b ratio 1–($\bar{x}$ = 1.9 ± 0.3)–3 (n = 54). **Asexual morph**: Undetermined.

Material examined: Bolivia, Cochabamba Department, Tiraque Province, Parque Nacional Carrasco, Camino de los Nubes-Cotany Alto road, 17° 17′ 28″ S, 65° 44′ 05″ W, 4146 m, open high Andean vegetation, on saxicolous *Lecanora rupicola* species complex, 2 December 2014, A. Flakus 26078 (KRAM-L 73247 **holotype**, LPB **isotype**); Department La Paz, Nor Yungas Province, Pongo, S slope, rocky stream with grasslands and *Polylepis* sp., 16° 19′ 26″, 67° 57′ 18″, 3700 m, on grey *Lecanora rupicola* on rocks, 25 May 2011, J. Etayo 26875, 26876 (LPB, herb. Etayo).

GenBank number: LSU: OR133231

Notes: Our phylogenetic analyses (Fig. 63) based on LSU dataset confirmed the phylogenetic placement of our collection (KRAM-L 73247) in *Polycoccum* (Polycoccaceae) grouped with *P. clauzadei* and several species of *Clypeococcum*. Ertz et al. (2015) mentioned the phylogenetic placement of *P. clauzadei* within *Clypeococcum* and consider as a wrong identification. Further phylogenetic analyses are required to clarify the phylogeny of *P. clauzadei.*

This new collection is characterized by strongly developed, vegetative hyphae, radially spreading over the host thallus, 4–8-spored asci, and broadly ellipsoid, dark greenish-grey to brown, verrucose ascospores. Morphology of our collection fits to *Clypeococcum* by aggregated ascomata covered by a common clypeus, persistent pseudoparaphyses and dark-pigmented septate ascospores (Hawksworth 1977; Hawksworth and Diederich 1988). Our collection however, differs from other *Clypeococcum* species by having strongly developed vegetative hyphae radially spreading over the host thallus, 4–8-spored asci, dark greenish-grey to brown, 1-septate, strongly verrucose ascospores of size 10–($\bar{x}$ = 18.6 ± 2.1)–24 × 8–($\bar{x}$ = 9.8 ± 0.6)–11 µm, and its host association on *Lecanora rupicola*. Similar vegetative hyphae (but less developed) have been observed and described for *C. bisporum* form Alaska and Siberia (Zhurbenko 2009a). *Clypeococcum bisporum* is a parasite of *Cetraria laevigata* and *Flavocetraria cucculata* and comprises 2-spored asci with larger and narrower ascospores [(17–)20–27(–35) × (4–)5–5.5(–6) µm, l/b ratio = (3.0–)3.6–5.3(–7.8)]. The members of *Clypeococcum* are mainly parasites of macrolichens, such as *Cetraria*, *Flavocetraria*, *Parmotrema*, *Umbilicaria* and *Xanthoparmelia*. Only four species of *Clypeococcum* are known to be parasites of microlichens viz. *C. epimelanostolum* (of *Buellia melanostola*), *C. galloides* (of *Lecidea* s. lat.), *C. placopsiiphilum* (of *Placopsis*) and *C. hypocenomycis* (of *Hypocenomyce scalaris*) (Hawksworth 1980; Øvstedal and Hawksworth 1986; Grube and Hafellner 1990; Etayo 2017). Despite the different host preferences above species differ in several characteristics from our collection. *Clypeococcum epimelanostolum* has smaller ascomata (90–120 µm diam.), much smaller 4-spored asci (30–35 × 12–15 µm) and smaller ascospores (8–10 × 5–7 µm) (Øvstedal and Hawksworth 1986). *Clypeococcum galloides* is characterized by (2–)4-spored asci of size 48–60 × 10–12 µm and small ascospores reaching 11.5–14(–16) × 5.5–7(–8) µm (Etayo 2017). *Clypeococcum hypocenomyces* develops consistently 8-spored smaller asci (45–55 × 12–15 µm) and smaller ascospores (9–)10–12(–13) × (4–)5–6(–6.5) µm (Hawksworth 1980). *Clypeococcum placopsiiphilum* differs in its small ascomata reaching about 100 µm diam., 8-spored

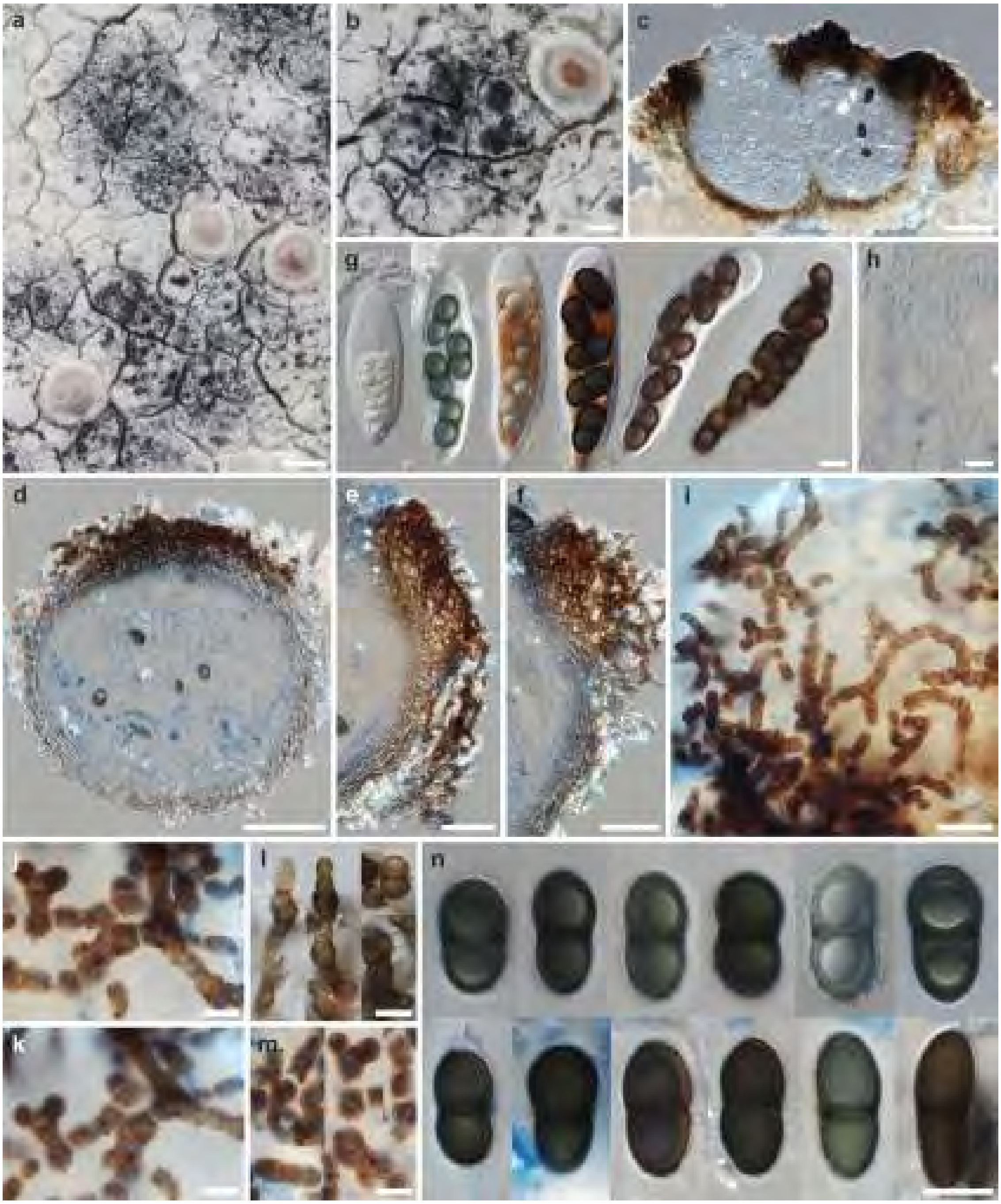


Fig. 62 ***Clypeococcum lichenostigmoides*** (KRAM-L 73247; **holotype**). **a**–**b** Habit of ascomata and vegetative hyphae radially spreading over the thallus of *Lecanora rupicola*. **c** section of two aggregated pseudothecia covered by thick common clypeus (mounted in distilled water). **d** Section of single pseudothecium showing prosoplectenchymatous wall (mounted in LPCB). **e** Pseudothecial wall with dark brown vegetative hyphae proliferating from its basal part (mounted in LPCB). **f** Pseudothecial wall with dark brown vegetative hyphae proliferating from its apical part (mounted in LPCB). **g** 4–8-spored asci mounted in Lugol's solution pretreated by 10% KOH. **h** Branched and anastomosing pseudoparaphyses (mounted in LPCB). **i** Vegetative hyphae (mycelium) immersed in the host thallus (mounted in LPCB). **j**–**k** Vegetative hyphae mounted in LPCB. (**j** With visible septation, **k** Showing verrucose walls). **l**–**m** Conidia produced by vegetative hyphae (**l** mounted in 10% KOH **m** mounted in LPCB). **n** Ascospores mounted in distilled water (upper row) and LPCB (lower row). Scale bars: a = 500 μm, b = 250 μm, c–d = 50 μm, e, f, i = 25 μm, g, h, j–n = 10 μm

Fig. 63 Phylogenetic reconstruction of the systematic position of *Clypeococcum lichenostigmoides* within Polycoccaceae inferred from ML analyses of nuLSU rDNA dataset. *Laurera megasperma* (Trypetheliaceae) was used as outgroup. Bold branches represent either bootstrap values ≥ than 70 and/or Bayesian posterior probabilities ≥ than 0.95

asci and smaller ascospores of 15.5–18 × 8–10 µm (Øvstedal and Hawksworth 1986; Grube and Hafellner 1990). Therefore, we introduce our collection as *Clypeococcum lichenostigmoides*.

Aspergillaceae Link

We follow the latest treatment and updated accounts of Aspergillaceae in Hyde et al. (2019a), Houbraken et al. (2020), and Crous et al. (2021).

Penicillium Link.

The generic name *Penicillium* was introduced by Link (1809) and designated *P. expansum* as the type species. Conventional morphology-based identification positioned this genus in Trichocomaceae (Pitt and Samson 1993). Houbraken and Samson (2011) segregated Trichocomaceae and placed *Penicillium* in Aspergillaceae along with its sister genus *Aspergillus*. Although, the well-defined key characteristics were noted in *Penicillium*. However, species circumscription is problematic due to outdated keys, and valid species list and the absence of a verified complete sequence database. Furthermore, Visagie et al. (2016) redefined the circumscription of *Penicillium* following a polyphasic taxonomic approach. Strict protocols were established for media, incubation conditions, macro and micromorphology and genes for identification and phylogeny. Recently, the classification of *Penicillium* was redefined by Houbraken et al. (2020). They segregated the genus into two subgenera which are *Aspergilloides* and *Penicillium*, comprise 32 sections and 100 sections respectively. In this study, we described six *Penicillium* species that reported in India for the first time.

Penicillium globosum L. Cai, Houbraken & X.Z. Jiang, in Diao et al., Cladistics: https://doi.org/10.1111/cla.12365, 16 (2018).

Index Fungorum number: IF818149; *Facesoffungi number*: FoF11432; Fig. 64

Holotype: HMAS 247726

Culture characteristics: Colonies growing after 5 days at 25 ± 2 °C on following agar media: **CYA** colonies medium growing, sulcate, slightly umbonate towards centre, filiform mycelia, cottony, mycelium greyish green (26E4), 11–12 mm in diam.; margins irregular, deep; sporulation greyish green (27E5) to white (26A1); exudate absent; soluble pigment absent; reverse filamentous, mycelia deep green (29E8) with the outline of white, sporulation greyish green (25D4) to cream (4A3). **MEA** colonies medium growing, velutinous, flat, powdery, dull green (26D3) mycelia, 13–14 mm in diam.; margins regular; sporulation greyish green to ocean green with the white periphery, often raised centrally; exudates absent; soluble pigments absent; reverse mycelia oyster grey (2C2), yellowish-white (1A2), yellowish-grey (3B2), pistachio green (28C4), greyish-green (29B3), sporulation white (29A1). **CYAS** colonies slow-growing, floccose, cottony, umbonate, mycelia greyish green (26B1), 10 mm in diam.; margin irregular; sporulation greyish green (26C3) and white; exudates absent; soluble pigments absent; reverse wrinkled, white (6D4) mycelia, brownish beige in between periphery and mycelia, sporulation white (6A1). **OA** colonies fast-growing, slightly suppressed, powdery, mycelia greyish green (26E5), 20 mm in diam.; margin regular; sporulation white (26A1) to greenish-white (26A2); exudates absent; soluble pigments absent; reverse mycelia white, sporulation greenish-white (27A2). **CZ** colonies slow-growing, powdery, flat, cream (4A3), 3–5 mm in diam.; margin irregular; exudates absent; soluble pigments absent; reverse yellowish-white (4A2) mycelia, sporulation cream (4A3). **DG18** colonies slow-growing, flat, cottony, mycelium silver white (2B2), 8–9 mm diam.; margin irregular; sporulation whit; exudates absent; soluble pigments absent; reverse mycelia silver white (2B3), sporulation white. **YES** colonies fast-growing, sulcate, cottony, umbonate towards mycelia, filiform mycelia, mycelia greyish green, 24–25 mm diam.; margin irregular; sporulation white; exudates absent; soluble pigments absent; reverse filamentous, mycelia jade green (27E5), sporulation white. **CREA** colonies flat, cottony, orange white (5A2) mycelia,

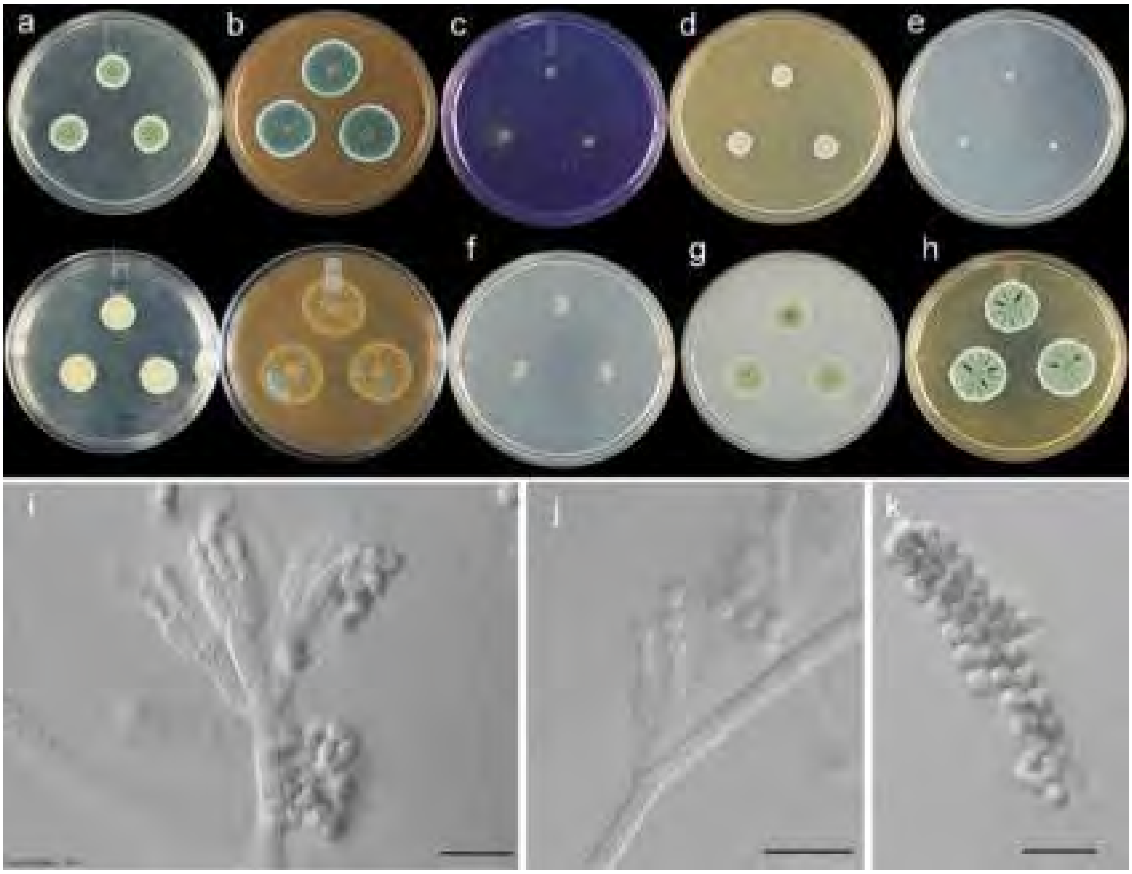


Fig. 64 ***Penicillium globosum*** (NFCCI 5061). **a, b** Colonies after 5d at 25 ± 2 °C on CYA, MEA surface view (above) and reverse view (below). **c**–**h** Surface view of colony on CREA, CYAS, CZA, DG18, OA, YES. **i** Biverticillate penicilli. **j** Monoverticillate penicilli. **k** Conidia. Scale bar: i–k = 10 µm

8–9 mm in diam.; margin irregular; sporulation white; reverse pastel yellow (3A4), mycelia greyish orange (5D6), white sporulation; acid production present.

Micromorphology: *Conidiophores* predominantly biverticillate, rarely monoverticillate; *stipes* rough walled, 40–150 × 3.2–4 µm. *Metulae* 2–4 per stipe, predominantly divergent, 7.5–20.5 × 2.5–4 µm. *Phialides* ampulliform, 2–19 per metulae, 7.5–13 × 2.5–4 µm. *Conidia* smooth, globose to subglobose, 3.4–4.1 × 2.5–3.8 µm; *sclerotia* not observed.

Material examined: India, Tamil Nadu, Madurai City, (09° 55′ 35″ N 78° 07′ 23″ E), from soil sample, 6 August 2019, K.C. Rajeshkumar and S. Raveendran, NFCCI 5061.

Substrates and distribution: In acidic soil in China and Australia; rainforest soil from Malaysia; industrial installations in Netherlands; soil in *Citrus* grove in Florida, USA (Calabon et al. 2022), soil and freshwater from Korea (Pangging et al. 2021).

GenBank numbers: ITS: OK342120, *BenA*: OL652653, *CaM*: OM948800, *rpb2:* OL652657.

Notes: Based on concatenated phylogenetic analyses of ITS, *BenA*, *CaM*, and *rpb2* gene loci, our strain (NFCCI 5061) aligns with the type strain of *Penicillium globosum* (CBS144639) and *P. cataractum* (CBS 140974). These two *Penicillium* species shared identical ITS sequences (Diao et al. 2018) and therefore, both species grouped together in the ITS phylogeny.

Our collection and type strain of *P. globosum* share the same morphological characters, such as biverticillate penicilli, globose to sub-globose conidia and smooth ornamentation. Therefore, we identified our collection as *P. globosum* and this is the first report of *P. globosum* from India.

Penicillium hirayamae Udagawa, J. Agric. Soc. Tokyo Nogyo Daigaku 5: 6. (1959)

Index Fungorum number: IF302402; *Facesoffungi number*: FoF 11431; Fig. 65

Holotype: CBS 229.60

Culture characteristics: Colonies growing after 5 days at 25 ± 2 °C on following agar media: **CYA** colonies slow growing, deep radial sulcations, cottony, velvety, flat, mycelium white 8–9 mm in diam.; margins irregular; sporulation greyish green (26E4); exudate absent; soluble pigment absent; reverse filamentous, mycelia reddish-orange (7A6), sporulation yellowish-white (2A2). **MEA** colonies medium growing, cottony, radially sulcate, flat, velutinous to somewhat floccose, mycelia chrome yellow (3A8),12–14 mm in diam.; margins irregular; sporulation yellow (3A6) to reddish-yellow (4A6); exudates present; soluble pigments absent; reverse mycelia yellow (3A6), sporulation white. **CYAS** colonies slow-growing, slightly sulcate, floccose, umbonate, mycelia yellow (3A7), 12–13 mm in diam.; margin irregular, deep; sporulation dark green (26F5); exudates absent; soluble pigments absent; reverse wrinkled, light yellow (3A5). **OA** colonies slow-growing, cottony, sporulation white, mycelia reddish yellow (3A5),7–8 mm in diam.; margin regular, flat; exudates present, deep yellow (4A8); soluble pigments absent; reverse mycelia pastel yellow, sporulation light yellow (4A4). **CZ** colonies slow-growing, flat, cottony, flat, mycelia greyish yellow (4B6), sporulation white, 3 mm in diam.; margin irregular; exudates absent; soluble pigments absent; **DG18** colonies slow-growing, cottony, smooth, planar, mycelium light yellow (3A5), 5–6 mm diam.; margin irregular; exudates absent; soluble pigments absent; reverse white. **YES** colonies slow-growing, floccose, umbonate, radiating sulcate, sporulation greenish-white, mycelia pastel yellow (3A4), 18 mm diam.; margin irregular; exudates absent; soluble pigments absent; colony reverse rhizoid, white. **CREA** colonies cottony, slightly umbonate, suppressed, half mycelia yellow (3A8) and greyish green (26E4), 5 mm in diam.; margin irregular; acid production present; soluble pigment present, light yellow (3A4); reverse colony flat, mycelia yellowish red (8B8), sporulation yellow (3A8).

Micromorphology: *Conidiophores* strictly monoverticillate, borne from funiculose aerial hyphae. *Stipes* 10–50 × 2.5–3 µm, smooth-walled, with apices usually vesiculate. *Phialides* ampulliform, 5 – 8 per conidiophore, 6 – 10 × 2 – 2.5 µm. *Conidia* sub-spheroidal, 1.5 – 3 × 1.5 – 2.5 µm, smooth-walled, borne in long columns.

Hosts and distribution: Milled rice from Thailand, South Africa

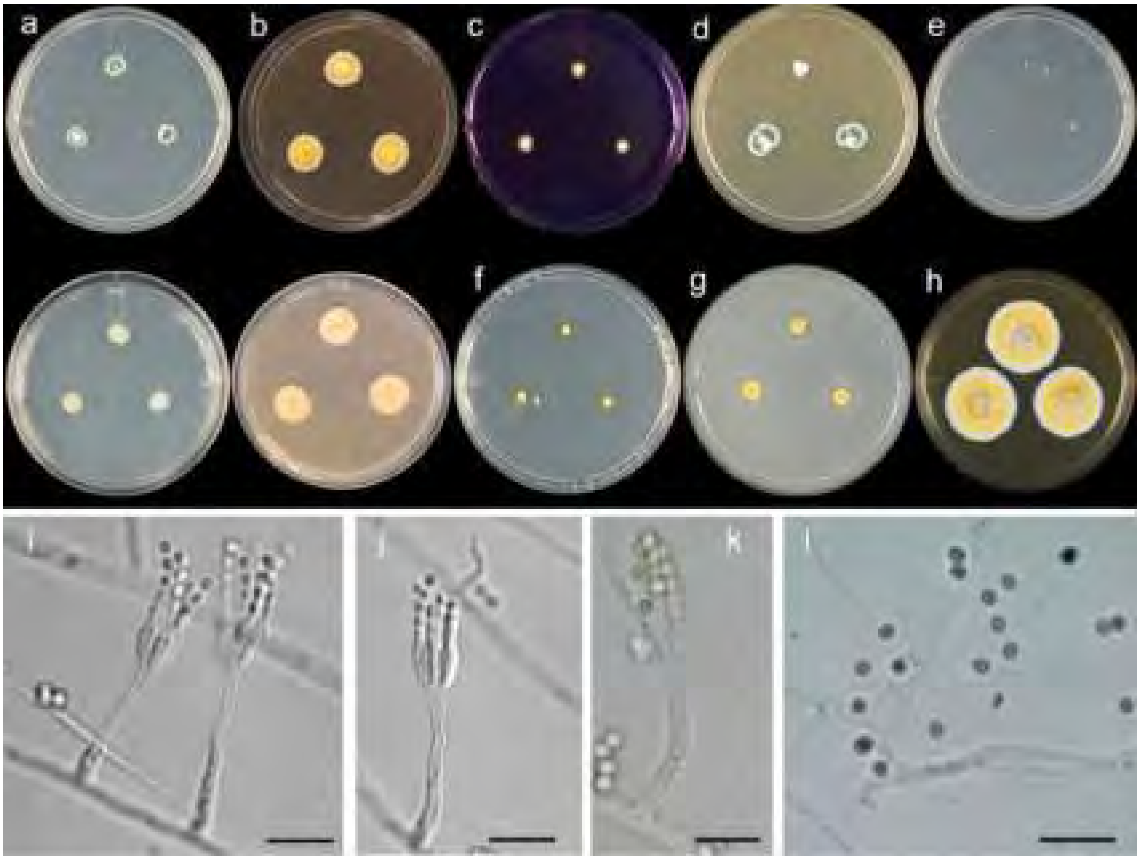


Fig. 65 ***Penicillium hirayamae*** (NFCCI 5062). **a, b** Colonies after 5 days at 25 ± 2 °C on CYA and MEA surface view (above) and reverse view (below). **c**–**h** Surface view of colony on CREA, CYAS, CZA, DG18, OA, YES. **i**–**k** Monoverticillate penicilli. **l** Conidia. Scale bar: i–l = 10 µm

Material examined: India, Maharashtra, Thane (19° 12′ 57″ N, 72° 59′ 31″ E) from soil, 26 December 2017, K.C. Rajeshkumar and Nikhil Ashtekar, NFCCI 5062.

GenBank numbers: ITS: OK342195, *BenA*: OL652652, *CaM*: OM948801, *rpb2:* OL652656.

Notes: Our isolate (NFCCI 5062) clustered with the type stain of *Penicillium hirayamae* (CBS 22960) in the combined ITS, *BenA*, *CaM*, and *rpb2* loci analyses with ML/BI = 100%/1.00 statistical support. Similarly, both strains have the same morphological features such as strictly monoverticillate conidiophore branching pattern and sub-spheroidal conidia with smooth ornamentation. Therefore, we identified our isolate (NFCCI 5062) as *P. hirayamae* and this is the first record of this species from India.

Penicillium raperi G. Sm., Trans. Br. Mycol. Soc. 40(4): 486 (1957)

Index Fungorum number: IF302421; *Facesoffungi number*: FoF 11433; Fig. 66

Holotype: CBS 281.58

Culture characteristics: Colonies growing after 5 days at 25 ± 2 °C on following agar media: **CYA** colonies medium growing, deep radial sulcations, cottony, slightly, umbonate, cottony, velutinous to floccose, mycelium white, 11–12 mm in diam.; margins regular, deep; sporulation pale yellowish-white (2A2); exudate absent; soluble pigment absent; reverse filamentous, mycelia brown (6F4), sporulation white. **MEA** colonies medium growing, velutinous, slightly umbonate, cottony, (1C4) light grey mycelia, radially sulcate, often raised centrally, velutinous to somewhat floccose, 18–20 mm in diam.; margins regular; sporulation greyish white (6A1); exudates absent; soluble pigments absent; reverse radiate, cream (4A3). **CYAS** colonies moderate growing, floccose, radially sulcate, slightly suppressed, mycelia pale grey (3B1), white, pale grey (3B1), 18–20 mm in diam.; margin regular, deep; sporulation white; exudates absent; soluble pigments absent; reverse wrinkled, mycelia brownish grey (6F8), cream sporulation. **OA** colonies moderate growing, planar, filiform mycelia, cottony, suppressed, mycelia greyish green (29B4), 18–20 mm in diam.; margin regular; sporulation white; exudates colourless; soluble pigments absent; reverse white greyish brown (6D3), sporulation pale yellow

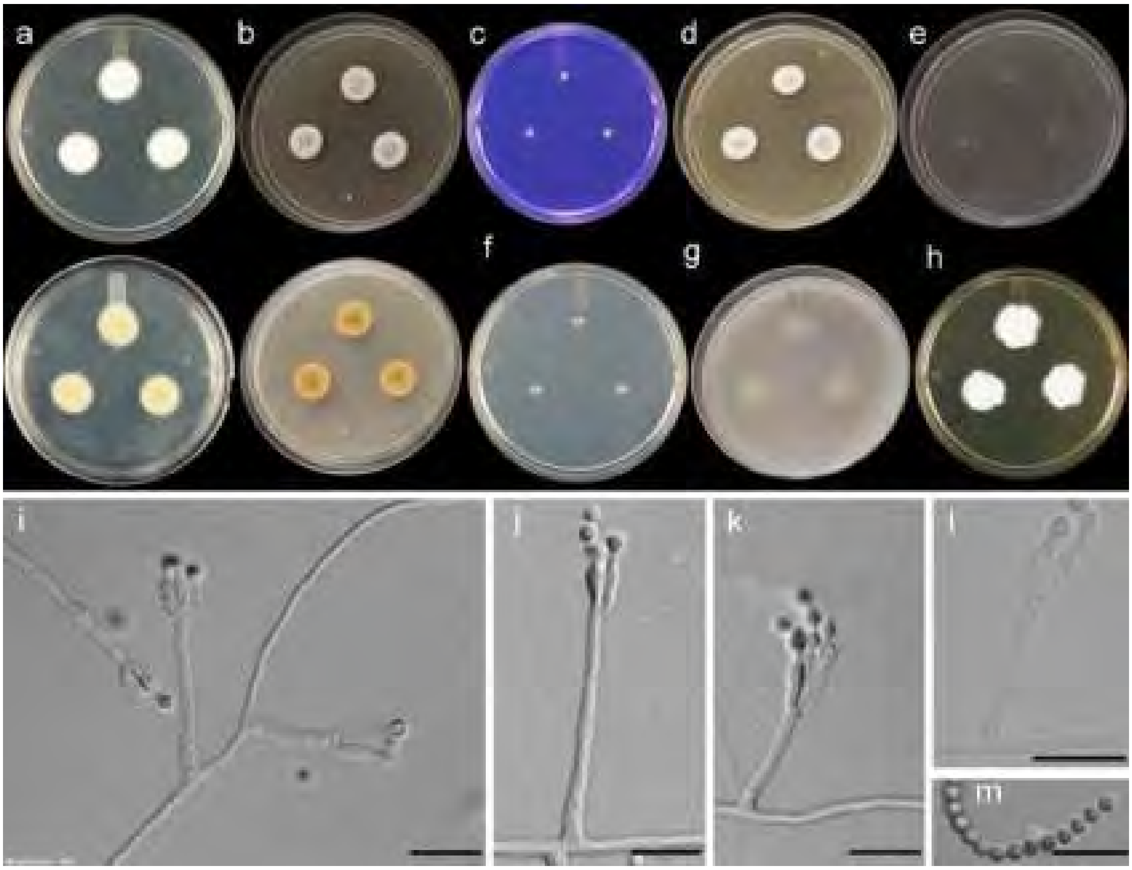


Fig. 66 ***Penicillium raperi*** (NFCCI 5066). **a, b** Colonies after 5 days at 25 ± 2 °C on CYA and MEA obverse and reverse. **c – h** CREA, CYAS, CZA, DG18, OA, YES. **i – l** Monoverticillate penicilli. **m** Conidia. Scale bar: i – m = 10 µm

(2A3). **CZ** colonies slow-growing, flat, granular, radiate, cottony, flat, pale yellowish-white (2A2) mycelia, 9 mm in diam.; margin irregular; sporulation white; exudates absent; soluble pigments absent; reverse pastel yellow (2A4) mycelia, white sporulation. **DG18** colonies slow-growing, planar, mycelium white, 4–5 mm diam.; margin regular; exudates absent; soluble pigments absent; reverse white (1A1). **YES** colonies medium growing, floccose, cottony, umbonate, slightly sulcate, mycelia pale yellow (4A3), sporulation medium grey (4E1), 20–21 mm diam.; margin irregular; exudates absent; soluble pigments absent; reverse wrinkled, mycelia golden (4B6), pastel yellow (3A4), sporulation pale yellow (3A3). **CREA** colonies 4—5 mm in diam.; margin regular; acid production present.

***Micromorphology**: Conidiophores* predominantly monoverticillate with occasionally a divaricate branch. *Stipes* smooth-walled, slender and long (200–800 × 2.0–3.0 µm), with vesicular apices up to 3—5 µm, vesicle bearing 6 – 10 phialides. *Phialides* ampulliform with a distinct neck, 8–11.5 × 3–4 µm. *Conidia* smooth or finely rough-walled, globose to broadly ellipsoidal 2.5–3.5 × 2–3 µm.

Material examined: India, Jammu and Kashmir, Kishtwar (33° 28′ 58″ N, 75° 50′ 51″ E), from soil, 20 March 2019, K.C. Rajeshkumar and Nikhil Ashtekar, NFCCI 5066.

Substrates and distribution: Soil in Great Britain

GenBank numbers: ITS: OK345044, *BenA*: OL652648, *CaM*: OM948805, *rpb2*: OL652654.

Notes: In the multilocus phylogenetic analyses of the ITS, *BenA*, *CaM* and *rpb2* genes shows that our isolate (NFCCI 5066) clustered with the neotype stain of *Penicillium raperi* (NRRL2674 = CBS 218.58) with ML/BI = 100%/1.00 statistical support. Further, NFCCI 5066 has similar morphological characters with the neotype such as predominantly monoverticillate branching with smooth and globose conidia. Hence, we identified our collection (NFCCI 5066) as *P. raperi* based on the morphological and phylogenetic evidence and this is the first report of this species from India.

Penicillium menonorum S.W. Peterson, in Peterson, Orchard & Menon IMA Fungus 2(2): 122. (2011)

Index Fungorum number: IF519297; *Facesoffungi number*: FoF 11434; Fig. 67

Holotype: BPI881018

Culture characteristics: *Colonies* growing after 5 days at 25 ± 2 °C on following agar media: **CYA** colonies medium growing, slightly umbonate, cottony, velutinous to floccose, mycelium pea green (29D5) to greyish green (29D4), 10–11 mm in diam.; margins irregular, deep; sporulation greenish green (26D2) and white; exudates absent; soluble pigments absent; reverse filamentous, half dark green (28F8) and white colony. **MEA** colonies medium growing, velutinous, flat, umbonate, powdery, white, grey (27C1) with a combination of jade green (27E5) mycelia, 12–14 mm in diam.; margins irregular; sporulation greyish green (27C3), dark green (27F4) in between mycelia and sporulation; exudates absent; soluble pigments absent; reverse wrinkled, reverse mycelia brown (6E8), white sporulation. **CYAS** colonies moderate growing, floccose, slightly umbonate, green (28A6) mycelia, 15–18 mm in diam.; margin irregular, deep; sporulation white; exudates absent, soluble pigments absent; reverse wrinkled, reverse mycelia golden yellow (5B7), sporulation white. **OA** colonies slow-growing, planar, flat, cottony, suppressed, mycelia grey (28C1), 19 mm in diam.; margin irregular; sporulation white, green (28C6) between mycelia and sporulation; exudates colourless; soluble pigments absent; reverse white, mycelia clay (5D5), pastel green between mycelia and sporulation. **CZ** colonies slow-growing, flat, cottony, pastel yellow (3A4) mycelia, 9–10 mm in diam.; margin regular; sporulation white; exudates absent; soluble pigments absent; reverse white (1A1). **DG18** colonies slow-growing, planar, flat, cottony, suppressed, mycelium white, 8–10 mm diam.; margin irregular; exudates absent; soluble pigments absent; reverse white (1A1). **YES** colonies fast-growing, floccose, radiating sulcation, slightly umbonate, 23–25 mm diam.; margin irregular; sporulation white, half mycelia and sporulation greyish green (28E5) and half pale green (25A3); exudates absent; soluble pigments absent; reverse wrinkled, white sporulation, half dull green (26E4) to cream (4A3) mycelia and sporulation. **CREA** colonies umbonate, cottony, mycelia yellowish-white (3A2), 10–12 mm in diam.; margin regular; sporulation white; exudates present, chrome yellow, signal yellow (3A8); soluble pigment pastel yellow (3A4); acid production present; reverse deep orange to orange chrome, mycelia orange, sporulation white.

Micromorphology: *Conidiophores* monoverticillate, smooth-walled, hyaline, 5–20 × 1.5–2.0 µm, with an apical whorl of 2–5. *Phialides* 5–9 × 2.5–3.5 µm. *Conidia* spherical to subspherical, 2–3.5 µm, with roughened to rugose ornamentation.

Substrates and distribution: China, Korea, and USA

Material examined: India, Meghalaya, Shillong (25° 33′ 39″ N, 91° 52′ 57″ E) from soil, 8 August 2018, K.C. Rajeshkumar, Nikhil Ashtekar, NFCCI 5064.

GenBank numbers: ITS: OK342221, *BenA*: OL652650, *CaM*: OM948803.

Notes: In the concatenated phylogenetic analyses of ITS, *BenA*, *CaM*, and *rpb2* genes shows that our isolate (NFCCI 5064) clustered with the type stain of *Penicillium menonorum* (NRRL50410) with ML/BI = 100%/1.00 statistical support. Morphologically, both strains share the same characters such as monoverticillate conidiophores with spherical conidia having roughened ornamentation. Therefore, we identified our isolate (NFCCI 5064) as *P. menonorum* based on the morphological and phylogenetic evidence and this is a new report of this species from India.

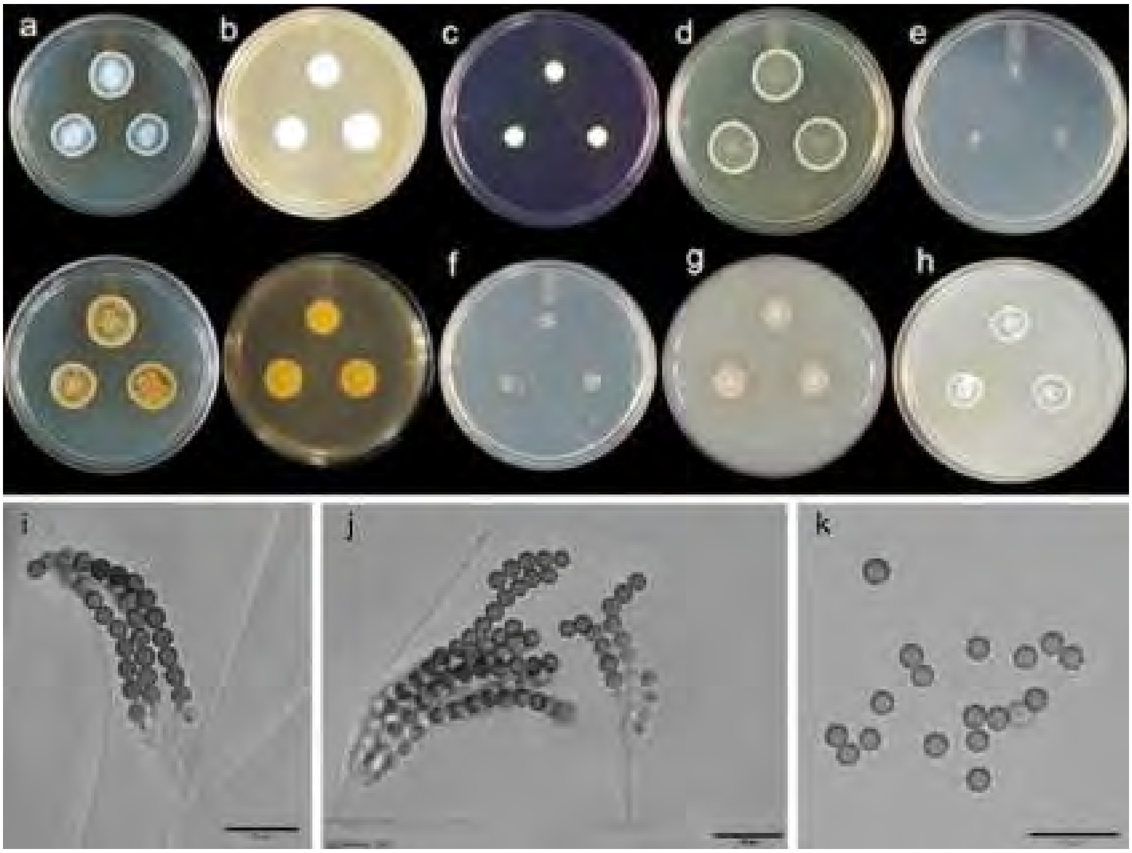


Fig. 67 ***Penicillium menonorum*** (NFCCI 5064). **a, b** Colonies after 5 day at 25 ± 2 °C on CYA and MEA obverse and reverse. **c–h** CREA, CYAS, CZA, DG18, OA, YES. **i–j** Monoverticillate penicilli with conidia. **k** Conidia. Scale bar: i–k = 10 µm

Penicillium steckii K.W. Zaleski, Bull. Int. Acad. Polon. Sci., Ser. B., Sci. Nat.1927: 469. 1927.

Index Fungorum number: IF278769; *Facesoffungi number*: FoF 11348; Fig. 68

Holotype: IMI 40583

Culture characteristics: Colonies growing after 5 days at 25 ± 2 °C on following agar media: **CYA** colonies slow-growing, umbonate, cottony, 2–4 mm in diam.; margins irregular; sporulation white; exudates colourless; soluble pigments absent; reverse wrinkled, cream. **MEA** colonies slow-growing, radially sulcate, velutinous, umbonate, powdery, mycelia pale white(1A1), 19 mm in diam.; margins regular; sporulation white, dark green (27F6) between mycelia and sporulation; exudate absent; soluble pigment absent; reverse wrinkled, mycelia ivory/natural/platinum blonde sand (4B3), sporulation white. **CYAS** colonies slow-growing, floccose, umbonate, cottony, mycelia pastel green (25A4), 9 mm in diam.; margin irregular; sporulation greenish-white (25A2); exudate absent; soluble pigment absent; reverse wrinkled, mycelia dark green (30F8), sporulation pale orange (6A3). **OA** colonies medium growing, flat, granular, powdery, mycelium grey (29E4), 12 mm in diam.; margins regular; sporulation white, greyish green (29E4) in between mycelia and sporulation; exudates colourless; soluble pigment absent; reverse mycelia greyish green, white sporulation (29A1). **CZ** colonies slow-growing, flat, granular, mycelium white (1A1), 13 mm in diam.; margins irregular; exudate absent; soluble pigment absent; reverse white (1A1). **DG18** colonies slow-growing, flat, cottony, suppressed, mycelium white (1A1), 7–9 mm in diam.; margin regular; exudates absent; soluble pigments absent; reverse white (1A1). **YES** colonies medium growing, floccose, radially sulcate, umbonate, cottony, mycelium dull green (29E3), 10–11 mm in diam.; margins irregular; sporulation white and greenish-grey (27C2) in mycelia and sporulation; exudate absent; soluble pigment absent; reverse wrinkled, mycelia dull green (27E4) to white, sporulation pale yellow. **CREA** colonies slow-growing, flat, powdery, mycelia greenish-white (26A2), pastel green (26B4) towards mycelia, 8–10 mm in diam.; margin irregular; sporulation white; acid production present, soluble pigment, pale yellow (3A3); reverse wrinkled, radiate, white sporulation (1A1), mycelia and sporulation, maize yellow (4A6) and olive-brown (4D4).

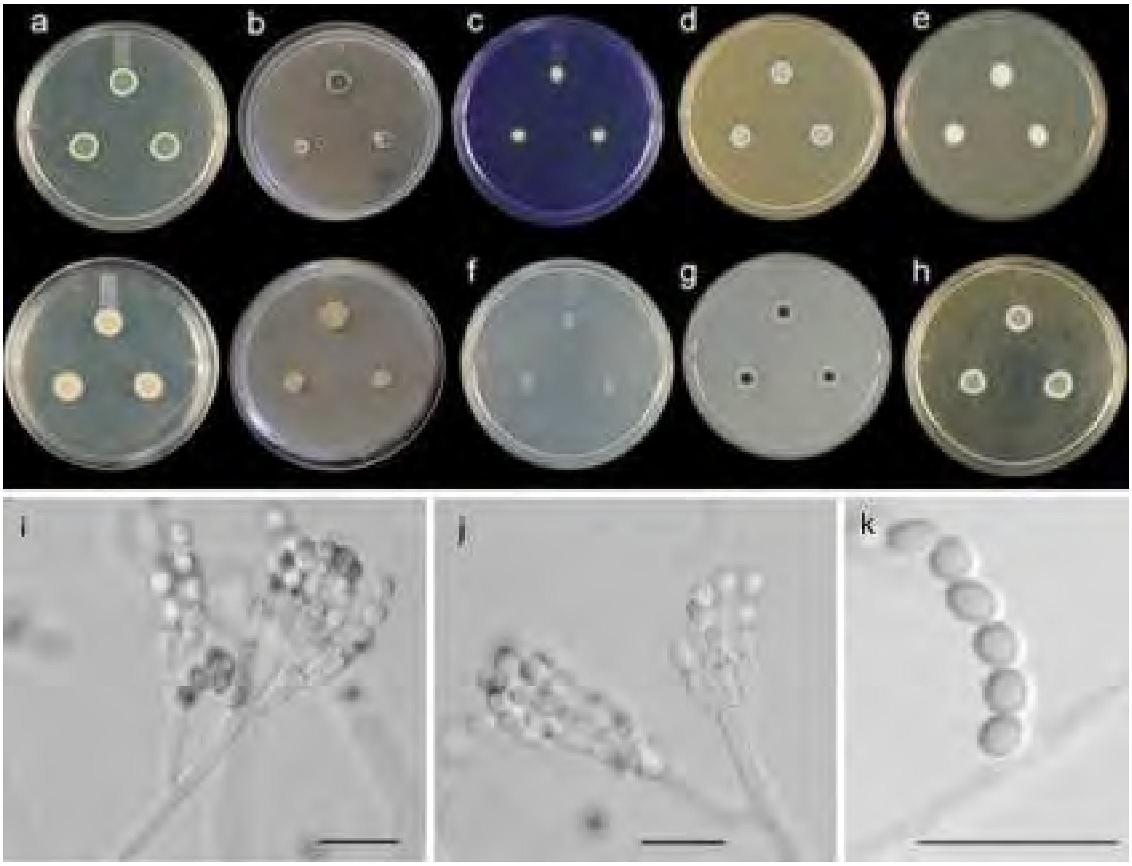


Fig. 68 ***Penicillium steckii*** (NFCCI 5065). **a, b** Colonies after 5 days at 25 ± 2 °C on CYA and MEA obverse and reverse. **c**–**h** CREA, CYAS, CZA, DG18, OA, YES. **i, j** Biverticillate conidiophore. **k** Conidia. Scale bar: i–k = 10 µm

Micromorphology: *Conidiophores* arising from mycelium mat, predominant symmetrically biverticillate, terverticillate structures abundantly produced in fresh isolates. *Stipes* smooth, width 2–3 µm. *Metulae* in whorls of 2–4, 12–16 × 2–2.7 µm. *Phialides* ampulliform, 7.5–10 × 2–2.5 µm. *Conidia* 2–2.5 × 1.8–2.5 µm, smooth-walled, globose to subglobose.

Material examined: India, Maharashtra, Pune (18° 31′ 47″ N, 73° 48′ 59″ E), from soil, 12 September 2018, K.C. Rajeshkumar, NFCCI 5065.

Substrates and distribution: Bermuda, Egypt, Indonesia, Japan, Netherlands, Panama, Slovenia, and Venezuela

GenBank numbers: ITS: OK345037, *BenA*: OL652649, *CaM*: OM948804.

Notes: The concatenated phylogenetic analyses of ITS, *BenA*, *CaM*, and *rpb2* genes reveals that our isolate (NFCCI 5065) clustered with the type stain of *Penicillium steckii* (CBS 26055) with ML/BI = 100%/1.00 statistical support. Further, both strains share the same characters such as bi-to terverticillate conidiophore branching with globose to subglobose conidia with a smooth ornamentation. Hence, we identified our collection (NFCCI 5065) as *P. steckii* based on morphology and phylogenetic analyses and this is the first report from India.

Penicillium subrubescens Houbraken, Mansouri, Samson & Frisvad, Antonie van Leeuwenhoek 103(6): 1354 (2012)

Index Fungorum number: IF801306; *Facesoffungi number*: FoF 11349; Fig. 69

Holotype: CBS H-21029

Culture characteristics: Colonies growing after 5 days at 25 ± 2 °C on following agar media: **CYA** colonies medium growing, floccose, sporulation turquoise white (24A2), 18 mm in diam.; margins irregular; exudates colourless; soluble pigments absent; reverse wrinkled, butter yellow (4A5). **MEA** colonies medium growing, radially sulcate, velutinous, sporulation pale yellow (1A3), 22 mm in diam.; margins irregular; exudate absent; soluble pigment absent; reverse sulcate, butter yellow (4A5). **CYAS** colonies slow-growing, floccose, mycelium white (1A1), 9 mm in diam.; margin irregular; exudate absent; soluble pigment absent; reverse greyish yellow (4B6). **OA** colonies medium growing, flat, granular, mycelium white, 6 mm in diam.; margins irregular; sporulation yellowish-white (1A2); exudates

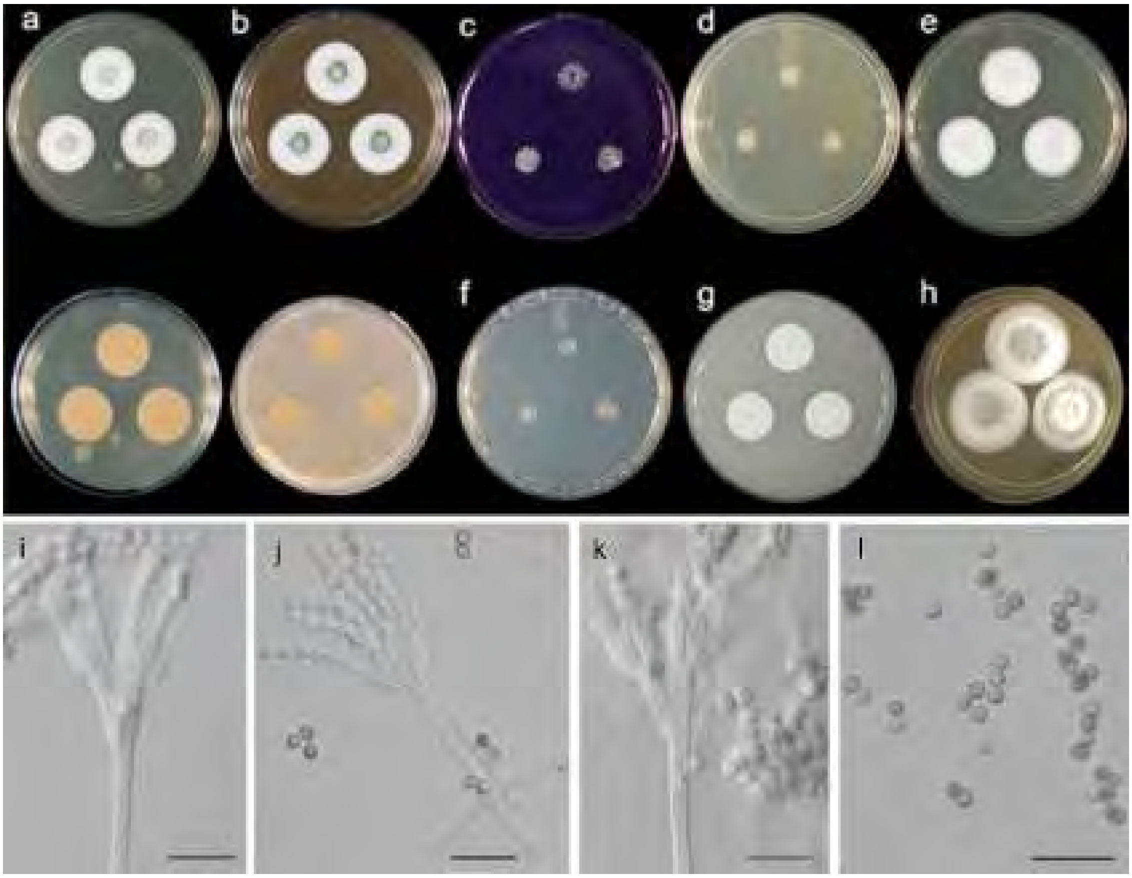


Fig. 69 ***Penicillium subrubescens*** (NFCCI 5063). **a, b** Colonies after 5 days at 25 ± 2 °C on CYA and MEA surface and reverse view. **c**–**h** CREA, CYAS, CZA, DG18, OA, YES. **i** monoverticillate conidiophore. **j**–**k** biverticillate conidiophore. **l** Conidia. Scale bar: i–l = 10 µm

colourless; soluble pigment absent; reverse yellowish-white (1A2). **CZ** colonies slow-growing, flat, granular, mycelium white (1A1), 13 mm in diam.; margins irregular; exudate absent; soluble pigment absent; reverse white (1A1). **DG18** colonies slow-growing, flat, mycelium white (1A1), 6 mm in diam.; margin irregular; exudate absent; soluble pigment absent; reverse white (1A1). **YES** colonies medium growing, floccose, mycelium white (1A1), 21 mm in diam.; margins irregular; sporulation orange white (5A2); exudate absent; soluble pigment absent; reverse wrinkled, sulcate, butter yellow (4A5). CREA 25 °C, 5 day, in darkness: Colonies slow-growing, flat 10 mm in diam.; margin irregular; acid production absent; sporulation yellowish-white (3A2); reverse white (1A1).

Micromorphology: Conidiophores predominantly biverticillate, often with one or more additional branches that also have symmetrically biverticillate structures; stipes coarsely roughened, 150–400 × 2.5–4 µm; metulae in verticils of 3 to 6, walls roughened, both equal and unequal in length, 10–15 (− 20) × 2.0– 3.5 µm; phialides ampulliform with distinct neck, with walls occasionally roughened, 7.0–9.5 × 2.0–3.5 µm; conidia subglobose to broadly ellipsoidal, smooth or finely roughened, 2.5–3.0 × 2.0–2.7 µm.

Material examined: India, Uttarakhand, Almora (29° 35′ 15″ N, 79° 35′ 46″ E), from soil, 27 February 2019, K.C. Rajeshkumar, NFCCI 5063.

Substrates and distribution: Soil of an artichoke field in Jerusalem, soil of *Helianthus tuberosus* field in Canada, Finland, Tanzania, and USA

GenBank numbers: ITS: OK345037, *BenA*: OL652649, *CaM*: OM948804, *rpb2:* OL652655.

Notes: The concatenated phylogenetic analyses of ITS, *BenA*, *CaM*, and *rpb2* genes placed our isolate (NFCCI 5063) along with the type stain of *Penicillium subrubescens* (CBS H-21029). Further, both strains have identical morphological characters such as, predominant symmetrically biverticillate conidiophore, globose to ellipsoidal conidia and smooth ornamentation. Therefore, we identified our isolate as *P. subrubescens* and this is the first record of *P. subrubescens* from India (Fig. 70).

Geoglossales Zheng Wang, C.L. Schoch & Spatafora

The monotypic order Geoglossales is typified by Geoglossaceae Corda. Members in this order are saprobes in terrestrial habitat (Hustad et al. 2013).

Geoglossaceae Corda

Species in Geoglossaceae are terrestrial and broadly known as "earth tongues" (Hustad et al. 2011). The species in Geoglossaceae are generally characterized by dark brown to black, small, club-shaped fruiting bodies with light-brown to dark-brown, multiseptate ascospores (Schoch et al. 2009). This family comprises eight genera viz. *Geoglossum* Pers., *Glutinoglossum* Hustad, A.N. Mill., Dentinger & P.F. Cannon, *Hemileucoglossum* Arauzo, *Leucoglossum* S. Imai, *Maasoglossum* K.S. Thind & R. Sharma, *Sabuloglossum* Hustad, A.N. Mill., Dentinger & P.F. Cannon, *Sarcoleotia* S. Ito & S. Imai and *Trichoglossum* Boud. There are circa 100 species in this family.

Trichoglossum Boud.

The genus *Trichoglossum* is typified by *T. hirsutum* (Pers.) Boud. *Trichoglossum* species are characterized by black or dark brown, club-shaped apothecia, inoperculate, amyloid asci, hymenial setae (presence in both ascogenous and sterile portions), apically curved or coiled, septate paraphyses and fusoid, septate ascospores. They are saprobes in soil (Mains 1954). There are 24 species listed under this genus (Index Fungorum 2023). We introduce a new *Trichoglossum* species in this study.

Trichoglossum beninense De Kesel, Hustad, A.N. Mill., Fedosova & V. Kučera, ***sp. nov.***

Index Fungorum number: IF557835; *Facesoffungi number*: FoF 13917; Fig. 71

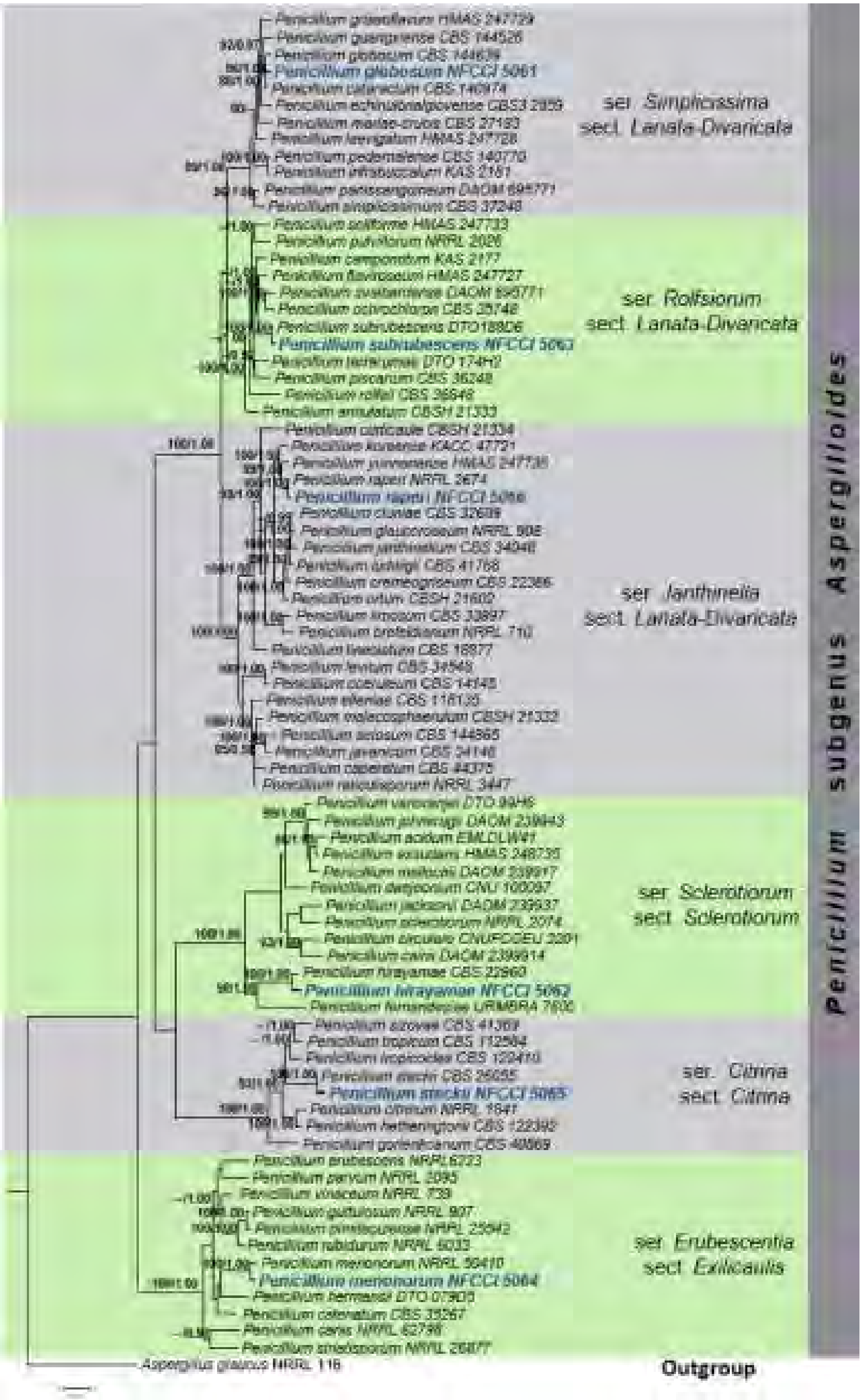
Etymology: epithet refers to Benin, West-African country where the type was found.

Fruiting bodies develop on sandy soil with some humus, usually under *Uapaca guineensis* Müll.Arg., *U. togoensis* Pax (Phyllanthaceae), *Berlinia grandiflora* Hutch. & Dalziela (Caesalpiniaceae), and *Isoberlinia doka* Craib & Stapf (Caesalpiniaceae). **Sexual morph**: *Ascomata* 20–45 mm high, capitate, stipitate, dry, hairy, black, locally with a greenish hue. *Ascigerous part* capitate or spoon-shaped, 1/5–1/3 of the total ascoma length, black, compressed, fresh with greyish-white context becoming slightly orange in longitudinal section, sharply delimited from the stipe, surface smooth and appears hairy due to discharged ascospores. *Stipe* 14–37 × 1–1.5 mm, cylindrical, terete or oval in cross section, slender, hirsute, with dark brown to black setae, when fresh blackish-orange in longitudinal section. *Hymenial layer* (230–)240–250(–260) µm thick. *Stipe surface* formed by inflated cells (13–40 × 5–12 µm) or by short chains (2–3 cells where the last cell is the most inflated) and between them setae of 120–180 × 5–11 µm (rarely up to 250 µm long), stipe base covered by dark ground mycelium, in young ascocarps sometimes ascending the stipe, composed of thin, black hyphae (33–62 × 2–2.5 µm). *Hymenial setae* rare, blackish-brown, tapered at the apex usually with protuberance (6–19 µm) in the basal part, thick-walled, (100–)125–218(–280) × (5–)5.5–7.5(–8) µm, (5–)20–30(–40) µm protruding above hymenium or (5–)25–40(–100) µm below surface of the hymenium, density above hymenium (0–)0.5(–2) pieces per 500 µm^2, density in hymenium (0–)1–2(–3) pieces per 500 µm^2. *Paraphyses* longer than asci, straight, sparsely septate, 2–4 µm wide in the middle part, hyaline at basal part, pale brown at the apex. *Apical cells of paraphyses* curved to circinate, sometimes club-shaped, slightly inflated, seldom branched (35–)47–73(–84) × (3)4.2–6.3(–8.5) µm, pale brown. *Asci* cylindrical-clavate, narrowed at the base, (201–)213–245(–268) × (15–)16–19(–25) µm, Q = (8.8–)9.8–13(–14.8), unitunicate, inoperculate, 8-spored, with euamyloid ascoapical apparatus and slightly amyloid wall in Melzer and IKI, arising from croziers. *Ascospores* elongate, subfusiform to fusiform, narrowed to the ends, sometimes slightly curved, initially 5–7-septate and (71–)122–166(–180) × (4–)4.9–6.1(–6.9)–6 µm, Q = (13.5–)22.3–30.5(–35.4) and when matured only 15-septated and (112–)139–165(–180) × (4.5–)5.1–6.1(–6.9) µm, Q = (17.6–)24.2–30.8(–35.4), brown, smooth (all measurements of microscopic characters refer to material observed in 5% KOH). **Asexual morph**: Undetermined.

Material examined: Benin, Atakora Province, Kota, N10° 12.770′ E1° 26.750′, alt. 512 m, steep and rocky gallery forest with *Uapaca guineensis* (Phyllanthaceae) on soil with humus, 15 September 2001, A. De Kesel, ADK 3172 (BR5020149821538 **holotype** deposited at BR); *ibid.*, 10° 12.680′ N 1° 26.723′ E, alt. 518 m, forest gallery with *U. guineensis* (Phyllanthaceae) and *Berlinia grandiflora* (Caesalpiniaceae), on soil, near stream and waterfall, 29 August 1997, A. De Kesel, ADK 2015 (BR5020074861746); Togo, Centrale Province, Fazao National Park, 08° 41.133′ N 0° 45.623′ E, alt. 625 m, rivulet associated woodland, on a slope, dominated by *U. togoensis* (Phyllanthaceae) and *Isoberlinia doka* (Caesalpiniaceae), on soil of the vertical bank of the rivulet, 19 July 2007, A. De Kesel, ADK 4439 (BR5020163771352).

GenBank numbers: ITS: OP355329, OP355330, LSU: OP355337

Notes: The ITS and LSU sequence data of our collection give *Trichoglossum* species as the closest matches in NCBI. The genus *Trichoglossum* is characterized by the hirsute look of the fertile part of ascomata. In our material the setae, responsible for this hirsute look, are relatively short and distributed infrequently in the hymenium and stipe. The 5–7-septate ascospores are clearly shorter (80–125 µm) than those with 15 septa (139–165 µm). The other *Trichoglossum* species with eight-spored asci and


Penicillium griseoflavum HMAS 247729
Penicillium guangxiense CBS 144526
Penicillium globosum CBS 144639
Penicillium globosum NFCCI 5061
Penicillium cataractum CBS 140974
Penicillium echinulonalgiovense CBS3 2859
Penicillium mariae-crucis CBS 27193
Penicillium laevigatum HMAS 247728
Penicillium pedernalense CBS 140770
Penicillium infrabuccalum KAS 2161
Penicillium [illegible] DAOM 695771
Penicillium simplicissimum CBS 37248
Penicillium soliforme HMAS 247733
Penicillium pulvillorum NRRL 2026
Penicillium camponotum KAS 2177
Penicillium flavoroseum HMAS 247727
Penicillium [illegible] DAOM 695771
Penicillium ochrochloron CBS 35748
Penicillium subrubescens DTO188D6
Penicillium subrubescens NFCCI 5063
Penicillium terrarumae DTO 174H2
Penicillium piscarium CBS 36248
Penicillium rolfsii CBS 36848
Penicillium annulatum CBSH 21333
Penicillium cinticaule CBSH 21334
Penicillium koreense KACC 47721
Penicillium yunnanense HMAS 247735
Penicillium raperi NRRL 2674
Penicillium raperi NFCCI 5066
Penicillium cluniae CBS 32689
Penicillium glaucoroseum NRRL 908
Penicillium janthinellum CBS 34048
Penicillium ludwigii CBS 41768
Penicillium cremeogriseum CBS 22366
Penicillium ortum CBSH 21602
Penicillium limosum CBS 33897
Penicillium brefeldianum NRRL 710
Penicillium lineolatum CBS 18877
Penicillium levitum CBS 34548
Penicillium coeruleum CBS 14145
Penicillium elleniae CBS 118135
Penicillium malacosphaerulum CBSH 21332
Penicillium setosum CBS 144865
Penicillium javanicum CBS 34148
Penicillium caperatum CBS 44375
Penicillium reticulisporum NRRL 3447
Penicillium vanoranjei DTO 99H6
Penicillium johnkrugii DAOM 239943
Penicillium acidum EMLDLW41
Penicillium exsudans HMAS 248735
Penicillium mallochii DAOM 239917
Penicillium daejeonium CNU 100097
Penicillium jacksonii DAOM 239937
Penicillium sclerotiorum NRRL 2074
Penicillium circulare CNUFCGEU 3201
Penicillium cainii DAOM 239914
Penicillium hirayamae CBS 22960
Penicillium hirayamae NFCCI 5062
Penicillium fernandesiae URMBRA 7606
Penicillium sizovae CBS 41369
Penicillium tropicum CBS 112584
Penicillium tropicoides CBS 122410
Penicillium steckii CBS 26055
Penicillium steckii NFCCI 5065
Penicillium citrinum NRRL 1841
Penicillium hetheringtonii CBS 122392
Penicillium gorlenkoanum CBS 40869
Penicillium erubescens NRRL 6223
Penicillium parvum NRRL 2095
Penicillium vinaceum NRRL 739
Penicillium guttulosum NRRL 907
Penicillium pimiteouiense NRRL 25542
Penicillium rubidurum NRRL 6033
Penicillium menonorum NRRL 50410
Penicillium menonorum NFCCI 5064
Penicillium hermansii DTO 07905
Penicillium catenatum CBS 35267
Penicillium ceris NRRL 62798
Penicillium striatisporum NRRL 26877
Aspergillus glaucus NRRL 116
100/1.00
100/1.00
100/1.00
ser. Simplicissima
sect. Lanata-Divaricata
ser. Rolfsiorum
sect. Lanata-Divaricata
ser. Janthinella
sect. Lanata-Divaricata
ser. Sclerotiorum
sect. Sclerotiorum
ser. Citrina
sect. Citrina
ser. Erubescentia
sect. Exilicaulis
Outgroup
Penicillium subgenus Aspergilloides

◂**Fig. 70** Phylogeny inferred using combined dataset of ITS, *BenA*, *CaM*, and *rpb2* of *Penicillium* subgenus *Aspergilloides* in RAxML. The matrix had 1447 distinct alignment patterns with 15.76% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.224185, C = 0.284056, G = 0.262355, T = 0.229404; substitution rates AC = 1.095739, AG = 3.139871, AT = 1.227232, CG = 0.748372, CT = 4.755400, GT = 1.0; gamma distribution shape parameter α = 0.299261. Bootstrap support for ML equal to or greater than 80%, Bayesian posterior probabilities (BI) equal to or greater than 0.9 are shown at the nodes. The tree is rooted to *Aspergillus glaucus* (NRRL 116). The newly generated sequences are indicated in blue bold

15-septated ascospores are *T. cheliense* F.L. Tai, *T. gracile* Pat., *T. hirsutum* (Pers.) Boud., *T. jejuense* S.H. Lee, *T. longisporum* F. L. Tai, *T. persoonii* F.L. Tai, *T. septatum* Ekanayaka, Q. Zhao & K.D. Hyde, *T. sinicum* F.L. Tai, *T. variabile* (E.J. Durand) Nannf., and *T. yunnanense* L.F. Tai (Ekanayaka et al. 2017; Prabhugaonkar and Pratibha 2017; Lee et al. 2021; Chakraborty et al. 2022). Our material differs from these species in having very sparsely distributed setae in the hymenium and short setae on the stipe surface. The orange coloring in the longitudinal section is also noteworthy. The field surveys indicate that this species only occurs in steep forest galleries with relatively cool and wet conditions during the long dry season (October–March). Ascomata are produced very late in the second half of the rainy season (July–September). It seems to prefer deep shade and develops on sandy soil with some humus, always under ectomycorrhizal trees *Berlinia grandiflora*, *Isoberlinia doka*, *Uapaca guineensis* and *U. togoensis*. Edibility is unknown.

Phylogenetic evidences reveal that our collections form a distinct clade between several undescribed *Trichoglossum* species with ML/BI = 100%/1.00 statistical supports. Therefore, we introduce our material as *T. beninense* sp. nov. This species is only known from Benin and Togo in Africa (Fig. 72).

Laboulbeniomycetes Engl.

Laboulbeniales Lindau

This order includes more than 2,100 species described as obligate ectosymbionts on Arthropods. The majority of hosts are insects, mostly Coleoptera and Diptera, less frequently mites (Acarina) and millipedes (Diplopoda).

Laboulbeniaceae G. Winter

This family consists mostly of terrestrial species that sexually reproduce with simple or compound endogenous antheridia. Santamaria and Pedersen (2021) listed 147 genera in this family.

Laboulbenia Mont. & C.P. Robin

Laboulbenia is by far the largest genus among the Laboulbeniales, with about 680 accepted species, representing almost one third of all known species in the order. The species of *Laboulbenia* occur on various families of beetles (Coleoptera), but are also found on flies (Diptera), true bugs (Hemiptera), ants (Hymenoptera), termites (Isoptera), cockroaches (Blattodea), crickets (Orthoptera), and mites (Acarina) (Kaishian et al. 2020; Kong et al. 2020; Santamaria and Pedersen 2021). There have been very few published sequences of species in this large genus to date, with most of the taxa, including the type species, lacking this molecular information. In this study, we introduce nine new species of *Laboulbenia* based on morphology.

Laboulbenia caprina A. Weir, M. McHugh & W. Rossi, ***sp. nov.***

Index Fungorum number: IF900424; *Facesoffungi number*: FoF 14178; Fig. 73

Etymology: referring to the peculiar modification of the perithecial lip cells, that resemble the horns of a goat (= *capra* in Latin).

Thallus erect, small, compact, hyaline to light brown with dark apical region to the perithecium, insertion cell and some appendage cells. Total length 150–183 µm. *Basal cell (I)* mostly hyaline with thin band of pale orange brown near the foot. Cell curved and tapered towards the foot, shape variable but typically broader distally, 20–50 × 20–35 µm. *Cell II* hyaline to tinged with pale brown, broader than long, 13–20 × 28–40 µm. *Cell III* hyaline or infused with brown along the outer edge, quadrate, 18–23 × 20–30 µm. *Cell IV* similar to cell III in coloration, smaller, 13–23 × 13–20 µm. *Cell V* mostly hyaline, wedge-shaped, 13–18 × 5–10 µm. *Appendages* formed above a dark, flat insertion cell with paler brown interior. Outer appendage basal cell light brown to hyaline, quadrate, 8–13 × 8–13 µm, giving way distally to a hyaline to dark brown suprabasal cell. The latter broader than long, 10–13 × 8–10 µm, deeply suffused along the base and outer margin and gives rise distally to usually two, hyaline, septate, branches (longest appendage 78 µm). Inner appendage basal cell completely hyaline, quadrate, slightly smaller overall than outer appendage basal cell, 5–13 × 8–10 µm, giving rise to two branches, one on each side, which themselves bifurcate to form a short, compact, tuft of branchlets reaching nearly to the tip of the perithecium (longest appendage 70 µm). *Perithecium* stalk cell (VI) hyaline to tinged with pale brown, rectangular, 8–20 × 25–33 µm. Perithecium ranges from brown to hyaline, short, squat, straight or slightly inflated about the middle, 88–108 × 33–53 µm. Apical region largely opaque with outer margin bulging slightly beneath the two distinct, curved, and hooked lip cells.

Material examined: Indonesia, Sulawesi Utara Province, Dumoga-Bone National Park, Toraut forest, at light, II. 1985, P. M. Hammond, on the margin of the right elytron of *Coptodera* sp. (BM(NH) Code No. 4.67) (Coleoptera,

Fig. 71 ***Trichoglossum beninense*** (BR5020149821538, **holotype**). **a** Ascospores. **b** Paraphyses. **c** Setae. **d** Hymenium. **e** Asci showing euamyloid reaction of the ascoapical apparatus. **f** Elements of the stipe surface. **g** Fresh ascomata. **h** Habitat of *T. beninense.* (a–d, f in 5% KOH, e in IKI). Scale bars: a–f = 10 µm, g = 1 cm

Carabidae, Lebiini), K(M) 43521, **holotype**; *ibid*. Sulawesi Utara Province, Dumoga-Bone National Park, Plot C, el. ca. 400 m, II. 1985, P. M. Hammond, on the margin of the right elytron of *Coptodera* sp. (BM(NH) Code No. 4.67), AW 308 in SYR, **paratype**.

Notes: Fifteen mature thalli have been examined on the margin of the right elytron of *Coptodera* sp. This new species may be compared to a group of species viz. *Laboulbenia catascopi* Thaxt., *L. coptoderae* Thaxt., *L. flagellata* Peyr., and *L. obliquata* Thaxt. reported on *Coptodera* sp. collected from Central and South America (Thaxter 1896, 1908). Our collections (K(M) 43521, AW 308 in SYR) differ from each of these species in having a much shorter, more compact thallus with cell II distinctly broader than long (Fig. 73). Additionally, all of these taxa lack the very distinct hooked, lip cells at the tip of the perithecium which our collections comprise. The appendages of our collections bear some similarity with *L. coptoderae*, but lacking the heavy pigmentation found in both the outer and inner appendage branches. Therefore, we introduce these collections as *Laboulbenia caprina* sp. nov.

Laboulbenia clavulata W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: IF900425; *Facesoffungi number*: FoF 14179; Fig. 74

Etymology: From Latin clavula, which means "small club", referring to the habitus of the fungus.

Perithecium grayish brown, very dark in older thalli; the rest of the fungus is pale brown, variably darker, especially in older specimens, along the outer margin of cell III and IV and much paler in the lower portion of cell I. Basal cell of the receptacle (cell I) elongate and almost cylindrical,

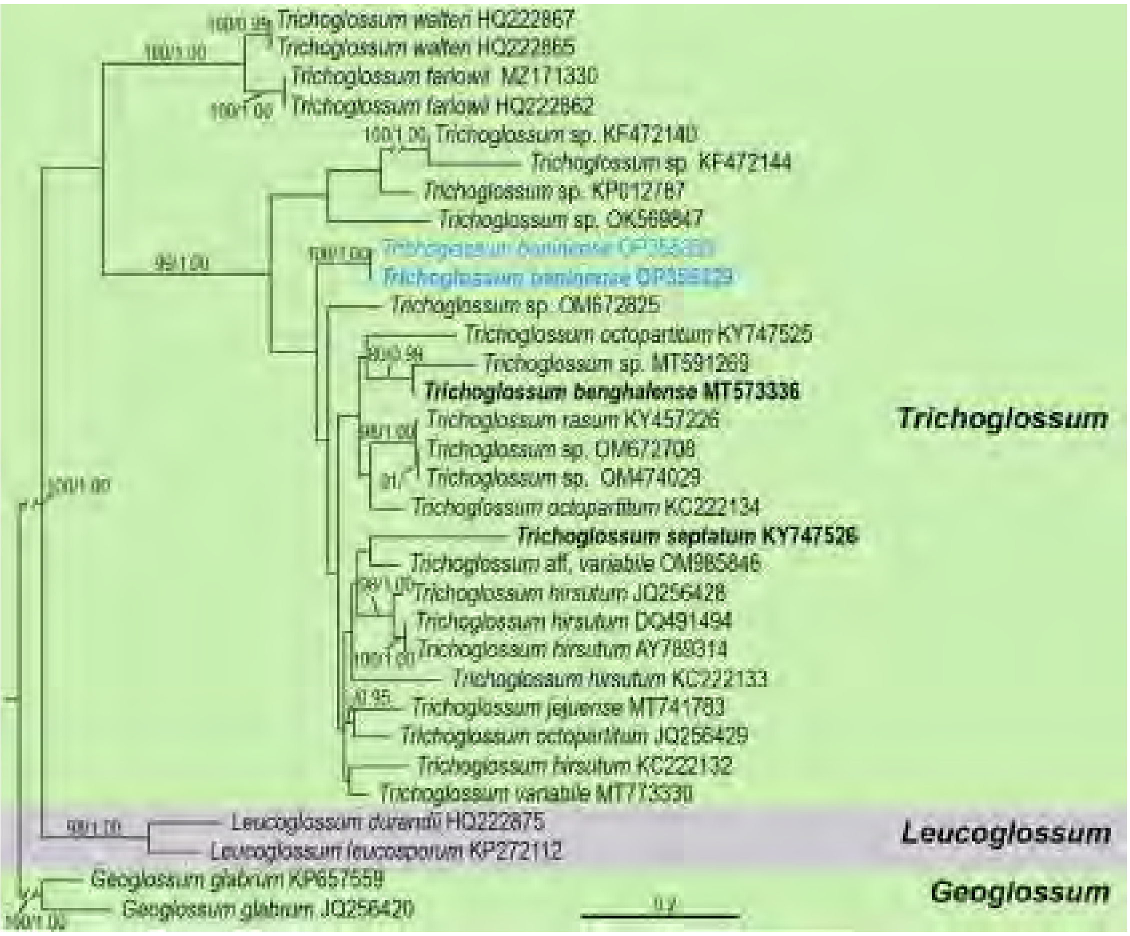


Fig. 72 Phylogram generated from maximum likelihood analysis based on ITS sequence data for *Trichoglossum* and several closely related genera in Geoglossaceae. Thirty-two specimens are included in the analyses. The matrix comprised aligned 703 characters, which was reduced to 535 characters including gaps after elimination of 168 characters by TrimAl v.1.2b. The tree is rooted with *Geoglossum glabrum* (ILLS 61038 and ILLS 72358). The best-fit AICc-selected models of evolution is TVM+I+G. The best scoring RAxML tree has a final likelihood value of − 5633.290401. The matrix had 352 distinct alignment patterns with 5.13% undetermined characters and gaps. Estimated base frequencies were as follows: A = 0.237638, C = 0.234066, G = 0.231049, T = 0.297247; substitution rates AC = 0.994448, AG = 3.586652, AT = 1.129458, CG = 0.458687, CT = 3.969106, GT = 1.0; gamma distribution shape parameter α = 0.808425. To remove the prestationary posterior probability distribution burn-in of 10% (ESS = 3621.7) was estimated with Tracer to be sufficient. Alignments and phylogenies were deposited in TreeBASE (http://treebase.org) under the submission ID 29628. Type specimens are in bold and newly generated sequences are in blue. Bootstrap support for ML equal to or greater than 80% and BI equal to or greater than 0.95 are given above the nodes

sometimes bent above the foot. Cell II about as long as the previous, slightly enlarged above, separated from cell III by a short, transverse septum and from cell VI by a much longer, oblique and slightly concave septum. Cell III about as long as cell II but narrower, its inner margin more or less concave. Cell IV slightly longer than cell III, its upper outer angle somewhat prominent below the insertion cell. Cell V relatively large, with the upper, convex margin free between the perithecium and the oblique insertion cell, which is narrow and thick. Outer appendage consisting of a large lower cell about twice as long as broad, followed by a slightly longer cell which gives rise to two elongate branches that are similar in size, but differ in colour, with the outer branch darker, sometimes distinctly so; these branches are invariably broken in mature thalli. Basal cell of the inner appendage much smaller than the outer, bearing a single, slender antheridium soon replaced by a simple branch much shorter and slenderer than the branches of the outer appendage. Cell VI small, subquadrate or irregularly trapezoidal. *Perithecium* elliptical, relatively narrow, with the whole inner margin united with the receptacle, the free, blackish tip tapering to a rounded apex, the lips outwardly oblique, hyaline about the pore. Length from foot to perithecial apex 265–395 µm; longest appendage 485 µm; perithecium 115–155 × 55–70 µm; ascospores about 55 µm.

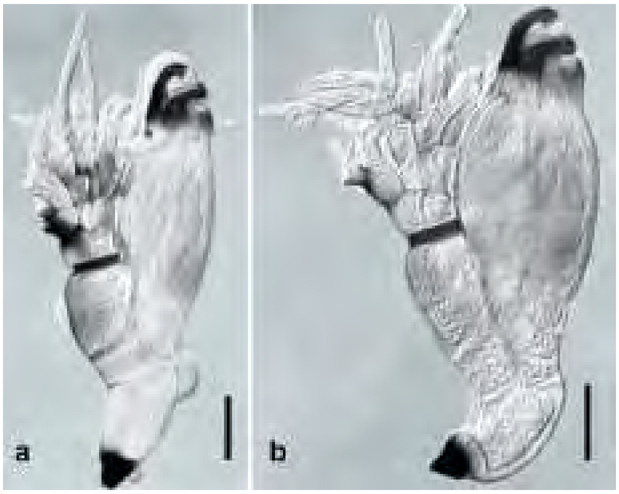


Fig. 73 ***Laboulbenia caprina*** (K(M) 43521, **holotype**). **a, b** Mature thalli. Scale bars: a, b = 25 µm

Fig. 74 ***Laboulbenia clavulata*** (CAMB WR1804a, **holotype**). **a** Thallus from the type slide, from the elytra of the host-insect. **b** Thallus from the isotype slide (FI WR1804b), from the abdomen of the host-insect. Scale bars = 50 µm

Material examined: Australia, Tasmania, Crade Mt., 21.I.1991, *leg*. M. Daccordi, at the apex of the elytra of *Agonica simsoni* Sloane (Coleoptera, Carabidae, Peleciini) (CAMB WR1804a, **holotype**; FI WR1804b, **isotype**).

Notes: Among the few species of *Laboulbenia* with the inner margin totally united with the receptacle but disjointed from the insertion cell, the most similar species to our collection (CAMB WR1804a) is *L. schizogenii* Thaxt., which was described on insects of the family Carabidae subfamily Scaritinae from USA and more recently reported from South America and West Africa (Thaxter 1896; Rossi and Leonardi 2018). However, our collection differs from *Laboulbenia schizogenii* by having more numerous branches of the appendages, for the thinner insertion cell, for the perithecial tip not strongly contracted above the venter, and for cell IV not prominent below the insertion cell (Fig. 74). Therefore, we introduce this collection (CAMB WR1804a) as *Laboulbenia clavulata* sp. nov. A picture of *Laboulbenia clavulata* has been already published (as *Laboulbenia* n. sp.) in Vigna-Taglianti and Rossi 1999.

Laboulbenia cobiae W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: IF900429; *Facesoffungi number*: FoF 14180; Fig. 75

Etymology: Named after the student of the Diopsidae Cobi Feijen (The Netherlands), who supplied us with the insect bearing the new species of fungus.

Thallus sigmoid, hyaline or almost so, with the perithecium light gray and the appendages brown. Adhesive organ (foot) with a hyaline, contrasting spot in the middle. Basal cell of the receptacle (cell I) curved, about three times longer than broad. Cell II slightly to distinctly larger than the previous one. Cell III much smaller, barrel-shaped, almost 1.5 times longer than broad. At the septum separating cell II from cell III the receptacle has an evident indentation. Cell IV + V similar to, but slightly shorter than cell III and completely free from the perithecium. Insertion cell very narrow and thick. Basal cell of the outer appendage quite large and expanding distally, giving rise to 4 branches consisting of elongate cells darker on the outer side and separated by blackish septa; these branches divide repeatedly forming a fan-shaped tuft of branchlets with hamate tip overcome by a disorganized hyaline matter. Inner appendage consisting of a small basal cell which gives rise to two elongate

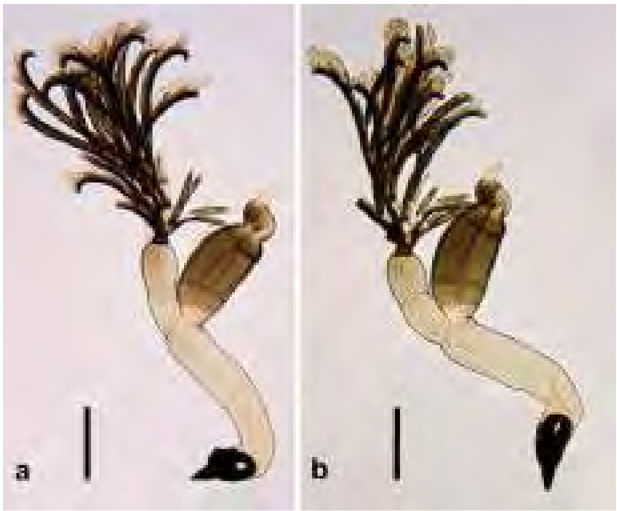


Fig. 75 ***Laboulbenia cobiae*** (FI WR4128, **holotype**). **a, b** Mature thalli. Scale bars: a, b = 50 µm

cells, each bearing distally a pair of grayish, elongate and bottle-shaped antheridia. Cell VI very small and oblique. Perithecial basal cells also small, forming a narrowing below the perithecial body. The latter asymmetrical, with the outer (ventral) margin straight or slightly concave and the inner (dorsal) convex, tapering abruptly upward forming a distinct constriction, above which the enlarged tip appears as two bulky, rounded, unequal lobes, the inner of which is larger and bears a digitiform, curved, hyaline outgrowth. Length from foot to tip of perithecial outgrowth 210–240 µm; from foot to tip of appendages 340–375 µm; longest appendages 175 µm; perithecium including basal cells, without outgrowth 95–100 × 35–40 µm; perithecial outgrowth 14–16 µm; antheridia 26–28 µm.

Material examined: Sri Lanka, Badulla Distr., Girandurakotte Circuit Bungalow 10 mi. NNE Mahiyanganaya, UV trap, 4–7.IX.1980, *leg.* K.V. Krombein et al., at the apex of the abdomen of a female specimen of *Diopsis* nr. *indica* Westwood (Diptera, Diopsidae) (FI WR4128, **holotype**).

Notes: Our collection (FI WR4128) is distinguishable from any other described species for the large, rounded upper portion of the perithecium subtended by a marked constriction. The perithecial outgrowth is also an uncommon feature in the genus *Laboulbenia*, although it is frequent in other genera of the Laboulbeniales. Our collection (FI WR4128) can be compared with *Laboulbenia gratiellae* W. Rossi, which was described *Teleopsis* spp. from Malaysia and Thailand (Rossi 1987). The two parasites have appendages with a similar structure, although these are more numerous in *Laboulbenia gratiellae*. Moreover, in the latter species cells III and IV are undivided but separated from cell V, while it is the contrary in our collection. Therefore, we introduce this collection (FI WR4128) as *Laboulbenia cobiae* sp. nov.

More information about the taxonomy of *Laboulbenia* species on *Diopsis indica* in Sri Lanka has been included in Feijen and Feijen (2020). A large collection of Sri Lankan Diopsidae has been studied by H. Feijen and C. Feijen and four specimens among 168 females (2.3%) and 16 out of 108 males (14.8%) were infected by Laboulbeniales (H. Feijen, pers. com.). This rate of infection is relatively high for oriental stalk-eyed flies, while the infection on African populations of the same family of insects is usually higher (Rossi and Feijen 2018).

Laboulbenia cosmodisci A. Weir, M. McHugh & W. Rossi, ***sp. nov.***

Index Fungorum number: IF900430; *Facesoffungi number*: FoF 14181; Fig. 76

Etymology: From Latin: referring to the name of the host beetle.

Thallus erect to sigmoidal, pale grayish brown to dark brown; total length from foot to tip of perithecium 325–375 µm. Receptacle composed of the usual arrangement of five superposed cells. *Basal cell* (I) brown with an orange tinge, slightly curved, and tapering towards the foot, about three times longer than broad, 60–88 × 18–33 µm. Cell II grayish brown to hyaline, more elongate than cell I, becoming slightly broader distally, 78–98 × 25–38 µm, giving way above to cell III and the perithecial stalk cell (VI). Cell III grayish brown to brown, two to three times as long as broad, rectangular but broadening distally 55–90 × 20–43 µm, giving way distally to cell IV. Cell IV grayish brown to almost hyaline, two to three times as long as broad, 60–85 × 18–38 µm. Cell V gray to hyaline, small, wedge-shaped, 28–33 × 10–25 µm. Appendages formed above a thick black, flattened insertion cell that is not directly connected to the perithecium. Outer appendage basal cell hyaline, twice as long as broad, 15–20 × 15 µm, giving rise to another, equal, superposed cell which in turn bears distally, two long, flexuous, septate, hyaline branches. Inner appendage basal cell hyaline, only slightly longer than broad, smaller than the outer appendage basal cell, 10–13 × 8–10 µm, giving way distally to a subequal cell, which in turn bears two short and usually 1–2 celled hyaline branchlets producing paired antheridia terminally. *Antheridia* 5 × 8 µm, hyaline, flask-shaped, borne terminally in pairs on the inner appendage. *Perithecium stalk cell* (VI) brown to gray, quadrate, 25–40 × 35–40 µm. *Perithecium* grayish brown to dark brown, completely free, with insertion cell close to perithecial apex, 135–175 × 45–60 µm, with opaque, sub-terminal region, and hyaline, rounded,

Fig. 76 Mature thallus of ***Laboulbenia cosmodisci*** (K(M) 43519, **holotype**). Scale bar = 100 µm

outwardly-directed lip cells. One thallus is much larger than the others reaching to 690 µm from foot to tip of perithecium. In other respects, though, this outlier thallus shares characteristics with the typical thalli as described above.

Material examined: Indonesia, Sulawesi Utara Province, Dumoga-Bone National Park, Plot A, lowland forest, el. ca. 200 m, Pitfall trap, 10–17.IV.1985, P.M. Hammond, on the elytra of *Cosmodiscus* sp. (BM(NH) Code No. 4.56) (Coleoptera, Carabidae, Pterostichini), K(M) 43519, **holotype**; AW 281 in SYR, **isotype**; Sulawesi Utara Province, Dumoga-Bone National Park, Hog's Camp, el. ca. 492 m, at light, IX.1985, P.M. Hammond, on the pronotum of *Cosmodiscus* sp. (BM(NH) Code No. 4.56), AW 280 in SYR, **paratype**. Sulawesi Utara Province, Dumoga-Bone National Park, nr. Kotamubagu, Daanau Mooat, el. ca. 1200 m, Pitfall trap, 21–23.X.1985, P.M. Hammond, on the pronotum of *Cosmodiscus* sp. (BM(NH) Code No. 4.56), AW 282 in SYR, **paratype**. Sulawesi Utara Province, Dumoga-Bone National Park, Plot A, lowland forest, el. ca. 200 m, Flight interception trap, 30.X – 06.XI.1985, P.M. Hammond, on the elytra and pronotum of *Cosmodiscus* sp. (BM(NH) Code No. 4.56), AW 290 in SYR, **paratype**.

Notes: Twenty-five thalli at various stages of development have been examined on the elytra and pronotum of various specimens of a single species of *Cosmodiscus*. The elongate receptacular cells produce a thallus where the insertion cell is at the level of the perithecial apex, and not below the middle as in the majority of *Laboulbenia* species. Our collections may be compared with *Laboulbenia erecta* Thaxt., and differ in having a much longer basal cell of the receptacle cell (I) and the non-flattened, somewhat tapered perithecial tip with distinctly out-turned lip cells (Fig. 76). Therefore, we introduce these collections as *Laboulbenia cosmodisci* sp. nov.

Laboulbenia omalii A. Weir, M. McHugh & W. Rossi, ***sp. nov.***

Index Fungorum number: IF900431; *Facesoffungi number*: FoF 14182; Fig. 77

Etymology: From Latin referring to the name of the host beetle.

Thallus erect, small, completely hyaline except for portions of the perithecium, the insertion cell, and the foot. Total length from foot to tip of perithecium 163–170 µm. Receptacle cell I completely hyaline, trapezoidal, tapering slightly towards the foot, longer than wide, 18–20 × 13 µm. Cell II completely hyaline, rectangular, becoming more rounded near the distal septum with cells III and VI, twice as long as wide, 38–40 × 15–18 µm. Cell III also hyaline, rectangular or quadrate, to somewhat rounded, 23 × 15–18 µm, giving way distally to cell IV. Cell IV completely hyaline, rectangular, separated from cell V by a vertical septum, 20 × 13–15 µm. Cell V hyaline, small, wedge-shaped, 8–10 × 5–8 µm. *Appendages insertion cell* dark brown to black, positioned at an angle to the main axis of the thallus, relatively thick. *Appendage* outer basal cell much larger than inner basal cell, hyaline, with an outer distal black septum, rounded to bell-shaped, giving way to a smaller, hyaline, triangular cell from its inner face, and producing a single cell above the outer black distal septum. Cell derived from inner face can give rise to one or two superposed, flattened cells. Inner basal cell smaller, hyaline, more flattened than outer, giving way distally to a single cell that then produces two smaller cells, each of which gives rise to a broad, squat antheridium with very short neck and with nip-shaped apices. *Perithecium stalk cell* (VI) hyaline, curved, quadrangular, slightly wider than long, 10–12 × 15 µm. *Perithecium* short, symmetrical, slightly inflated, hyaline to smoky black, the dark suffusion particularly prevalent along the upper outer margin and sub-terminally beneath the hyaline, obtuse, lip-cells, that are subtended by a blackish area on the inner side.

Fig. 77 Thallus of ***Laboulbenia omalii*** (K(M) 43522, **holotype**). Scale bar = 25 µm

Material examined: Indonesia, Sulawesi Utara Province, Dumoga-Bone National Park., Plot C, el. ca. 400 m, fallen fruit of *Ficus* sp., II.1985, P. M. Hammond, on the tergites of an unidentified rove beetle (BM(NH) Code No. 20.6) (Coleoptera, Staphylinidae, Omaliinae), K(M) 43522, **holotype**.

Notes: Only two mature and two immature thalli have been examined from the tergites of the host. Approximately, 680 species have been described in the genus *Laboulbenia* and only about 5% are known on hosts in family Staphylinidae. It is obvious that they do not form a monophyletic group, as even the three found on Omaliinae [*L. geodromychi* Baumgartner, *L. omalii* (described here), and *L. richardii* W. Rossi & Santam.] are unrelated. The presumed antheridia may be intercalary on the inner appendage in contrast to the typical external formation of these organs in this genus. The structure of the receptacle and the presence of the typical insertion cell leave no doubt as to the generic placement of this new species (Fig. 77). The structure of the appendage in our collection is distinct not only from the two species previously described on Omaliinae and from any of the more than 30 species on Staphylinidae, but also from all other known species of *Laboulbenia*. Therefore, we introduce this collection as *Laboulbenia omalii* sp. nov.

Laboulbenia nilotica W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: IF900432; *Facesoffungi number*: FoF 14183; Fig. 78

Etymology: The name of the species comes from the Nile river, in whose waters were collected the host insects.

Thallus olive-gray, with darker perithecium and paler cell II, IV, V, and lower portion of cell I. Basal cell (cell I) slightly shorter than the suprabasal (cell II); at the transverse septum separating these cells the receptacle is slightly inflated, then distinctly narrowed because of the concave margin of upper cell on the dorsal side. The septum dividing cell II from cell III is short and slightly oblique, while the septum between cell II and cell VI is more oblique and much longer. Cell III broadly shaped like an inverted trapeze, slightly longer than broad. Cells IV and V small, subequal, separated by a vertical septum. Insertion cell quite thin, not joined to the perithecium. *Appendages* broken in all the numerous examined thalli. The basal cell of the outer appendage is relatively large, divided from the outer branch by a black ring. Cell VI about twice broader than long. *Perithecium* ovoid, twice longer than broad, the tip not distinguished ending in a rounded apex with the hyaline ostiole distinctly turned outwards, subtended by irregular darker areas more extended on the dorsal side. Length from foot to perithecial apex 215–320 µm; perithecium 95–120 × 50–60 µm.

Fig. 78 Mature thalli of ***Laboulbenia nilotica*** (FI WR1244a, **holotype**). Scale bars = 50 µm

Material examined: Uganda, near Nile River, Murchison Falls National Park, 28.VII.1971, *leg.* N. Sanfilippo, on Orectogyrus (*Trichogyrus*) *oscari* Apetz (Coleoptera, Gyrinidae) (FI 1244a, **holotype**; FI WR1244b, 1244c 1245a, 1245b, 1245c, **paratypes**).

Notes: Our collection is quite different from all the other species of *Laboulbenia* associated with hosts in family Gyrinidae. It is also clearly distinct from the six species reported on insects of the genus *Orectogyrus*, none of which has blackened insertion cell (Thaxter 1908). Our collection has constricted basal portion of the receptacle and this character can occur in *Laboulbenia strangulata* Thaxt. that was described on *Orectochilus* sp. from Timor and India. However, *Laboulbenia strangulata* has a longer and distinctly concave insertion cell joined to the perithecium, very unequal and larger cells IV and V, the latter of which is extended upwards, and completely different branches of the appendages (Thaxter 1908). Our collection bears a superficial resemblance with *L. pedicellata* Thaxt., a common and widespread fungus occurring on ground beetles, from which is easily distinguished among other features by the different shape of the perithecial apex and the thick insertion cell joined to the perithecium (Fig. 78). Thus, we introduce our collection as *Laboulbenia nilotica* sp. nov.

Laboulbenia robusta W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: IF900433; *Facesoffungi number*: FoF 14184; Fig. 79

Etymology: From Latin *robustus* = strong, robust.

Thallus slightly sigmoid, colored dirty yellow, with the perithecium becoming darker with age. *Basal cell* of the receptacle (cell I) regularly expanding distally, almost three times as long as maximum width. *Cell II* much larger, separated by cell III by a very short, transverse septum and by cell VI by a much longer, oblique and concave septum. *Cell III* relatively small, almost twice longer than broad, tapering below. *Cell IV* similar in size to cell III. *Cell V* relatively large, wedge-shaped, with the inner margin partially free between the perithecium and the very oblique and thick insertion cell. Basal cell of outer appendage quite large, about twice longer than broad, giving rise to two branches which divide dichotomously forming four long, slender, straight, subequal branchlets formed by elongated cells. Inner appendage consisting of a basal cell distinctly smaller than the basal cell of the outer appendage,

Fig. 79 ***Laboulbenia robusta*** (FI WR1588, **holotype**). **a, b** Mature thalli. Scale bars: a, b = 100 µm

producing by repeated dichotomous divisions a large and sometimes dense tuft of short branchlets, each bearing apically a hyaline, bottle-shaped antheridium. *Cell VI* irregularly quadrangular, about as long or slightly longer than maximum width. *Perithecium* less than half free, its ventral margin evenly convex, forming a slight external prominence between the second and third wall-cells tiers, above which it is abruptly contracted in a blackened and subconical tip which ends in a rounded apex, the lips with hyaline edges turned obliquely outwards. Length from foot to perithecial apex 395–530 µm; longest appendages 470 µm; perithecium 150–195 × 60–85 µm.

Material examined: Australia, Joondalup Lake, 25 km N to Perth, 1.XII.1990, *leg.* W. Rossi, on *Pseudoceneus iridescens* (Castelnau) (Coleoptera, Carabidae, Pterostichinae) (FI WR1588, **holotype**).

Notes: The distinctive characters of our collection (FI WR1588) are the branching pattern and length of the outer appendage, the dense tuft of antheridia on the inner appendage and the absence of sterile branches on the same and the very oblique insertion cell distinctly free from the perithecium. Our collection bears a superficial resemblance with *Laboulbenia anchonoderi* Thaxt., which occurs on *Anchonoderus* sp. (Carabidae, Lebiinae) from Central and South America (Thaxter 1908). The latter fungus is paler and slenderer, with cells III and VI more elongated, the perithecium free for about two thirds, and the inner appendage bearing elongate, sterile branches (Fig. 79). Therefore, we introduce our collection as *Laboulbenia robusta* sp. nov.

Laboulbenia similis A. Weir, M. McHugh & W. Rossi, ***sp. nov.***

Index Fungorum number: IF900434; *Facesoffungi number*: FoF 14185; Fig. 80

Etymology: From Latin: referring to the similarity of this species with *Laboulbenia stigmatophora* described in this same contribution.

Thallus mostly erect to slightly sigmoid, with brown punctation especially in cell I and below the perithecium. Total length from foot to tip of perithecium, 140–230 µm. *Receptacle Cell I* suffused with brown near to the foot, becoming hyaline in the middle, and heavily punctate with

Fig. 80 Mature thallus of ***Laboulbenia similis*** (K(M) 43520, **holotype**). Scale bar = 50 µm

brown along the septum with cell II and on the outer margins, rectangular to slightly curved and tapering towards the foot, forming a distinct stalk, 38–50 × 13–20 µm. *Cell II* located directly above cell I, hyaline to slightly mottled to darkly punctate especially along the outer margin, rectangular to quadrate, 25–33 × 15–23 µm. *Cell III* hyaline to mottled with brown spots, triangular, 18–25 × 13–20 µm, giving rise distally to cell IV. *Cells IV* and *V* hyaline or variably punctate, both longer than broad and separated from each other by an almost vertical septum. Cell IV 18–28 × 13–20 µm, Cell V 23–33 × 8–13 µm. Appendages formed above a brown, narrow, flattened insertion cell that is usually at the same level with the base of the perithecium. Outer basal cell large, hyaline, barrel-shaped, 13–15 × 13–15 µm, giving way to a larger superposed, hyaline to pale brown cell, which in turn produces two long, sturdy, septate appendages. Inner appendage basal cell much smaller than outer, 10–13 × 8–10 µm, hyaline to pale brown giving way distally to a pale brown suprabasal cell of equal size or longer. The suprabasal cell bears two short, flexuous branches which may support antheridia. *Perithecium stalk cells* (VI and VII) relatively large, bulging outwards and deeply punctate with dark brown along the outer margin. *Perithecium* largely suffused with brown with darker blotches subterminally below the rounded lip cells. Perithecium 100–120 × 40–53 µm, basally constricted, then more or less straight, and finally abruptly tapering to the narrow apex with two crest-like protrusions emerging from the outer margin just below the abruptly tapered apical region. Apex erect, overall dark, and not distinctly turned inwards.

Material examined: Indonesia, Sulawesi Utara Province, Dumoga-Bone National Park, Plot A, lowland forest, el. ca. 200 m, Base camp, I.1985, P.M. Hammond, on the edge of the elytra of *Hyphaereon* cf. *timidus* Darlington (BM(NH) Code No. 4.74) (Coleoptera, Carabidae, Harpalini), K(M) 43520, **holotype**; AW 241 in SYR, **isotype**.

Notes: Eleven mature and two immature thalli have been examined on the edge of the elytra of *Hyphaereon* cf. *timidus*. Thalli of our collection (K(M) 43520) are apparently similar to *Laboulbenia stigmatophora* A. Weir, M. McHugh & W. Rossi which is described in this study. However, our collection differs from *Laboulbenia stigmatophora* by the orientation and colour of the perithecial tip and in the detail of the appendages, with our collection having more erect and darker perithecial tip and more robust and less branched appendages. The combination of deeply punctate receptacular cells, perithecial morphology and coloration, and relatively simple, rigid appendage branches make our collection a distinguished species from others species in the genus. Thus, we introduce our collection as *Laboulbenia similis* sp. nov.

Laboulbenia stigmatophora A. Weir, M. McHugh & W. Rossi, ***sp. nov.***

Index Fungorum number: IF900435; *Facesoffungi number*: FoF 14186; Fig. 81

Etymology: From Greek: adjective, meaning "bearer of dots".

Thallus erect to slightly sigmoid, total length from foot to tip of perithecium 220–325 µm. Receptacle deeply punctate throughout. *Cell I* distinct, hyaline to deep brown with dark punctations merging on outer margin to form a dark brown edge that continues for the length of the receptacle, Cell I tapering towards the foot and forming a distinct stalk to the thallus, 2–3 times longer than broad, 43–73 × 18–30 µm. Remaining receptacle cells not well distinguished, heavily punctate with brown becoming confluent along the outer margin, a small punctate, but paler region remaining immediately below the insertion cell. Insertion cell usually small, free from, and located towards the base of, the perithecium. *Appendages* typically light brown to hyaline. Outer appendage basal and suprabasal cells relatively large, basal 15–20 × 15–18 µm, suprabasal 18–23 × 15–18 µm. The latter giving way to usually 2–4 very long (to 370 µm) flexuous, septate, and drawn out branches. Inner appendage basal cell hyaline, rectangular, 8–13 × 8–10 µm, smaller than outer appendage basal cell. Inner appendage suprabasal cell relatively small, giving way to shorter branchlets that typically form a tuft and on which the antheridia may arise. Antheridia not observed. *Perithecium* 113–145 × 53–65 µm, straight, inflated, broadest just below the neck with two crest-like protrusions emerging from the outer margin just below the abruptly tapered apical region. Apex distinctly angled inwards. Basal region of venter smokey-grey, mid- and upper portion usually pale yellow (but occasionally smokey-grey to chocolate brown), the neck blackened with paler, hyaline, obtuse lip cells.

Material examined: Indonesia, Sulawesi Utara Province, Dumoga-Bone National Park, Plot A, lowland forest,

Fig. 81 ***Laboulbenia stigmatophora*** (K(M) 43517, **holotype**). **a, b** Mature thalli. Scale bars: a, b = 50 µm

el. ca. 200 m, Flight Interception Trap, 30.X – 06.XI.1985, P.M. Hammond, on the posterior margin of the left elytron of *Loxandrus* sp. (BM(NH) Code No. 4.165) (Coleoptera, Carabidae, Pterostichini) (K(M) 43517, **holotype**; AW 299 in SYR, **isotype**. Sulawesi Utara Province, Dumoga-Bone National Park, Plot A, lowland forest, el. ca. 200 m, Flight Interception Trap, 01–08.V.1982, P.M. Hammond, on the outer margin of the left elytron of *Loxandrus* sp. (BM(NH) Code No. 4.165), AW 245 in SYR, **paratype**. Same locality, Edward's Camp, 03–11.IV.1985, P.M. Hammond, on the outer margin of the left elytron of *Loxandrus* sp. (BM(NH) Code No. 4.165), AW 289 in SYR, **paratype**.

Notes: Eight, mature thalli have been examined on different samples of *Loxandrus* sp. and all of them were on or around the outer margin of the left elytron. There are four species of *Laboulbenia* known from the species of *Loxandrus* in Central and South America viz. *Laboulbenia decoromanorum* Balazuc, *L. flagellata* Peyr., *L. loxandri* Thaxt., and *L. polyphaga* Thaxt. However, our collections (K(M) 43517, AW 299 in SYR, AW 245 in SYR, AW 289 in SYR) differ from above species by their overall thallus morphology and in the shape, coloration, and punctation of portions of the thallus. Further, our collections are morphologically somewhat similar to *Laboulbenia helluodis* Thaxt. and *L. similis*. However, our collections differ from *L. helluodis* in the overall shape of the receptacle, and in the formation of a dense tuft of branches in the appendage The differences with *L. similis* are described above in the notes for that species (Fig. 81). Interestingly, even though, our collections are morphologically allied with *L. similis*, their hosts are not closely related and, are often found together in the same habitat, lending support to the idea of a host shift (Rossi 2011). Returning to the characteristics of *L. stigmatophora*, the heavily punctate receptacle, the distinctive perithecium, and the extremely long, flexuous, appendage branchlets easily serve to distinguish this new species from all other known species of *Laboulbenia*. These collections are distinguished as an unidentified species and we introduce this collection as *Laboulbenia stigmatophora* sp. nov.

Lecanoromycetes O.E. Erikss. & Winka

Ostropomycetidae V. Reeb, Lutzoni & Cl. Roux

Ostropales Nannf.

Ostropales was introduced by Nannfeldt (1932). This order is typified by Stictidaceae and comprised with two more families viz. Phaneromycetaceae and Spirographaceae. Currently, this order comprises 32 genera.

Stictidaceae Fr.

Members of Stictidaceae are small, drought-tolerant fungi inhabited in mostly bark, wood and rock substrates (Wedin et al. 2004). They are mainly saprobes and some are lichenized or lichenicolous fungi (Fernández-Brime et al. 2018). Some species are ocationally lichenized whereas individuals of the same fungus occur as saprobic or facultatively lichenized species depending on the substrate (Wedin et al. 2004). The sexual morphs of Stictidaceae are characterized by ascomata with crystalline excipular incrustations and long, filiform ascospores (Wedin et al. 2005). Twenty-two genera were accepted by Thiyagaraja et al. (2021) with molecular data.

Stictis Pers.

Stictis species are distributed in tropical and temperate regions (Joshi et al. 2012). These species occur as saprophytes or lichenized fungi on dead twigs, leaves, fern fronds, grasses, and herbaceous stems (Wedin et al. 2004; Li and Hou 2016). Sexual morph of *Stictis* is characterized by the orbicular ascoma opening by a pore, periphysoids in apothecial margins that extend down the whole length, a hymenium that splits from the margin when dry with a thick crystalline layer in the ascoma margin and a non-parasitic niche. Phylogenetic analyses in Lu et al. (2021) and Thiyagaraja et al. (2021) based on combined LSU, ITS and mtSSU genes confirmed that *Stictis* species are polyphyletic and the phylogeny of this study also confirm it. There are 357 epithets listed in Index Fungorum (2023).

Stictis anomianthi N.I. de Silva, Lumyong & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900477; *Facesoffungi number*: FoF 14187; Fig. 82

Saprobic on dead twigs of *Anomianthus dulcis* (Dunal) J.Sinclair. **Sexual morph**: *Apothecia* 250–350 µm high × 600–700 µm diam. ($\overline{x}$ = 270 × 650 µm, n = 10), initially immersed, opening by entire pore at maturity, subglobose. *Disc* deeply cupulate, pale creamy, with white pruinose margin. *Exciple* comprising thin layer of hyaline, hyphal tissue, extending under the hymenium and with crystalliferous upper part. *Hymenium* 20–25 µm wide ($\overline{x}$ = 22 µm, n = 10), comprising hyaline cells of *textura prismatica*. *Hamathecium* comprising asci and paraphyses. *Paraphyses* hyaline, 1–2 µm wide ($\overline{x}$ = 1.4 µm), numerous, long filiform, unbranched, aseptate. *Asci* 90–110 × 6–8 µm ($\overline{x}$ = 100 × 7 µm, n = 20), unitunicate, 8-spored, cylindrical, rounded apex with sessile or short pedicel. *Ascospores* 45–55 × 2–3 µm ($\overline{x}$ = 49 × 2.4 µm, n = 30), hyaline, fusiform, 6–8-septate, smooth, no gelatinous sheath observed, tapering towards the base. **Asexual morph**: Unknown.

Material examined: Thailand, Chiang Rai Province, on dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N.I. de Silva, AND8 (HKAS 107096, **holotype**).

GenBank numbers: LSU: OQ975316; ITS: OQ980248

Notes: A new species of *Stictis* is described as *S. anomianthi* and determined to be genetically distinct based on

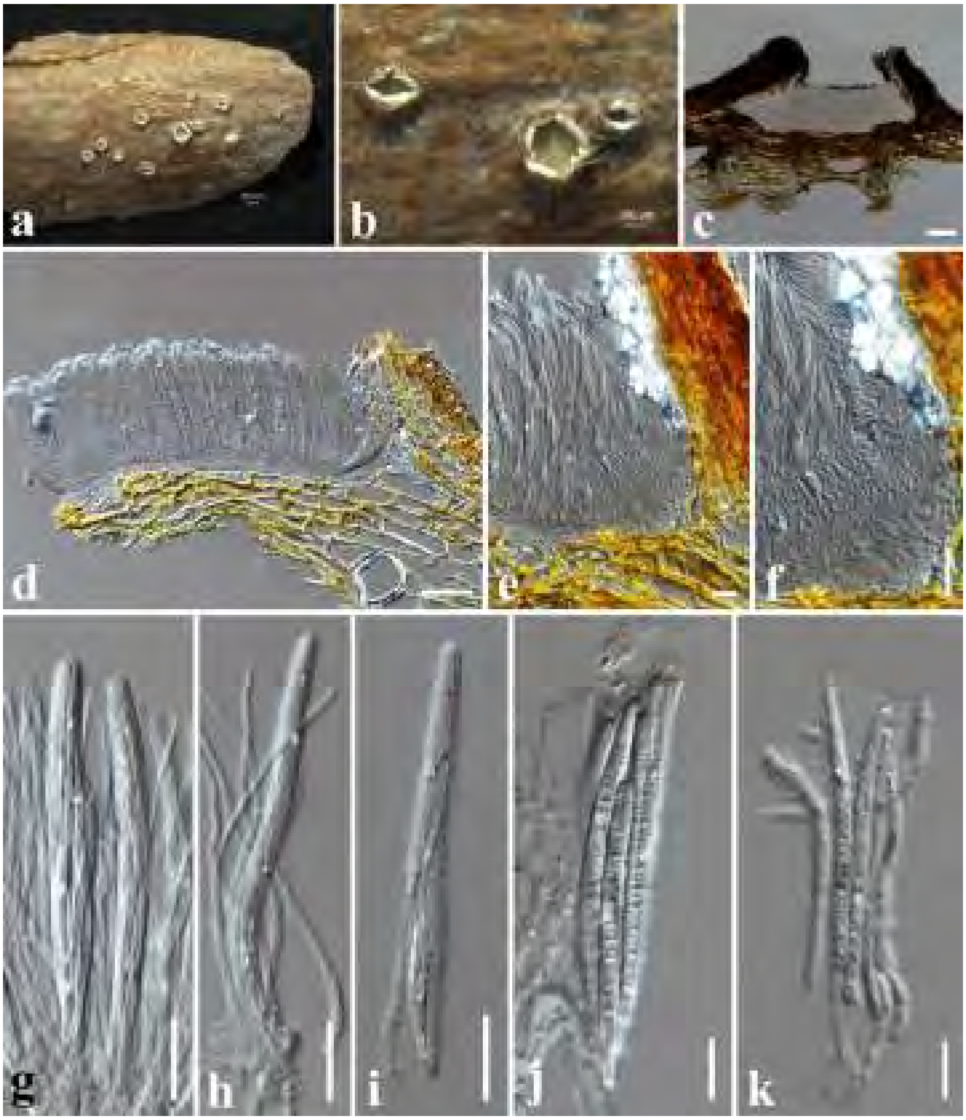


Fig. 82 ***Stictis anomianthi*** (HKAS 107096, **holotype**). **a, b** Appearance of ascomata on substrate. **c, d** Vertical section through an ascoma. **e, f** Vertical sections of peridium. **g**–**i** Paraphyses and asci. **j**, **k** Ascospores. Scale bars: a = 500 µm, b = 200 µm, c = 100 µm, d = 50 µm, e–i = 20 µm, j, k = 10 µm

phylogenetic analyses of combined of LSU, ITS and mtSSU sequence data (Fig. 83). Phylogenetically, *Stictis anomianthi* (HKAS 107096) closely related to *S. anhuiensis* (HOU 1233a and HOU 1233M) with 94% ML support. *Stictis anhuiensis* was isolated from on fallen needles of *Cunninghamia lanceolata* (Cupressaceae) in Anhui Province, China (Li et al. 2016). However, *S. anomianthi* is clearly distinct from *S. anhuiensis* in having larger asci and ascospores. *Stictis anomianthi* has larger asci (90–110 × 6–8 µm) and 45–55 × 2–3 µm ascospores than *S. anhuiensis* has small asci (50–70 × 3.5–5 µm) and ascospores (32–50 × 1–1.5 µm) (Li et al. 2016). *Stictis anhuiensis* has aseptate ascospores and similarly, both *S. pusilla* and *S. sarothamni* have aseptate ascospores (Li et al. 2016). However, *Stictis anomianthi* has septate ascospores.

Class Leotiomycetes O.E. Erikss. & Winka

Subclass Leotiomycetidae P.M. Kirk et al.

Helotiales Nannf. ex Korf & Lizoň

Helotiales was established by Nannfeldt (1932) to accommodate discomycetous species of Ascocortiaceae, Caliciaceae, Dermateaceae, Geoglosssaceae, Helotiaceae, Hemiphacidiaceae, Hyaloscyphaceae, Orbiliaceae and Sclerotiniaceae (Kimbrough 1970). The advance of molecular phylogenetic studies excluded Geoglossaceae, Calicaceae and Orbiliaceae from Helotiales (Wedin and Tibell 1997; Erikson et al. 2003; Wang et al. 2006). Helotiales comprises apothecial, cleistothecial (Galán et al. 2015) and perithecial species (Digby and Goos 1987). They are mostly found as saprobes, while some are as pathogens, endophytes and mutualists (Hernándes-Restrepo et al. 2017; Suija and Motiejūnaitė 2017; Tanney and Seifert 2020). Helotiales is the well-studied order in Leotiomycetes and currently encompass 38 families (Quandt and Haelewaters 2021).

Mollisiaceae Rehm

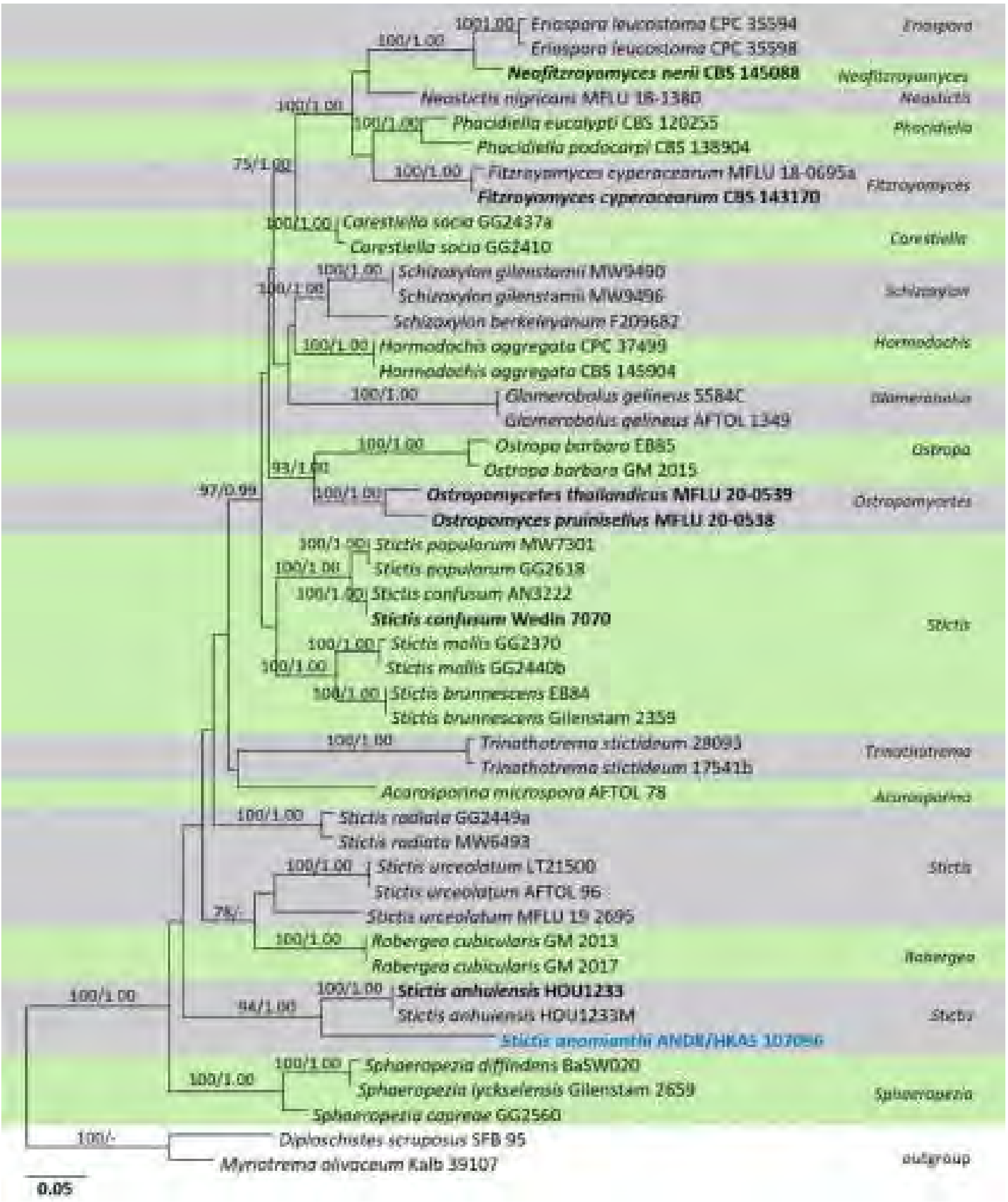


Fig. 83 Phylogram generated from the maximum likelihood analysis based on combined LSU, ITS and mtSSU sequence data representing selected genera of Stictidaceae. Related sequences are taken from Thiyagaraja et al. (2021). *Diploschistes scruposus* (SFB 95) and *Myriotrema olivaceum* (Kalb 39107) are used as the outgroup taxa. Forty-seven strains are included in the combined gene analyses comprising 3,380 characters after alignment (LSU=930, ITS=560, mtSSU=700). The best RAxML tree with a final likelihood value of − 22,586.790930 is presented. The matrix had 1503 distinct alignment patterns, with 47.53% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.241216, C = 0.242934, G = 0.273292, T = 0.242558; substitution rates AC = 1.074003, AG = 2.167182, AT = 1.275282, CG = 0.844529, CT = 5.569289, GT = 1.0; gamma distribution shape parameter α = 0.509718. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are given above the nodes. New strain is indicated in blue bold

Most species in this family are saprobes or root endophytes and it also includes endophytes of other plant tissues (Tanney and Seifert 2020). Mollisiaceae is one of poorly studied family and hence its taxonomy remains with limited understanding. Multigene phylogenetic studies suggested that the family contains more overlooked diversity (Tanney and Seifert 2020). Currently, this family includes 19 genera with around 400 species (Wijayawardene et al. 2022).

Phialocephala W.B. Kendr.

Kendrick (1961) introduced the dematiaceous hyphomycete genus *Phialocephala* for a group of morphologically distinct species previously accommodated in *Leptographium*. *Phialocephala* is typified by *P. dimorphospora* W.B. Kendr. This genus is morphologically distinguished by enteroblastic, basipetal conidiogenesis and a stationary conidiogenous locus (phialides) that gradually thickens towards the apex (Johnston et al. 2014). Currently, there are 39 accepted species in this genus (Species Fungorum 2023). *Phialocephala* species are often isolated from roots and decayed wood in heathlands, forests and alpine ecosystems across north temperate and boreal regions and rarely reported from tropical regions (Tanney et al. 2016).

Phialocephala chinensis Senan., N. Yapa & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900436; *Facesoffungi number*: FoF 14188; Fig. 84

Etymology: based on the region where the sample was collected.

Saprobic on dead stem of unidentified plant. **Sexual morph**: Undetermined. **Asexual morph**: *Mycelia* 4–5 µm diam., consisting of brown, smooth, thick-walled, branched, septate hyphae sometime slightly constricted at the septa, sometimes 3–5 in bundles. Synanamorphic with diplococcium-like and phialocephala-like (on culture). diplococcium-like synanamorph: *Conidiophores* 6–8 µm wide, macronematous, erect, solitary or clusters, branched, cylindrical, multiseptate, constricted at the septa, brown, smooth, thick-walled, sometimes with vertical or irigular

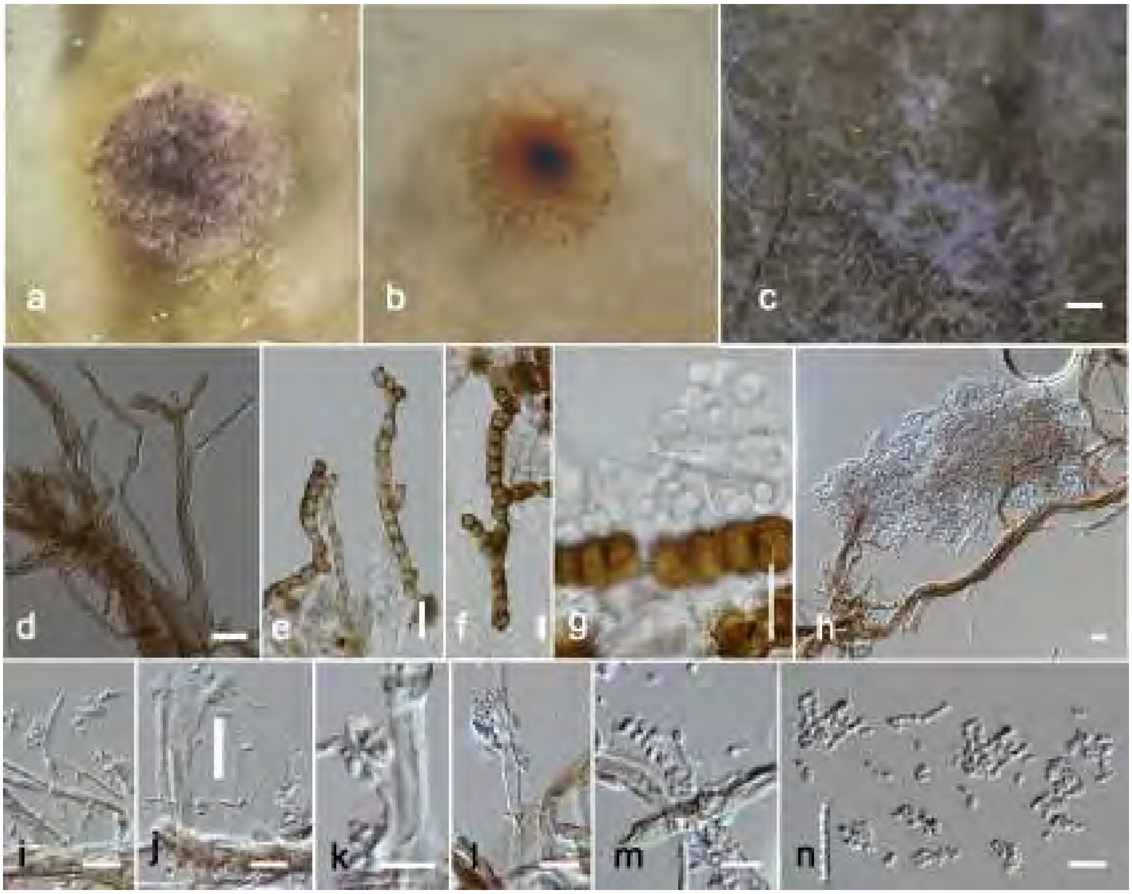


Fig. 84 ***Phialocephala chinensis*** (MHZU 22-0087, **holotype**). **a** Surface view of culture on PDA. **b** Reverse view of culture on PDA. **d** Vegitative hyphae. **c, h** Synnemata of phialocephala-like synanamorph (on culture). **g**, **i–m** Conidia attached to conidiogenous cells. **n** Conidial chains. **e, f** Synnemata of diplococcium-like synanamorph (on substrate). **g** Conidia attached to conidiogenous cells. Scale bars: c = 50 µm, d–n = 10 µm

striations, densely branched at maturity. *Conidiogenous cells* 5–12.5 × 2–3.5 µm, phialidic, cylindrical, monoblastic or polyblastic, integrated, terminal or intercalary, extensions sympodial, with 1–2 conidiogenous loci, septate, hyaline, smooth-walled. *Conidia* 2–4 × 3–6 µm ($\bar{x}$ = 3.5–5 µm, n = 20), globose to oval, unicellular, hyaline, smooth-walled, multiguttulate. Phialocephala-like synanamorph: *Synnemata* arising on hyphae, erect, unbranched, dark brown, up to 40–60 µm high, conidia produce on upper half of the synnemata. *Conidiophores* 1–3 µm wide, erect, pale brown, smooth, cylindrical, thick-walled, branched, septate. *Conidiogenous cells* monoblastic or polyblastic, integrated, terminal or intercalary, extensions sympodial, with single conidiogenous loci. *Conidia* 2–3 × 3–5 µm, blastic, globose to oval, hyaline, smooth-walled, unicellular, in chains later separate into single conidia.

Culture characteristics: Colonies on PDA reached 2 cm diam., after 30 days incubated in dark at 25 °C; circular, flat, smooth margin, white, little aerial mycelial clots, becoming brown when mature, dark brown synnemata with white conidial mass visible; reverse pale brown middle with creamy margin.

Material examined: China, Guangdong Province, Shenzhen City, Nanshan District, Yangtai Forest Park Mountain, 22° 39´21.26″ N 113° 57´18.53″ E, decaying stem of unidentified plant, 18 June 2020, I.C. Senanayake, 1026 (MHZU 22-0087, **holotype**), ex-type cultures ZHKUCC 22-0153, ZHKUCC 22-0157.

Genbank numbers: ITS: OR164942, OR164943, LSU: OR164970, OR164971.

Notes: Combined gene analysis of ITS, LSU and *tef1-α* showed that our isolates (ZHKUCC 22-0153, ZHKUCC 22-0157) clustered with *Phialocephala hiberna* (Basionym: *Cadophora hiberna* Bills) (CBS 110521), but genetically distinct forming a well-supported clade with ML/BI = 98%/0.90 statistical support. The base pair difference in ITS locus between our collection and type strain of *Phialocephala hiberna* is 2.56%.

Morphologically, our collection and *Phialocephala hiberna* are distinct from each other. *Phialocephala hiberna* forms distinct sporodochium on substrate while our collection forms synnemata. Further, we observed diplococcium-like and phialocephala-like anamorphs (synanamorphs) from our collection. *Phialocephala hiberna* produce broadly elliptical, pale olive-brown, eguttulate, smaller (2–3.5 × 1.5–2 µm) conidia while our collection produce large, globose, hyaline, sometime guttulate conidia. Therefore, we introduce our collection as a new *Phialocephala* species, *P. chinensis* (Fig. 85).

Pezizellaceae Velen.

Pezizellaceae was established by Velenovský (1934) with *Calycina* as the type genus. There are 23 genera in the genus (Wijayawardene et al. 2022). Species in Pezizellaceae are characterized by morphological sexual morph: sessile to stipitate apothecia, filiform paraphyses, cylindrical to cylindrical-clavate asci with calycina-like apical ring, and fusoid to ellipsoid ascospores (Velenovský 1934; Baral and Rämä 2015; Martínez-Gil and Baral 2018). Asexual morph of Pezizellaceae members are reported as chalara-like hypomycetes (Baral 2016; Guatimosim et al. 2016; Ekanayaka et al. 2019; Lestari and Chethana 2022).

Calycina Nees ex Gray

Calycina is typified by *C. herbarum* (Pers.) Gray which is formerly known as *Peziza herbarum* (Persoon 1794; Gray 1821; Dumont 1972). *Calycina* is characterized by the sexual morph with bright-coloured apothecia, gelatinized ectal excipulum, filiform paraphyses, cylindrical asci, and hyaline, fusoid to ellipsoid ascoscpores (Baral and Marson 2005; Baral and Rämä 2015; Suija and Motiejūnaitė 2017; Lestari and Chethana 2022). Species in *Calycina* are saprobes on dead plant materials (Dumont 1972; Quijada and Beltrán-Tejera 2017), pathogens in living plants (Crous et al. 2019) and lichenicolous species (Suija and Motiejūnaitė 2017).

Calycina papaeana Lestari & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900437; *Facesoffungi number*: FoF13908; Fig. 86

Etymology: Epithet represents Pa Pae sub-district where the specimen was collected.

Saprobic on decaying root of an unidentified plant. **Sexual morph**: *Apothecia* 165–487 × 145–450 µm ($\bar{x}$ = 143.4 × 229 µm, n = 10), dark yellow in dry condition, arising singly or in small cluster, stipitate. *Receptacle* cupulate, olivaceous dark brown to black. *Stipe* 1–2 × 0.5–1 mm in dry condition, concolorous with receptacle, rugose. *Disc* yellow, shallow cupulate, slighly concave. *Ectal excipulum* 23–50 µm ($\bar{x}$ = 31.8 µm, n = 10), composed of thin-walled, hyaline to pale brown cells of *textura porrecta*. *Medullary excipulum* 23–57 µm ($\bar{x}$ = 39.2 µm, n = 10) in lower flanks, composed of thin-walled, hyaline cells of *textura oblita*. *Hymenium* 62–75 µm ($\bar{x}$ = 70.1 µm, n = 10), hyaline. *Paraphyses* 1.2–2.3 µm in diam. ($\bar{x}$ = 1.7 µm, n = 10), filiform with occasional subclavate swells at the apex, sometimes branched at the base, guttulate. *Asci* 38–58 × 3–6 µm ($\bar{x}$ = 50.2 × 4.6 µm, n = 10), 8-spored, unitunicate, cylindrical, rounded, amyloid, with long substipitate base, arising from croziers. *Ascospores* 4–9 × 2–5 µm ($\bar{x}$ = 5.7 × 3.2 µm, n = 15), ellipsoid, uniseriate or partially biseriate, hyaline, biguttulate, rounded at both ends. **Asexual morph**: Undetermined.

Material examined: Thailand, Chiang Mai Province, Pa Pae sub-district, Mushroom Research Center, 8 September 2020, Anis S. Lestari, CM 11 (MFLU 23-0015, **holotype**)

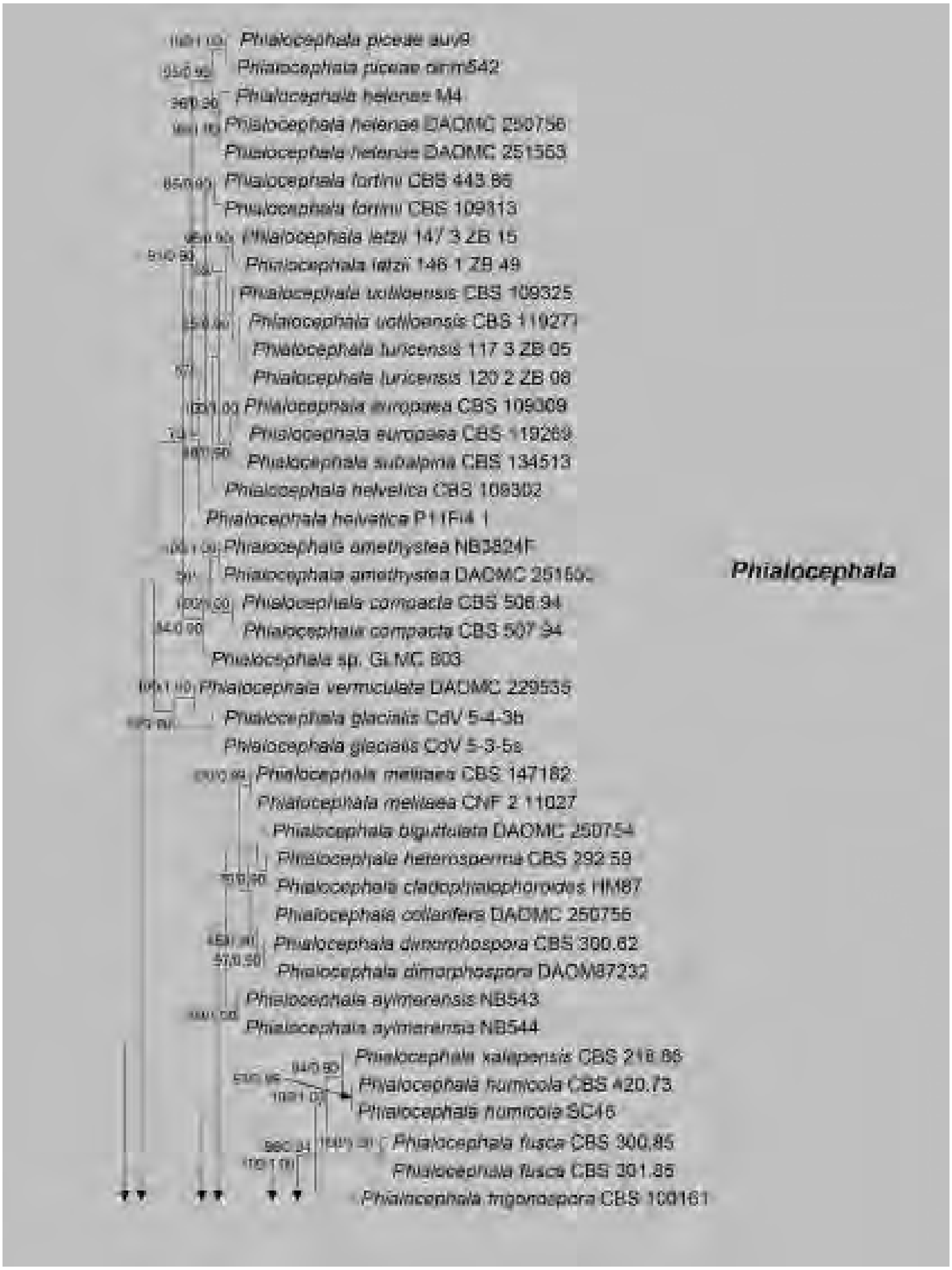


Fig. 85 The best scoring RAxML tree with a final likelihood value of − 14,938.532372 for combined dataset of ITS (521 bp), LSU (850 bp) and *β-tubulin* (588 bp) sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses. The tree is rooted with *Leotia lubrica* (AFTOL ID 1). The matrix had 1013 distinct alignment patterns with 52.57% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.255331, C = 0.228833, G = 0.278368, T = 0.237468; substitution rates AC = 1.157479, AG = 2.182775, AT = 1.284773, CG = 0.936220, CT = 5.805724, GT = 1.0; gamma distribution shape parameter α = 0.333593. Ex-type strains are in bold and newly generated sequences are in red. Bootstrap support for ML equal to or greater than 50% and BYPP equal to or greater than 0.90 are given above the nodes

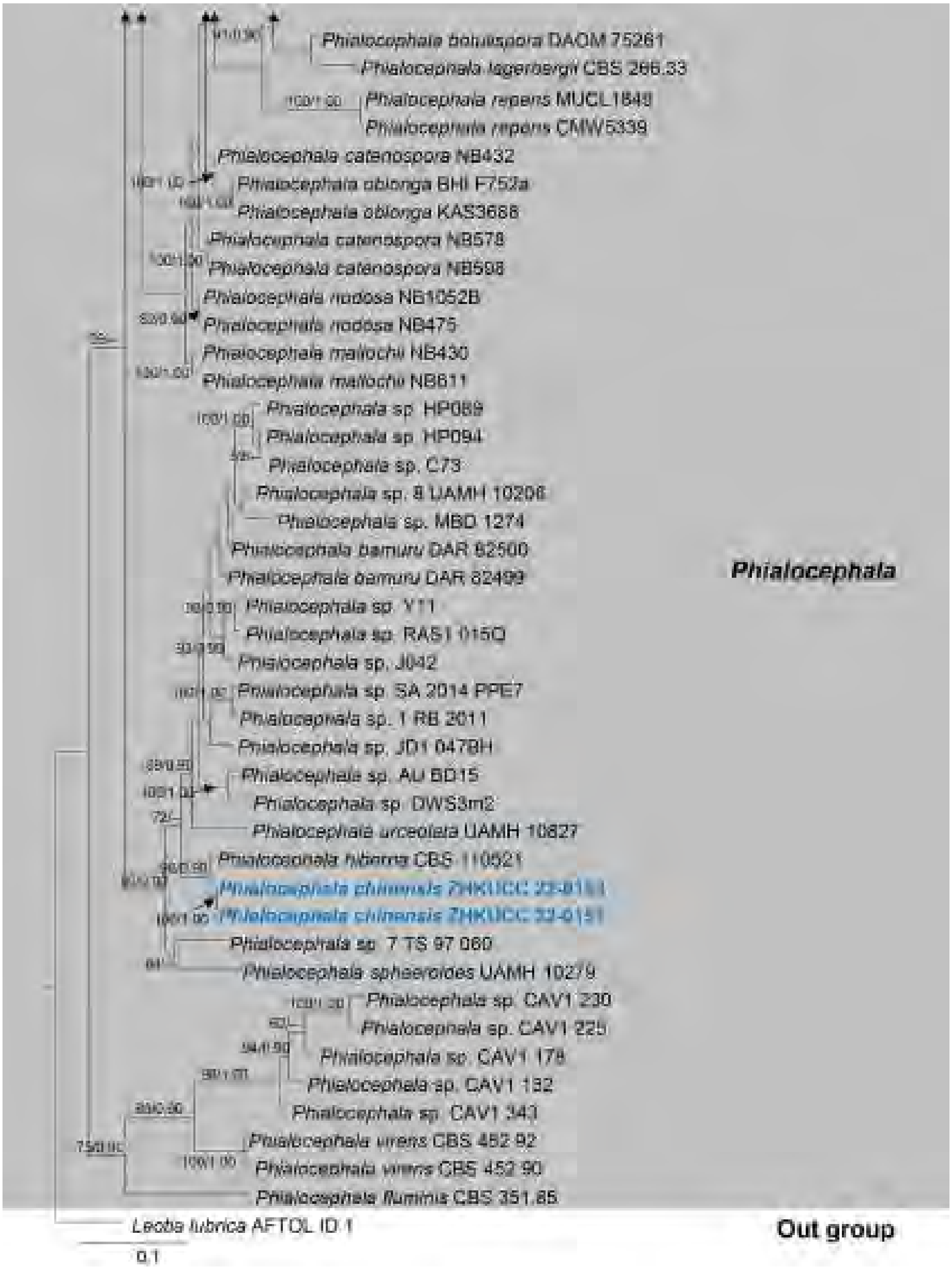


Fig. 85 (continued)

GenBank numbers: ITS: OQ079546, LSU: OQ079547

Notes: The ITS and LSU sequences of our collection (MFLU 23-0015) show *Calycina* species as the closest matches with NCBI. Our collection forms a distinct lineage in the combined ITS and LSU sequence analyses with ML/BI = 91%/0.99 statistical support (Fig. 87). The nucleotide differences in ITS and LSU sequences of our collection and phylogenetically close *Calycina* species are listed in Table 3.

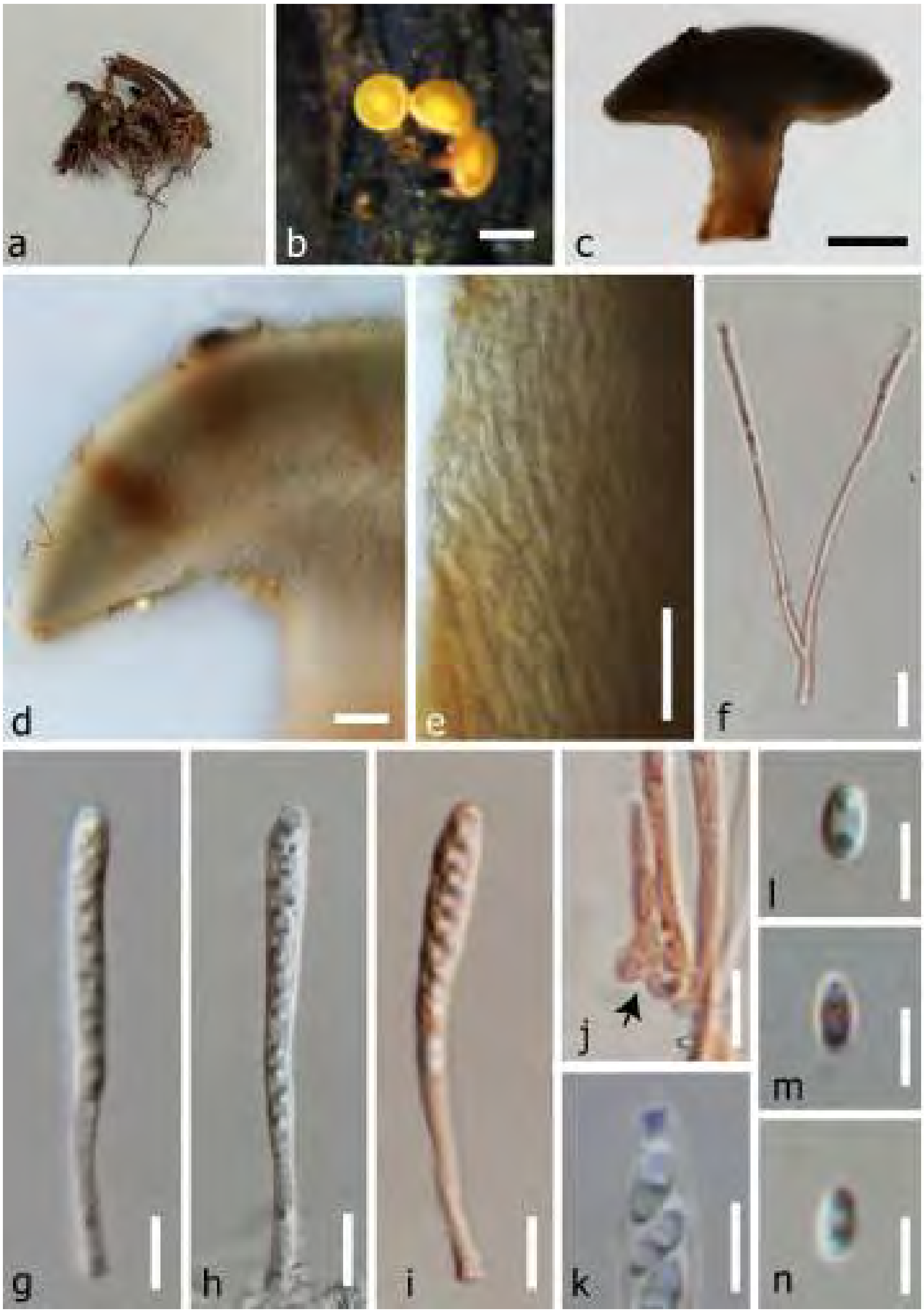
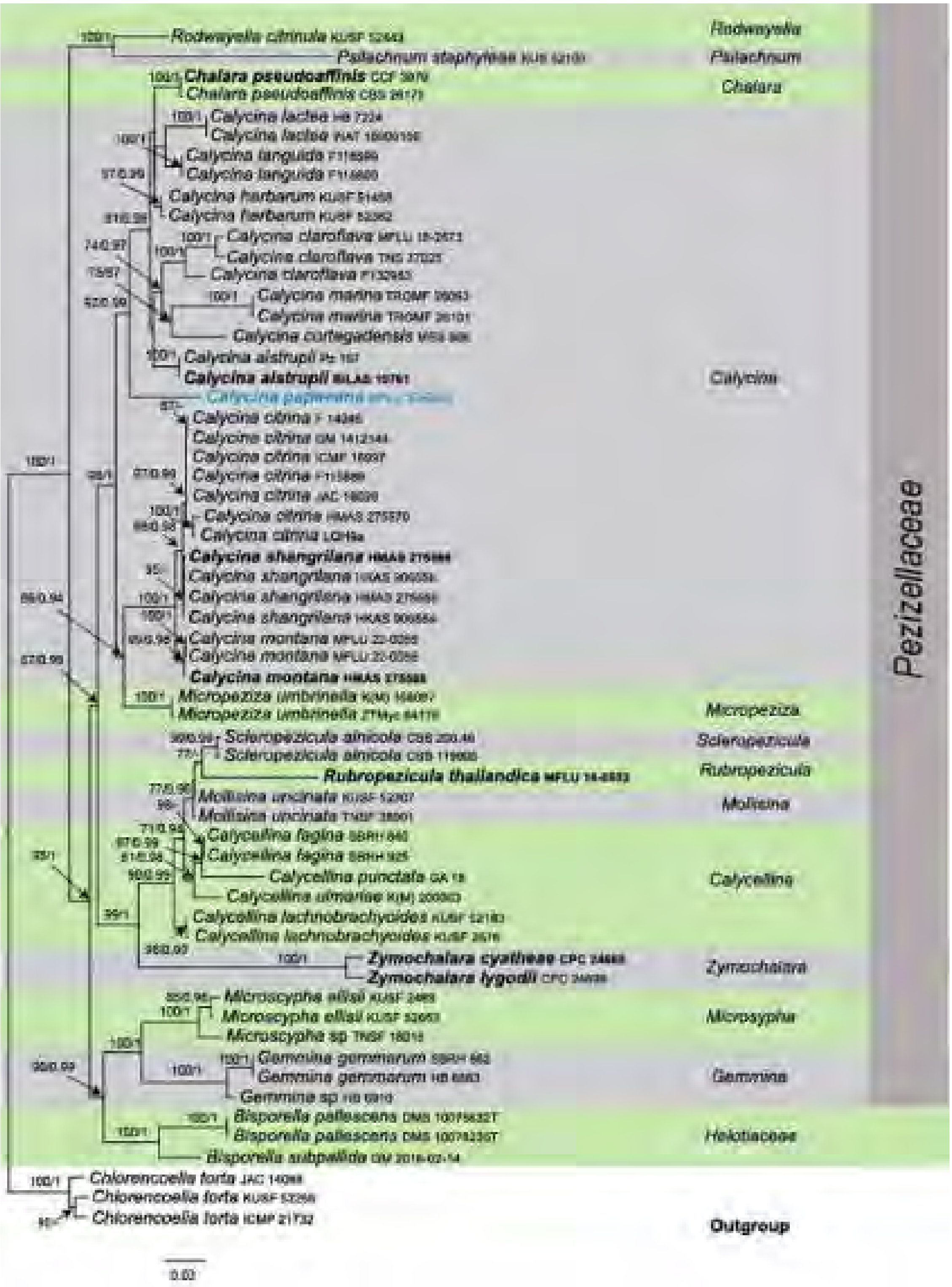


Fig. 86 ***Calycina papaeana*** (MFLU 23-0015, **holotype**). **a** Examined material. **b** Apothecia on the substrate. **c** Vertical cross-section through the apothecium. **d** Close up of hymenium at the margin **e** Ectal excipulum cells. **f** Paraphyses. **g–i** Asci (**i**. mounted in Congo red). **j** Crozier at the base of a young ascus (arrowed). **k** Ascal tip (J + without KOH treatment). **l–n** Ascospores. Scale bar: b = 380 µm, c = 200 µm, d = 60 µm, e = 25 µm, f–n = 10 µm

Our collection morphologically fits with *Calycina* by having gelatinized ectal excipulum, filiform paraphyses, cylindrical asci with apical rings and ellipsoidal ascospores (Baral and Marson 2005; Baral and Rämä 2015; Suija and Motiejūnaitė 2017; Lestari and Chethana 2022).

Despite the ITS and LSU base pair differences (Table 2), our collection distinguished from *Chalara pseudoaffinis*, *Calycina lactea*, *C. languida*, *C. herbarum*, *C. claroflava*, *C. cortegadensis* and *C. alstrupii* (Table 3). The sexual morph is absence for *Chalara pseudoaffinis* and it only characterized by chalara-like asexual morph (Koukol 2011). Our collection is characterized by its stipitate apothecia which is differed from species with sessile apothecia viz. *C. alstrupii, C. claroflava* and *C. marina* (Baral and Rämä 2015; Quijada and Beltrán-Tejera 2017; Suija and Motiejūnaitė 2017). Asci of our collection arise from crozier and *C. languida* and *C. cortegadensis* produce asci from simple septa (Baral 2021). Ascospores of our collection are ellipsoid with biguttules and *C. herbarum* and *C. lactea* are characterized with their multiguttulate, fusoid ascospores (Baral 2013; Dominguez 2017). Therefore, we introduce our collection as *Calycina papaeana* sp. nov.



Pezizomycetidae Locq.

Pezizomycetes O.E. Erikss. & Winka

Pezizales J. Schröt.

Pezizales contains apothecial, cleistothecial or perithecial species and some species with enclosed ascomata occur in underground known as truffles. Most members release ascospores through the apical operculum of the asci excluding the hypogeous taxa. The aseptate ascospores are diversed in shapes, from globose to naviculate with smooth or ornamented walls (Pfister and Healy 2021). Most Pezizales taxa are saprobic on organic materials, mutualistic as

◂**Fig. 87** The best scoring RAxML tree with a final likelihood value of − 8091.026 based on the combined ITS and LSU sequence data of taxa in Pezizellaceae. The tree is rooted with members of Cenangiaceae (*Chlorencoelia torta* JAC 14068, KUSF 52256 and ICMP 21732). The tree topology of RAxML is identical with Bayesian analysis. Sixty strains were included in the data set which comprised 1322 characters (466 characters for ITS and 854 characters for LSU including the gap regions). The matrix had 901 distinct alignment patterns with 68.15% undetermined characters and gaps. Estimated base frequencies were as follows: A = 0.2424, C = 0.1082, G = 0.3617, T = 0.9371; substitution rates AC = 2.2394, AG = 3.3421, AT = 2.2394, CG = 1.0, CT = 8.6577, GT = 1.0; gamma distribution shape parameter α = 0.688. The new species is indicated in blue bold. Bootstrap value (ML) is greater than 70% and Bayesian posterior probabilities (BI) greater than 0.90 are given at the nodes

mycorrhizae, endophytes, and parasitic on plants (Pfister and Healy 2021). Pezizales contains 23 families (Pfister and Healy 2021). Some members within Pezizales are economically important, such as morels, the bachu mushrooms, and truffles, while some are toxic, such as *Gyromitra* spp.

Sarcosomataceae Kobayasi

This family is characterized by brown or black, discoid to cupulate, leathery to gelatinous apothecia, coloured hymenial hairs or setae, operculate, inamyloid asci, and globose, ellipsoid or suballantoid ascospores with smooth or ornamented walls (Zeng et al. 2021). Anamorph states are *Conoplea* or possibly *Strumella* (Pfister and Healy 2021; Zeng et al. 2021). There are eight genera within this family, with *Korfiella* and *Selenaspora* lacking molecular data (Pfister and Healy 2021).

Urnula ailaoshanensis J. R. Lu, Y. Zhang & Q. Zhao, in Lu, Yu, Zhou, Lu, Zhang & Zhao, Phytotaxa 619(1): 91 (2023)
Index Fungorum number: IF 900885; *Facesoffungi number*: FoF 14797; Fig. 88

Saprobic on dead, rotten wood surrounded by mosses. **Sexual morph**: *Apothecia* 2–5 cm diam., up to 1.5–3 cm high, scattered to gregarious, sessile to subsessile. *Receptacle* cupulate to turbinate, dark at receptacle surface, margin conspicuous, involute, entire, or undulate when young. *Hymenium* glabrous, deep ocher to dark brown with matt surface or reddish brown with lacquer gloss, nearly smooth. External surface velvety, towards juncture to stem folded or veined, veins joined to give the reticulate appearance, blackish to brownish black. *Ectal excipulum* 100–270 µm broad, of *textura globulosa* to *textura angularis*, composed of yellowish brown, dark brown to black cells, 22–35 × 8–21 µm broad, with two type hairs; 1) 3–5.5 µm broad, cylindrical, septate, dark brown, long hairs (hyphoid hairs), with dark granules on the surface; 2) 4–6.5 µm broad, subhyaline to yellow brown or dark brown, short hairs (true hairs), with smooth walls and rounded ends. *Medullary excipulum* 480–1,650 µm broad, of *textura intricata*, hyaline to yellowish-brown, composed of 3.5–5.5 µm broad hyphae. *Paraphyses* 1.5–3.5 µm diam., subhyaline to yellow brown, filiform, septate, longer than asci, apex slightly enlarged, irregular protuberances, and amorphous pigment in the upper part, 2.5–5 µm broad. Setae 3–5.5 µm diam., brown, filiform to narrowly cylindrical, straight, aseptate. *Asci* 410–600 × 20–30 µm, 8-spored, operculate, cylindrical, with a long stalk, J- apical ring. *Ascospores* (29.0–) 31–35 (–36.7) × (13.5–) 14.5–16.5 (–17.0) µm (Q = 1.89–2.37, Q = 2.13±0.14), subfusiform ellipsoid, inequilateral, rarely equilateral, uniseriate, hyaline, smooth-walled, 1–3-guttulate, or multi-guttulate. **Asexual morph**: Unknown.

Material examined: China, Yunnan Province, Puer City, Jingdong County, Ailao Mountain, on unidentified dead wood, 28 August 2021, Hongli Su, SHL-1 (HKAS 125550). *ibid.* 24 August 2022, Le Luo, LL 453 (HKAS 125897).

GenBank numbers: ITS: OP850045, OP850046; LSU: OP850224, OP850225.

Notes: Our collections clustered with the holotype collection of *Urnula ailaoshanensis* with bootstrap support (ML/BI = 82%/0.99) (Lu et al. 2023). The ITS and LSU sequence data of our collection is identical to the sequences derived from holotype. Therefore, we identified our collection as *U. ailaoshanensis*. However, our collection shows few morphological differences from holotype in hymenium, ectal excipulum, hairs, paraphyses and ascospores. Hence, we provide an emendation to the prologue. Hymenium in our collection is deep ocher to dark brown without lacquer gloss and external surface is not velvety, towards juncture to stem. Our collection contains two different kind of hairs viz. dark brown, long, hyphoid hairs with dark granules on the surface and subhyaline to yellow brown or dark brown, short, true hair with smooth walls and rounded ends. Ascospores in our collection are evenly distributed within the ascus while ascospores in holotype collection mostly concentrated into the upper part of asci. Ascospores of our collection are subfusiform, 1–3-guttulate, or multi-guttulate while illustration of holotype collection does not contain any guttulate (Lu et al. 2023).

Urnula ailaoshanensis is morphologically distinguished from other Urnula species by cupulate to turbinate apothecia with two type excipular hairs, deep ocher to dark brown or reddish brown with lacquer gloss hymenium, subfusiform, inequilateral ascospores with 1–3 guttules. Further, Urnula ailaoshanensis is phylogenetically close to *Urnula himalayana* and *U. versiformis*. However, these two species morphologically differ from *Urnula ailaoshanensis* (Wang and Huang 2015; Wang et al. 2018; Lu et al. 2023) (Fig. 89).

Tarzettaceae Ekanayaka, K.D. Hyde, Q. Zhao & E.B.G. Jones

Based on analysis of combined LSU, SSU, ITS, *tef*1-α and *rpb2* sequence data, Ekanayaka et al. (2018) introduced Tarzettaceae for the *Tarzetta-Geopyxis* lineage, with *Tarzetta* (Cooke) Lambott as its type genus. Macromorphologically, Tarzettaceae is characterized by apothecial or truffle-like, epigeous or hypogeous, cupulate to bladder-like

Table 2 Comparison of ITS and LSU sequences of closely related *Calycina* species with our collection

Species	ITS (%)	LSU (%)
Calycina alstrupii (BILAS 10761)	13.09	1.52
Chalara pseudoaffinis (CCF3979)	9.22	1.87
Calycina lactea (HB7224)	8.79	N/A
Calycina languida (F116599)	8.79	N/A
Calycina herbarum (KUSF51458)	7.29	1.52
Calycina claroflava (F132983)	9.22	N/A
Calycina marina (TROMF26093)	10.94	3.99
Calycina cortegadensis (MSS 906)	12.23	1.99

ascomata. Microscopically, the paraphyses are filiform, septate, slightly swollen at the apices and branched. The asci are operculate to sub-operculate or indehiscence, amyloid or nonamyloid, cylindrical, 8-spored, and the ascospores are globose to ellipsoid, and guttulate.

Tarzetta (Cooke) Lambotte

Tarzetta was established by Cooke (1879) as a subgenus of *Peziza* Fr. and later combined to the genus *Tarzetta* by Lambotte (1888). Its type species is *Tarzetta catinus* (Holmsk.) Korf & J.K. Rogers. *Tarzetta* was originally circumscribed as a member of the Pyronemataceae. Using four-gene phylogeny, Pyronemataceae was demonstrated as a paraphyletic group and then *Tarzetta* was placed in *Tarzetta*-*Geopyxis* lineage (Hansen et al. 2013; Wang et al. 2016; Kumar et al. 2017). Ekanayaka et al. (2018) introduced the new family Tarzettaceae to accommodate *Geopyxis*, *Hydnocystis*, *Hypotarzetta*, *Paurocotylis*, *Stephensia*, and *Tarzetta* based on phylogenetic analyses of five combined loci of ITS, LSU, SSU, *tef*1-α, and *rpb2* regions. Currently, *Tarzetta* comprises 21 species that have a widespread distribution in north temperate region (Kirk et al. 2008; Ekanayaka et al. 2018; van Vooren et al. 2019). In China, only four species have been reported, i.e., *Tarzetta catinus*, *T. confusa*, *T. cupularis*, and, *T. linzhiensis* (Kirk et al. 2008; Zhuang 2014; Hyde et al. 2021). The apical ends of the paraphyses often used as an important diagnostic character to separate species in *Tarzetta*. However, van Vooren et al. (2019) suggested that the morphology of paraphyses may differ with the age of the collection or the area of hymenium that we observed. We introduce two new *Tarzetta* species in this study.

Tarzetta tibetensis F.M. Yu, & Q. Zhao ***sp. nov.***

Index Fungorum number: IF900470; *Faceoffungi number*: FoF14239; Fig. 90

Etymology: Named after Tibet, China, where the type specimen was collected.

Saprobic on soil. **Sexual morph**: *Apothecia* up to ca. 10 mm broad, stipitate, cupuliform, scattered, hymenium light yellow, cream yellow, receptacle surface greyish yellow to greyish brown. *Margin* crenate and eroded, with brown tooth. *Subhymenium* and *medullary excipulum* thin, brown, cells of *textura intricata*, with hyaline hyphae, 2.5–5.0 µm wide. *Ectal excipulum* 6.5–29.5 µm diam., with cells of *textura subglobulosa/angularis*, hyaline to light brown, organized in small pyramidal brownish warts. *Asci* 215–320 × 11–17 µm, 8-spored, cylindrical, long narrowed to the base, croziers, operculate, inamyloid. *Paraphyses* 2.0–4.5 µm diam. wide, filiform, separate, branched, as long as asci, straight, hyaline, irregular at the top, digitate or with lateral bumps, the widest point at the apex 3.0–6.0 diam. *Ascospores* 14.5–21.5 × 8.5–11.5 µm ($\overline{x} = 18.5 \times 10.0$ µm, n = 50), ellipsoid, blunt rounded at both ends, uniseriate, hyaline, smooth, containing two or more small guttules that fuse into one at maturity. **Asexual morph**: Undetermined.

Material examined: China, Tibet, Shigatse City, Yadong Country, on soil, 2 July 2022, 27° 25′ 52.3487″ N, 88° 59′ 58.8944″ E, 3632 m a.s.l., F.M. Yu, FM22-109 (HKAS 127118, **holotype**), FM22-232 (HKAS 127117, **paratype**).

GenBank numbers: ITS: OQ422965, OQ417936, LSU: OQ418059, OQ418058.

Notes: The sequence data of our collections (HKAS 127117 and HKAS 127118) reveal species in *Tarzetta* as the closest matches with NCBI. Phylogenetic analyses of the combined ITS and LSU sequences (Fig. 92) showed that our collections formed a well-supported distinct subclade which is sister to the subclade comprising *Tarzetta cupularis*, *T. catinus*, *T.* cf. *cupularis*, *T. melitensis*, *T. scotica*, and *T. spurcata*. However, morphologically our collections are distinct from phylogenetically close species (Table 4). There are four *Tarzetta* species viz. *T. catinus*, *T. confusa*, *T. cupularis* and *T. linzhiensis* have been reported in China. The apical ends of paraphyses in our collections are irregular with digitate or lateral bumps, which were distinctly different from other *Tarzetta* species collected in China. Therefore, we introduce our collections as *Tarzetta tibetensis* sp. nov.

Tarzetta urceolata L. Lei, & Q. Zhao ***sp. nov***.

Index Fungorum number: IF900471; *Faceoffungi number*: FoF14240; Fig. 91

Etymology: The epithet refers to its urceolate apothecia.

Saprobic on a humus layer covered with moss. **Sexual morph**: *Apothecia* ca. 20 mm broad, stipitate, urceolate, scattered, hymenium greyish brown when fresh, receptacle surface whitish, yellowish grey to olive grey, with finely white-powdery. *Margin* involute when mature. *Subhymenium* and *medullary excipulum* 287–345 µm, well-developed, cells of *textura intricata*, with hyaline hyphae 2.5–8.5 µm wide. *Ectal excipulum* ca. 300 µm, cells of *textura subglobulosa/angularis*, with 7–26 µm wide, hyaline to brown, organized in small pyramidal brownish warts. *Asci* 400–437 × 13–17.5 µm, 8-spored, cylindrical,

Table 3 Morphological comparison of *C. papaena* with other fungal species phylogenetically closely related

Species	Apothecia	Asci	Ascospores	Asexual morph	References
Calycina alstrupii	Sessile	Cylindrical to subcylindrical, J +, arising from simple septa, 8-spored	5–7 × 1.5–2.5; ellipsoid, obtuse or with apices attenuated at one or both ends, hyaline, uniseriate	N/A	Suija and Motiejūnaitė (2017)
Calycina claroflava	Sessile	Cylindric-clavate, rounded apex, J-, arising from simple septa	7–12.5 × 2–3; subcylindrical to fusoid, hyaline, obtuse to narrow ends, 1-septate, uniseriate to biseriate	N/A	Quijada and Beltrán-Tejera (2017)
Calycina cortegadensis	Short stipe	Cylindrical to subcylindrical, a conical or obtuse apex, J +, arising from simple septa	Ellipsoid, hyaline, obtuse apices, aseptate, uniseriate to biseriate	N/A	Crous et al. (2019)
Calycina herbarum	Short stipe	Cylindric to cylindrical clavate, J +	Fusoid, guttulates (more than 2-guttules)	N/A	Han et al. (2014), Uzun et al. (2014)
Calycina lactea	Stipitate	Cylindric with subclavate at the top, J + (IKI), arising from croziers (not clear), 8 spored but only with 2–4 mature ascospores	Fusoid with 1–3 septate and guttulate	N/A	Baral (2013)
Calycina languida	Short stipe	Cylindrical with long base, J + (IKI), arising from simple septa	Fusoid mostly with two big guttules and small guttules, partially biseriate to uniseriate, aseptate	N/A	Baral (2021)
Calycina marina	Sessile	Cylindrical clavate with rounded apex, arising from simple septa	Subcylindrical to subfusoid or ellipsoid, obtuse at both ends, uniseriate to biseriate	N/A	Baral and Rämä (2015)
Calycina papaeana	Stipitate	Cylindrical with rounded apex, J + (MLZ without KOH treatment) arising from crozier, 8 spored	Fusoid to ellipsoid, bigutulate	N/A	This study
Chalara pseudoaffinis	N/A	N/A	N/A	Multiseptate conidiophore, phialide lageniform with cyclindric phialoconidia	Koukol (2011)

MLZ Melzer agent, *IKI* Iodine-Potassium Iodide, *N/A* not available, size in µm

Fig. 88 ***Urnula ailaoshanensis*** **a** Habitat. **b**–**e** Examined material (**b**, **c** HKAS 125550; **d**, **e** HKAS 125897). **f** Ectal excipulum and partly medullary excipulum. **g** Smooth hairs (true hairs). **h** Hairs with granules on the surface (hyphoid hairs). **i** Hymenium. **j** Paraphyses. **k** Apex of asci. **l** Setae (hymenium hair). **m**, **n** Asci. **o**–**r** Ascospores. Scale bars: f, h = 50 µm, g, k, l = 30 µm, i, m, n = 150 µm, j = 100 µm, o–r = 20 µm

long narrowed to the base, croziers, operculate, inamyloid. *Paraphyses* 2.5–4.5 µm wide, filiform, separate, branched, as long as asci, apex enlarged or constrictive slightly, straight or curved at the apex. *Ascospores* 8.5–13.5 × 6.5–9 µm (= 11.5 × 8.0 µm, n = 50), subglobose, broad ellipsoid to ellipsoid, hyaline, smooth. **Asexual morph**: Undetermined.

Material examined: China, Tibet, Nyingchi County, Chayu City, on ground covered with moss, 15 July 2022, 28° 36′ 35.0415″ N, 98° 5′ 22.2463″ E, 4107 m a.s.l., F.M. Yu, FM22-244 (HKAS 127116, **holotype**).

GenBank numbers: ITS: OQ422966, LSU: OQ418060.

Notes: Our collection (HKAS 127116) clustered with *Tarzetta linzhiensis* with ML/BI = 100%/1.00 statistical support (Fig. 92) in combined ITS and LSU gene analyses. The nucleotide comparison of sequences of our collection and *T. linzhiensis* reveals 9.33% in ITS and 1.55% in LSU. Morphologically, our collection differs from *T. linzhiensis* by its longer asci (400–437 µm *vs.* 310–385 µm), and smaller (8.5–13.5 × 6.5–9 µm *vs* 18.5–22.5 × 10–13.5 µm) ascospores.

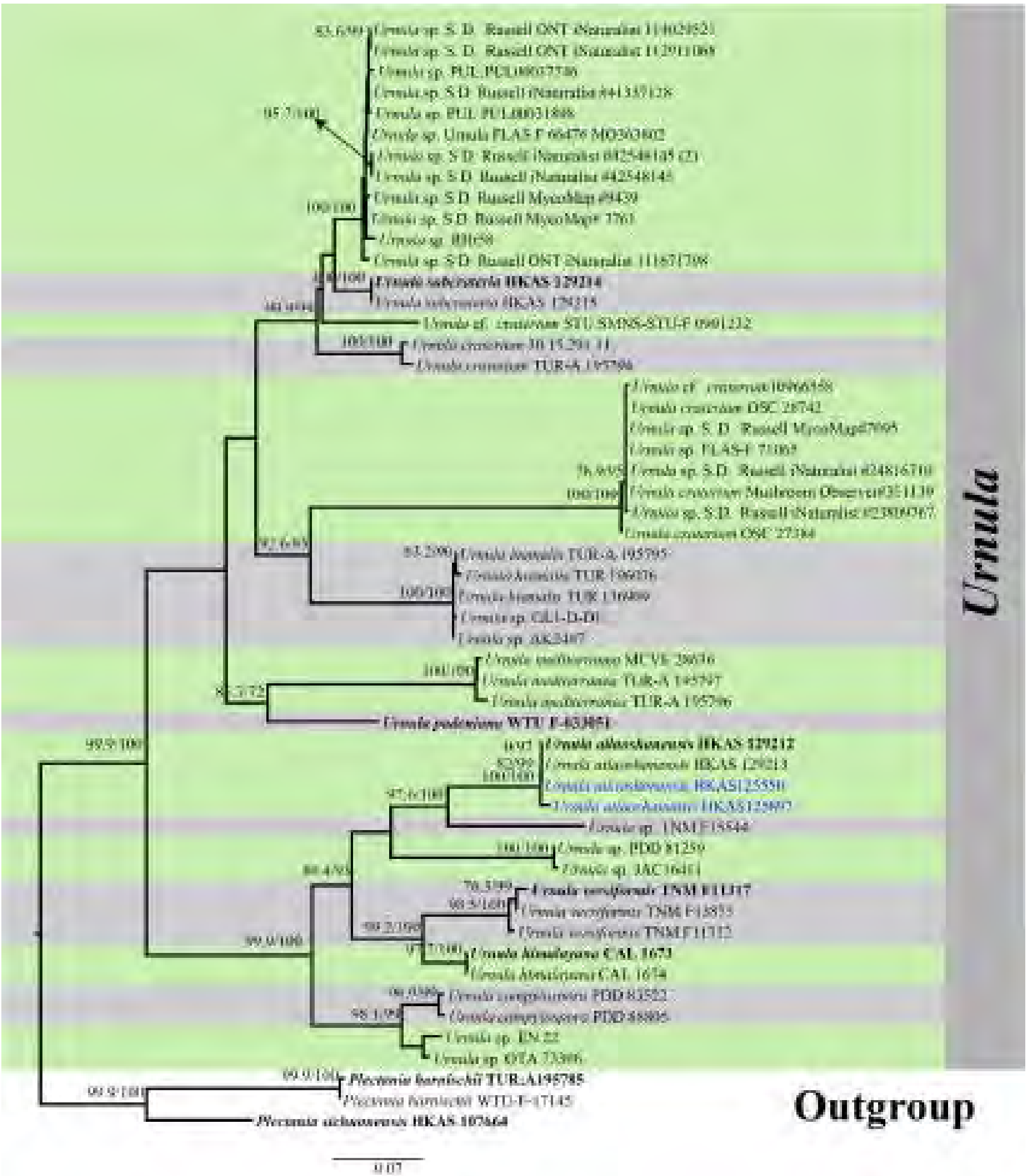


Fig. 89 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Fifty-three strains are included in the combined analyses which comprised 1,828 characters (ITS: 987 bp; LSU: 841 bp). Both the Maximum likelihood (ML) and Bayesian analyses yielded similar tree topologies, and only the tree inferred from ML analysis is shown in Fig. 89. Bootstrap support values for ML ≥ 80% and Bayesian posterior probabilities greater than 0.95 are indicated at the nodes. The tree is rooted with *Plectania harnischii* (TUR: A195785 and WTU-F-17145) and *P. sichuanensis* (HKAS 107664). The newly generated sequences are indicated in blue bold and type strains are in bold.

Therefore, we introduce this collection as a novel species *Tarzetta urceolata* based on morphology and phylogeny.

Sordariomycetes O.E. Erikss. & Winka

Diaporthomycetidae Senan., Maharachch. & K.D. Hyde

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

The order Coniochaetales has been proposed based on Coniochaetaceae (Huhndorf et al. 2004), and except Coniochaetaceae, this order includes Cordanaceae Nann. Cordanaceae was previously classified in the order Cordanales, and it was treated as a synonym of Coniochaetales (Hongsanan et al. 2017).

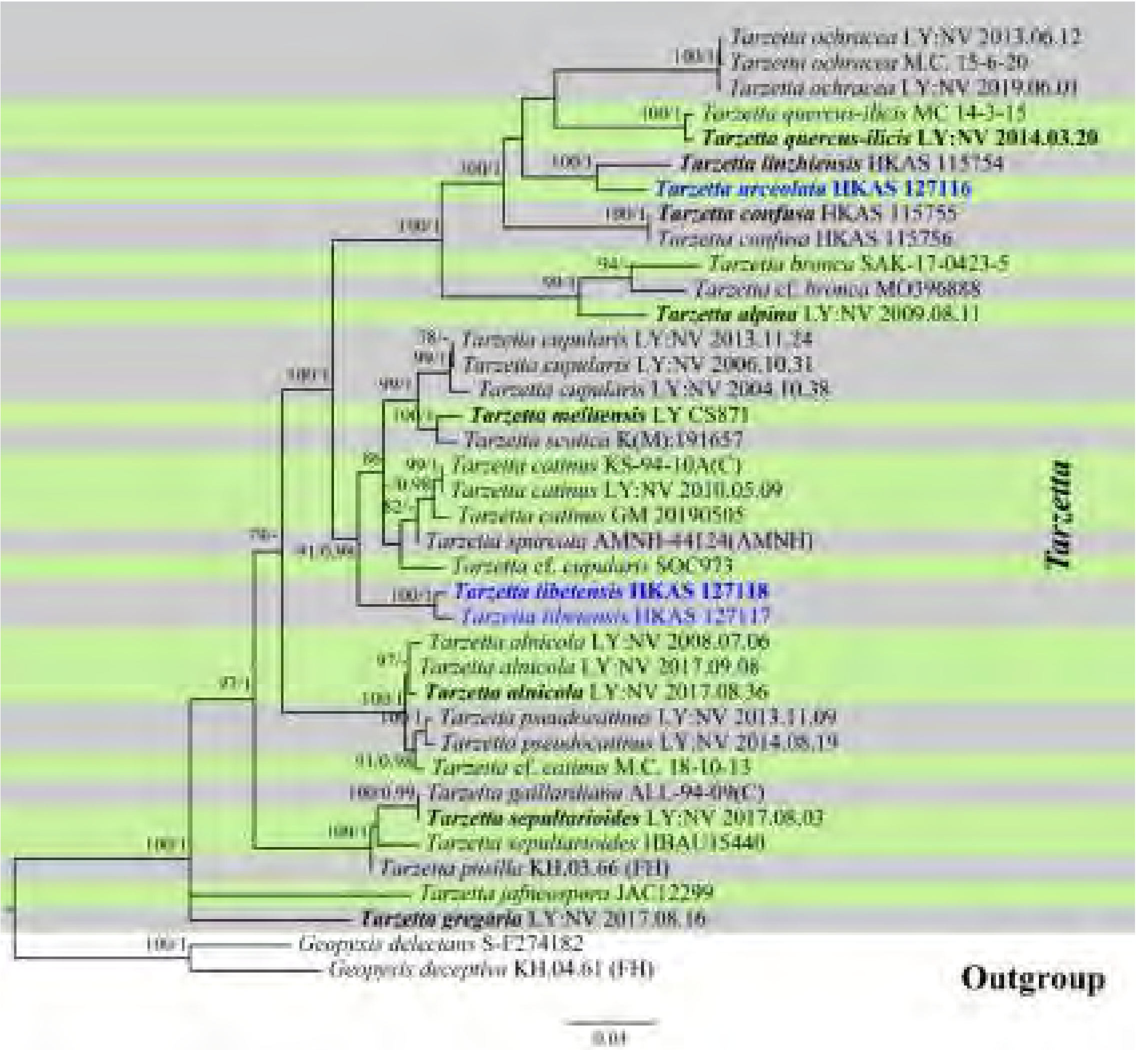


Fig. 90 ***Tarzetta tibetensis*** (HKAS 127118, **holotype**). **a–c** Typical mature specimens. **d** Anatomic structure of a portion of an apothecium. **e, f** Asci and paraphyses. **g–j** Asci. **k** Paraphyses. **l** Apex of ascus. **m** Ascospores. Scale bars: a–c = 0.5 cm, d–f = 200 μm, g, h = 100 μm, i = 50 μm, j = 20 μm

Coniochaetaceae Malloch & Cain

Coniochaetaceae was established by Malloch and Cain (1971) and comprises two genera as *Barrina* and *Coniochaeta* (Hyde et al. 2020a). The family is accommodated in Coniochaetales (Huhndorf et al. 2004). Species of Coniochaetaceae are usually saprobic or pathogenic in plants and animals (Damm et al. 2010; Samarakoon et al. 2018). Coniochaetaceae species also produce potent antibiotics, and some strains were evaluated to have a high potential for biological detoxification of lignocellulosic biomass (Segeth et al. 2003; López et al. 2004; Friebes et al. 2016).

Coniochaeta (Sacc.) Cooke

The genus *Coniochaeta* was introduced and typified by *C. ligniaria* (Grev.) Cooke (Cooke 1887). Members of this pleomorphic genus distribute globally (García et al. 2006; Damm et al. 2010; Raja et al. 2012; Vázquez-Campos et al. 2014; Réblová et al. 2016; Nasr et al. 2018; Harrington et al. 2019) with a wide range of hosts and substrates, such as butter, faeces, wood, soil, uranium wastewater, plants, and lichens (Weber et al. 2002; García et al. 2006; Vázquez-Campos et al. 2014; Harrington et al. 2019). Some *Coniochaeta* species are also known to be human and animal pathogens (de Hoog et al. 2000; Perdomo et al. 2013; Troy et al. 2013). The sexual morph of *Coniochaeta* is characterized by dark brown to black, pyriform ostiolate or globose non-ostiolate ascomata with setae and unicellular, smooth ascospores with an elongated germ slit (García et al. 2006; Asgari et al. 2007) while the asexual morphs of *Coniochaeta* produce phialidic conidiogenous cells (Checa et al. 1988; Damm et al. 2010; Khan et al. 2013). Currently, there are 117 species in *Coniochaeta* (Species Fungorum 2023).

Table 4 Morphological comparisons of *Tarzetta* species closely related to our collections

Species	Size of asci µm	Paraphyses	Ascospores	Geographical distribution	References
T. catinus	270–300 × 13–15	2–3 µm wide, filiform, slightly enlarged at the apex, straight, separate	17–23 × 9.5–13 µm, ellipsoid slightly narrow at both ends, 2-guttulate	Worldwide	Zhuang (2014)
T. confusa	310–365 × 14–17	2–3.5 µm wide, filiform	13.5–15.5 × 8–9 µm, ellipsoid, 2-guttulate	China (Tibet)	Hyde et al. (2021)
T. cupularis	290–310 × 15–20	2–4 µm wide at apex, 2–2.5 µm wide at base, filiform, slightly enlarged at the apex, straight, separate	18–24 × 12.5–16 µm, ellipsoid to broad ellipsoid with rounded ends	Worldwide	Zhuang (2014)
T. linzhiensis	310–385 × 15–20	2–3 µm wide, filiform, septate, straight	18.5–22.5 × 10–13.5 µm, ellipsoid, 2-guttulate turn to one at maturity	China (Tibet)	Hyde et al. (2021)
T. melitensis	280–325 × 14–19	Filiform, slightly inflated at the top, 3–7 µm diam., straight, simple or occasionally forked at the base, hyaline	(21.3) 22.9–26.5 × 12.2–13.4 µm, ellipsoid with tapered ends to subfusoid, hyaline, smooth, rather thick-walled, containing two large oil drops, with numerous small guttules	Malta	van Vooren et al. (2019)
T. urceolata	400–437 × 13–17.5	2.5–4.5 µm wide, filiform, separate, branched, as long as asci, apex enlarged or constrictive slightly, straight or curved at the apex	8.5–13.5 × 6.5–9 µm, subglobose to broad ellipsoid to ellipsoid	China (Tibet)	This study
T. scotica	N/A	N/A	(19)–20–23 × (9.5)–10.5–12.5(–13) µm, ellipsoid	Worldwide	Yao and Spooner (2002)
T. spurcata	N/A	Often swollen at apex, becoming lobed or irregularly branched, usually extending beyond the asci, entangled or adhering in bunches	21–25(–26.5) × (10)–11–12.5(–13.5) µm, ascospores ellipsoid to subfusoid	The British Isles	Yao and Spooner (2002)
T. tibetensis	215–320 × 11–17	2–4.5 µm diam., filiform, separate, branched, length similar to ascus height,straight, irregular at the apex, digitate or with lateral bumps with 3–6 diam. µm at the widest point	14.5–21.5 × 8.5–11.5 µm, ellipsoid, blunt rounded at both ends, 1-guttulate at maturity	China (Tibet)	This study

Fig. 91 *Tarzetta urceolata* (HKAS 127116, **holotype**). **a** Typical mature specimens. **b** Anatomic structure of a portion of an apothecium. **c** Hymenium. **d** Subhymenium, medullary excipulum, and ectal excipulum. **e** Asci and paraphyses. **f** Asci. **g** Paraphyses. **h** Upper part of paraphyses. **i** Ascospores. Scale bars: a = 2.5 cm, b–d = 200 µm, f = 100 µm, g, h = 50 µm, i = 20 µm

Coniochaeta riskali-shoyakubovii Samarak., Gafforov, Teshaboeva & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900163; *Facesoffungi number*: FoF10746; Fig. 93

Etymology: riskali-shoyakubovii (Lat.) in honor of Uzbekistan scientist, Prof. Shoyakubov Riskali Shoyakubovich (1944–2015) for his contribution to the botanical research of Uzbekistan.

Holotype: TASM 6166

Saprobic on a dead branch of *Acer* sp. **Sexual morph**: *Ascomata* 135–370 µm diam. ($\bar{x}$ = 262 µm, n = 12), forming conspicuous groups in cracks of bark or erumpent through the bark, or growing solitarily, superficial or semi-immersed in the bark, often with only the ostiole visible, black, with somewhat rough surface, globose. *Ostiole* centric, depressed, densely filled with 2–3.3 µm ($\bar{x}$ = 2.5 µm, n = 15) wide, periphyses. *Peridium* 30–60 µm ($\bar{x}$ = 46 µm, n = 10), thick brittle when dry, softer when rehydrated, two-layered, inner layer consisting of hyaline to subhyaline,

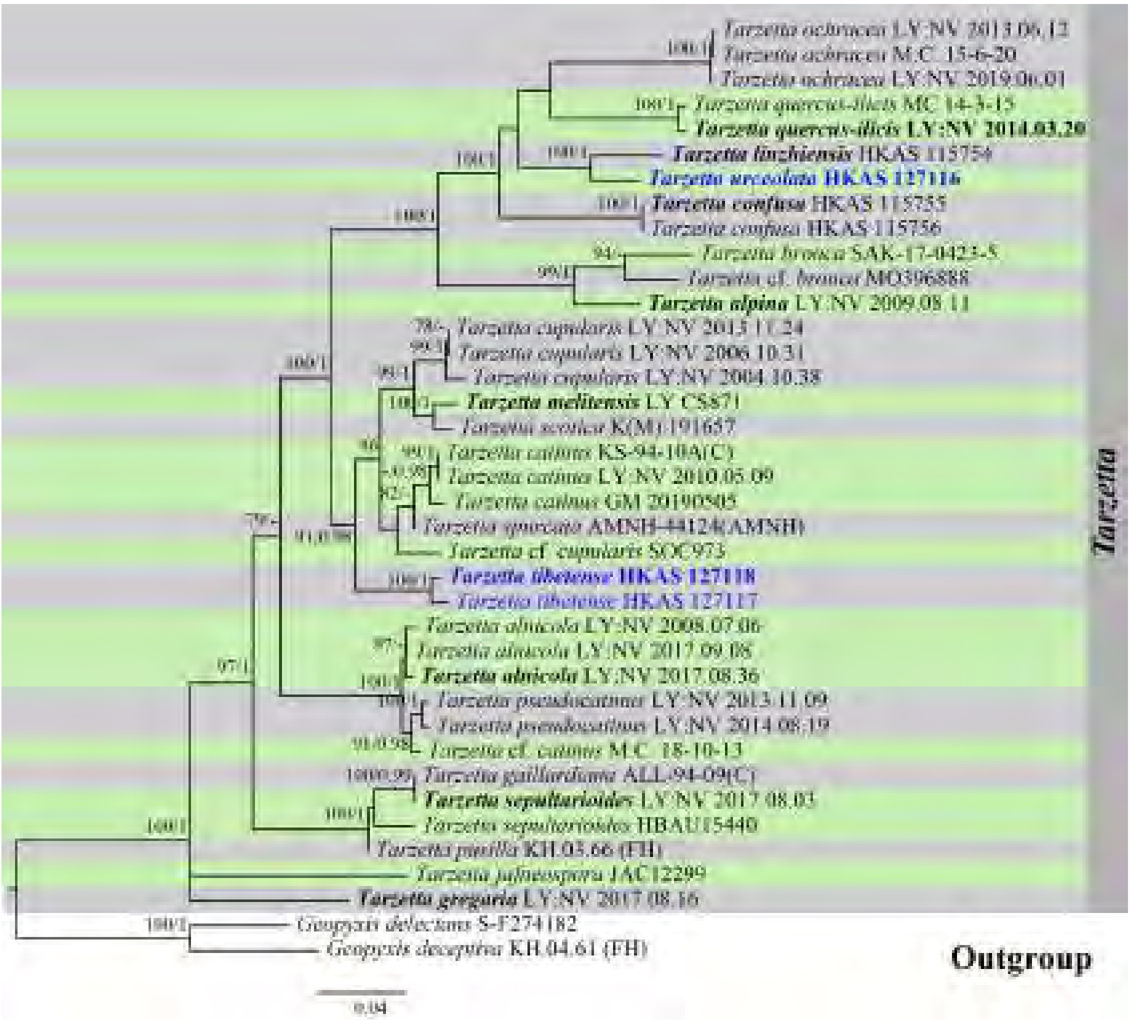


Fig. 92 Phylogram generated from maximum likelihood analysis based on the combined ITS and LSU sequence data representing the species of *Tarzetta* and related taxa. Thirty-eight taxa were included in the combined locus alignment that comprised 1681 characters (LSU: 878, ITS: 803). The best scoring RAxML tree with a final likelihood value of − 9181.759191 is presented. The matrix had 632 distinct alignment patterns, with 25.03% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.266168, C = 0.225813, G = 0.277987, T = 0.230032; substitution rates: AC = 1.673745, AG = 2.397809, AT = 1.502043, CG = 1.309663, CT = 4.583265, GT = 1.0; gamma distribution shape parameter α = 0.218698. Bootstrap support for ML equal to or greater than 75% and BI equal to or greater than 0.95 are given above the nodes. *Geopyxis deceptiva* (FH KH.04.61) and *G. delectans* (S-F274182) were used as the outgroup taxa. The newly generated sequence is indicated in blue bold. The ex-type strains are in bold

strongly compressed cells, outer layer consisting of densely packed, moderately thick-walled, brown cells, tending to be darker and more isodiametric towards the outside; near the ostiole some protruding, thick-walled, elongated, apically rounded cells and sparse, pale, often apically darker, septate, hairs present, become dark green in 5% KOH. *Hamathecium* comprising numerous, 2–2.8 µm ($\overline{x}$ = 2.4 µm, n = 25) wide, filamentous, septate, blunt paraphyses. *Asci* 85–120 × 6.5–9.5 µm ($\overline{x}$ = 105 × 8 µm, n = 15), 8-spored, unitunicate, cylindrical, short pedicellate, apical ring inconspicuous, J- apical ring in Melzer's reagent. *Ascospores* 10–14 × 4.5–6.5 µm ($\overline{x}$ = 12 × 6 µm, n = 35), overlapping uniseriate, ellipsoid, slightly laterally compressed, dark brown, with a conspicuous, straight germ slit across the entire length, smooth-walled, without sheath or appendages. **Asexual morph**: Undetermined.

Material examined: Uzbekistan, Surxondaryo Region, Boysun District, Qizilnaur Village, South-Western Hissar Mountains, on the dead branch of *Acer* sp. (Sapindaceae), 13 May 2016, Yusufjon Gafforov and Shaxnoza Teshaboeva YG-S31 (TASM 6166, **holotype**; MFLU 17-0051, **isotype**).

GenBank numbers: ITS: OQ355014, LSU: OQ355012, SSU: OQ355013, *tef*1-α: OQ354721.

Notes: The morphological characters of *Coniochaeta riskali-shoyakubovii* fit into the generic concept of *Coniochaeta* in having globose ascomata, cylindrical asci, and

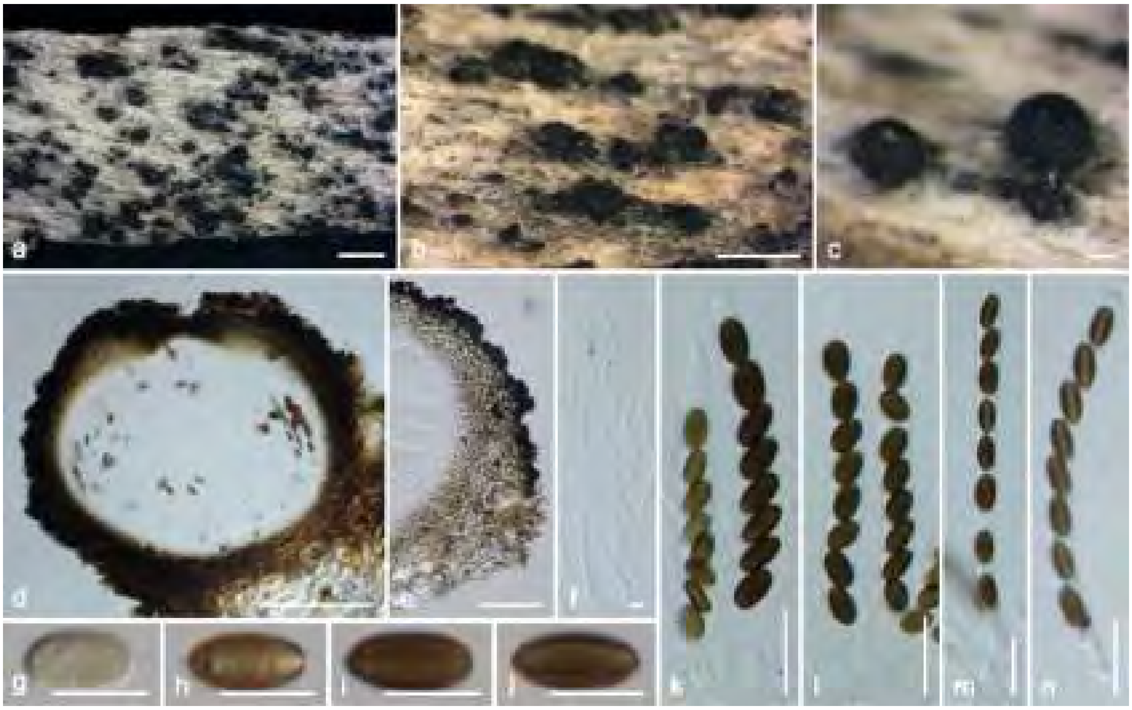


Fig. 93 ***Coniochaeta riskali-shoyakubovii*** (MFLU 17-0051, **isotype**). **a–c** Appearance of ascomata on the substrate. **d** Vertical sections of ascoma. **e** Peridium. **f** Paraphyses. **g–j** Ascospores. **k–n** Asci. Scale bars: a = 1,000 µm, b = 500 µm, c,d = 100 µm, e = 50 µm, k–n = 20 µm, g–j = 10 µm, f = 5 µm

ellipsoid ascospores with a straight germ slit across the entire length. *Coniochaeta coluteae* has ascomata with globe-like outer structures, an absence of setae, a long ostiolar neck, and oval to ellipsoid ascospores, which differ from those of *C. riskali-shoyakubovii* (Samarakoon et al. 2018). The combined LSU-ITS phylogenetic analyses show that our collection (TASM 6166) clusters as basal to the *C. coluteae* (MFLUCC 17-2299)-*Coniochaeta* sp. (ZHKUCC 22-0086) with 53% ML, 0.97 BI statistical support (Fig. 94). BLASTn search of the LSU of *C. riskali-shoyakubovii* is similar to those of *C. rosae* (MFLUCC 17-0806, 99.4% similarity) and *C. mutabilis* (CBS 206.73, 99% similarity), while ITS is similar to that of *C. mongoliae* (CGMCC 3.20250, 97% similarity). In recent studies, new *Coniochaeta* species have been introduced from Uzbekistan including *C. acaciae* (*Acacia* sp.), *C. baysunika* (*Rosa* sp.), *C. coluteae* (*Colutea paulsenii*), and *C. rosae* (*Rosa* sp.) (Samarakoon et al. 2018; Wanasinghe et al. 2018). Therefore, we introduced our collection as a new species, *C. riskali-shoyakubovii* from Uzbekistan.

Diaporthales Nannf.

Diaporthales was introduced by Nannfeldt (1932) and it forms a well-supported, monophyletic clade within Diaporthomycetidae (Senanayake et al. 2018). Currently, Diaporthales comprises 32 families (Senanayake et al. 2017, 2018; Yang et al. 2017a; Braun et al. 2018; Fan et al. 2018; Wijayawardene et al. 2022). This order is characterized by sexual morphs with solitary or aggregated perithecia sometimes with long papilla, 2–32-spored, unitunicate asci having a conspicuous refractive ring and the asexual morphs are generally coelomycetous, although rarely hyphomycetous (Rossman et al. 2007; Senanayake et al. 2018). Taxa in this order are saprobes, endophytes, and pathogens on plants, animals or in soil and occur in terrestrial or aquatic habitats (Senanayake et al. 2017).

Cryphonectriaceae Gryzenh. & M.J. Wingf.

Cryphonectriaceae was described by Gryzenhout et al. (2006a) and known as important canker pathogens of plants in the Melastomataceae and Myrtaceae (Myrtales). The best known of these is *Cryphonectria* that causes notorious chestnut blight (Anagnostakis 1987; Ali et al. 2018). Cryphonectriaceae is able to undergo host jumps or shifts between native and cultivated trees (Gryzenhout et al. 2006b; Ali et al. 2018). The genera in Cryphonectriaceae are characterized by orange stromata and purple reaction in 3% KOH, this is different from other families in Diaporthales (Jiang et al. 2019). Currently, 27 genera are accepted in Cryphonectriaceae (Wijayawardene et al. 2022).

Cryphonectria (Sacc.) Sacc. & D. Sacc.

Cryphonectria is known as one of the important phytopathogenic genera worldwide, and was introduced to accommodate *Nectria abscondita* and *N. variicolor*, but the type species were not designated (Saccardo and Saccardo 1905; Jiang et al. 2018). Gryzenhout et al. (2005) proposed *C. parasitica* as the type species of *Cryphonectria* and it is the causative agent of chestnut blight. The sexual characteristic features of *Cryphonectria* are gregarious or single, semi-immersed, erumpent, orange, ascostromata, unitunicate, cylindrical-fusoid to clavate, pedicellate asci with 8-spores, with distinct, J- refractive rings, and ellipsoid, fusoid to cylindrical, aseptate to 1-septate ascospores, not constricted at septa, which are hyaline, or seldom brown (Jiang et al. 2020). The characteristic features of asexual morph of *Cryphonectria* are pyriform, globose, subglobose to pulvinate loculate conidiomata, cylindrical conidiophores with bulbous base, phialidic or ampulliform conidiogenous cells, and aseptate, hyaline, cylindrical conidia (Jiang et al. 2020). There are 16 *Cryphonectria* species in the Species Fungorum (2023) and it has been assumed *Cryphonectria decipiens* and *Cryphonectria naterciae* are the same species (Rigling and Prospero 2018).

Cryphonectria kunmingensis Lu L., K.D. Hyde & Tibpromma, ***sp. nov.***

Index Fungorum number: IF900438; *Facesoffungi number*: FoF 10843; Fig. 95

Etymology: based on the location where the fungus was collected.

Saprobic on dead stem of unidentified plant. **Sexual morph**: *Ascostromata* (excluding neck) 300–660 × 240–420 µm ($\bar{x}$ = 526 µm, n = 342), single, semi-immersed, orange, oval to irregular. *Perithecia* immersed, single or aggregated, subglobose or irregular, multi-loculate, with long necks, ostiolar canal sometimes immersed in ascostromatic tissues, or come out from the substrate, orange. *Neck* composed of umber stromatic cells of *textura porrecta*. *Peridium* consists of two distinct layers, cells of *textura angularis*, outer layer dense, thick, yellow to pale brown, inner layer 4–5-layered, hyaline. *Hamathecium* 6–9 µm wide ($\bar{x}$ = 7 µm, n = 20) consists of a cellular, septate, hyaline, paraphyses attached at base. *Asci* 55–70 × 8–10 µm ($\bar{x}$ = 64.5 × 8.9 µm, n = 20), 8-spored, unitunicate, cylindrical, hyaline, with distinct J- refractive ring, no stalk. *Ascospores* 9.5–15 × 3–5 µm ($\bar{x}$ = 13 × 4.2 µm, n = 20), overlapping uniseriate to biseriate, ellipsoid, 1–2-septate when mature, constricted at septa, hyaline, smooth-walled, without a mucilaginous sheath. **Asexual morph**: Undetermined.

Culture characteristics: colonies on PDA reaching 60 mm diam., after 4 weeks in 20 °C, circular, flat, lobate, pale yellow, flocculent, front view pale yellow, reverse view orange, turning pale yellow towards the margin, produced pigments in the culture.

Material examined: China, Yunnan Province, Kunming City, Chang chong Mountain, on dead stem of unidentified plant, 20 June 2021. Li Lu, CCS 4, (HKAS 121976, **holotype**), ex-type culture KUMCC 21-0216.

GenBank numbers: ITS: ON359918, ON359919; LSU: ON340718, ON340719; *β-tubulin*: ON599004, ON5999005; *rpb*2: ON599000, ON599001; *tef1-α*: ON599002, ON599003

Notes: In the combined ITS, LSU, *rpb2*, *β-tubulin* and *tef1-α* gene analysis, our collection (HKAS 121976) formed a distinct subclade (Fig. 96) with MP/BI = 98%/1.00 bootstrap support. ITS sequence of our strain is 93.6% similar to *Cryphonectria nitschkei* (GQ290656) while LSU is 99.6% similar to *C. nitschkei* (AF408341). The blast results of *tef1-α* is 90% similar to *C. macrospora* (AY308952), *rpb*2 is 96.5% similar to *Chromendothia citrina* (DQ862015) and *β-tubulin* is 92% similar to *Cryphonectriaceae* sp. (JQ862910). Morphologically, our collection is similar to general characters of *Cryphonectria* (Jiang et al. 2020), however, it differs from other *Cryphonectria* species in having 2-septate ascospores. In addition, our ascospores (9.5–15) are longer compared to the morphologically similar species *C. nitschkei* (8.5–12.5) (Myburg et al. 2004). Therefore, we introduce our collection as a new species, *Cryphonectria kunmingensis*. Four species have been collected from China viz. *C. japonica*, *C. neoparasitica*, *C. quercus* and *C. quercicola* and this is the fifth species.

Cytosporaceae Fr.

Cytosporaceae was introduced by Fries (1825) and placed into Diaporthales, which comprises phytopathogens and saprobes (Wehmeyer 1975; Barr 1978; Eriksson 2001; Castlebury et al. 2002). Hyde et al. (2020c) accepted six genera in this family.

Cytospora Ehrenb.

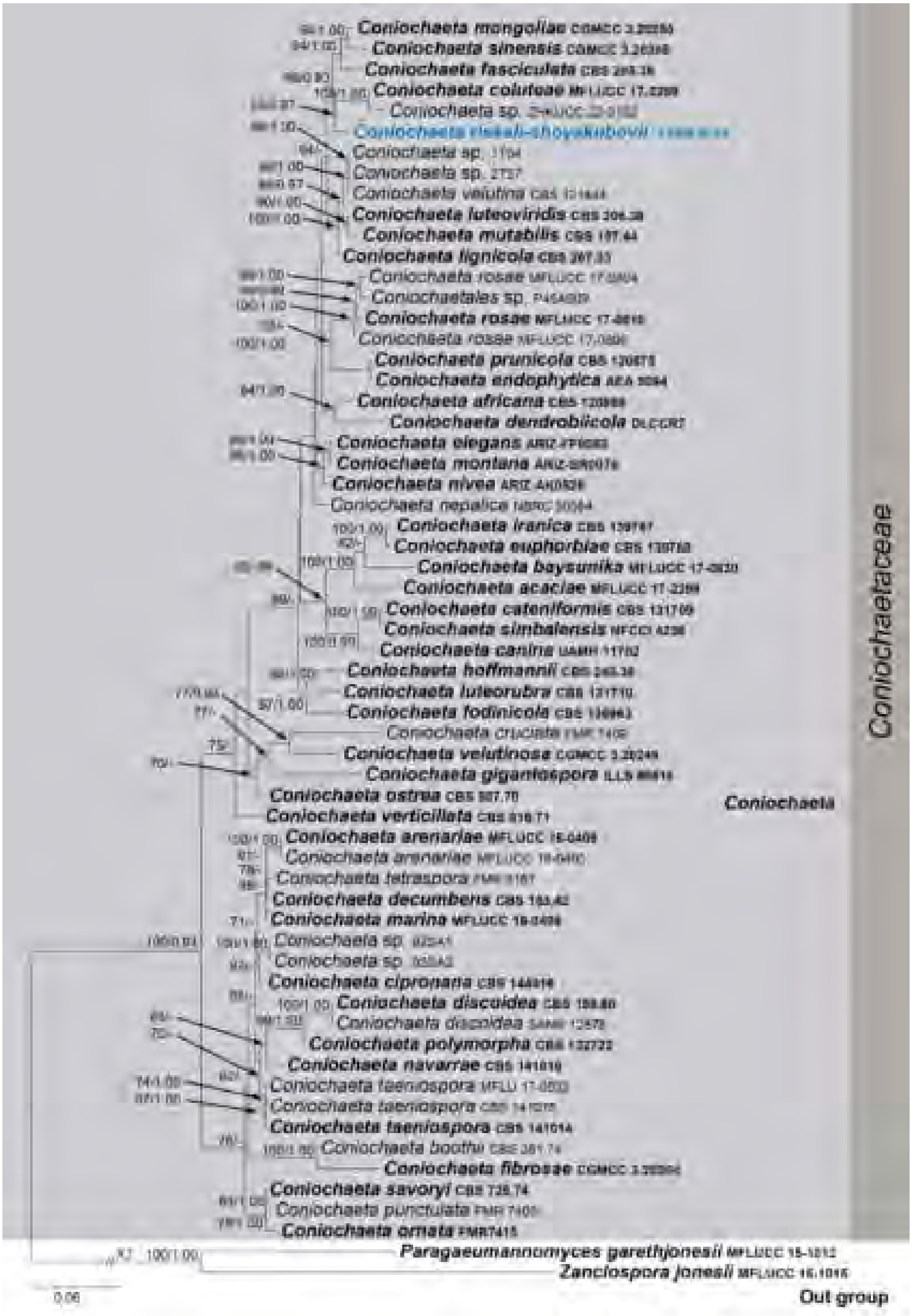
Cytospora was introduced by Ehrenberg (1818) and typified by *C. chrysosperma* (Pers.) Fr. Most *Cytospora* species are important plant pathogens (Adams et al. 2005; Fan et al. 2020). Cytospora-canker is a destructive disease of numerous hosts and causes serious economic losses. *Leucostoma*, *Valsa*, *Valsella*, and *Valseutypella* have been treated as the synonyms of *Cytospora* (Rossman et al. 2015; Senanayake et al. 2017; 2018). Identification of *Cytospora* species is difficult due to insufficient phylogenetic understanding and overlapping morphological characteristics (Pan et al. 2020). Currently, there are 340 accepted species in *Cytospora* (Species Fungorum 2023).

Cytospora lumnitzericola Norph., T.C. Wen & K.D. Hyde, in Norphanphoun, Raspé, Jeewon, Wen & Hyde, MycoKeys 38: 104 (2018)

Index Fungorum number: IF554778; *Facesoffungi number*: FoF 04603; Fig. 97

Holotype: MFLU 18-1227

Saprobic on dead stem of unidentified plant. **Sexual morph**: *Stromata* indistinct, immersed in bark. *Ascostromata*


Coniochaeta mongoliae CGMCC 3.20250
Coniochaeta sinensis CGMCC 3.20248
Coniochaeta fasciculata CBS 205.38
Coniochaeta coluteae MFLUCC 17-2299
Coniochaeta sp.
Coniochaeta iskali-shoyakubovii
Coniochaeta sp. 1194
Coniochaeta sp. 2757
Coniochaeta velutina CBS 121444
Coniochaeta luteoviridis CBS 206.38
Coniochaeta mutabilis CBS 157.44
Coniochaeta lignicola CBS 267.33
Coniochaeta rosae MFLUCC 17-0804
Coniochaetales sp. P45A929
Coniochaeta rosae MFLUCC 17-0815
Coniochaeta rosae MFLUCC 17-0806
Coniochaeta prunicola CBS 120875
Coniochaeta endophytica AEA 9094
Coniochaeta africana CBS 120868
Coniochaeta dendrobiicola DLCCR7
Coniochaeta elegans ARIZ-FF0083
Coniochaeta montana ARIZ-SR0078
Coniochaeta nivea ARIZ-AH0526
Coniochaeta nepalica NBRC 30584
Coniochaeta iranica CBS 139767
Coniochaeta euphorbiae CBS 139768
Coniochaeta baysunika MFLUCC 17-0830
Coniochaeta acaciae MFLUCC 17-2298
Coniochaeta cateniformis CBS 131709
Coniochaeta simbalensis NFCCI 4236
Coniochaeta canina UAMH 11762
Coniochaeta hoffmannii CBS 245.38
Coniochaeta luteorubra CBS 131710
Coniochaeta fodinicola CBS 136963
Coniochaeta cruciata FMR 7409
Coniochaeta velutinosa CGMCC 3.20249
Coniochaeta gigantospora ILLS 60816
Coniochaeta ostrea CBS 507.70
Coniochaeta verticillata CBS 816.71
Coniochaeta arenariae MFLUCC 18-0409
Coniochaeta arenariae MFLUCC 18-0410
Coniochaeta tetraspora FMR 6167
Coniochaeta decumbens CBS 153.42
Coniochaeta marina MFLUCC 18-0408
Coniochaeta sp. 3Z5A1
Coniochaeta sp. 3G5A2
Coniochaeta cipronana CBS 144016
Coniochaeta discoidea CBS 158.80
Coniochaeta discoidea SANK 12878
Coniochaeta polymorpha CBS 132722
Coniochaeta navarrae CBS 141016
Coniochaeta taeniospora MFLU 17-0830
Coniochaeta taeniospora CBS 141015
Coniochaeta taeniospora CBS 141014
Coniochaeta boothii CBS 381.74
Coniochaeta fibrosae CGMCC 3.20250
Coniochaeta savoryi CBS 725.74
Coniochaeta punctulata FMR 7409
Coniochaeta ornata FMR7415
Paragaeumannomyces garethjonesii MFLUCC 15-1012
Zanclospora jonesii MFLUCC 15-1016
Coniochaetaceae
Coniochaeta
Out group
0.06
100/1.00
94/1.00
75/-
70/-
97/1.00
77/-
87/1.00
74/1.00

◂**Fig. 94** Phylogenetic tree generated from maximum likelihood analysis (RAxML) based on a combined LSU-ITS sequence dataset. Sixty-one strains are included in the combined analyses, which comprise 1392 characters (827 for LSU and 565 for ITS) after alignment. *Paragaeumannomyces garethjonesii* (MFLUCC 15-1012) and *Zanclospora jonesii* (MFLUCC 15-1015) are used as the outgroup taxa. Single gene analyses were also performed to compare the topology and clade stability with combined gene analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian inference analysis. The best RaxML tree with a final likelihood value of − 7641.0294 is presented. The matrix had 511 distinct alignment patterns, with 69.9% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.2322, C = 0.2618, G = 0.3022, T = 0.2039; substitution rates AC = 1.4010, AG = 1.9398, AT = 1.3856, CG = 1.3748, CT = 8.4597, GT = 1.0; gamma distribution shape parameter α = 0.479. Bootstrap values for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (the rounding of values to 2 decimal proportions) from Bayesian inference analysis are labeled on the nodes. Ex-type strains are in bold. The new isolate is in blue

200–250 × 140–180 µm diam., erumpent in host tissue, scattered, solitary or aggregated, mostly in pairs, uni- or multiloculate, with ostiolar neck. *Ostiole* 70–100 µm long, central, sometime slanted on substrate, sometime straight, inner layer covered with hyaline, filamentous periphyses. *Peridium* comprising two layers; inner, hyaline, compressed, cells of *textura angularis*, outer, brown, cells of *textura angularis. Hamathecium* comprising cellular, anastomosed paraphyses. *Asci* 25–30 × 5–7 µm ($\bar{x}$ = 27 × 6 µm, n = 15), 8-spored, unitunicate, clavate to elongate obovoid, with a J-, refractive apical ring. *Ascospores* 5–6 × 1–1.5 µm ($\bar{x}$ = 5.6 × 1.3 µm, n = 20), biseriate, elongated oblong, unicellular, hyaline, smooth-walled. **Asexual morph**: Norphanphoun et al. (2018).

Culture characters: Colonies on PDA reaching 2.5 cm diameter after 2 days at 25 °C, circular to irregular, medium dense, flat, slightly raised, with edge undulate, fairly fluffy, white from above, light yellow from below; not producing pigments in agar.

Material examined: China, Guangdong Province, Guangzhou City, Baiyun Mountain (23° 09′ 35″ N 113° 17′ 40″ E), on dead stem of unidentified plant, 15 July 2021, I.C. Senanayake, 76 (MHZU 22-0088), living cultures ZHKUCC 22-0154, ZHKUCC 22-0158.

GenBank numbers: ITS: OR164918, OR164919, LSU: OR164960, OR164961, *tef*1-α: OR166280, OR166281.

Hosts and distribution: Thailand (Phetchaburi Province), on leaf spot of *Lumnitzera racemosa* (Norphanphoun et al. 2018).

Notes: The combined ITS, LSU and *tef1-α* gene analysis (Fig. 98) shows that our isolates (ZHKUCC 22-0154, ZHKUCC 22-0158) grouped with the type strain of *Cytospora lumnitzericola* with ML/BI = 99%/1.00 statistical support. ITS sequences of our isolates reveal one base pair differences with holotype collection and LSU sequences are identical. Our isolates did not sporulate on media and the sexual morph of *C. lumnitzericola* is unknown. The colony characters of ex-type culture of *Cytospora lumnitzericola* was described on MEA (Norphanphoun et al. 2018) while our cultures were grown on PDA. However, based on the identical molecular data, we determined that our collection is the sexual morph of *C. lumnitzericola.* Our collection was obtained from a dead stem as a saprobe while the type collection was from spots of living leaves (Norphanphoun et al. 2018). However, further collections and pathogenicity testing need to confirm the life mode of this fungus.

Diaporthaceae Höhn. ex Wehm.

The family Diaporthaceae encompasses numerous endophytes and phytopathogens of a wide variety of plants causing diseases (Lamprecht et al. 2011; Gomes et al. 2013; Dai et al. 2014; Voglmayr and Jaklitsch 2014). This family was introduced by Höhnel (1917) with type genus *Diaporthe* Fuckel and placed in Diaporthales (Höhnel 1917; Castlebury et al. 2002). Currently, there are 15 genera accepted in this family viz. *Apioporthella* Petr., *Apiosphaeria* Höhn., *Chaetoconis* Clem., *Chiangraiomyces* Senan. & K.D. Hyde, *Diaporthe*, *Hyaliappendispora* Senan. et al., *Leucodiaporthe* M.E. Barr & Lar.N. Vassiljeva, *Mazzantia* Mont., *Ophiodiaporthe* Y.M. Ju et al., *Paradiaporthe* Senan. et al., *Phaeocytostroma* Petr., *Phaeodiaporthe* Petr., *Pustulomyces* D.Q. Dai et al., and *Stenocarpella* Syd. & P. Syd. (Senanayake et al. 2017, 2018; Hyde et al. 2020a).

Diaporthe Fuckel

= *Diaporthe* Nitschke

Diaporthe which is typified by *D. eres* Nitschke, is a species rich genus occur in a diverse range of host plants as endophytes, pathogens and saprobes (Gomes et al. 2013). *Diaporthe* proposed over *Phomopsis* (Rossman et al. 2015). Many species are morphologically similar containing numerous cryptic species and however, genetically distinct (van Rensburg et al. 2006; Udayanga et al. 2011; Jayawardena et al. 2018; Yang et al. 2018). Norphanphoun et al. (2022) revised this genus and assigned the species in to several species complexes based on the combined sequence data of ITS, *tef1-α*, *β-tubulin*, *calmodulin* and *histone* H3. There are plenty of *Diaporthe* species have been collected and introduced from China and here we introduce three new species collected from China (Figs. 99, 100).

Diaporthe angustiapiculata Senan., ***sp. nov***.

Index Fungorum number: IF900439; *Facesoffungi number*: FoF 14191; Fig. 101.

Etymology: based on the narrowed apex of conidiogenous cells.

Saprobic on petiole of *Phoenix roebelenii* O'Brien. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 375–520 × 580–610 µm ($\bar{x}$ = 500 × 600 µm,

Fig. 95 ***Cryphonectria kunmingensis*** (HKAS 121976, **holotype**). **a**–**c** Ascostromata on the host surface. **d** Cross section of ascostromata. **e** Peridium. f Paraphyses. **g**–**j** Asci (stained in Congo Red reagent). **k** J⁻ Refractive ring (stained in Melzer's reagent). **l** Germinated ascospore. **m**–**q** Ascospores (stained in Congo Red reagent). **r** Upper and reverse views of colonies on PDA. Scale bars: d = 300 µm, e = 30 µm, f = 25 µm, g–l = 20 µm, m–q = 5 µm

n = 10), superficial, scattered on substrate, solitary, compressed subglobose, dark brown, coriaceous, ostiolate, papillate. *Conidiomatal wall* comprises pale brown, thick-walled, cells of *textura angularis*. *Conidiophores* reduce to conidiogenous cells. *Alpha conidiogenous cells* 19–27 × 4–6 µm ($\overline{x}$ = 25 × 5 µm), phialidic, terminal, bottle-shaped with narrowed apex, no visible periclinal thickening, straight, aseptate, unbranched, densely aggregated, hyaline,

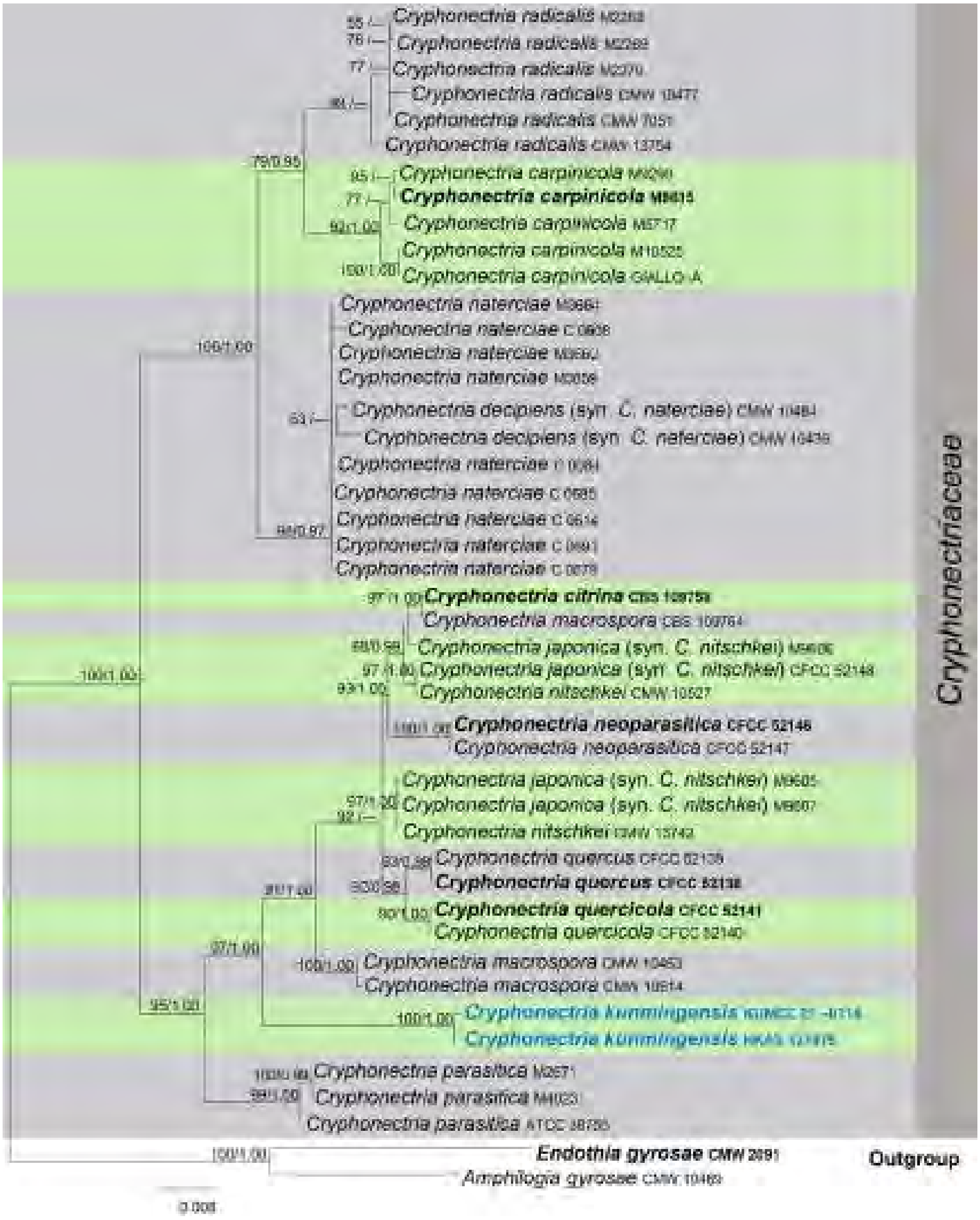
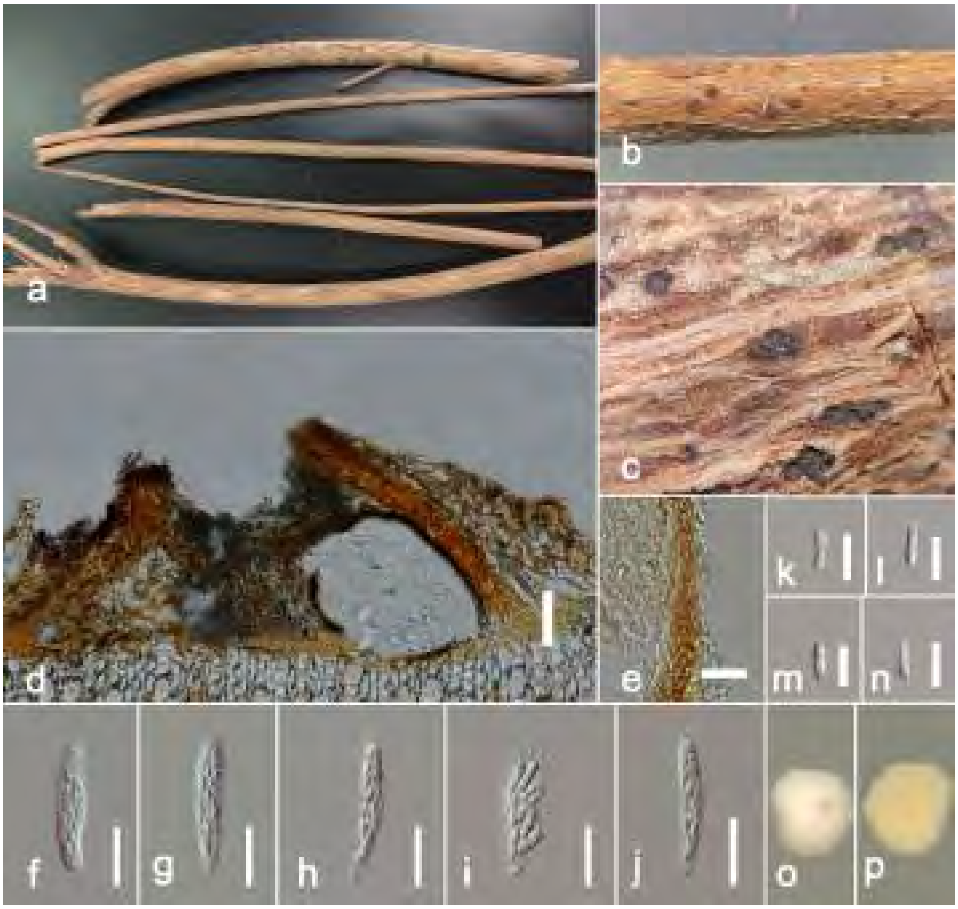


Fig. 96 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *rpb2*, *β-tubulin* and *tef1-α* sequence data. 45 taxa were included in the combined analyses, which comprised 3280 characters (LSU = 869 bp, ITS = 569 bp, *rpb2* = 1,113 bp, *β-tubulin* = 475 bp, *tef1-α* = 254 bp) after alignment. The best scoring RAxML tree with a final likelihood value of − 7795.712285 is presented. The matrix had 510 distinct alignment patterns, with 48.97% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.227853, C = 0.275760, G = 0.262261, T = 0.234126; substitution rates: AC = 1.967589, AG = 4.751144, AT = 3.030078, CG = 1.335415, CT = 15.093804, GT = 1.0; gamma distribution shape parameter α = 0.02. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (the rounding of values to 2 decimal proportions) from Bayesian inference analysis are labelled at each node. Ex-type strains are in black bold, while the new isolate is indicated in blue bold. The tree is rooted to *Amphilogia gyrosae* (CMW 10469) and *Endothia gyrosae* (CMW 2091)

Fig. 97 ***Cytospora lumnitzericola*** (MHZU 22-0088). **a** Examined material. **b, c** Ascomata on substrate. **d** Vertical cross section of ascoma. **e** Peridium. **f–j** Asci. **k–n** Ascospores. **k** Surface view of colony on PDA. **l** Reverse view of colony on PDA. Scale bars: d = 50 µm, e–n = 10 µm



thick-walled. *Alpha conidia* 6–9 × 3–5 µm (x̄ = 7 × 4.5 µm), lower end round, upper end pointed, aseptate, distinct biguttulate, hyaline. *Beta conidia* not observed.

Culture characteristics: Colonies on PDA reaching 3 cm diam. after 10 days in dark at 25 °C, floccose, flat, circular, entire margin, white, wooly aerial mycelia, reverse off-white, no pigments produced.

Material examined: China, Guangdong Province, Guangzhou City, Danxia Mountain, on petiole of *Phoenix roebelenii* (Arecaceae), 23 September 2021, I.C. Senanayake, 2R (MHZU 22-0110, **holotype**), ex-type cultures ZHKUCC 22-0184, ZHKUCC 22-0194.

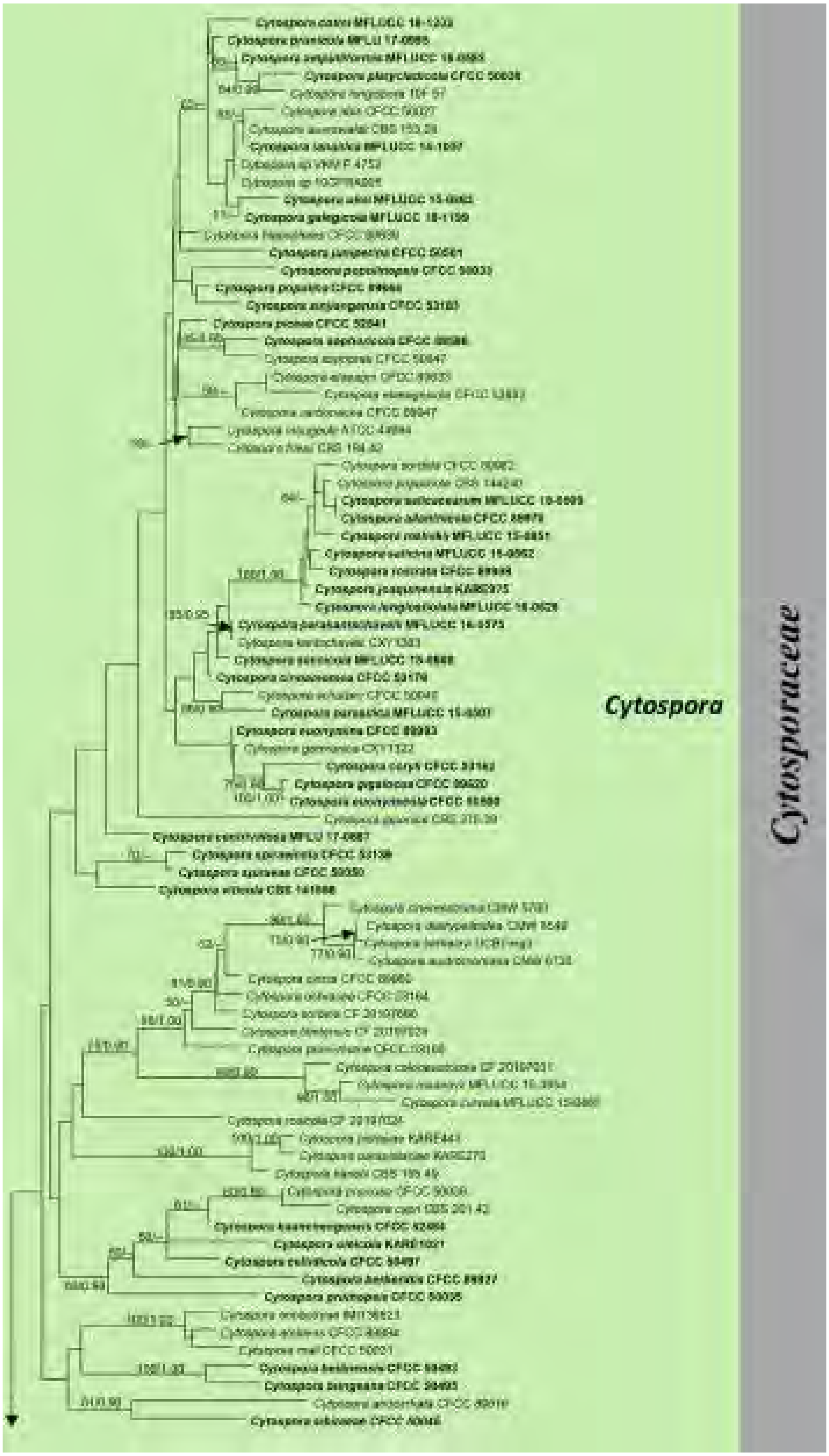
GenBank numbers: ITS: OR164920, OR164921, *tef*1-α: OR166269, OR166270, *β-tubulin*: OR166309, OR166310, *calmodulin*: OR166299, OR166300.

Notes: The combined gene analysis of ITS, *β-tubulin*, *tef1-α* and *cal* (Fig. 99) shows that our isolates (ZHKUCC 22-0184, ZHKUCC 22-0194) grouped with *Diaporthe apiculatum*, *D. gardeniae*, *D. charlesworthii* which is basal to *D. eres* species complex with ML/BI = 93%/0.99 bootstrap support. The base pair differences of ITS, *β-tubulin*, and *tef1-α* locus between our isolates and *D. apiculatum* revealed that 1.69%, 10.27%, 12.46%, and for *D. gardeniae* are 3.7%, 13.5%, N/A, while these differences for *D. charlesworthii* are 3.5%, 5%, 12% respectively. Phylogenetic network from the concatenated dataset based on the LogDet transformation and the NeighborNet algorithm, inferred by SplitsTree shows that our isolates do show any recombination with the species members in the *Diaporthe eres* species complex and other well-delimitated species (Fig. 100c).

Diaporthe apiculatum has scattered or aggregated, globose conidiomata, 3–6-layered conidiomatal wall, cylindrical conidiogenous cells with visible periclinal thickening and subcylindrical beta conidia (Song et al. 2019) while our species comprises compressed, subglobose conidiomata, 6–9-layered conidiomatal wall with *textura angularis* cells, ampulliform conidiogenous cells with prominent, narrowed apex and absence of beta conidia. *Diaporthe apiculatum* produces a cyan-white compact mycelial colony with crenate margins after several days and it then developed into a colony with a dull white to pale olivaceous-grey surface patched on PDA at 25 °C for a week in the dark due to the aerial mycelia which is different from our isolates.

Diaporthe gardeniae comprises oval to oblong alpha conidia (7.5–16 × 2.5–4.5 µm), and hyaline, aseptate, line-type beta conidia. However, our collection comprises

Fig. 98 The best scoring RAxML tree with a final likelihood value of − 25,165.404246 for combined dataset of ITS (609 bp), LSU (876 bp) and *tef1-α* (663 bp) sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses. The tree is rooted with *Diaporthe eres* (CBS 160.32). The matrix had 1009 distinct alignment patterns with 45.55% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.253307, C = 0.281105, G = 0.240277, T = 0.225311; substitution rates AC = 1.354317, AG = 2.316471, AT = 1.518768, CG = 0.880462, CT = 5.395950, GT = 1.0; gamma distribution shape parameter α = 0.210813. Ex-type strains are in bold and newly generated sequences are in red. Bootstrap support for ML equal to or greater than 50% and BI equal to or greater than 0.90 are given above the nodes



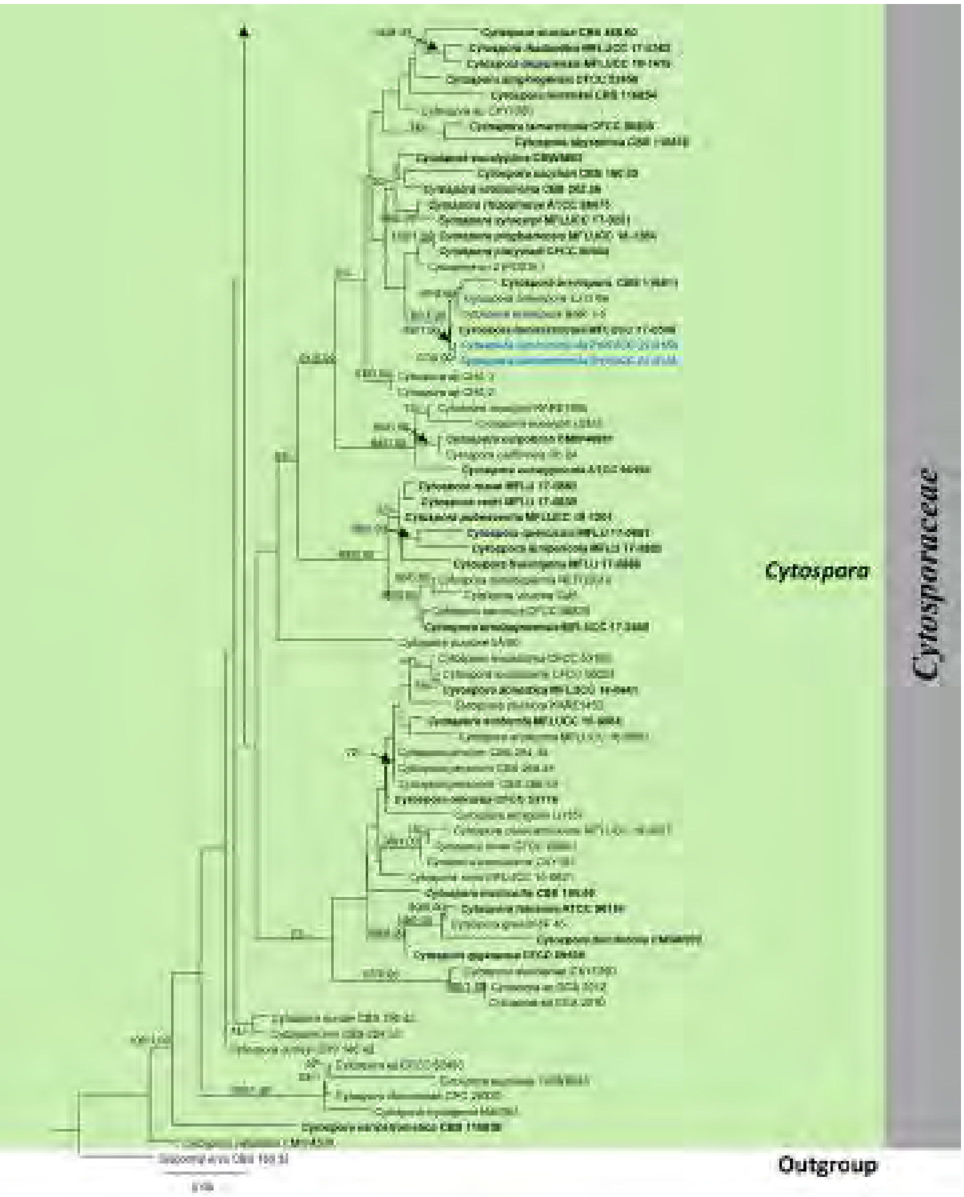


Fig. 98 (continued)

rounded alpha conidia (6–9 × 3–5 µm) with lower end is rounded while upper end is pointed. Our collection did not produce beta-conidia. *Diaporthe gardeniae* causes stem cankers on *Gardenia jasminoides* (Fang et al. 2022). *Diaporthe charlesworthii* comprises conidiomata with distinct necks up to 1 mm, 2-septate, branched, hyaline to subhyaline conidiophores, cylindrical conidiogenous cells (15–35 × 1.5–3 µm), fusiform to cylindrical alpha conidia (7–9.5 × 2–2.5 µm) and abundant beta conidia (Thompson et al. 2015) while our collection has short, indistinct necks, conidiophores reduced to conidiogenous cells, round alpha conidia (19–27 × 4–6 µm) and absent of beta conidia. Further, *Diaporthe phoenicis* and *D. pseudophoenicicola* have been collected from *Phoenix* sp. (Gomes et al. 2013; Dissanayake et al. 2017). There is no sequence data for *Diaporthe phoenicis* and *D. pseudophoenicicola* clustered distantly in the phylogenetic tree. *Diaporthe phoenicis* was collected from the petioles of *Phoenix dactylifera* L. and it has been described only from its sexual morph (Patouillard 1987). Therefore, morphological characters cannot be compared. Hence, we introduce this *Diaporthe* species as *D. angustiapiculata* sp. nov.

Diaporthe arecae (H.C. Srivast., Zakia & Govindar.) R.R. Gomes, Glienke & Crous, Persoonia 31: 16 (2013), emended.

Index Fungorum number: IF 802924; *Facesoffungi number*: FoF 14193; Fig. 102

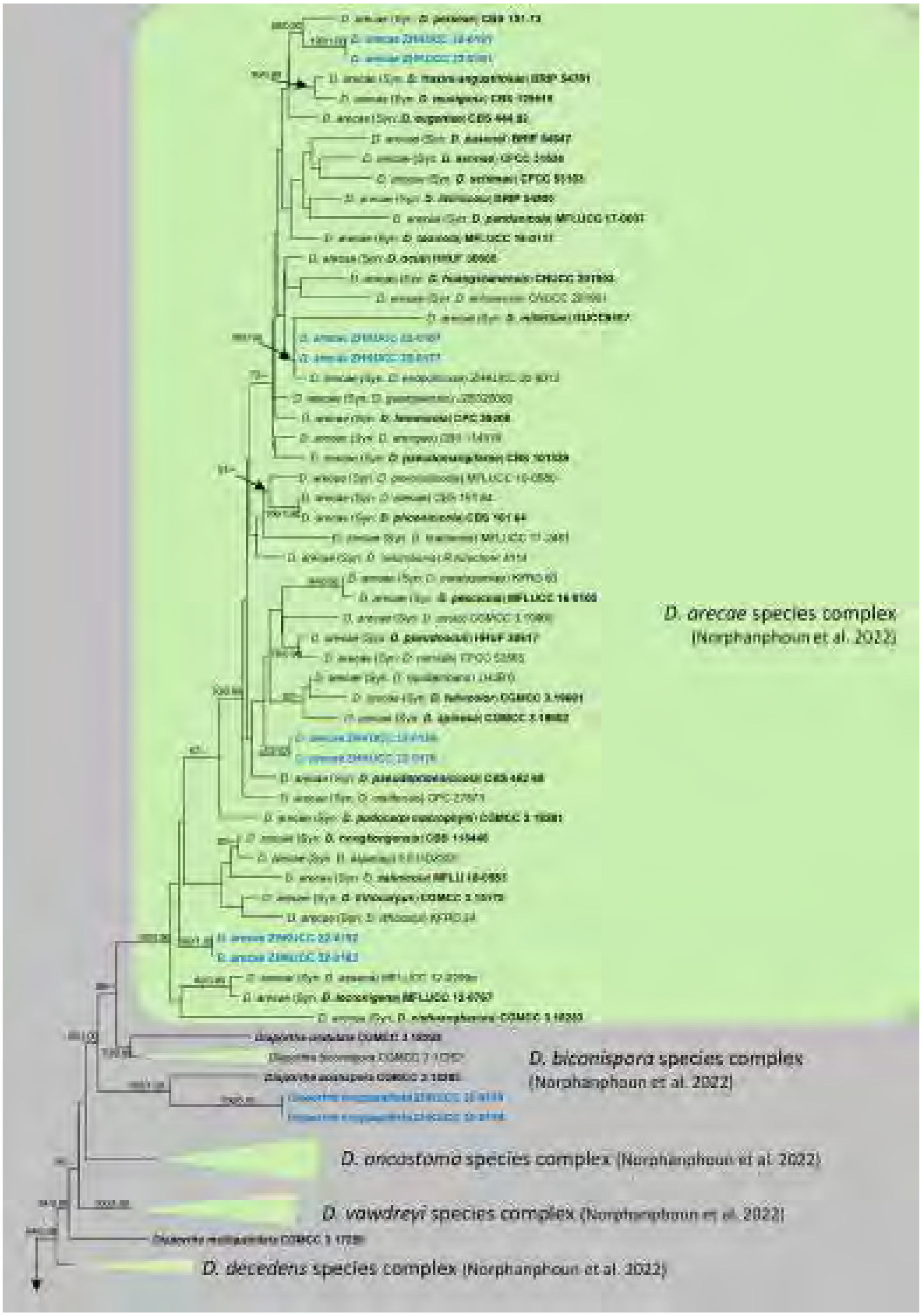


Fig. 99 Phylogram generated from maximum likelihood analysis based on combined ITS, *β-tubulin*, *tef*1-*α* and *cal* sequence data which comprised 1801 characters (ITS = 590, *β-tubulin* = 399, *tef*1-*α* = 401, *cal* = 411). The best scoring RAxML tree with a final likelihood value of − 66,138.215080 is presented. The matrix had 1373 distinct alignment patterns, with 21.86% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.220620, C = 0.327829, G = 0.221919, T = 0.229632; substitution rates: AC = 1.155068, AG = 3.569724, AT = 1.178946, CG = 0.924185, CT = 4.411577, GT = 1.0; gamma distribution shape parameter α = 0.524319. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (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 blue bold. Except *D. arecae* species complex, other all species complexes are compressed. The tree is rooted to *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt)

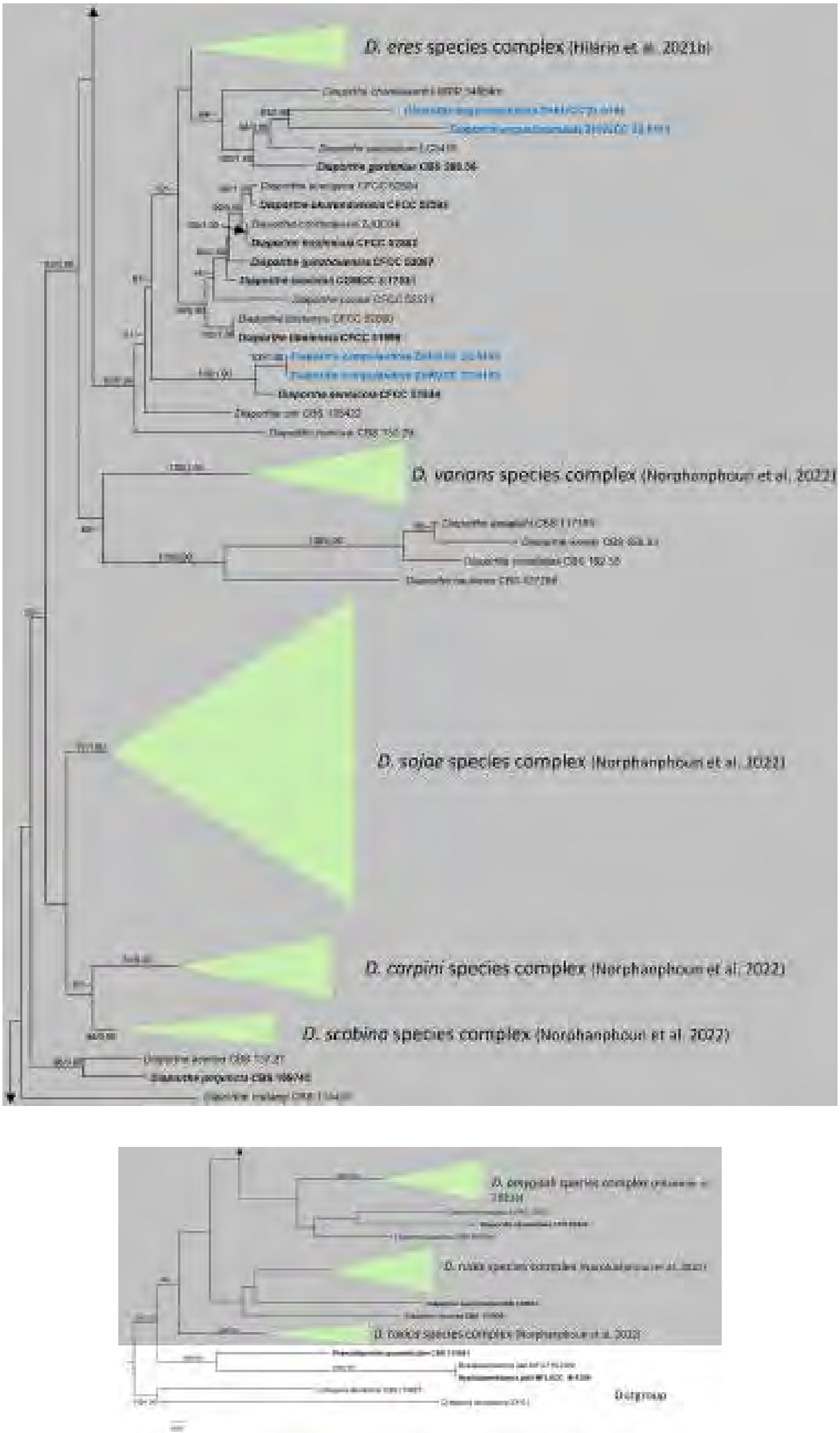


Fig. 99 (continued)

Saprobic on dead leaves of monocotyledon plants**. Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 60–320 × 120–160 µm ($\bar{x}$ = 255 × 148 µm, n = 10), immersed just beneath the epidermis, scattered on substrate, solitary, subglobose, compressed globose to irregular, dark brown, coriaceous, ostiolate. *Conidiomatal wall* 10–17 µm wide ($\bar{x}$ = 15 µm, n = 10), comprises pale brown, thick-walled, cells of *textura angularis*. *Conidiophores* reduce to conidiogenous cells. *Alpha conidiogenous cells* 7–13 × 2–3 µm ($\bar{x}$ = 11 × 2.5 µm), annellidic, with visible periclinal thickening, collarets not flared, terminal, ampulliform, slightly tapered towards the apex, straight, aseptate, unbranched, densely aggregated, hyaline, thick-walled. *Alpha conidia* 3.7–7 × 2.2–2.8 µm ($\bar{x}$ = 6.3 × 2.6 µm, n = 20), fusoid, ends pointed, aguttulate to biguttulate, hyaline, unicellular. *Beta conidiogenous cells* 7–11 × 3–4 µm ($\bar{x}$ = 10 × 3.5 µm), phialidic, terminal, cylindrical, slightly tapered towards the apex, straight, aseptate, unbranched, densely aggregated, hyaline, thick-walled. *Beta conidia* 8–15 × 1–2 µm ($\bar{x}$ = 12 × 1.5 µm), filiform, hamate or slightly curved, base truncate, tapering towards one apex, hyaline, aseptate.

Culture characteristics: Colonies on PDA reaching 6 cm diam. after 10 days in dark at 25 °C, floccose, flat, circular, filiform margin, white, filamentous mycelia spread out from the center, reverse off-white, no pigments produced.

Material examined: China, Guangdong Province, Guangzhou City, Baiyun Mountain (23° 09′ 35″ N 113° 17′ 40″ E), on leaves of *Cycas* sp. (Cycadaceae), 16 August 2021, I.C. Senanayake, 102-1, (MHZU 22-0110), living cultures ZHKUCC 22-0182, ZHKUCC 22-0192; Danxia Mountain, on leaves of *Livistona chinensis* (Arecaceae), 23 September 2021, I.C. Senanayake, 48 (MHZU 22-0105), living cultures ZHKUCC 22-0177, ZHKUCC 22-0187; Nansha District, near Baihuitian reservoir, on leaves of *Trachycarpus fortunei* (Arecaceae), 15 July 2021, I.C. Senanayake, 45 (MHZU 22-0104), living cultures ZHKUCC 22-0176, ZHKUCC 22-0186; Shenzhen City, Nanshan District, Yangtai Mountain Forest Park, 22° 39′ 21.26″ N 113° 57′ 18.53″ E, on leaves of *Dypsis lutescens* (Arecaceae), 23 September 2021, I.C. Senanayake, 101-2, (MHZU 22-0109), living cultures ZHKUCC 22-0181, ZHKUCC 22-0191.

GenBank numbers: ITS: OR164924, OR164925, OR164930, OR164931, OR164932, OR164933, OR164926, OR164927. *β-tubulin*: OR166305, OR166306, OR166303, OR166304, OR166311, OR166312. *tef1-α*: OR166273, OR166274, OR166275, OR166276. *cal*: OR166295, OR166296.

Notes: The phylogenetic analysis (Fig. 99) showed that our isolates clustered with in the *Diaporthe arecae* species complex. Phylogenetic network from the concatenated dataset based on the LogDet transformation and the NeighborNet algorithm, inferred by SplitsTree also shows that our isolates clustered with the species members of the *Diaporthe arecae* species complex and they are distinct from other well-delimitated species (Fig. 100a). Our collections share similar characters and all of them were collected from monocotyledons plants in Guangdong Province, China. Therefore, we emended *Diaporthe arecae* species complex providing additional data.

Diaporthe campylandrae Senan., ***sp. nov.***

Index Fungorum number: IF900440; *Facesoffungi number*: FoF 14192; Fig. 103

Etymology: based on the host plant *Campylandra*.

Saprobic on dead leaves of *Campylandra chinensis* (Baker) M. N. Tamura et al. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 100–115 × 100–110 µm ($\bar{x}$ = 109 × 102 µm, n = 10), immersed, scattered on substrate, solitary, globose, dark brown to black, coriaceous, ostiolate, apapillate or indistinct papillate. *Conidiophores* reduce to conidiogenous cells. *Conidiogenous cells* 9–11 × 1–2 µm ($\bar{x}$ = 9.8 × 1.8 µm, n = 20), annellidic, without visible periclinal thickening, collarets very flared, cylindrical to ampulliform, slightly tapered towards the apex, frills-like structure remain at apex, straight or sinuous, aseptate, densely aggregated, terminal, hyaline, thick-walled. *Alpha conidia* 2–3 × 1.5–2 µm ($\bar{x}$ = 2.5 × 1.7 µm, n = 20), fusiform or oval, both ends obtuse or acute, aguttulate to small, biguttulate, hyaline, unicellular. *Beta conidia* not observed.

Culture characteristics: Colonies on PDA reaching 3 cm diam. after 10 days in dark at 25 °C, floccose, flat, circular, entire margin, white, wooly aerial mycelia concentrate at the center, reverse off-white, no pigments produced.

Material examined: China, Guangdong Province, Guangzhou City, Baiyun Mountain (23° 09′ 35″ N 113° 17′ 40″ E), on dead leaves of *Campylandra chinensis* (Convallariaceae), 16 August 2021, I.C. Senanayake, 11-2 (MHZU 22-0111, **holotype**), ex-type cultures ZHKUCC 22-0183, ZHKUCC 22-0193.

GenBank numbers: ITS: OR164922, OR164923, *tef1-α*: OR166271, OR166272, *cal*: OR166297, OR166298, *β-tubulin*: OR166307, OR166308.

Notes: Our isolates (ZHKUCC 22-0183, ZHKUCC 22-0193) clustered with *Diaporthe sennicola* (CFCC 51634) in the combined ITS, *β-tubulin*, *tef1-α* and *cal* gene analysis (Fig. 99) with ML/BI = 100%/1.00 bootstrap support. The base pair differences of ITS, *β-tubulin*, *tef1-α* and *cal* between our isolates and *Diaporthe sennicola* revealed 2.37%, 1%, 4.23%, 1.94% respectively. Phylogenetic network from the concatenated dataset based on the LogDet transformation and the NeighborNet algorithm, inferred by SplitsTree shows that our isolates do not have any recombination with *D. sennicola* and related well-delimitated species (Fig. 100b). Morphologically, our

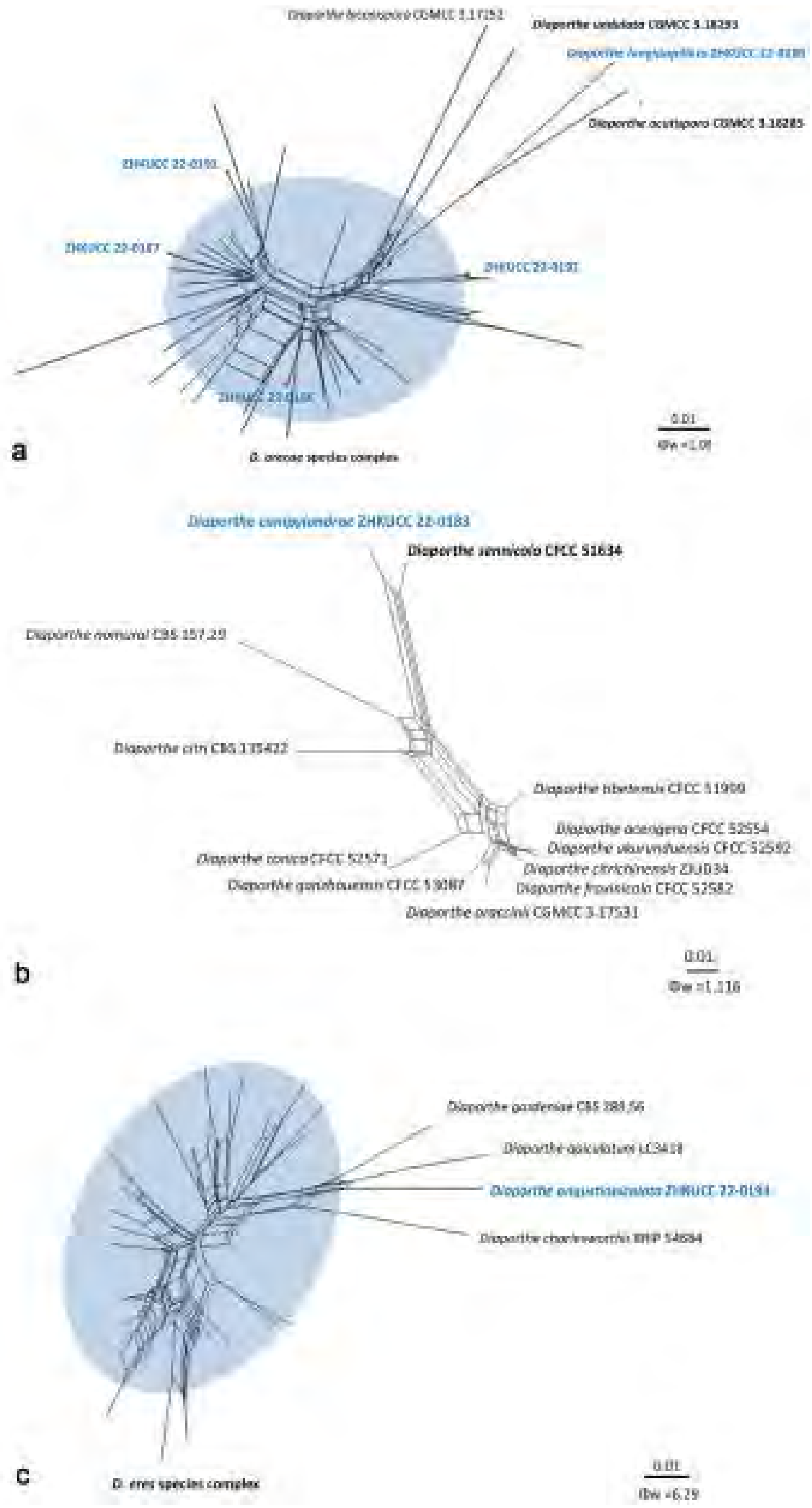


Fig. 100 Phylogenetic network from the concatenated data (ITS, *β-tubulin*, *tef*1-*α*, *cal*) representing the structure of the **a** *Diaporthe arecae*, **c** *D. eres* species complexes and other well-delimitated species **b** the newly generated *Diaporthe* strains, based on the LogDet transformation and the NeighborNet algorithm, inferred by SplitsTree. The scale bar represents the expected number of substitutions per nucleotide position

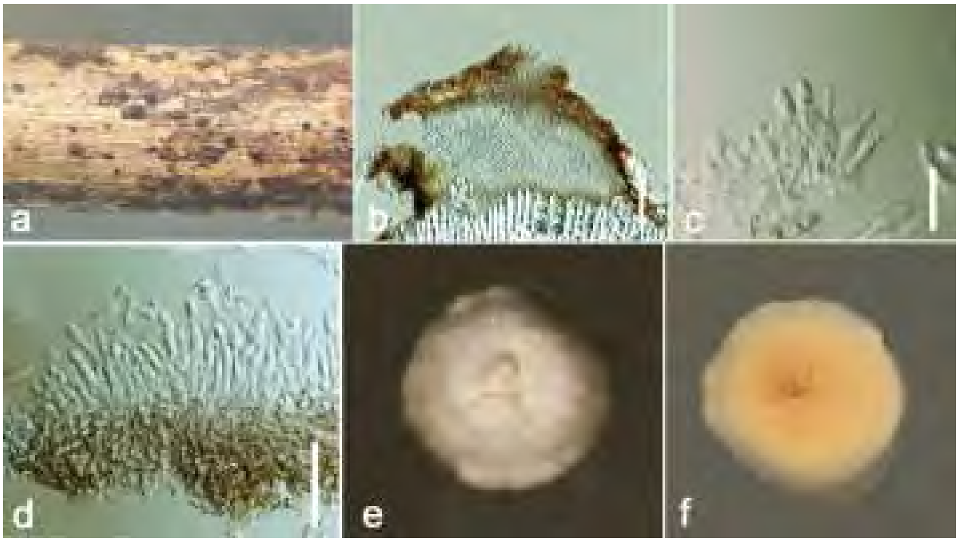


Fig. 101 ***Diaporthe angustiapiculata*** (MHZU 22-0110, **holotype**). **a** Conidiomata on substrate. **b** Cross section of conidioma. **c, d** Conidia attached to conidiogenous cells. **e** Surface view of colony on PDA. **f** Reverse view of colony on PDA. Scale bars: b = 250 µm, c, d = 20 µm

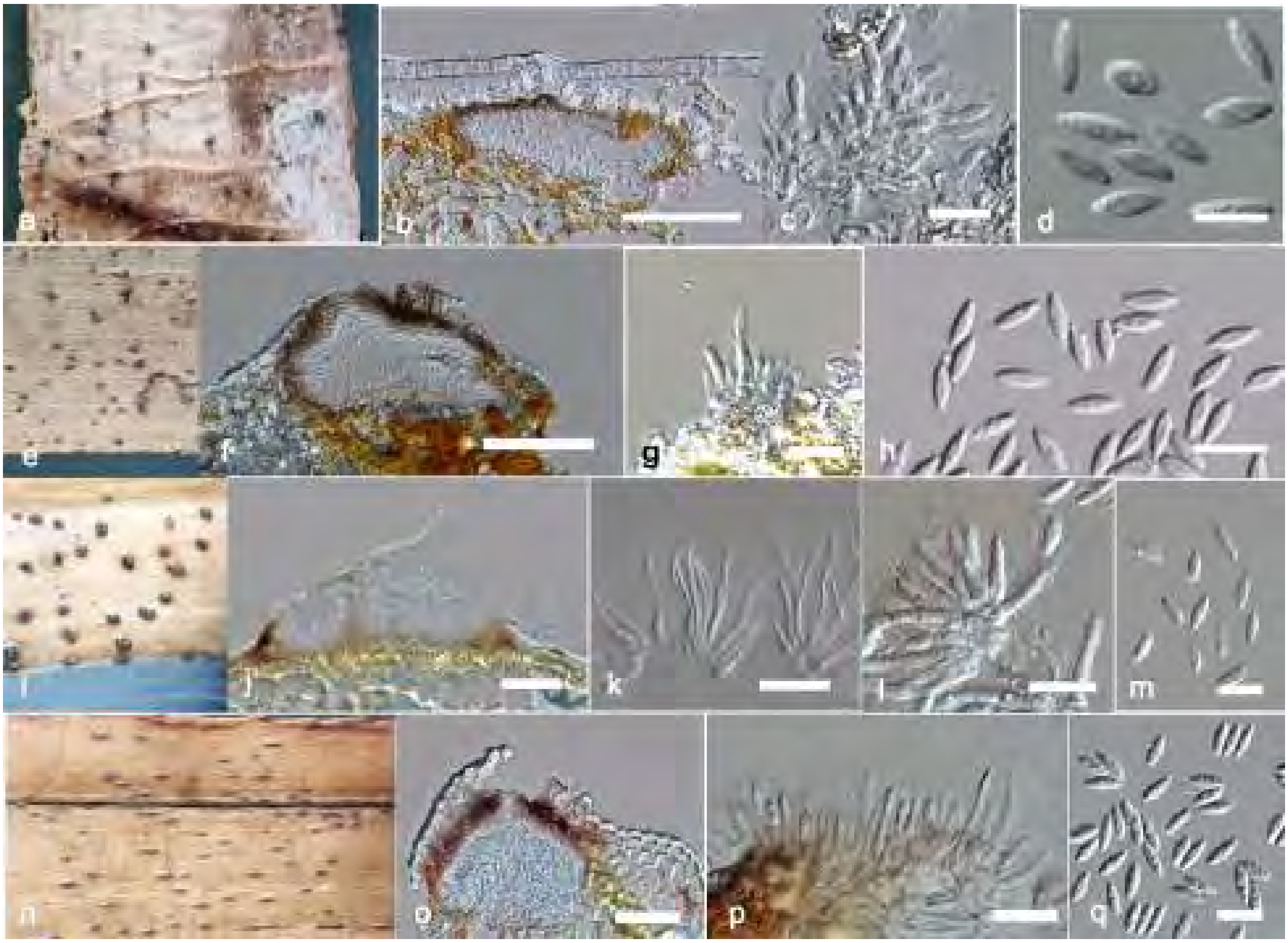


Fig. 102 ***Diaporthe arecae*** (MHZU 22-0109 (**a**–**d**); MHZU 22-0104 (**e**–**h**); MHZU 22-0109 (**i**–**m**), MHZU 22-0105 (**n**–**q**). **a, e, i, n** Conidiomata on substrates. **b, f, j, o** Cross sections of conidiomata. **k** Beta conidia attached to conidiogenous cells. **c, g, l, p** Alpha **c**onidia attached to conidiogenous cells. **d, h, m, q** Alpha conidia. Scale bars: b, f, j, o = 100 µm, c, g, l, p, k, d, h, m, q = 15 µm

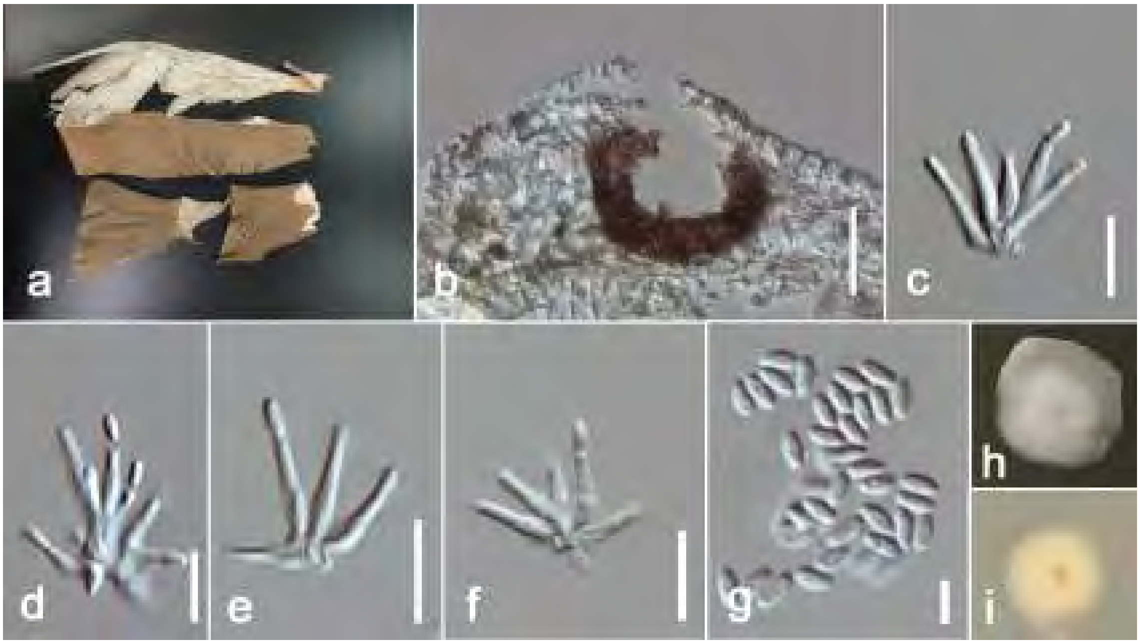


Fig. 103 ***Diaporthe campylandrae*** (MHZU 22-0111, **holotype**). **a** Examined material. **b** Cross section of conidioma. **c–f** Conidia attached to conidiogenous cells. **g** Conidia. **h** Surface view of colony on PDA. **i** Reverse view of colony on PDA. Scale bars: b = 70 µm, c–f = 10 µm, g = 2.5 µm

collection differs from *Diaporthe sennicola* by globose conidiomata immersed in substrate, absence of ectostromatic disc and conidiophores with fusiform to oval aguttulate conidia while *D. sennicola* has compressed globose conidiomata, dark brown, flat ectostromatic disc, phialidic, branched conidiophores and ellipsoidal, conspicuously biguttulate conidia (Yang et al. 2017a). Further, colonies of *D. sennicola* are initially flat with white felty aerial mycelia and turn to white compact furcate mycelia at the centre and auburn furcate mycelia at the irregular margin while our isolates have circular, white colonies with entire margin. Therefore, we introduce our collection as a new *Diaporthe* species, *D. campylandrae*.

Diaporthe longipapillata Senan., ***sp. nov.***

Index Fungorum number: IF900444; *Facesoffungi number*: FoF 14197; Fig. 104

Etymology: based on the long papilla of the ascomata.

Saprobic on dead twigs of unidentified plant. **Sexual morph**: *Ascomata* 620–946 × 350–500 µm ($\bar{x}$ = 370 × 490 µm, n = 10), perithecial, immersed to erumpent, scattered, solitary, globose, black, coriaceous, ostiolate with long, distinct papilla come out from the substrate. *Paraphyses* hyaline, cellular, dissolve when mature. *Asci* 80–90 × 16–19 µm ($\bar{x}$ = 87 × 17.5 µm, n = 30), 8-spored, unitunicate, elongate to clavate, sessile. *Ascospores* 19–23 × 5–7 µm ($\bar{x}$ = 22 × 6.3 µm, n = 50), overlapping biseriate, elongated to elliptical, two-celled, hyaline, often 4-guttulate with larger guttules at center and smaller ones at ends, dissolve when over mature. **Asexual morph**: Undetermined.

Culture characteristics: Colonies on PDA reaching 2 cm diam. after 10 days in dark at 25 °C, floccose, flat, circular, smooth margin, white, thick mycelial spreading over the colony; reverse off-white, no pigments produced.

Material examined: China, Guangdong Province, Guangzhou City, Haizhu District, Xiaogang park, on twigs of unidentified plant, 5 April 2021, I.C. Senanayake, 96 (MHZU 22-0108, **holotype**), ex-type cultures ZHKUCC 22-0180, ZHKUCC 22-0190.

GenBank numbers: ITS: OR164928, OR164929, *tef1-α*: OR166277, OR166278, *cal*: OR166301, OR166302, *β-tubulin*: OR166313, OR166314.

Notes: The combined gene analysis of ITS, *β-tubulin*, *tef1-α* and *cal* (Fig. 99) showed that our isolates (ZHKUCC 22-0180, ZHKUCC 22-0190) grouped with *Diaporthe acutispora* (CGMCC 3.18285) with ML/BI = 100%/1.00 support. The base pair differences of ITS, *β-tubulin*, *tef1-α* and *cal* genes between our isolates and *Diaporthe acutispora* revealed that 3.72%, 4.76%, 13.96%, and 6.32% respectively. Phylogenetic network from the concatenated dataset based on the LogDet transformation and the NeighborNet algorithm, inferred by SplitsTree shows that our isolates do not show any recombination with the species members in *Diaporthe arecae* species complex and other well-delimitated species (Fig. 100a). However, we only obtain the sexual

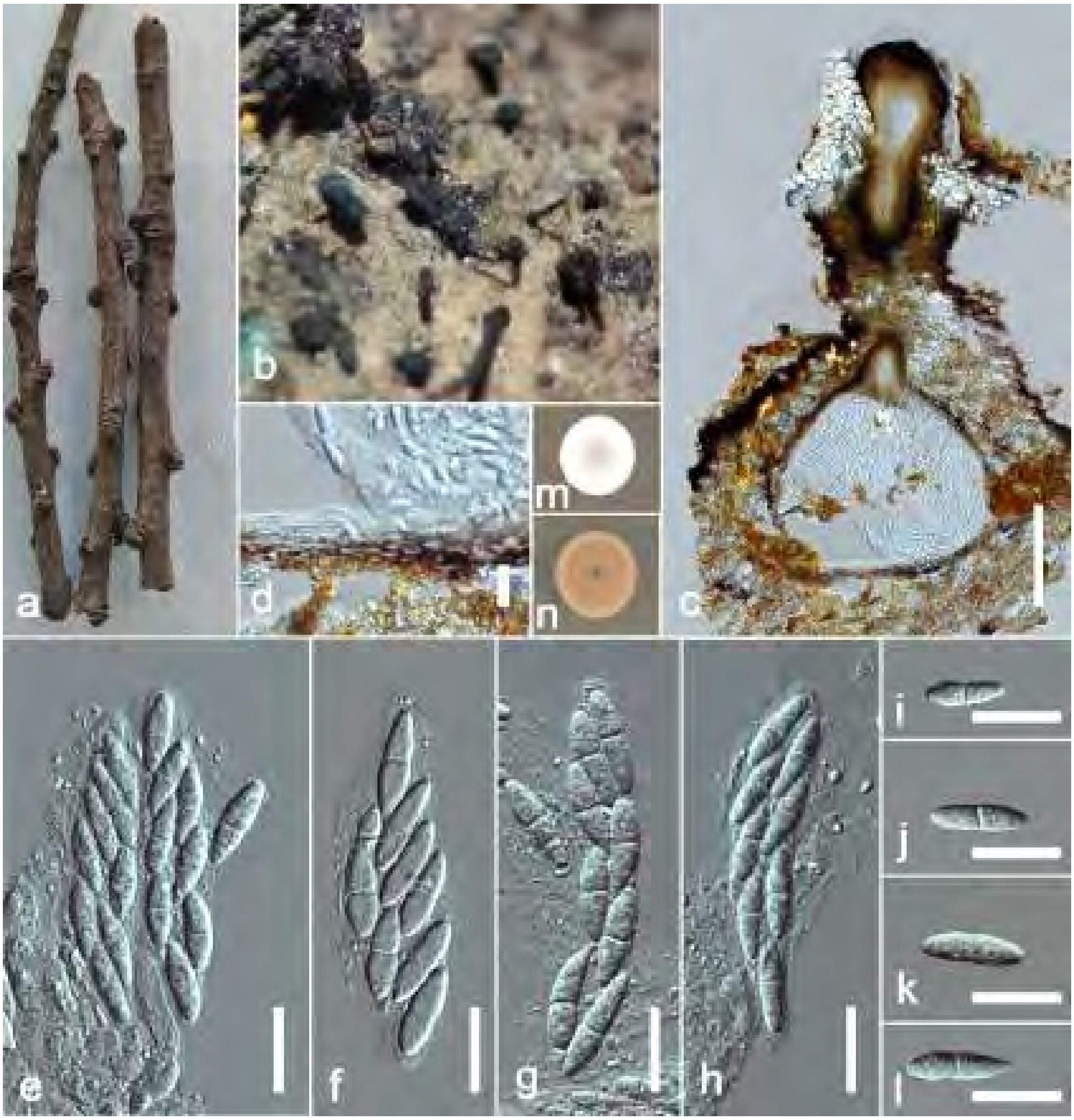


Fig. 104 ***Diaporthe longipapillata*** (MHZU 22-0108, **holotype**). **a** Examined material. **b** Ascomata on substrate. **c** Cross section of ascomata. **d** Peridium. **e–h** Asci. **i–l** Ascospores. **m** Surface view of colony on PDA. **n** Reverse view of colony on PDA. Scale bars: c = 200 µm, d = 50 µm, e–l = 20 µm

morph of our collection while *D. acutispora* was described from its asexual morph. Therefore, it is impossible to compare the morphology of our collection with *D. acutispora*. *Diaporthe acutispora* was collected from Yunnan Province, China on healthy leaves of *Coffea* sp. and *Camellia sasanqua* (Gao et al. 2017). Therefore, we introduce our collection as a new species of *Diaporthe*, *D. longipapillata*.

Togniniales Senan., Maharachch. & K.D. Hyde

The order Togniniales comprises only its type family Togniniaceae (Maharachchikumbura et al. 2015; Réblová et al. 2015). Multi-gene analyses showed that Togniniales is a distinct order in the subclass Diaporthomycetidae (Maharachchikumbura et al. 2015, 2016; Réblová et al. 2015). Species in this order have a worldwide distribution and are pathogens of plants and animals (Hoffmann and Voigt 2011; Kredics et al. 2011; Huang et al. 2018b).

Togniniaceae Réblová, L. Mostert, W. Gams & Crous

The monotypic family Togniniaceae was introduced to accommodate species of *Phaeoacremonium* (Réblová et al. 2004). *Phaeoacremonium* species occur in a wide range of hosts and habitats (Mostert et al. 2006; Damm et al. 2008). Most members in this family are plant, animal and human pathogens and some have been recorded on arthropods or in soil (Groenewald et al. 2001; Guarro et al. 2003; Hemashettar et al. 2006; Mostert et al. 2006; Damm et al. 2008; Gramaje et al. 2015). Currently, there are two genera accepted in this family viz. *Conidiotheca* Réblová & L Mostert and *Phaeoacremonium* W. Gams et al. (Hyde et al. 2020c).

Phaeoacremonium W. Gams, Crous & M.J. Wingf.

Phaeoacremonium was introduced by Crous et al. (1996) and it is typified by *P. parasiticum*. The sexual morph of *Phaeoacremonium* is *Tognini*a (Mostert et al. 2003; 2006; Pascoe et al. 2004) and *Phaeoacremonium* was conserved over *Togninia* based on its availability in nature and common usage of the name (Réblová et al. 2016). Species of *Phaeoacremonium* are basically characterized by black ascomata with a long neck, clavate to cylindrical asci with oval to ellipsoid, hyaline ascospores and straight or flexuous mononematous conidiophores with oval to reniform phialo-conidia (Marin-Felix et al. 2018; Spies et al. 2018). We introduce one new species in this study.

Phaeoacremonium chinensis Senan. & Kular., ***sp. nov.***

Index Fungorum number: IF900446; *Facesoffungi number*: FoF 14201; Fig. 105

Etymology: in reference to the region where sample has been collected, China.

Saprobic on decaying wood. **Sexual morph**: Undetermined. **Asexual morph**: *Mycelium* 2.5–3.5 µm wide, consisting of branched, septate, single hyphae, subhyaline to pale brown, smooth-walled. *Conidiophores* 20–25 µm long, 2.5–3.5 µm wide, arising from aerial or submerged hyphae, branched, each conidiophores often ending in a single terminal conidiogenous cells, occasionally also with lateral conidiogenous cells, erect, up to 4-septate, subhyaline to pale brown, paler towards the tip, smooth. *Conidiogenous cells* 2–3 µm long, 1–1.5 µm wide, terminal or lateral, monophialidic, smooth, mostly subulate, some navicular, tapering towards the apex, pale brown to olivaceous, collarettes. *Conidia* 3.5–4.5 × 2–2.5 µm, hyaline to olivaceous, allantoid or subcylindrical, unicellular.

Culture characteristics: Colonies reaching 5 cm diam. after 10 days at 25 °C. Colonies on PDA flat, circular, filiform margin, woolly with plenty of aerial mycelia, initially pale brown become dark brown when sporulate; reverse dark brown with filamentous hyphae at margin.

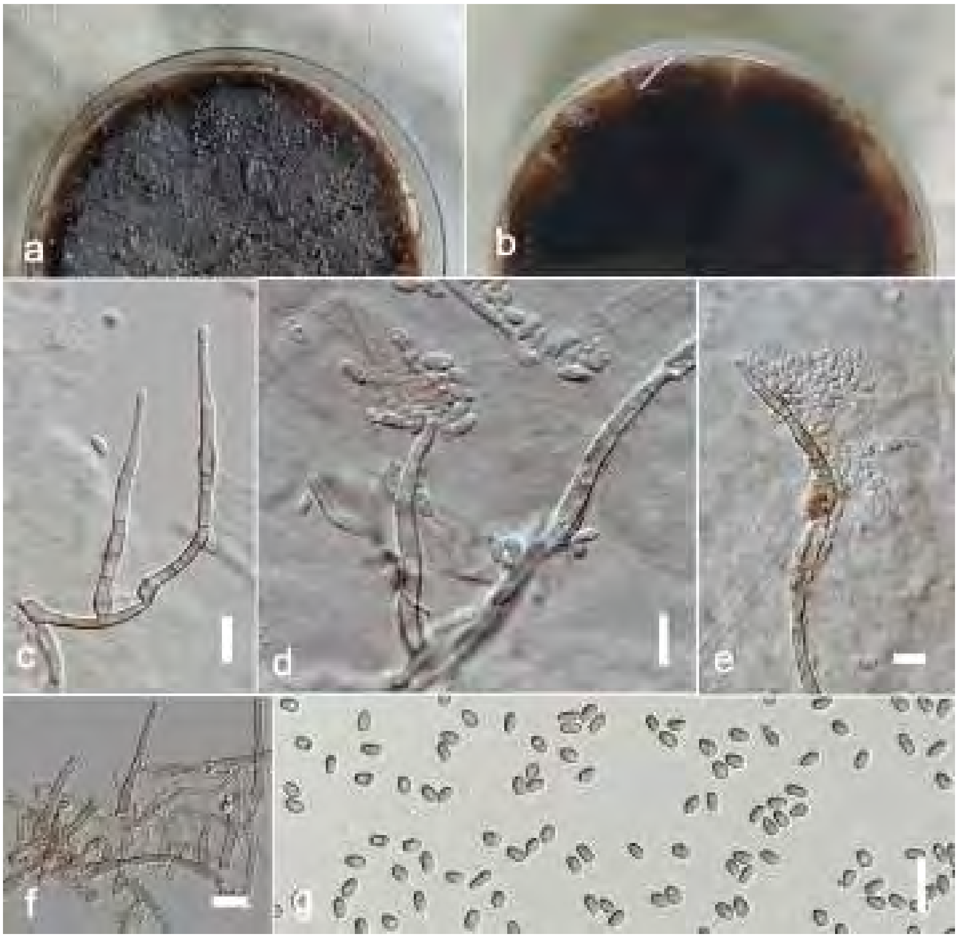


Fig. 105 ***Phaeoacremonium chinensis*** (MHZU 22-0083, **holotype**). **a** Surface view of the colony on PDA. **b** Reverse view of the colony on PDA. **c**–**f** Conidiophores attached to conidia. **g** Conidia. Scale bars: c–g = 10 µm

Material examined: China, Guangdong Province, Guangzhou City, Haizhu District, Xiaogang park, on bark of unidentified host, 5 April 2021, N.D. Kularathnage, NDK 2-1, (MHZU 22-0083, **holotype**), ex-type culture ZHKUCC 22-0149.

GenBank numbers: ITS: OR164913, LSU: OR164958, *tef1-α*: OR166282.

Note: The combined ITS, LSU and *β-tubulin* gene analyses (Fig. 106) shows that our collection is close to *Phaeoacremonium aquaticum* and *P. rubrigenum*, forming a distinct clade with ML/BI = 99%/1.00 statistical support. *Phaeoacremonium aquaticum* is only described from its sexual morph and this species was reported from Yunnan and Beijing Provinces in China on submerged wood in freshwater streams (Hu et al. 2012). Our collection shows 1.67% nucleotide differences in ITS with *P. aquaticum* and sequences of other genes are unavailable for *P. aquaticum.*

Our collection is distinct from *P. rubrigenum* by smooth-walled, mycelia absence of hyphal bundles, non-verrucose conidiogenous cells and hyaline to olivaceous, allantoid or subcylindrical conidia while *P. rubrigenum* has verrucose-walled hyphal bundles, tuberculate with warts up to 1 µm wide, verrucose conidiogenous cells and hyaline to pale brown, mostly ellipsoidal to cylindrical conidia (Essakhi et al. 2008). This species has been reported as a plant pathogen on *Vitis vinifera* from Croatia and as a human pathogen from USA. Therefore, our collection is significantly different from *Phaeoacremonium aquaticum* and *P. rubrigenum*. Thus, we introduce our collection as *Phaeoacremonium chinensis* sp. nov.

Glomerellales Chadef. ex Réblová, W. Gams & Seifert

Chadefaud (1960) proposed this order for a group of fungal endophytes and parasites of living plants with endostromatal to apostromatal ascomata and unicellular, hyaline ascospores. This order comprises three families viz. Australiascaceae Réblová & W. Gams, Glomerellaceae Locq. ex Seifert & W. Gams, and Reticulascaceae Réblová & W. Gams. (Réblová et al. 2011).

Plectosphaerellaceae W. Gams, Summerb. & Zare

The family Plectosphaerellaceae was introduced with *Plectosphaerella* as the type genus (Zare et al. 2007). This family includes numerous plant pathogenic genera and soil-borne fungal species. Twenty-two genera are currently accepted in this family (Giraldo and Crous 2019).

Plectosphaerella Kleb.

The genus *Plectosphaerella* was introduced based on the holomorphic species *P. cucumerina* (Lindf.) W. Gams, by Domsch and Gams (1972), which produces perithecia with elongate necks and the asexual morph with phialidic, mononematous conidiophores (Zare et al. 2007). There are 24 species listed under this genus (Species Fungorum 2023). *Plectosphaerella* species occur in different habitats including plants, animals and soil (Zhang et al. 2019). Here, we describe a new host and geographical record of *P. cucumerina*.

Plectosphaerella cucumerina (Lindf.) W. Gams, in Domsch & Gams, Fungi in Agricultural Soils: 160 (1972)

Index Fungorum number: IF320609; *Facesofungi number*: FoF12962; Fig. 107

Neotype: CBS H-7656, CBS 137.37 (ex-neotype)

Associated with leaf spots of *Bridelia* sp. **Sexual morph**: *Vegetative hyphae* 1.4–3 µm wide ($\bar{x}$ = 1.88, n = 40), hyaline to brown, smooth-walled, septate, branched. *Ascomata* developing on MEA, 145–150 × 120–147 µm ($\bar{x}$ = 148 × 130 µm, n = 5), superficial or immersed in culture colonies, scattered, solitary to gregarious, subglobose to ovoid, uni- or multi-loculate. *Peridium* 18–32 µm ($\bar{x}$ = 24.2 µm, n = 10) wide, composed of 1–3 layers, inner layers comprising hyaline to dark brown, pseudoparenchymatous cells of *textura angularis*, outer layers composed of thick, dark brown to black, cells of *textura angularis*. *Asci* 42–58 × 6–13 µm ($\bar{x}$ = 50.7 × 8.92 µm, n = 10), 8-spored, unitunicate, cylindrical to obpyriform, thick-walled at apex, with J-, sub-apical ring. *Ascospores* 6.75–14 × 2–3.65 µm ($\bar{x}$ = 7.46 × 2.85 µm, n = 30), hyaline, cylindrical to clavate or fusiform, with rounded apices and bases, smooth-walled, 1-septate, guttulate, slightly constricted in the middle. **Asexual morph**: *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6.5–10.5 × 4.8–6 µm ($\bar{x}$ = 8.2 × 5.57 µm, n = 5), enteroblastic, phialidic, solitary, ellipsoidal to ovoid, smooth-walled, hyaline to pale brown. *Conidia* only young conidia attached to conidiogenous cells observed. *Appressoria* not observed.

Culture characteristics: Colonies on MEA reaching approximately 70 mm diam. after 5 days at 25 °C, flat, entire margin, aerial mycelia, dense, fast-growing, pale orange with hyaline mycelium, reverse yellowish white.

Material examined: Thailand, Chiang Mai Province, Omkoi, on living leaves of *Bridelia* sp. (Phyllanthaceae), 16 October 2019, Gomdola D., (MFLU 22-0174, dry culture), living culture MFLUCC 22-0114.

Hosts and distribution: *Foeniculum vulgare*, *Helianthus annuus*, *Cucumis sativus*, *Medicago sativa*, *Lagenaria siceraria*, *Brassica oleracea*, *Lycopersicon esculentum*, *Phaseolus vulgaris*, *Platostoma palustre*, *Sedum* sp., *Solanum lycopersicum* from China; *Arabidopsis thaliana*, *Pyrus malus* from Switzerland; *Bambusa* sp. from Iran; *Dieffenbachia maculate*, *Phlox* sp. from New Zealand; *Galium spurium*, *Solanum melongena*, *Pisum sativum* from Canada; *Nicotiana tabacum* from Belgium; *Solanum tuberosum* from Pakistan; *Viola odorata* from Egypt; *Viola tricolor* from Netherlands; *Asparagus officinalis*, *Aquilegia flabellata*,

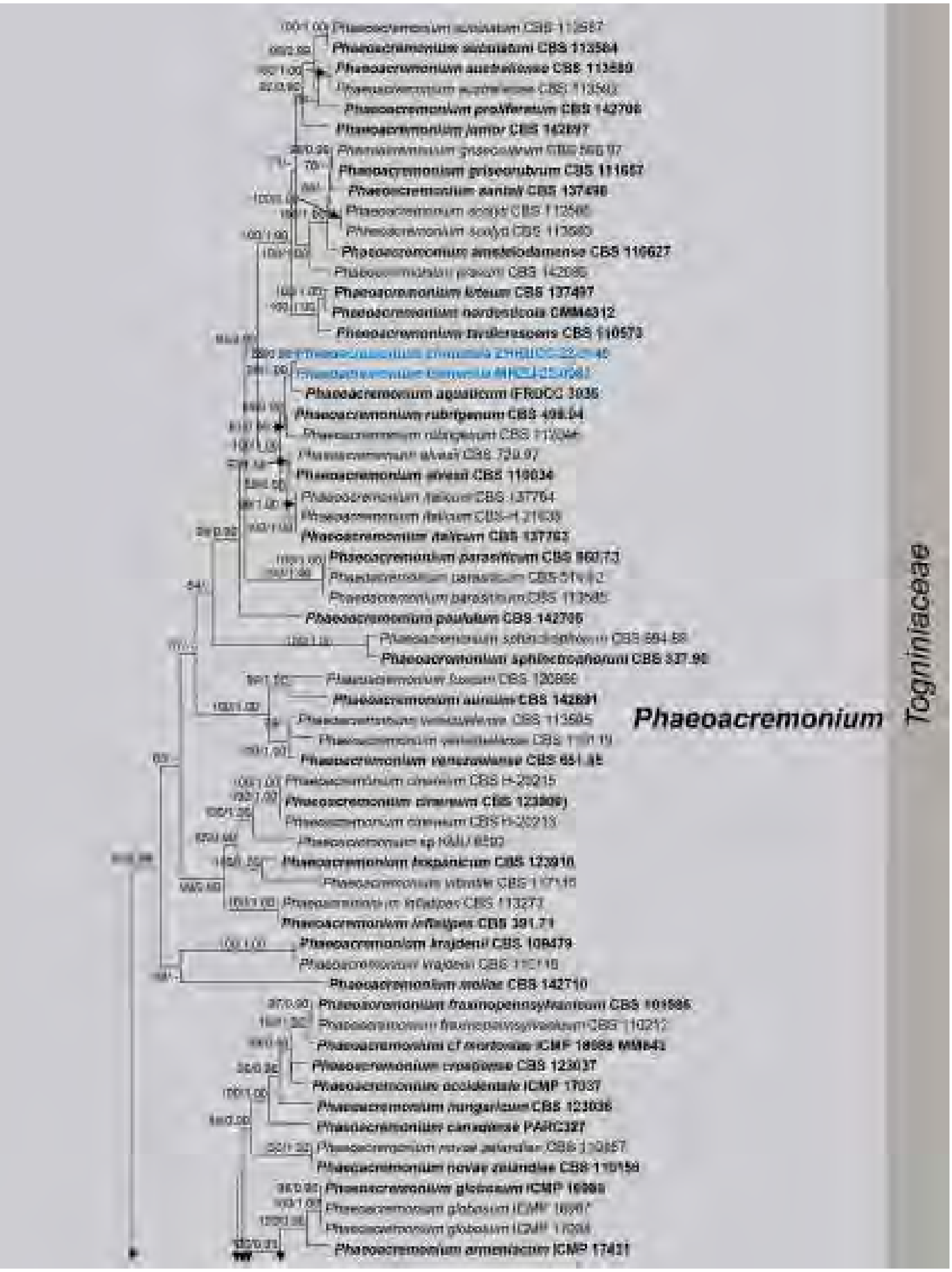


Fig. 106 The best scoring RAxML tree with a final likelihood value of − 20,111.099446 for combined dataset of ITS (415 bp) and LSU (1098 bp) sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses. The tree is rooted with *Pleurostoma richardsiae* (CBS 270.33). The matrix had 951 distinct alignment patterns with 40.73% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.224327, C = 0.285250, G = 0.263495, T = 0.226927; substitution rates AC = 1.643769, AG = 4.356590, AT = 1.491903, CG = 1.297038, CT = 5.507338, GT = 1.0; gamma distribution shape parameter α = 0.220723. Ex-type strains are in bold and newly generated sequences are in blue bold. Bootstrap support for ML equal to or greater than 50% and BI equal to or greater than 0.90 are given above the nodes

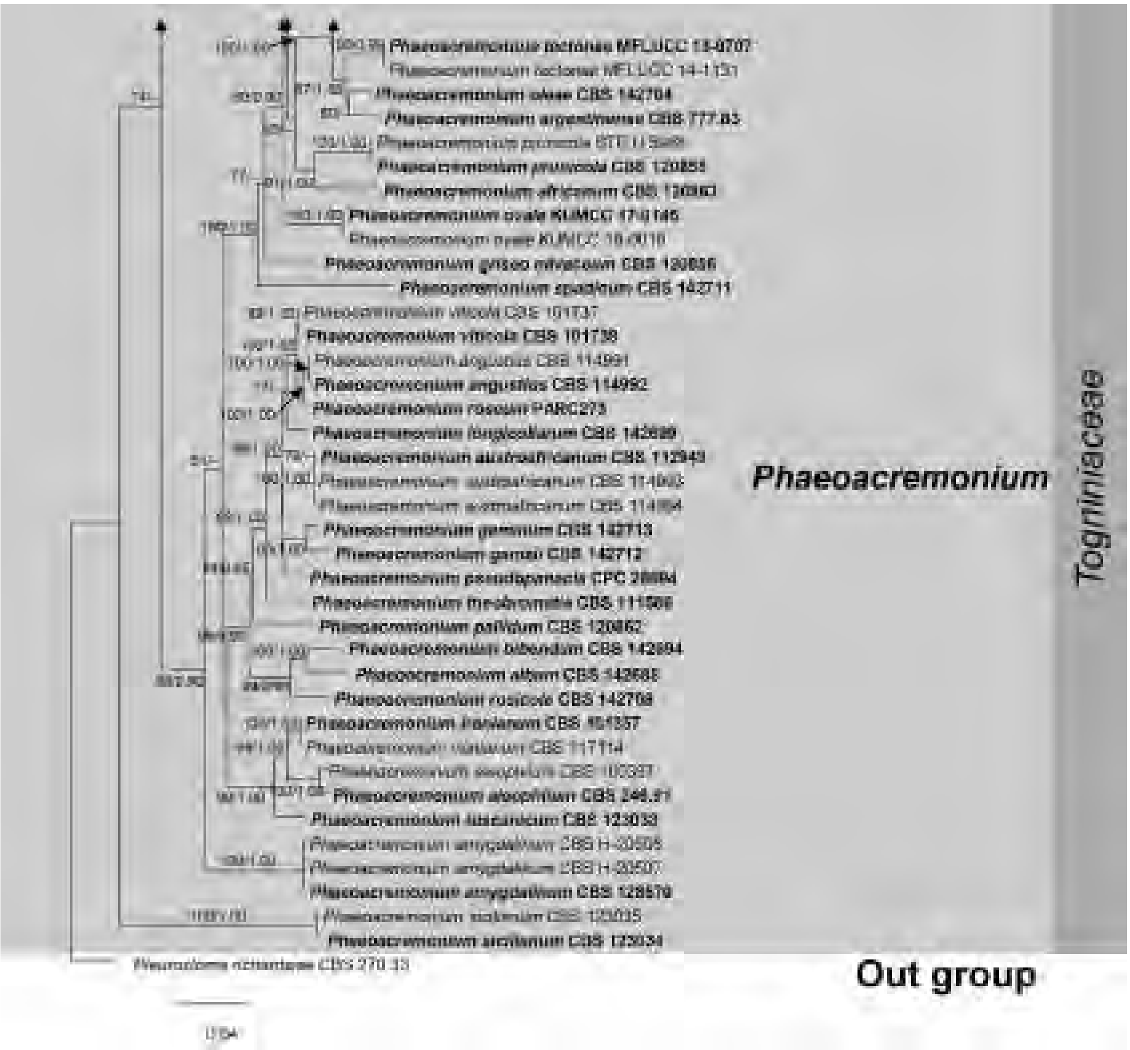


Fig. 106 (continued)

Diplotaxis tenuifolia, *Capsicum annuum*, *Cichorium endivia*, *Citrullus lanatus*, *Cucumis melo*, *Ocimum basilicum*, *Valerianella locusta*, *Petroselinum crispum*, *Solanum lycopersicum* from Italy; *Glycine max*, *Heterodera glycines*, *Heuchera sanguinea*, *Ocimum basilicum* from USA (Farr and Rossman 2023).

GenBank numbers: ITS: OP678332, LSU: OP678334

Notes: Our collection (MFLU 22-0174) clusters with the strains of *Plectosphaerella cucumerina* including the type strain in the combined ITS, LSU, *β-tubulin* and *tef*1-*α* locus analyses with ML/MP/BI = 98%/98%/1.00 bootstrap support. Morphologically, our collection fits to *P. cucumerina* by its sexual morphic characters (Carlucci et al. 2012). Therefore, we identified our collection as *P. cucumerina.*

There are several reports about disease of *P. cucumerina* that cause necrotic leaf spots on *Aquilegia flabellata* in Italy (Garibaldi et al. 2021), *Alfalfa* root rot, fennel root rot and Chinese cabbage wilt in China (Cai et al. 2021; Zhao et al. 2021; Gao et al. 2022). Here, our *P. cucumerina* collection associated with leaf spots of *Bridelia* sp. This is the first report of this species on living leaves of *Bridelia* sp. from Thailand and it is a new host and geographical record (Fig. 108).

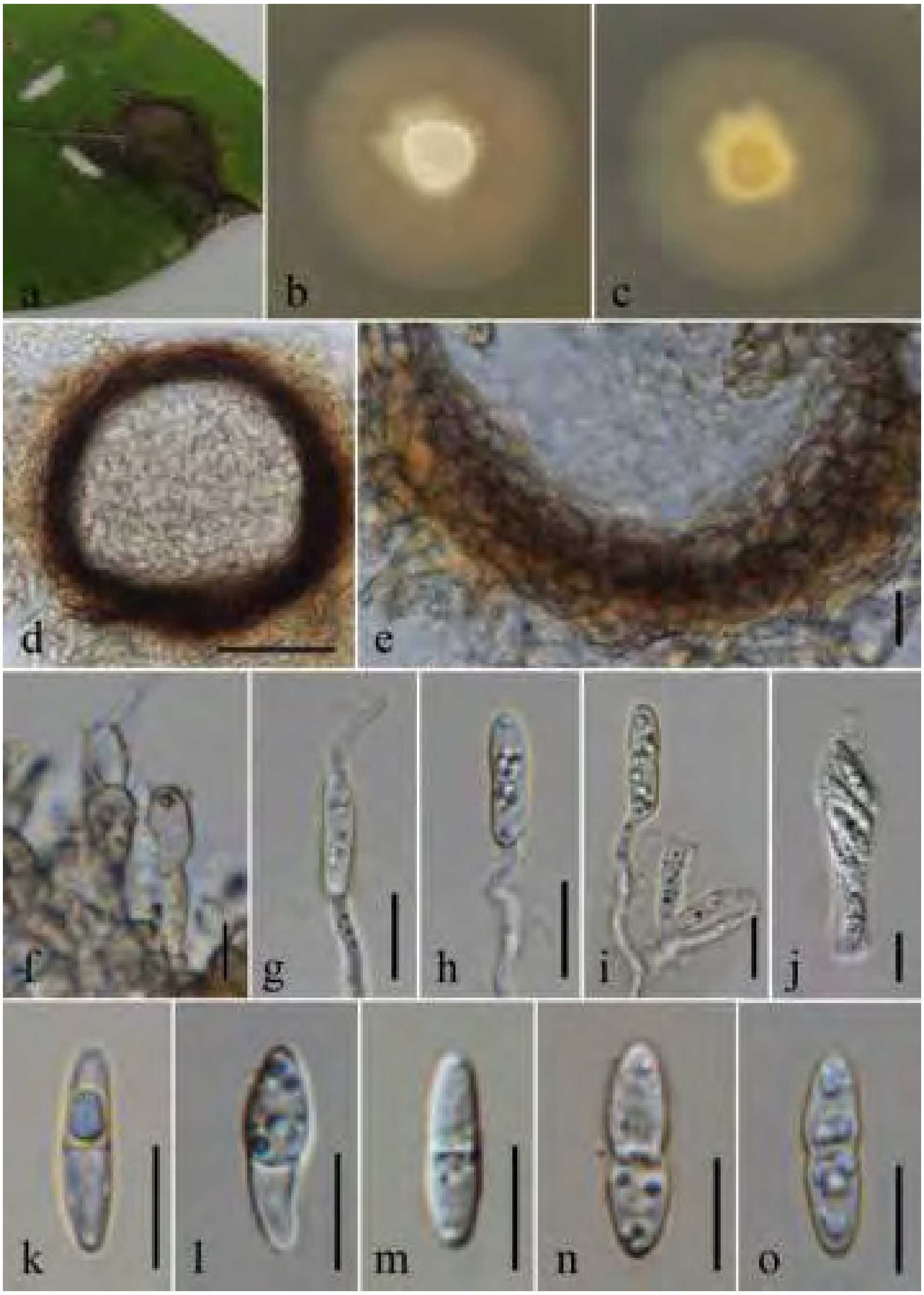
Hypocreales Lindau

Hypocreales was introduced by Lindau (1897). The order contains 15 families with about 320 genera (Wijayawardene et al. 2022).

Bionectriaceae Samuels & Rossman

Bionectriaceae is characterized by unilocular perithecia of white, pale yellow to pale brown, producing pigments which does not react with KOH, and are superficial or immersed in a substrate (Rossman et al. 1999). It includes 47 genera of which seven are lichenicolous (Diederich et al. 2018; Wijayawardene et al. 2022; Perera et al. 2023).

Fig. 107 ***Plectosphaerella cucumerina*** (MFLU 22-0174). **a** Examined material with leaf spots. **b** Surface view of colony on MEA. **c** Reverse view of colony on MEA. **d** Section through ascoma. **e** Peridium. **f** Conidiogenous cells attached to young conidia in culture. **g**–**i** Germinating ascospores. **j** Asci. **k**–**o** Ascospores. Scale bar. d = 50 µm e, g–o = 10 µm f = 5 µm



Pronectria Clem.

Pronectria is almost exclusively lichenicolous genus including 44 species (Diederich et al. 2018). It is characterized by astromatic pale perithecia without interascal filaments, immersed in lichen thalli or algal crust, and hyaline, mainly 1-septate ascospores produced in unitunicate asci (Rossman et al. 1999; Diederich et al. 2018). In this study, we introduce a new *Pronectria* species.

Pronectria loweniae Flakus, Etayo, Rodr. Flakus & Zhurb., ***sp. nov.***

Index Fungorum number: IF900452; *Facesoffungi number*: FoF 14203; Fig. 109

Etymology: The new species is named in honor to the eminent American mycologist Dr. Rosalind Lowen (New York), who studied the species for the first time together with Swedish lichenologist Dr. Rolf Santesson, for her important contribution to knowledge on lichenicolous Hypocreales.

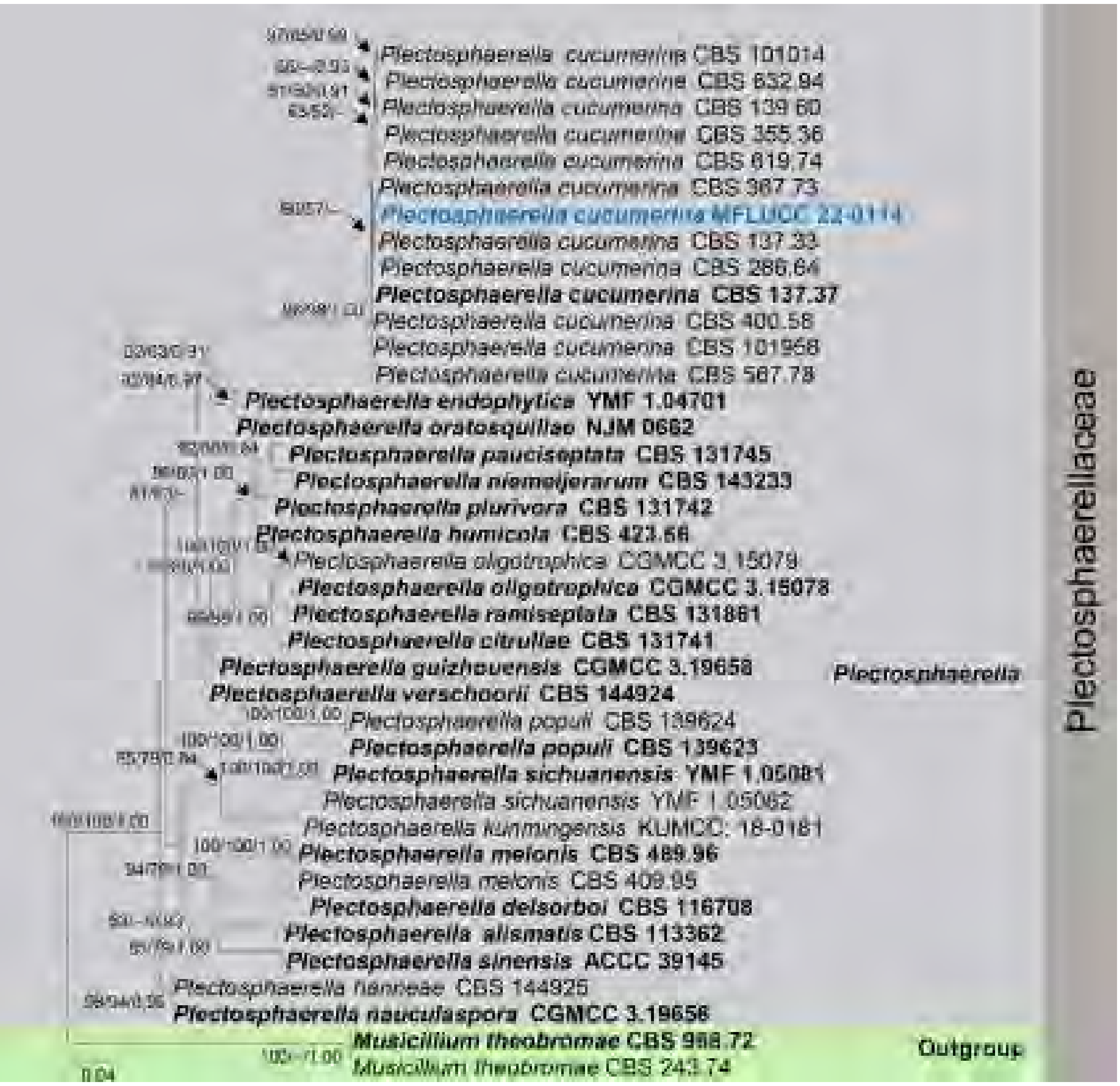


Fig. 108 The best scoring RAxML tree with a final likelihood value of − 9039.925089 for the combined dataset of ITS (473 bp), LSU (793 bp), *β-tubulin* (317 bp) and *tef*1-*α* (455 bp) sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses. The tree is rooted with *Musicillium theobromae* (CBS 243.74 and CBS 968.72). The matrix had 515 distinct alignment patterns with 27.20% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.223589, C = 0.294693, G = 0.277902, T = 0.203817; substitution rates AC = 1.565720, AG = 2.080346, AT = 1.939801, CG = 0.818113, CT = 7.028180, GT = 1.0; gamma distribution shape parameter α = 0.184705. Ex-type strains are in bold and newly generated sequences are in blue bold. Bootstrap support for ML equal to or greater than 50% and BI equal to or greater than 0.90 are given above the nodes

Lichenicolous. Growing on discs of apothecia and occasionally adjacent parts of the thallus of lichen-forming fungi *Solorina bispora, S. saccata* and *S. spongiosa.* **Sexual morph**: *Ascomata* perithecia, growing on discs of apothecia and occasionally also adjacent parts of thallus of *Solorina* species, aggregated in small groups, subglobose to obpyriform, 120–250 µm wide, 110–220 µm tall, often shortly papillate, with distinct ostiole, erumpent and occasionally up to 1/3 exposed, pale yellowish, yellow- to apricot-orange, rarely also medium orange-brown or reddish orange, with projecting hyaline, thin-walled, septate hyphae 5–25 × 3–6 µm (sometimes radially spreading over the host hymenia as paler areas surrounding ostiolar regions). *Exciple* 20–25 µm wide below, up to 60 µm wide above, of cells 1–17 × 1–3 µm, consists of hyaline inner layer, composed of tangentially elongated, thin-walled cells (strongly inspersed by small orange oil droplets; the droplets sometimes observed additionally inside the asci and the whole ascomatal cavities) and hyaline to pale orange outer layer composed of tangentially elongated to isodiametric thick-walled cells, KOH–, lactic acid–. *Interascal filaments* scarce,

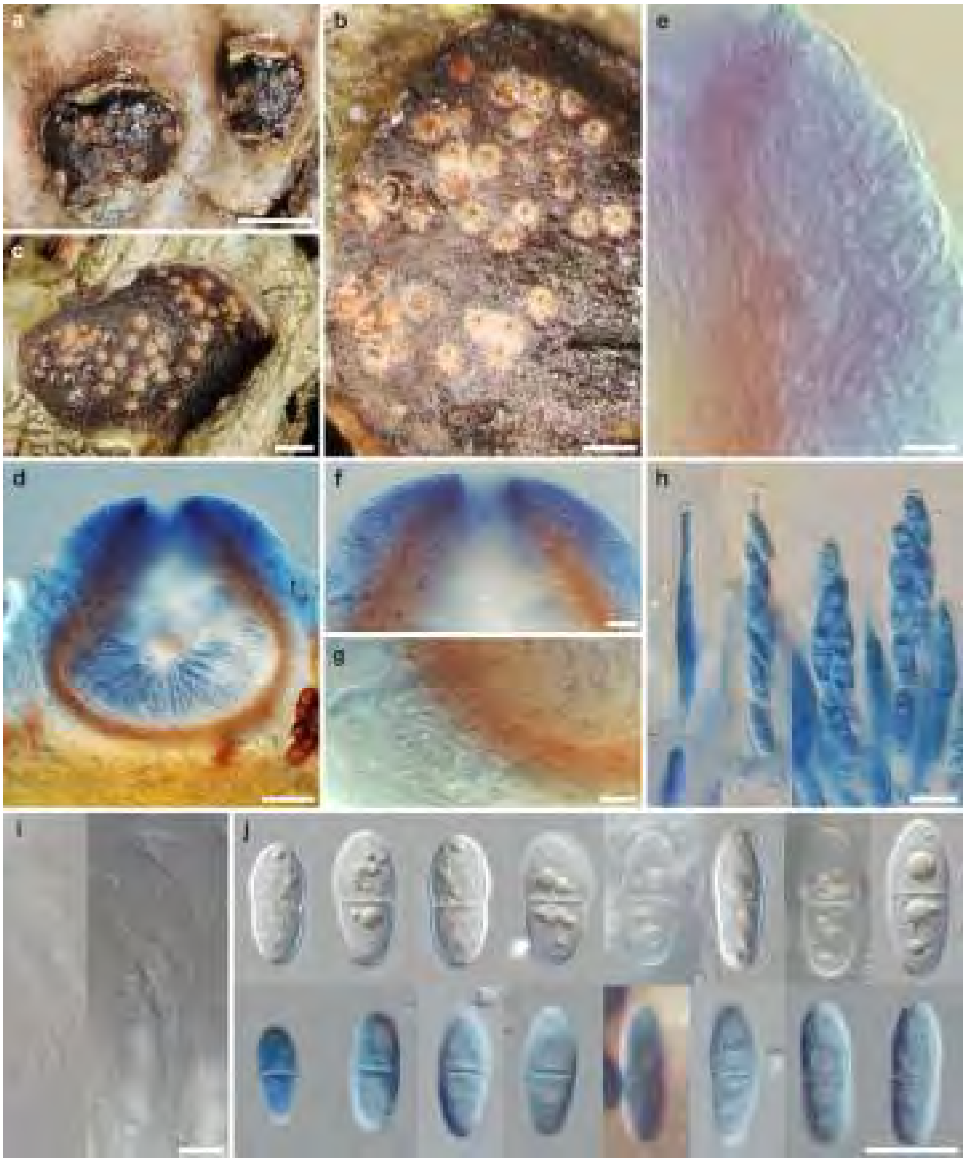


Fig. 109 ***Pronectria loweniae*** (KRAM-L 73248, **holotype**). **a**–**c** Habit of ascomata growing in hymenia of *Solorina saccata*. **d** Transversal section of ascoma showing exciple differentiated into inner layer inspersed by orange droplets and thickened apically outer layer (mounted in LPCB). **e** Thickened apical outer layer of exciple (mounted in LPCB). **f** Periphyses (mounted in LPCB). **g** Exciple divided into inner layer inspersed by orange droplets and hyaline outer layer (mounted in LPCB). **h** Asci (mounted in LPCB). **i** Interascal filaments (mounted in distilled water). **j** Ascospores mounted in distilled water (upper row) and LPCB (lower row). Scale bars: a–c = 500 µm, d = 50 µm, e–j = 10 µm

2–10 µm wide, hyaline, septate, constricted near septa. *Periphyses* hyaline, simple to branched, sometimes septate, 15–30 × 1–2 µm. *Asci* unitunicate, subcylindrical to elongate-clavate, truncate at the apex, 8-spored, 60–70 × 8–10 µm. *Ascospores* hyaline, elliptic to narrowly elliptic (sometimes almost fusiform), occasionally with slightly wider upper cell, smooth-walled, without evident gelatine coat, with pale orange guttules, 1-septate, usually slightly constricted at the septum (if observed in water), 10–($\bar{x}$ = 13.2 ± 1.8)–18 × 3–($\bar{x}$ = 5.1 ± 1.5)–8 µm, l/b ratio 1.5–($\bar{x}$ = 2.8 ± 0.7)–5 (n = 230) [in holotype: 11–($\bar{x}$ = 14.5 ± 1.6)–17 × 3.5–($\bar{x}$ = 5.6 ± 0.6)–6.5 µm, l/b ratio 2.2–($\bar{x}$ = 2.6 ± 0.3)–3.7 (n = 53)], diagonally uniseriate to biseriate in the ascus. **Asexual morph**: Undetermined.

Material examined: France, Arette, La Pierre St. Martin le Braca, hayedo-abetal close to road D-132, 42° 59′ 06″ N, 0° 44′ 38″ W, 1480 m, on terricolous *Solorina saccata* in limestone crack, 1 August 2018, P. Rodriguez-Flakus 4000, J. Etayo & A. Flakus (KRAM-L 73248, **holotype**, herb. Etayo, **isotype**); Canada, Nunavut: Ellesemere Is., Eureka, 80° 06′ N, 85° 38′ W, on *S. bispora* var. *subspongiosa*, 30 July 1999, N.V. Matveeva (LE 260160); *ibid.*, Black Top Ridge, 80° 04′ N, 85° 29′ W, 900 m, on *S. bispora* var. *subspongiosa*, 30 July 1999, F.J.A. Daniëls (LE 260039); Mongolia, Khubsugul Aimak, Renchinlkhumbe Somon, headwaters of Ar Khordolyn Gol River, NE slope of Khordolyn Sardig Nuru Range, 50° 53′ 32″ N, 99° 56′ 50″ E, 2050 m, on *S. saccata*, 15 July 2018, M.P. Zhurbenko 1885a (LE 309699a); 16 July 2018, M.P. Zhurbenko 1886 (LE 309700); Norway, Svalbard, Dickson Land, W coast of

Billefjorden, 7 km S of Pyramiden, near Nidedalselva river mouth, 78° 37′ N, 16° 20′ E, 2–100 m, on *S. bispora*, 23 July 2003, M.P. Zhurbenko 03329 (LE 260960); M.P. Zhurbenko 03333 (LE 261160); Russia, Arkhangelsk Region, Franz Josef Land, Hooker Is., Cape Sedov, 80° 20′ N, 52° 52′ E, on *S. bispora* var. *subspongiosa*, 2 August 1930, V.P. Savicz 9d (LE 207391); Krasnoyarsk Territory, Kara Sea, Vize Is., 79° 32′ N, 76° 50′ E, on *S. bispora* var. *subspongiosa*, 14 August 1930, V. P. Savicz 1607 (LE 207390); Taimyr Peninsula, Byrranga Mts, Zamknutaya River, 74° 37′ N, 98° 33′ E, 150 m, on *S. bispora* var. *subspongiosa*, 6 August 1995, M.P. Zhurbenko 95474 (LE 233942); N of Levinson-Lessing Lake, 74° 31′ N, 98° 36′ E, 400 m, on *S. bispora* var. *subspongiosa*, 20 August1995, M.P. Zhurbenko 95501b (LE 260299b); on *S. bispora* var. *bispora*, 22 August 1995, M.P. Zhurbenko 95500 (LE 260260); Republic of Sakha (Yakutia), Lower Lena River, Primorskii Range, Stolb meteostation, 72° 22′ N, 126° 42′ E, 50 m, on *S. bispora* var. *subspongiosa*, 4 August 1998, M.P. Zhurbenko 98368 (LE 260100); Samoilovskii (D'ieleekh Aryyta) Island, 72° 22′ N, 126° 29′ E, 10 m, 27 July 1998, M.P. Zhurbenko 98371 (LE 260080); USA, Alaska, Sagwon, 69° 26′ N, 148° 40′ W, 280 m, on *S. bispora* var. *bispora*, 7 August 2003, D.A. Walker (LE 260067); Kobuk Valley Wilderness, 67° 07′ N, 159° 03′ W, 40 m, on *S. bispora* var. *bispora*, 9 August 2000, M.P. Zhurbenko 00465 (LE 260277); 67° 06′ N, 159° 01′ W, 50 m, on *S. spongiosa*, 4 August 2000, M.P. Zhurbenko 00179 (LE 260028).

Additional material examined of P. robergei: Russia, Murmansk Region, Pyukhyakuru River, 66° 47′ N, 30° 00′ E, on *Peltigera canina*, 12 August 1986, T.A. Dudoreva (LE 233837); *ibid.* Nenets Autonomous Area, Khar'yaga oilfield, 67° 11′ 07″ N, 56° 29′ 37″ E, 70 m, on *P. aphthosa*, 25 July 2007, M.P. Zhurbenko 0727 (LE 210498); 67° 11′ 19″ N, 56° 29′ 53″ E, 70 m, on *P. aphthosa*, 22 July 2007, M.P. Zhurbenko 0728 (LE 210346); Komi Republic, headwaters of Pechora River, 62° 02′ N, 58° 05′ E, 180 m, on *P. praetextata*, 10 July 1997, M.P. Zhurbenko 97264 (LE 210237); 62° 05′ N, 58° 25′ E, 200 m, on *P. leucophlebia*, 7 July 1997, M.P. Zhurbenko 97279 (LE 210351); Krasnoyarsk Territory, 40 km NW of Krasnoyarsk, near Pogorelka Village, 56° 25′ N, 93° 00′ E, on *P. canina*, 20 July 2000, T.N. Otnyukova (LE 210259); Altai Republic, Kuderli Lake, 55° 52′ N, 88° 35′ E, 1700 m, on *Peltigera* sp., 10 June 1987, N.I. Zolotukhin (LE 207388a); Republic of Buryatia, Khamar-Daban Range, Temnik River, 51° 05′ N, 104° 55′ E, 1200 m, on *Peltigera* sp., 21 July 1994, G.P. Urbanavichyus (LE 207389); Spain, Navarra, Orbaiceta, Irati forest, coming up from Orbaiceta to Azpegui refuge, Ursario, on *Peltigera* sp., 43° 02′ 02″ N, 1° 12′ 50″, 1030 m., 13 September 2018, J. Etayo (Etayo 31406).

GenBank numbers: ITS: OR116443; LSU: OR133232.

Notes: Our new collection is characterized by small, pale yellowish-orange (rarely reddish orange), often finely papillate ascomata immersed in hymenia of various species of *Solorina* (likely without causing visibly damages to the host), exciple strongly inspersed by small, orange oil droplets with thickened in the apical part, and constantly smooth-walled ascospores.

Our phylogenetic analyses based on the concatenated dataset of LSU and ITS (Fig. 110) revealed that our collection clustered with *Pronectria* species within Bionectriaceae (Hypocreales). Further, it formed a sister clade to *Pronectria robergei* (growing on lichen in *Peltigera*) and *Protocreopsis freycinetiae* that growing on remnants of monocotyledonous plants (Rossman et al. 1999). The subclade formed by these three species, then sistered to a subclade with the saprobic species in genera *Lasionectriella* and *Ochronectria* and these phylogenetic placements are very similar to Rossman et al. (1999) and Lechat and Fournier (2016). Our collection clustered with *P. robergei* in our phylogenetic analyses (Fig. 110).

Pronectria robergei can be distinguish from our collection by having darker, reddish tinge, and large ascomata (240–340 µm wide, 250–320 µm high) mostly developing on thalli (only rarely on apothecia) of *Peltigera* species. *Pronectria robergei* usually damages the host thallus causing necrosis. The ascospores of *P. robergei* are smooth to spinulose (Rossman et al. 1999) while ascospores of our collection are smooth-walled. Zhurbenko (2009a) showed that the sizes of ascospores vary greatly in *Pronectria*. However, ascospores of *P. robergei* [10.5–($\bar{x}$ = 13.8 s = 2)–20 × 2.5–($\bar{x}$ = 4.2 s = 1.4)–7.5 µm, l/b ratio 2.1–($\bar{x}$ = 3.5 s = 0.8)–6 (n = 148)] are thinner and more elongated than our collection [10–($\bar{x}$ = 13.2 s = 1.8)–18 × 3–($\bar{x}$ = 5.1 s = 1.5)–8 µm, l/b ratio 1.5–($\bar{x}$ = 2.8 s = 0.7)–5 (n = 230)].

In addition to the sexual morphic stage, *P. robergei* reported from its specific anamorphic stage *Illosporium carneum* (Sikaroodi et al. 2001; Hafellner 2015; Diederich et al. 2018), occurring on various species of *Peltigera*, but never reported from any species of *Solorina*. Specimens that morphologically identical to our collection were reported as "*Pronectria solorinae* Lowen & R. Sant. (ined.)" from Austria, Canada, Germany, Norway, Russia and Sweden, growing on *Solorina bispora*, *S. saccata* and *S. spongiosa* (Santesson 1993; Zhurbenko and Santesson 1996; Hafellner 1999; Zhurbenko and Daniëls 2003; Alstrup et al. 2008; Brackel 2014). However, these specimens are different from *P. solorinae*.

Further, two morphologically similar hypocrean fungi were described from *Solorina*, viz. *Pronectria rolfiana* and *Xenonectriella lutescens*. Both of them differ from our collection by its ornamented, larger ascospores (21–26 × 10–13 µm) and the KOH + violet exciple with

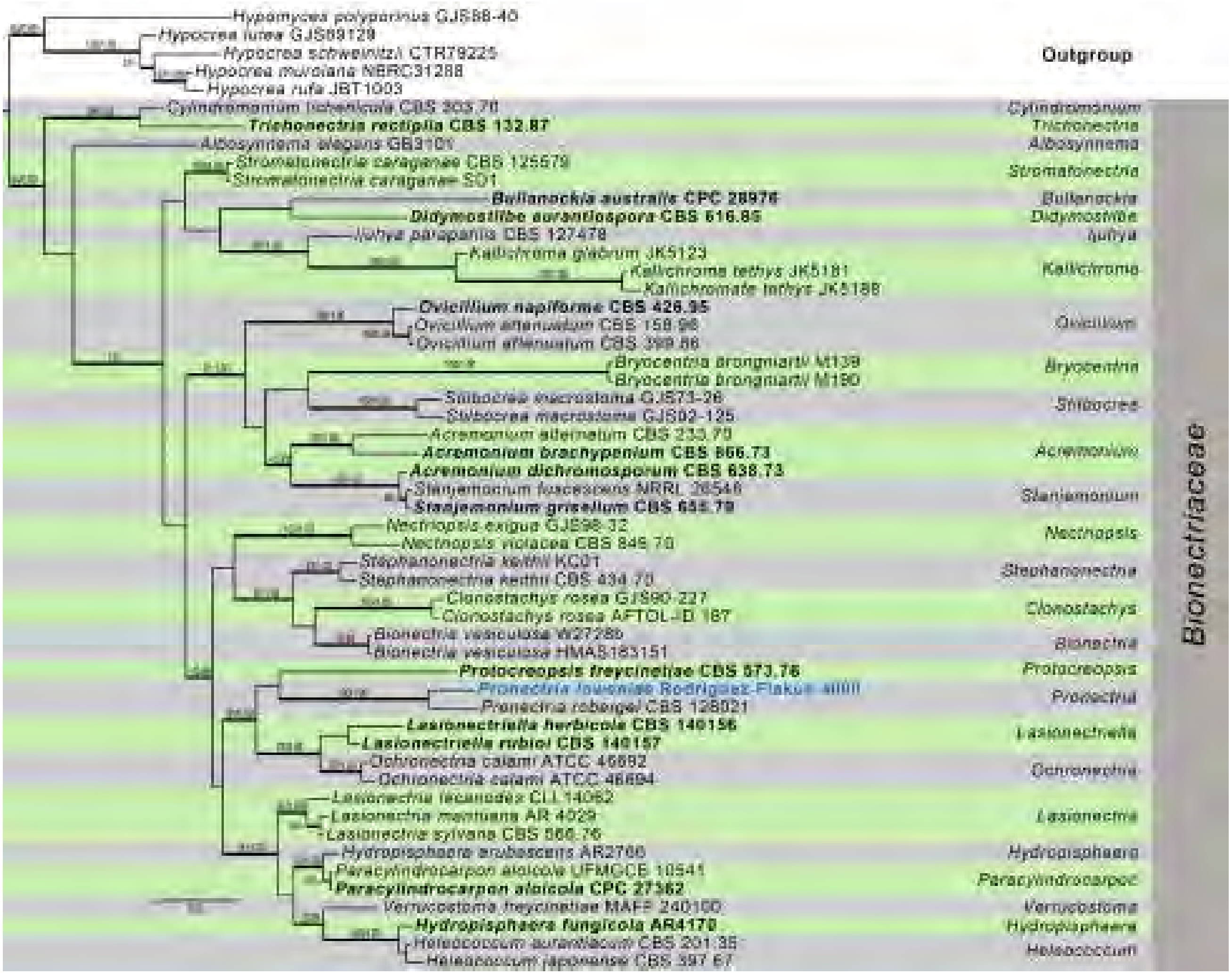


Fig. 110 Phylogenetic reconstruction of the systematic position of *Pronectria loweniae* within Bionectriaceae inferred from ML analyses of combined nuLSU and nuITS rDNA dataset. Species from the Hypocreaceae (*Hypocrea* and *Hypomyces*) were used as outgroup. Bold branches represent either bootstrap values ≥ 70 and/or Bayesian posterior probabilities ≥ 0.95

1-septate ascospores merging together into submuriform structures respectively (Zhurbenko 2009b; Etayo and Triebel 2010). Therefore, we introduce our collection as *Pronectria loweniae* sp. nov. This species widely distributes in the Northern Hemisphere. We have examined specimens from Canada, France, Mongolia, Norway, Russia and USA.

Hypocreaceae De Not.

Hypocreaceae was introduced by de Notaris (1844) and is typified by *Hypocrea* Fr. Members of this family are characterized by their brightly coloured, fleshy perithecial stromata (Rogerson 1970). The family comprises 17 genera and more than 450 species (Kirk et al. 2008; Wijayawardene et al. 2018; Hyde et al. 2020a).

Trichoderma Persoon

Trichoderma, the asexual morph of *Hypocrea* Fr. is an ecologically and economically important genus (Persoon 1794). This genus typified by *T. viride* Pers. Rifai (1969) provided the generic delineation of *Trichoderma*, based on microscopic characters. Currently, there are more than 340 species listed in the genus (Index Fungorum 2023). A recent review of *Trichoderma* species was published by Cai and Druzhinina (2021).

Trichoderma pyrrosiae Li Hua & Senan., ***sp. nov.***

Index Fungorum number: IF900453; *Facesoffungi number*: FoF 14204; Fig. 111

Isolated from leaves of *Pyrrosia lingua* (Thunb.) Farwell. **Sexual morph**: Not observed. **Asexual morph**: *Conidiophores* straight or slightly curved, many, often branched in pairs, branched 1–2 times, base width 2–4 µm, distance between adjacent two branches (5.5–)7–16(–24.5) µm, branches usually perpendicular to the main axis, terminating in 3–5 branches. *Phialides* (4–)5–9 × 2.5–4 µm, l/w ratio 2:1, ampulliform to lageniform in whorls, sometimes directly from the main axis. *Conidia* (3.5–)4–5 × 3–4 µm, aspect ratio 1.5:1, spherical to subglobose, thin-walled, white, smooth.

Material examined: China, Guangdong Province, Guangzhou City, Baiyun Mountain, 23° 11′ 13″ N 113° 17′ 51″ E, isolated from *Pyrrosia lingua* (Polypodiaceae), 16 August 2021, Li Hua (MHZU 22-0159, **holotype**); ex-type culture, ZHKUCC 22-0297.

Culture characteristics: Colonies on PDA reaching 8 cm diameter after 3 days at 25 °C, circular, smooth margin, green in the center, white at the margin, aerial hyphae hairy to floccose, dense at center, relative sparse at the margin. Chlamydospores or diffusing pigments not formed. The wood smell was occurred.

GenBank numbers: ITS: OQ980189, OQ980190

Notes: Our trichoderma-like species grouped with *Trichoderma asperellum* in the combined ITS, *rpb*2, and *tef*1-*α* sequence analyses (Fig. 112) with ML/BI = 96%/1.00 statistical support. However, our collection morphologically differs from the phylogenetically nearest species *T. asperellum* by its sterile secondary branches and the short phialides (5–9 *vs* 7–11.5). The nucleotide differences of *rpb*2 and *tef*1-α between our collection and *T. asperellum* revealed

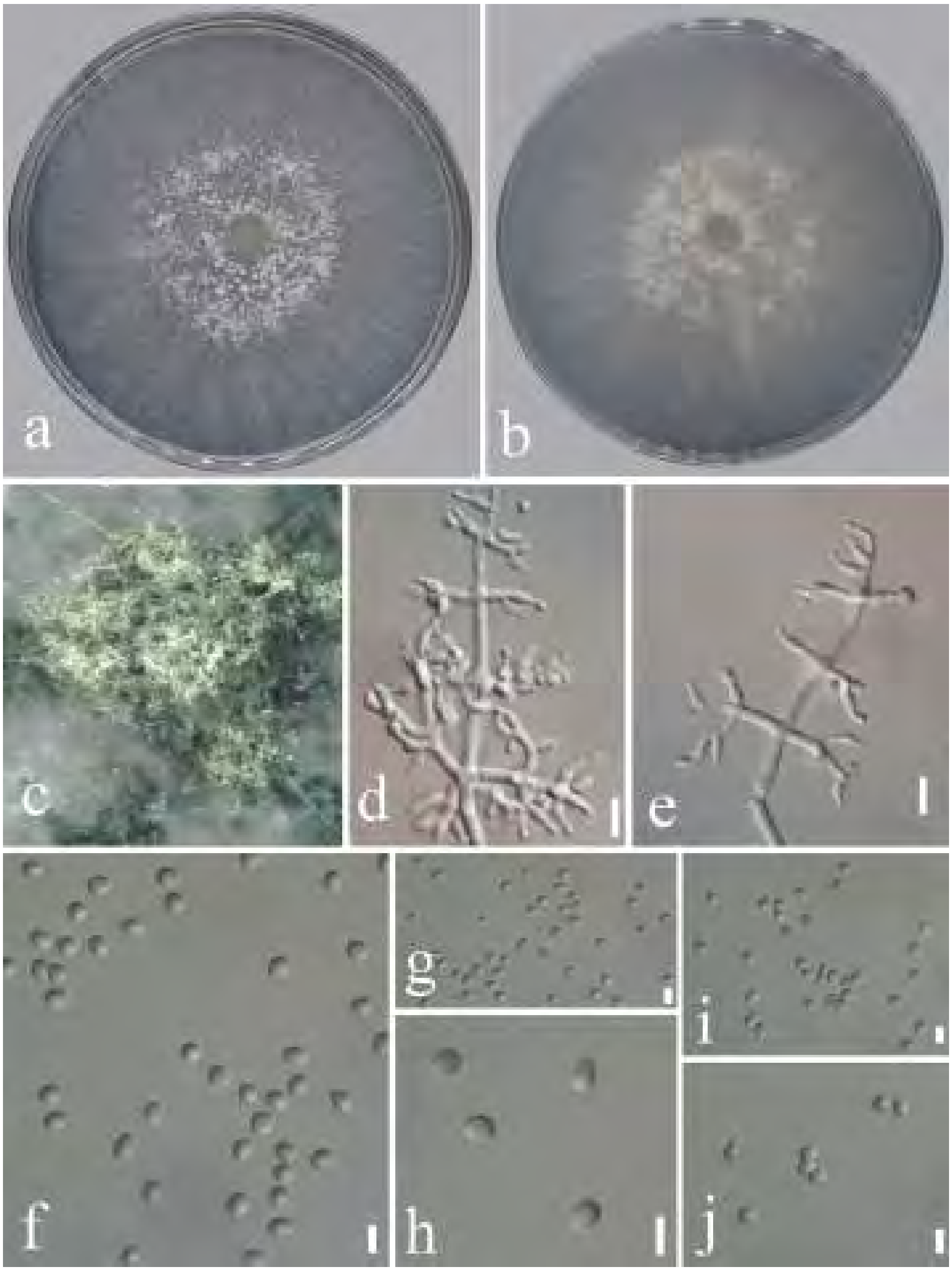


Fig. 111 ***Trichoderma pyrrosiae*** (MHZU 22-0159, **holotype**). **a** Surface view of culture on PDA. **b** Reverse view of culture on PDA. **c** Conidial mass on PDA. **d–e** Conidiophores, phialides and attached conidia. **f–j** Conidia. Scale bars: d–e = 10 cm, f–g, i–j = 5 µm, h = 15 µm

1.31% and 1.5% respectively and ITS sequences are identical. Therefore, we introduce our collection as *Trichoderma pyrrosiae* sp. nov.

Microascales Luttr. ex Benny & R.K. Benj.

Currently there are seven families and 103 genera in this order and we followed the outline of Hyde et al. (2020c).

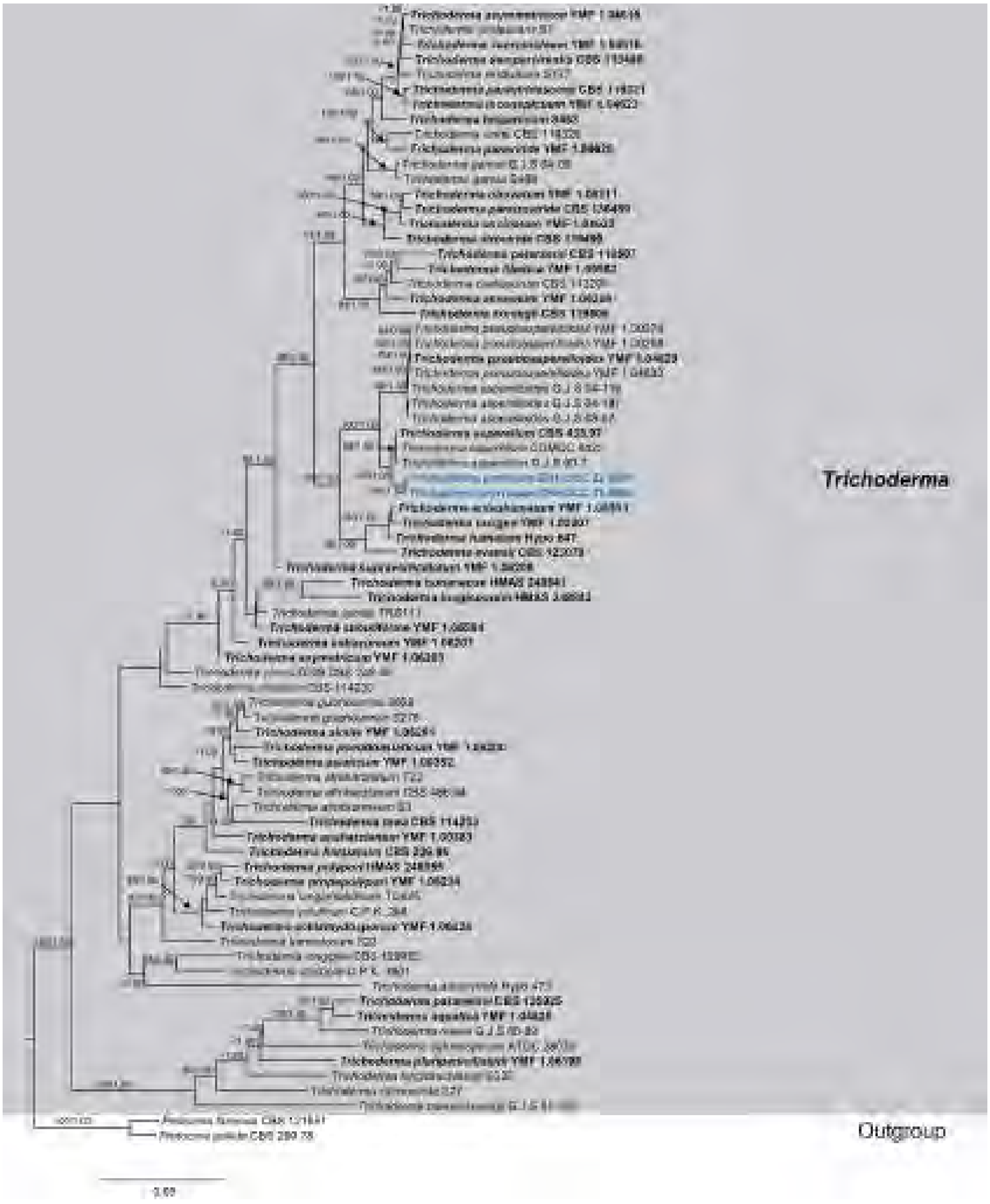


Fig. 112 Phylogenetic tree derived from maximum likelihood analyses of a combined ITS, *rpb*2 and *tef*1-α sequences. The aligned dataset comprised of 2626 characters including gaps (ITS = 463, *rpb*2 = 1067, *tef*1-α = 1,094). A best scoring RAxML tree was established with a final ML optimization likelihood value of − 20,692.436886. The matrix had 580 distinct alignment patterns with 15.62% undetermined characters or gaps. Estimated base frequencies were found to be: A = 0.233296, C = 0.282631, G = 0.255967, T = 0.228106; substitution rates AC = 0.898272, AG = 3.638367, AT = 0.947951, CG = 0.678561, CT = T: 5.576378, GT = 1.0. *Protocrea farinose* (CBS 121551) and *P. pallida* (CBS 299.78) were used as outgroup taxa. Newly generated isolates are indicated in blue bold. Bootstrap support for ML ≤ 75% and BI equal to or greater than 0.90 are given at the nodes

Microascaceae Luttr. ex Malloch

Microascaceae was circumscribed by Luttrell (1951). It comprises saprobic, plant and opportunistic human pathogenic fungi (de Hoog et al. 2011; Sandoval-Denis et al. 2013; Maharachchikumbura et al. 2016). Sandoval-Denis et al. (2016a, b) revised this family using combined LSU, ITS, *tef*1-α and *β-tubulin* gene analysis and proposed several new species and combinations in Microascaceae. Currently, there are 24 genera in this family and species are mainly saprobic, coprophilous and clinically important taxa.

Petriella Curzi

Petriella is morphologically closely resembling with *Microascus* (Zukal 1885), but differs by having hairy ascomata (Curzi 1930). *Petriella* is typified by *P. asymmetrica* Curzi and currently this genus comprises seven species (Index Fungorum 2023). *Petriella* was accepted in Microascaceae (Maharachchikumbura et al. 2015, 2016; Wijayawardene et al. 2017, 2018; Hyde et al. (2020c). *Petriella* species were collected as saprobes on dried branches of *Pyrus communis, Populus grandidentata, P. nigra* and on leaves of *Luzula* sp. from China (Honshu), Cyprus, Italy, Thailand and USA (Ontario) and on the dung of Cervidae from USA (Ontario) (Corlett and MacLatchy 1987; Lackner and de Hoog 2011). This study introduces a new *Petriella* species.

Petriella thailandica O. Karimi & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900454; *Facesoffungi number*: FoF 13983; Fig. 113.

Etymology: The name refers to Thailand, where the fungus was collected.

Saprobic on submerged wood in freshwater habitat. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiophores* 785–1,350 × 25–115 µm ($\bar{x}$ = 953 × 69 µm, n = 50), synnematous, erect, flexuous, olivaceous brown to dark brown, consisting individual conidiophores (50–90 µm), septate. *Synnemata* abundant, 785–1,350 × 25–115 µm. *Conidiogenous cells* 10–45 × 1–2.7 µm ($\bar{x}$ = 35 × 1.9 µm, n = 50), cylindrical to sub cylindrical, long, branched profusely at the apex. *Conidia* 1.7–7.4 × 1–2.7 µm ($\bar{x}$ = 4.4 × 1.7 µm, n = 100), aseptate, hyaline, smooth, variable, ellipsoidal, reniform, obovoid, cylindrical.

Culture characteristics: Colonies on PDA reaching 40 mm diam. after 14 days at 25 °C, circular, flat, smooth margin, initially white, turning to creamy; reverse white. Mucoid conidial mass observed after five weeks.

Material examined: Thailand, Chiang Rai, Phan District, Doi Pui Sai Khao, on decaying submerged wood, 27 September 2021, O. Karimi, STS5B40 (MFLU 23-0001, **holotype**), ex-type culture MFLUCC 23-0001.

GenBank numbers: ITS: OQ172252; LSU: OQ172248; *rpb2*: OQ200123; *β-tubulin*: OQ184744.

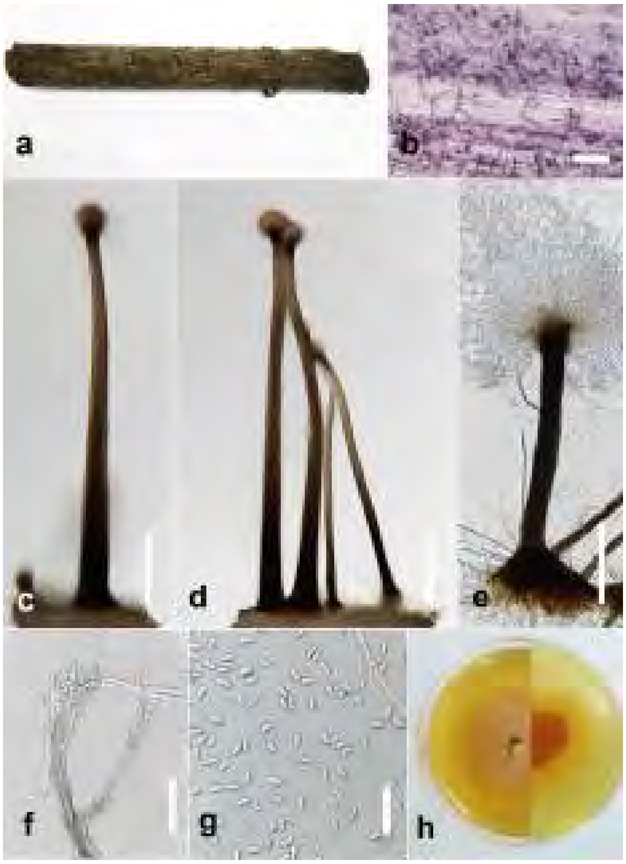


Fig. 113 ***Petriella thailandica*** (MFLU 23-0001, **holotype**). **a** Host substrate. **b** Synnemata on substrate. **c, d** Synnemata. **e, f** Conidiogenous cells. **g** Conidia. **h** Surface view of colony on PDA. Scale bars: b = 1 mm, c–f = 70 µm, f = 20 µm, g = 7 µm

Notes: Our petriella-like collection is morphologically similar to *P. lindforsii* Curzi and *P. guttulata* G.L. Barron & Cain. However, our collection differs from *P. lindforsii* in having long conidiophores (786–1,350 × 250–350 µm), and aseptate, ellipsoidal, reniform, obovoid to cylindrical, small conidia (1.7–7.4 × 1–2.7 µm) while *P. lindforsii* has mostly hyaline, cylindrical-oblong, large conidia (8–14 × 3.5–6 µm) with a papillate appendage at the proximal end (Barron et al. 1961). Our collection differs from *P. guttulata* in longer and wider synnemata (785–1350 × 25–115 µm vs 1000 × 6–25 µm) (Barron et al. 1961). In the combined ITS and LSU sequence analysis (Fig. 114) shows that our petriella-like collection forms a distinct clade and distant from *P. lindforsii* and *P. guttulata*. Therefore, we introduce this collection as *Petriella thailandica*.

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

The order Chaetosphaeriales was introduced by Huhndorf et al. (2004) based on the morphology and phylogeny. This order comprises four families viz. Chaetosphaeriaceae, Helminthosphaeriaceae, Leptosporellaceae and Linocarpaceae (Maharachchikumbura et al. 2016; Hernándes-Restrepo et al. 2017; Konta et al. 2017; Hyde et al. 2020c). Species of Chaetosphaeriales are mostly saprobes or pathogens in terrestrial and aquatic habitats, and sometimes reported as fungicolous species (Maharachchikumbura et al. 2016).

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

The family Chaetosphaeriaceae was introduced by Réblová et al. (1999) to accommodate *Chaetosphaeria* and its allied taxa and placed in the Sordariales. However, Huhndorf et al. (2004) placed Chaetosphaeriaceae in Chaetosphaeriales based on the molecular data. The asexual morph of Chaetosphaeriaceae is hyphomycetous and characterized

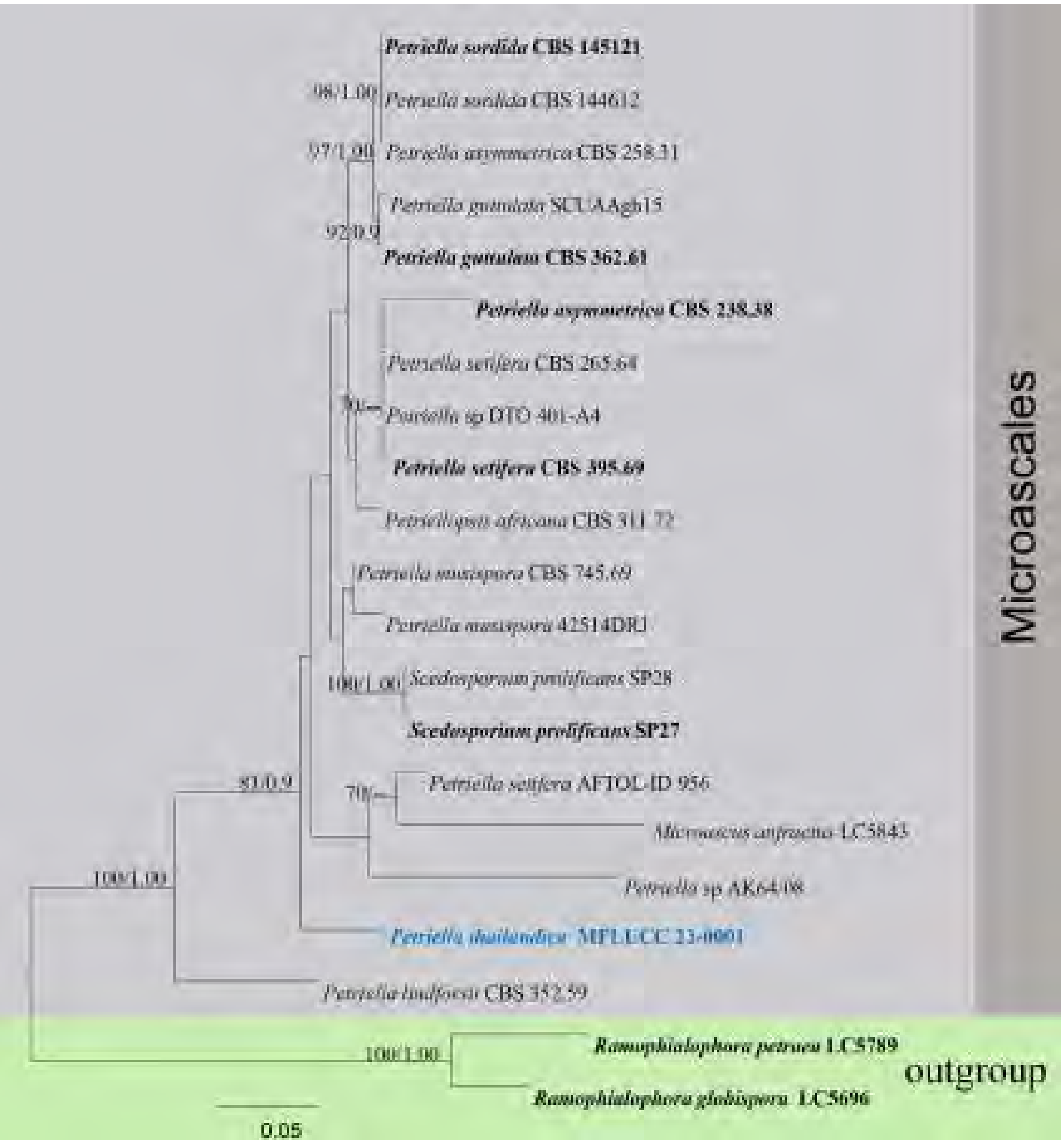


Fig. 114 The best scoring RAxML tree generated using ITS and LSU combined dataset with a final likelihood value of – 4609.603487 is presented.The tree is rooted with *Ramophialophora globispora* (LC5789) and *R. petraea* (LC5696). The ML bootstrap values > 60% and Bayesian posterior probabilities (PP) > 0.9 are noted at the nodes. The new species is in blue bold. Twenty taxa are included in the combined analyses which comprise a total of 1346 characters. The matrix had 345 distinct alignment patterns, with 25.06% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.252378, C = 0.240783, G = 0.285095, T = 0.221744; substitution rates AC = 1.743022, AG = 2.583205, AT = 1.866015, CG = 1.345319, CT = 7.144677, GT = 1.0; gamma distribution shape parameter α = 0.226347

by septate, branched or unbranched conidiophores with the monophialidic or polyphialidic, holoblastic or enteroblastic, smooth-walled conidiogenous cell (Réblová et al. 1999; Wu and Diao 2022). Currently, there are 43 genera in this family (Hyde et al. 2020c).

Paragaeumannomyces Matsush.

Paragaeumannomyces was introduced and typified by *P. sphaerocellularis* (Matsushima 2003). Currently, there are 15 species listed in Species Fungorum (2023). This genus is characterized by scolecosporous, multiseptate, asymmetrical, hyaline to light pink ascospores and unique three-layered ascomatal wall (Réblová et al. 2020). Members of the genus occur on decaying, decorticated plant materials (Matsushima 2003; Perera et al. 2016). Members of *Paragaeumannomyces* species are distributed worldwide and especially occur in Central America and Asia but were also encountered in the subtropical and temperate climate zones of Europe, Japan, New Zealand and North America.

Paragaeumannomyces panamensis (Huhndorf & F.A. Fernández) Réblová & A.N. Mill., in Réblová, Nekvindová, Fournier & Miller, MycoKeys 74: 32 (2020)

Basionym: *Chaetosphaeria panamensis* Huhndorf & F.A. Fernández

Index Fungorum number: IF836535; *Facesoffungi number*: FoF 02657; Fig. 115

Saprobic on decaying, submerged wood in freshwater stream. **Sexual morph**: *Ascomata* 180–260 × 285–265 µm ($\overline{x}$ = 235 × 210 µm, n = 10), scattered, solitary, superficial, globose to subglobose, ostiolate, slightly papillate, coriaceous, not collapsing when dry, black, setose, rough-walled. *Setae* scattered, cover entire ascomata, dark, stiff, pointed, 40–85 µm long ($\overline{x}$ = 62 µm, n = 30). *Peridium* 35–65 µm ($\overline{x}$ = 44 µm, n = 20), thick, one-layered, composed of large isodiametric to polygonal, brown to dark brown cells. *Asci* 85–137 × 9–15 µm ($\overline{x}$ = 104 × 11 µm, n = 20), 8-spored, unitunicate, cylindrical, rounded at the apex. *Ascospores* 50–70 × 2–4 µm ($\overline{x}$ = 62 × 3 µm, n = 20), filiform, loosely fasciculate, straight or slightly curved, 7-septate, early stage without constrictions at the septa but late stage has constrictions at the septa, rounded at both ends, apical end broader than the basal end, hyaline, smooth-walled. **Asexual morph**: Undetermined.

Culture Characteristics: Ascospores germinated on PDA within 12 h at 25 °C, germ tubes produced from both ends. Colonies on PDA reaching 27 mm diam. in 10 days at 28 °C, flat, circular, irregular margin, greyish green from above with white aerial mycelia, reverse dark grey with white margin.

Material examined: China, Guangdong Province, Guangzhou City, Baiyun Mountain, on sub-merged decaying wood in a freshwater stream, 16 August 2021, Jizhen Fu, BYS05 (MHZU 22-0084, **new geographical record**), living culture ZHKUCC 22-0150.

Hosts and distribution: On decorticated wood in Panama (Matsushima 2003) and on decorticated twigs of *Pinus* in Thailand (Perera et al. 2016).

GenBank numbers: ITS: OR164934, LSU: OR164962.

Notes: In the combined ITS, LSU and *tef1-α* gene analyses (Fig. 116) shows that our collection (ZKUH 22-0084) clustered with *Paragaeumannomyces panamensis* and morphology of our collection is identical to the holotype of *P. panamensis* (Matsushima 2003; Perera et al. 2016). Therefore, taxonomic affiliation of our collection with *P. panamensis* was confirmed based on morphology and phylogeny. However, *P. panamensis* only reported from Panama and Thailand and this is the first report of *P. panamensis* in China.

Xylariomycetidae O.E. Erikss. & Winka

Amphisphaeriales Hawksw. & O.E. Erikss.

The order Amphisphaeriales has been accepted in consecutive studies using multigene phylogenies in the subclass Xylariomycetidae (Senanayake et al. 2015; Samarakoon et al. 2016; Hongsanan et al. 2017; Crous et al. 2018). Hyde et al. (2020c) accepted Amphisphaeriaceae, Apiosporaceae, Beltraniaceae, Clypeophysalosporaceae, Cylindriaceae, Hyponectriaceae, Iodosphaeriaceae, Melogrammataceae, Phlogicylindriaceae, Pseudomassariaceae, Sporocadaceae, and Vialaeaceae.

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr

Apiosporaceae was introduced and typified by *Apiospora* Sacc. (Hyde et al. 1998) to accommodate taxa which comprise apiospores and a basauxic, arthrinium-like conidiogenesis (Samuels et al. 1981; Senanayake et al. 2015; Dai et al. 2017; Wang et al. 2018; Pintos et al. 2019). Currently, this family comprises three genera, viz. *Apiospora*, *Arthrinium* Kunze, and *Nigrospora* Zimm (Pintos and Alvarado 2021). Apiosporaceae comprises saprobes, pathogens on leaves, stems and roots of monocotyledon plants, mostly grasses, endophytes on plants, lichens, and marine algae, soil inhabitant or occasionally infect in humans (Seifert et al. 2011; Crous and Groenewald 2013; Pintos et al. 2019; Senanayake et al. 2020a; Feng et al. 2021). Therefore, species in Apiosporaceae are economically, environmentally and medicinally important (de Hoog et al. 2000; Jiang et al. 2018).

Apiospora Sacc.

Apiospora was introduced (Saccardo 1875) without designating a type species and Saccardo et al. (1931) later designated *A. montagnei* Sacc. as the lectotype of the genus. *Apiospora* species are cosmopolitan with wide range of hosts and substrates as endophytes, phytopathogens or saprobes

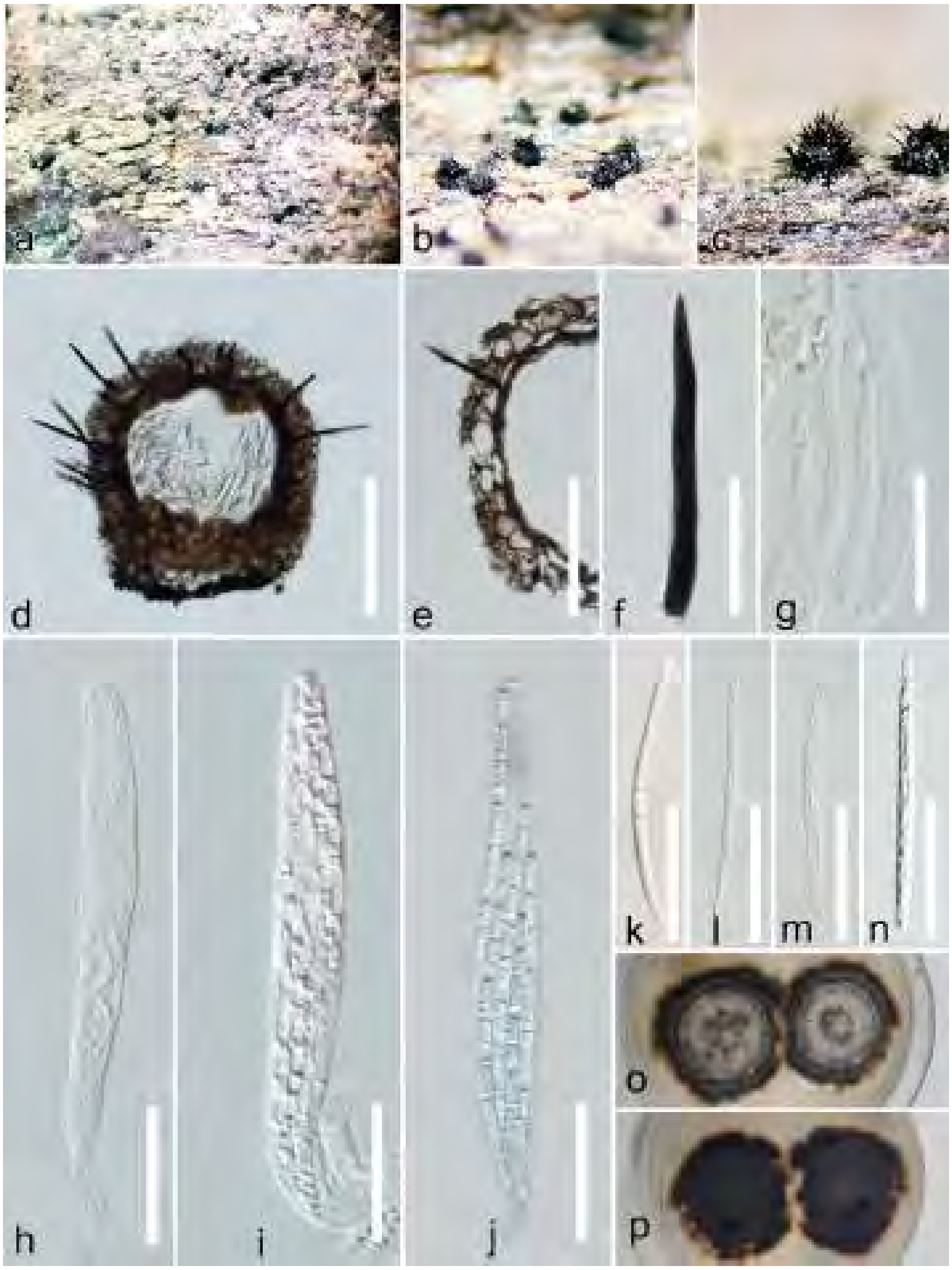


Fig. 115 ***Paragaeumannomyces panamensis*** (ZKUH 22-0084). **a–c** Ascoma on substrate. **d** Vertical cross section of ascoma. **e** Peridium. **f** Setae. **g** Paraphyses. **h–j** Asci. **k–n** Ascospores. **o** Upper view of colony on PDA. **p** Reverse view of colony on PDA. Scale bars: d–n = 20 μm

while some are lichen-associated, air or soil-borne (Dai et al. 2017; Wang et al. 2017, 2018; Hyde et al. 2020c; Senanayake et al. 2020a; Pintos and Alvarado 2021). A few species have been reported as animal and human pathogens that can cause Onychomycosis (Goodenough et al. 2017; Dyląg et al. 2017). Some species produce antifungal metabolites such as Apiosporamide (Alfatafta et al. 1994). The sexual morph of *Apiospora* is characterized by multi-locular, perithecial stromata with hyaline ascospores surrounded by a thick gelatinous sheath (Senanayake et al. 2015; Pintos and Alvarado 2021) while the asexual morph of this genus is characterized by basauxic conidiogenesis, with pale brown to brown, globose to sub-globose, obovoid to fusiform conidia (Hyde et al. 1998; Dai et al. 2016). *Apiospora* species share more similar morphological characters, thus it is required to have molecular data to distinguish species. *Apiospora* was synonymized under *Arthrinium* (Crous and Groenewald 2013). Pintos and Alvarado (2021) showed that some *Arthrinium* species form a monophyletic basal clade to *Apiospora* and this clade suggested as *Arthrinium* s. str. Currently there are 101 species in this genus (Species Fungorum 2023) (Fig. 117).

Apiospora cannae Senan., ***sp. nov.***

Index Fungorum number: IF900455; *Facesoffungi number*: FoF 14207; Fig. 118

Fig. 116 The best scoring RAxML tree with a final likelihood value of − 4292.869723 of combined ITS (415 bp) and LSU (1098 bp) sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses. The tree is rooted with *Chaetosphaeria fusiformis* (CBS 101429). The matrix had 693 distinct alignment patterns with 33.02% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.929735, C = 0.028634, G = 0.026025, T = 0.015606; substitution rates AC = 0.741911, AG = 0.356590, AT = 0.631883, CG = 0.458695, CT = 0.504294, GT = 1.0; gamma distribution shape parameter α = 0.563546. Ex-type strains are in bold and newly generated sequences are in blue bold. Bootstrap support for ML equal to or greater than 50% and BI equal to or greater than 0.90 are given above the nodes

Etymology: based on the host genus *Canna*.

Saprobic, isolated from leaves of *Canna* sp. **Sexual morph**: Not observed. **Asexual morph**: Sporulating on PDA, scattered, pale brown spore masses visible on cultures. *Hyphae* 2–3 µm diam., hyaline, branched, thick-walled, septate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 20–25 × 2.5–3.5 µm ($\bar{x}$ = 24 × 3 µm, n = 25), holoblastic, monoblastic, hyaline, cylindrical, straight, discrete, aseptate, smooth-walled. *Conidia* 5–8 µm ($\bar{x}$ = 7 µm, n = 20) globose in surface view, lenticular in side view, dark brown, smooth-walled, with a pale equatorial slit. *Sterile cells* 13–20 × 4–6 µm ($\bar{x}$ = 16 × 5 µm, n = 20) ellipsoid to elongated ovoid, brown, mixed among conidia.

Culture characteristics: Colonies on PDA reaching 5 cm diam. after 10 days in dark at 25 °C, circular to irregular, filamentous edge, white, fluffy aerial mycelial clots, reverse off-white, sporulate after 10 days.

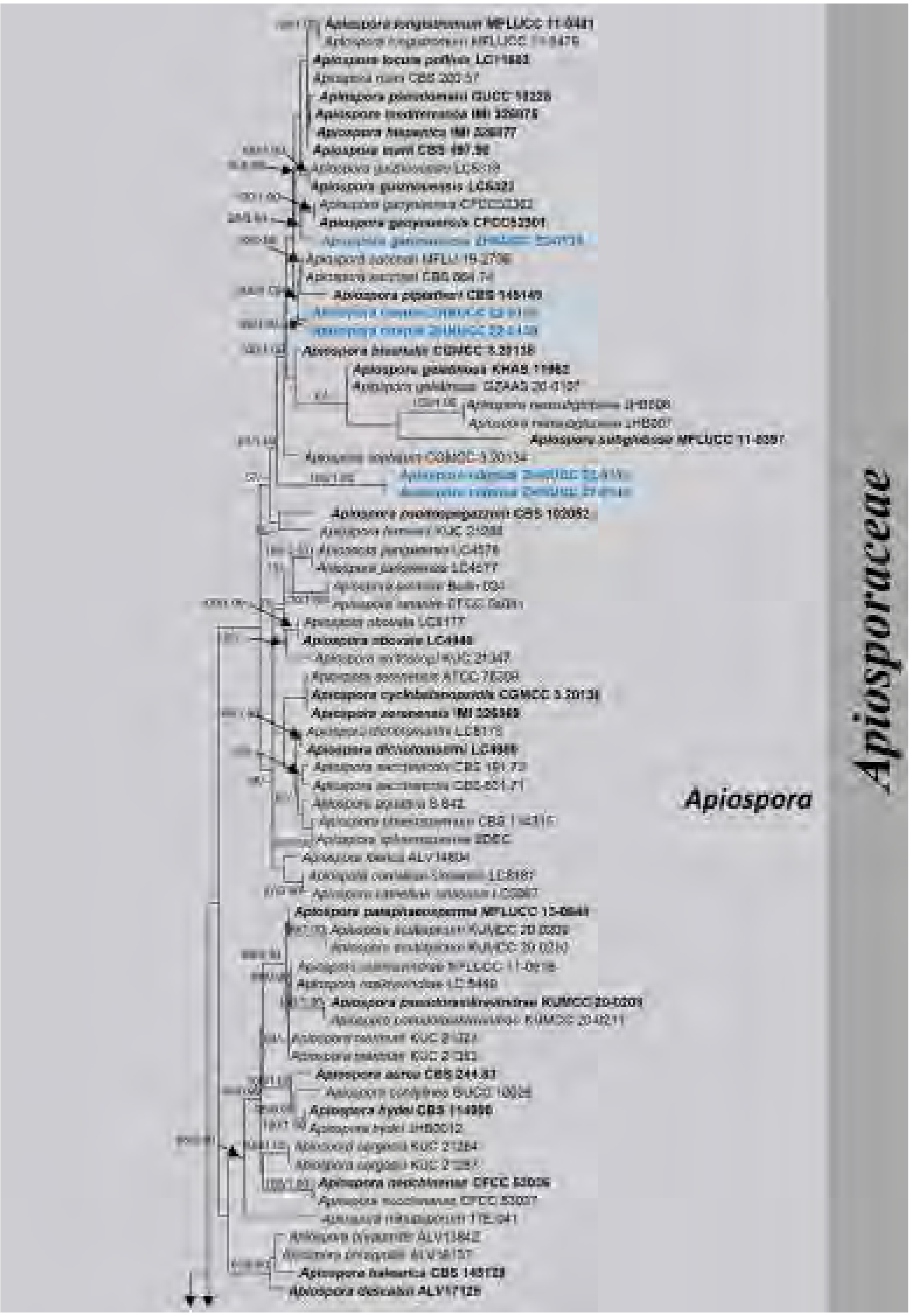


Fig. 117 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *β-tubulin* and *tef1-α* sequence data of 190 taxa, which comprised 2694 characters (ITS = 565, LSU = 862, *β-tubulin* = 444, *tef1-α* = 823). The best scoring RAxML tree with a final likelihood value of − 20,488.974413 is presented. The matrix had 917 distinct alignment patterns, with 25.57% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.229550, C = 0.267919, G = 0.242735, T = 0.259795; substitution rates: AC = 1.447018, AG = 2.737139, AT = 1.353872, CG = 1.119023, CT = 4.157776, GT = 1.0; gamma distribution shape parameter α = 0.215582. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (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 blue bold. The tree is rooted to *Sporocadus trimorphus* (CBS 114203)

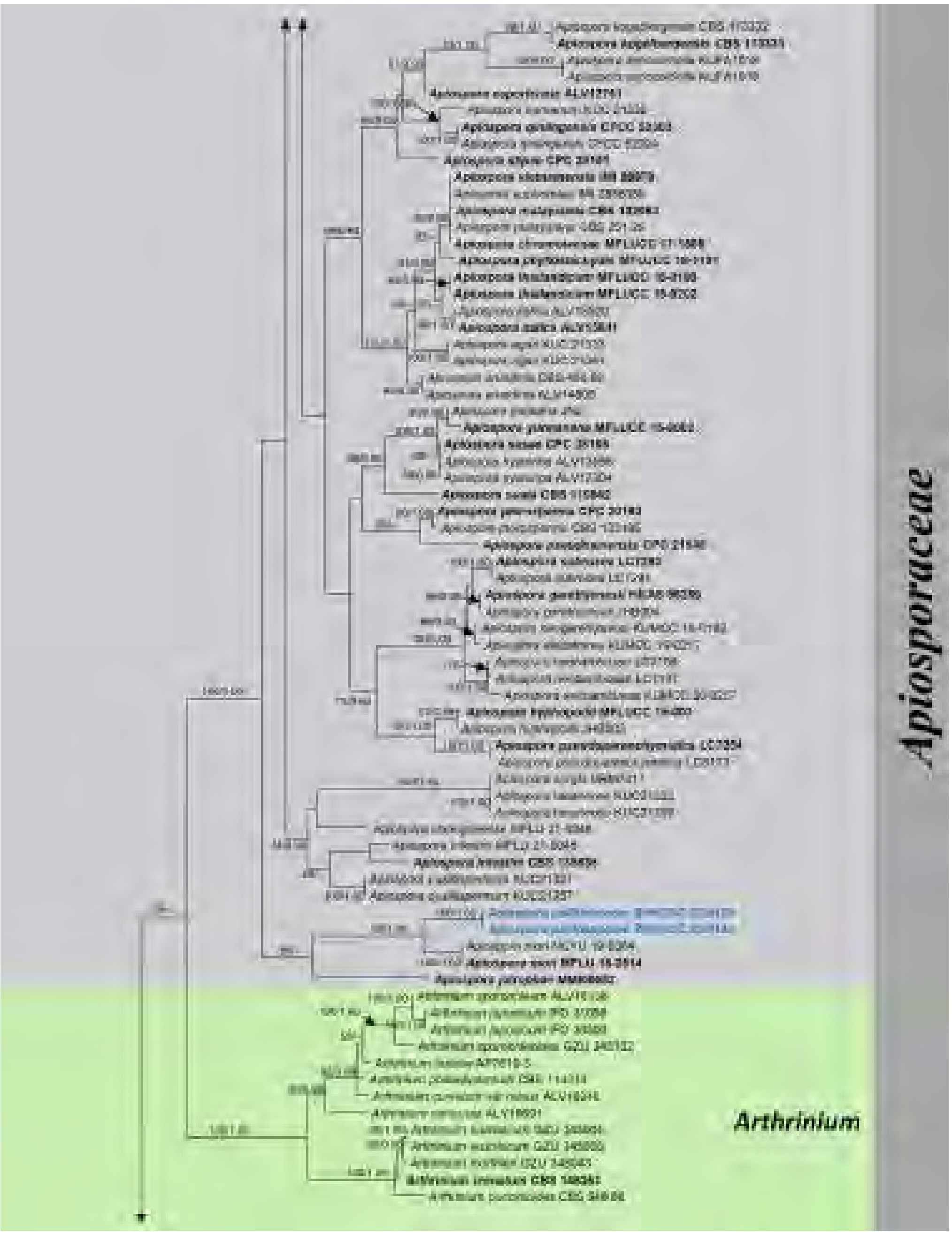


Fig. 117 (continued)

Material examined: China, Guangdong Province, Guangzhou City, Baiyun Mountain (23° 09′ 35″ N 113° 17′ 40″ E), leaves of *Canna* sp. (Cannaceae), 20 June 2021, I.C. Senanayake, 71–2 (MHZU 22-0070, **holotype**), ex-type cultures ZHKUCC 22-0127, ZHKUCC 22-0139.

GenBank numbers: ITS: OR164901, OR164902; LSU: OR164948, OR164949; *tef*1-*α*: OR166285, OR166286; *β-tubulin*: OR166321, OR166322.

Notes: The sequence data of ITS, LSU, *β-tubulin* and *tef*1-α of our collection (MHZU 22-0070) gives species in *Apiospora* as the closest matches with NCBI. The phylogenetic analysis (Fig. 117) showed that our isolate is genetically close, but distinct from *Apiospora sacchari* (CBS 301.49, CBS 212.30) and *A. piptatheri* (ALV13594) forming a distinct subclade with MP/BI = 100%/1.00 support. Morphologically, our collection (MHZU 22-0070) has solitary, cylindrical conidiogenous cells on hyphae while *Apiospora sacchari* has ampulliform to doliiform conidiogenous cells aggregated in clusters on hyphae proliferating sympodially with globose conidia (Crous and Groenewald

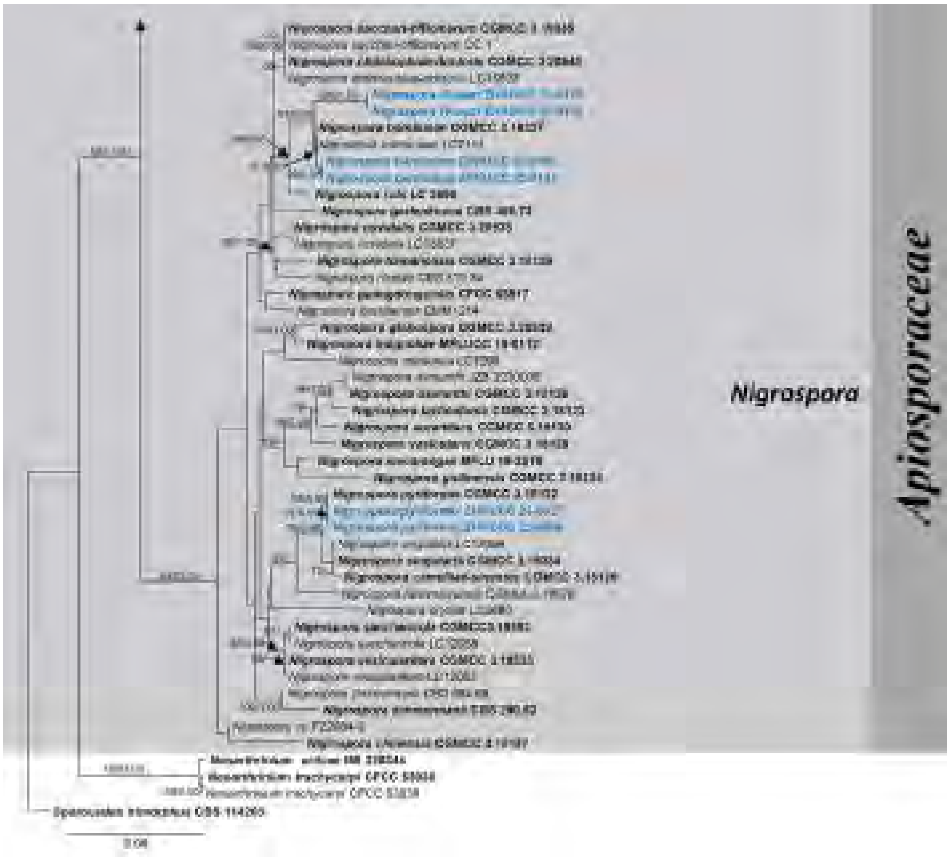


Fig. 117 (continued)

Fig. 118 ***Apiospora cannae*** (MHZU 22-0070, **holotype**). **a** Examined material. **b** Conidial clusters on surface. **c** Upper view of culture on PDA. **d** Reverse view of culture on PDA. **e**–**g** Conidia attached to conidiogenous cells. **h, i** Conidia. Scale bars: e–i = 10 μm

2013). However, *Apiospora piptatheri* comprises hyaline to brown, aggregated or solitary, ampulliform, cylindrical or doliiform conidiophore mother cells and basauxic, polyblastic, sympodial, cylindrical, discrete, short (6–27 µm) conidiogenous cells (Pintos et al. 2019) while our collection (MHZU 22-0070) absence with conidiophore mother cells and conidiophores, holoblastic, monoblastic, cylindrical, long conidiogenous cells (20–25 µm). *Apiospora sacchari* was reported from England, Indonesia, Japan and The Netherlands as saprobes on dead plant stems, soil and air, while *A. piptatheri* has been collected from Mallorca Island, Spain and South Korea from *Sargassum fulvellum* and dead stems of *Piptatherum miliaceum* respectively (Tsukada et al. 2011; Jiang et al. 2018; Elkhateeb et al. 2019; Kwon et al. 2021). Therefore, we introduce our collection as a new species, *Apiospora cannae*.

Apiospora elliptica Senan., ***sp. nov.***

Index Fungorum number: IF900456; *Facesoffungi number*: FoF 14208; Fig. 119

Etymology: based on the ellipsoidal shape of conidia.

Saprobic on dead stem of unidentified plant. **Sexual morph**: Undetermined. **Asexual morph**: *Conidial masses* scattered on substrate as irregular patches. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 15–25 × 2–3 µm ($\bar{x}$ = 22 × 2.3 µm, n = 20), phialidic, cylindrical, hyaline, smooth-walled. *Conidia* 10–15 × 7–10 µm ($\bar{x}$ = 12 × 8 µm, n = 20), fusiform, dark brown, smooth-walled, with a pale equatorial slit.

Culture characteristics: Colonies on PDA reaching 5 cm diam. after 5 days in dark at 25 °C, circular, flat, entire, white, less aerial mycelia, reverse off-white.

Material examined: China, Guangdong Province, Guangzhou City, Danxia Mountain, dead wood of unidentified plant, 20 June 2021, I.C. Senanayake, S2 4 (MHZU 22-0074, **holotype**), ex-type cultures ZHKUCC 22-0132, ZHKUCC 22-0145.

GenBank numbers: ITS: OR164905, OR164906; LSU: OR164952, OR164953; *tef*1-*α*: OR166284; *β-tubulin*: OR166323, OR166324.

Notes: The sequence data of ITS, LSU, *β-tubulin* and *tef*1-α of our collection (MHZU 22-0074) gives species in *Apiospora* as the closest matches with NCBI. The phylogenetic analysis (Fig. 117) showed that our isolate is genetically close, but genetically distinct from *Apiospora agaves* and another new *Apiospora* collection (MHZU 22-0073) obtained in this study forming a clade with ML/BI = 95%/1.00 statistical support. Our collection different from *Apiospora agaves* (MHZU 22-0075) by absence of conidiogenous mother cells and fusiform conidia. The other new collection (MHZU 22-0073) differs by having smooth-walled, fusiform conidia. Therefore, we introduce our collection as a new species, *Apiospora elliptica*.

Apiospora gaoyouensis (C.M. Tian & N. Jiang) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 205 (2021)

Index Fungorum number: IF837671; *Facesoffungi number*: FoF 14206; Fig. 120

Holotype: BJFC S1411

Saprobic, isolated from dead twigs of *Aster* sp. **Sexual morph**: *Ascomata* 100–140 µm high, 98–110 µm diam. ($\bar{x}$ = 126 × 108 µm, n = 10), pycnidia, solitary or paired, scattered, immersed, globose to subglobose, dark brown to black, coriaceous, ostiolate, papillate. *Peridium* 10–15 µm wide, composed of several layers of dark brown cells of

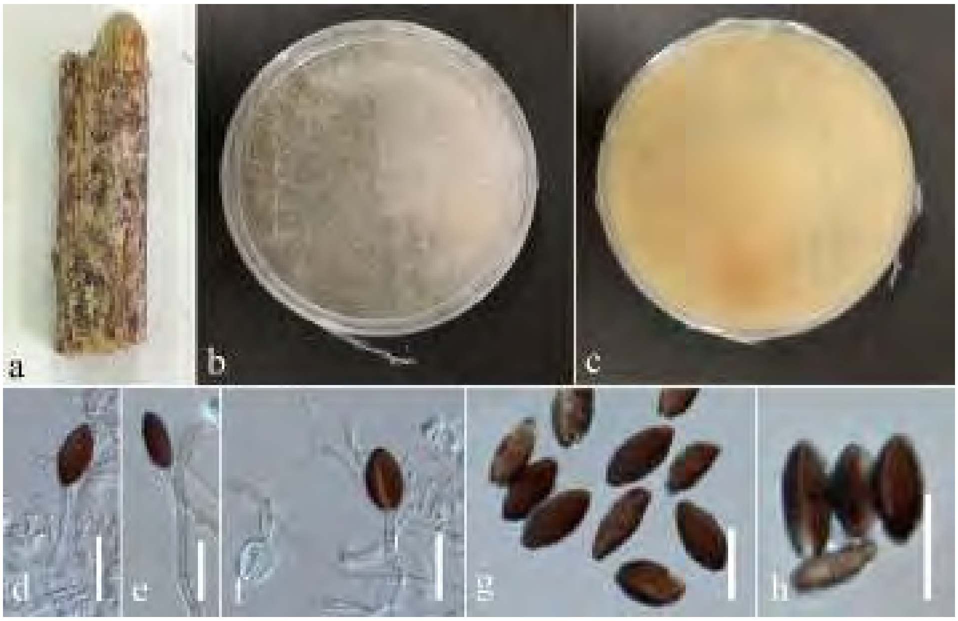


Fig. 119 *Apiospora elliptica* (MHZU 22-0074, **holotype**). **a** Examined material. **b** Surface view of colony. **c** Reverse view of colony. **d**–**f** Conidia attached to conidiogenous cells. **g, h** Conidia. Scale bars: d–h = 15 µm

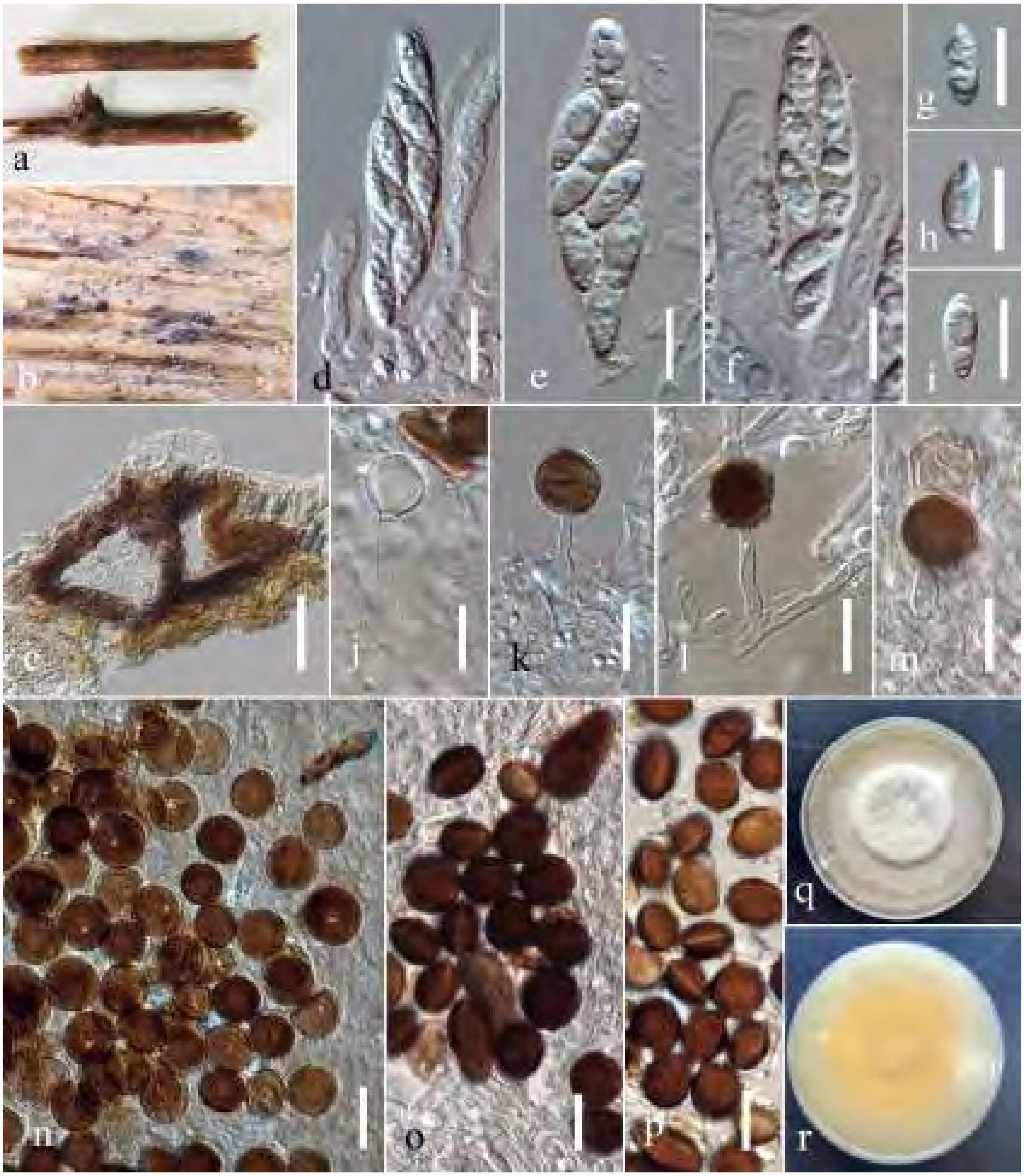


Fig. 120 ***Apiospora gaoyouensis*** (ZKUH 22-0076). **a** Examined material. **b** Ascomata on substrate. **c** Vertical cross section of ascoma. **d**–**f** Asci. **g**–**i** Ascospores. **j**–**m** Conidiogenous cells attached to the conidia. **n**–**p** Conidia. **q** Upper view of culture on PDA. **r** Reverse view of culture on PDA. Scale bars: c = 50 µm, d–i = 20 µm, j–o = 15 µm

textura angularis. *Hamathecium* 4–5 µm wide, comprising dense, hyaline, septate paraphyses. *Asci* 75–90 × 18–22 µm ($\bar{x}$ = 86 × 20 µm, n = 20), 8-spored, unitunicate, clavate to fusiform, apically rounded, with an indistinct pedicel. *Ascospores* 17–22 × 8–11 µm ($\bar{x}$ = 20 × 10 µm, n = 30), overlapping uniseriate to overlapping biseriate, oval to fusiform, obtuse at both ends, slightly wider in the middle, hyaline, 1-septate, non-constricted at the septum, straight, apiosporous, large upper cell with 1–2-guttules, small lower cell mostly aguttulate, smooth-walled, sheath absent. **Asexual morph**: Sporulate on PDA after two weeks, scattered, dark brown conidial masses visible on cultures. *Hyphae* 2–4 µm diam., hyaline, branched, thick-walled, septate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 20–35 × 1.5–2.5 µm ($\bar{x}$ = 25 × 2 µm, n = 25), holoblastic, monoblastic, hyaline, cylindrical, straight, discrete, aseptate, smooth-walled. *Conidia* dimorphic, 10–18 × 10–15 µm ($\bar{x}$ = 11 × 12 µm, n = 20), globose to subglobose, 7–10 × 18–21 µm ($\bar{x}$ = 10 × 20 µm, n = 25), elongated to pyriform, pale to dark brown, smooth-walled, with a longitudinal germ slit, wide pore at the ends of the slit. *Sterile cells* brown, elongated, mixed with conidia.

Culture characteristics: Colonies on PDA reaching 5 cm diam. after 7 days in dark at 25 °C, floccose, circular, edge entire, wooly aerial mycelia at the center, filamentous hyphae at the margin, initially white, becoming black when sporulate, reverse off-white.

Material examined: China, Guangdong Province, Guangzhou City, South China Botanical Garden (23° 11′ 12″ N 113° 21′ 51″ E), dead stem of *Aster* sp. (Asteraceae), 10 August 2021, I.C. Senanayake, S2 10-1 (MHZU 22-0076), living culture ZHKUCC 22-0133.

GenBank numbers: ITS: OR164907; LSU: OR164954; *tef*1-*α*: OR166283; *β-tubulin*: OR166325.

Notes: The sequence data of ITS, LSU, *β-tubulin* and *tef*1-α of our collection (MHZU 22-0076) gives species in *Apiospora* as the closest matches with NCBI. The phylogenetic analysis (Fig. 117) showed that our isolates clustered with type strain of *Apiospora gaoyouense* (CFCC52301, CFCC52302), with MP/BI = 94%/1.00 support. Except the larger size of conidiogenous cells and conidia, our collection (MHZU 22-0076) is similar to *Apiospora gaoyouense* and it was occurred from dead stem of *Aster* sp., while *A. gaoyouense* collected from leaves and culms of *Phragmites australis* from China as a saprobe. Therefore, we identified our collection as *A. gaoyouense* and this is the first report on *Aster* sp. further, we described the sexual morph of *A. gaoyouense* for the first time.

Apiospora pallidesporae Senan., ***sp. nov.***

Index Fungorum number: IF900457; *Facesoffungi number*: FoF 14209; Fig. 121

Etymology: based on the very pale brown conidia.

Saprobic on dead wood of unidentified host. **Sexual morph**: Undetermined. **Asexual morph**: Sporulate on PDA after three weeks, scattered, pale brown spore masses visible on cultures. *Hyphae* 2–3 µm diam., hyaline, branched, thick-walled, septate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 20–35 × 1.5–2.5 µm ($\bar{x}$ = 25 × 2 µm, n = 25), holoblastic, monoblastic, hyaline, cylindrical, straight, discrete, aseptate, smooth-walled. *Conidia* 8–15 × 10–12 µm ($\bar{x}$ = 10 × 10 µm, n = 20), hyaline to pale brown, globose to subglobose, smooth-walled, with a longitudinal germ slit.

Culture characteristics: Colonies on PDA reaching 5 cm diam. after 10 days in dark at 25 °C, floccose, edge entire, initially white, becoming black when sporulate, reverse off-white with black patches due to sporulation.

Material examined: China, Guangdong Province, Shenzhen City, Nanshan District, Mountain Yangtai Forest Park (22° 39′ 21.26″ N 113° 57′ 18.53″ E), dead wood of unidentified host, 15 July 2021, I.C. Senanayake, 98 (MHZU

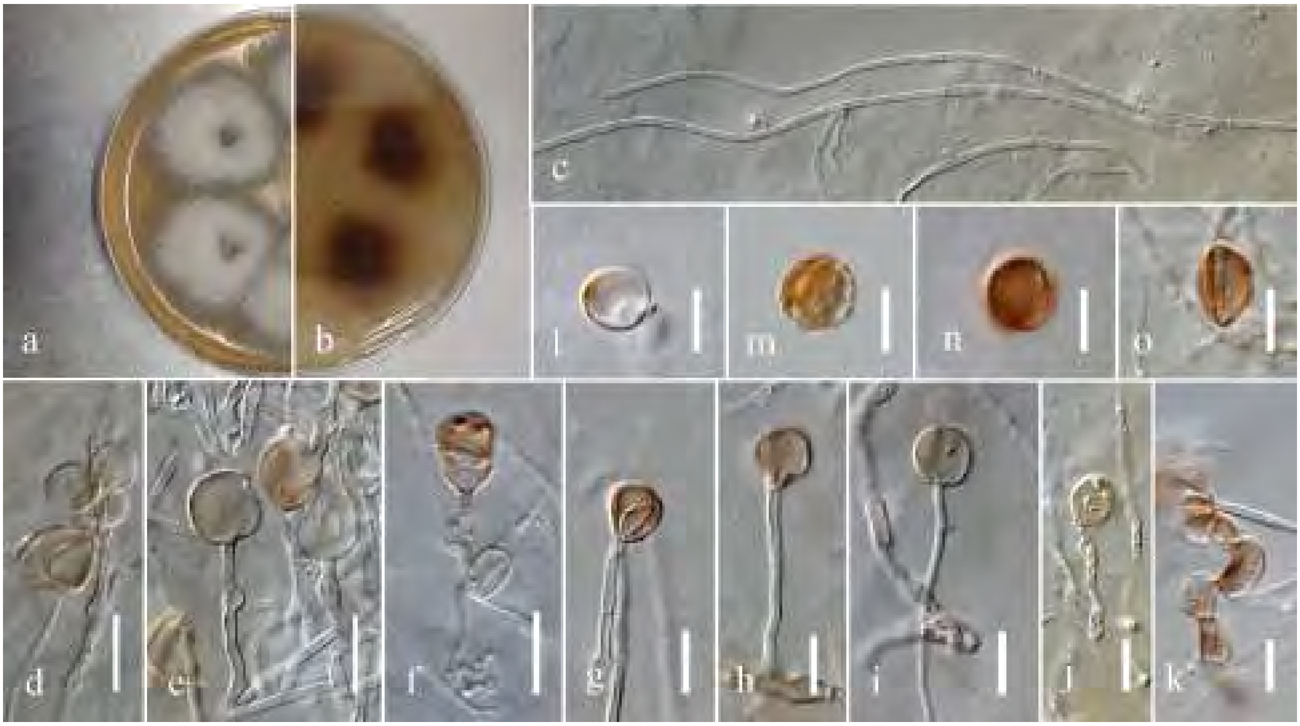


Fig. 121 ***Apiospora pallidesporae*** (ZKUH 22-0072, **holotype**). **a** Upper view of culture on PDA. **b** Reverse view of culture on PDA. **c** Hyphae. **d–j** Conidiogenous cells attached to the conidia. **k** Elongated sterile cells. **l–o** Conidia. Scale bars: d–o = 10 µm

22-0072, **holotype**), ex-type cultures ZHKUCC 22-0129, ZHKUCC 22-0142.

GenBank numbers: ITS: OR164903, OR164904; LSU: OR164950, OR164951.

Notes: The sequence data of ITS, LSU, *β-tubulin* and *tef*1-α of our isolates (ZHKUCC 22-0129, ZHKUCC 22-0142) give species in *Apiospora* as the closest matches with NCBI. The phylogenetic analysis (Fig. 117) showed that our isolates clustered with type strain of *Apiospora jatrophae* (CBS 134262) and *A. mori* (MFLU 18-2514, NCYU 19-0364), but forming a distinct subclade with MP/BI = 99%/1.00 support. Our collection (MHZU 22-0072) is different from *A. mori* by absence of conidiophores, long cylindrical conidiogenous cells and hyaline to pale brown, globose, large ($\bar{x}$ = 10 μm diam.) conidia while *A. mori* distinguishes by aggregated, hyaline to light brown sporodochia, short ($\bar{x}$ = 7 × 2.5 μm), hyaline to pale yellow, subcylindrical to doliiform conidiogenous cells and small ($\bar{x}$ = 5 μm diam.), dark brown conidia (Tennakoon et al. 2021). *Apiospora jatrophae* comprises ampulliform to lageniform conidiophore mother cells, thick-septated conidiophores and small ($\bar{x}$ = 7.5 μm diam.), dark brown conidia as clusters on hyphae (Sharma et al. 2014) while our collection has large ($\bar{x}$ = 10 μm diam.), hyaline to pale brown conidia. *Apiospora jatrophae* and *A. mori* collected from live petiole of *Jatropha podagrica* Hook. from India and dead leaves of *Morus australis* from China (Taiwan region) respectively. Therefore, we introduce this collection (MHZU 22-0072) as a new species, *Apiospora pallidesporae*.

Nigrospora Zimm.

The genus *Nigrospora* was introduced by Zimmerman (1902) for *N. panici*, which was isolated as an endophyte from leaves of *Panicum amphibium* in Indonesia. Species in this genus are cosmopolitan as phytopathogens, endophytes, and saprobes on different hosts including economically important crops (Wang et al. 2017; Hao et al. 2020; Hyde et al. 2020c). Some *Nigrospora* species are opportunistic pathogens causing onychomycosis in humans (de Hoog et al. 2000; Fan et al. 2009) and corneal ulcer (Kindo et al. 2014). There are 39 species listed in Species Fungorum (2023). Morphologically, species of *Nigrospora* are filamentous and dematiaceous taxa can be distinguished from other morphologically similar genera by producing highly pigmented, single conidium from conidiogenous cells (Wang et al. 2017). Species of *Nigrospora* have a great potential in bioactive secondary metabolite production with antileukemic, antileishmanial and antifungal activities (Metwaly et al. 2014).

Nigrospora bambusae Mei Wang & L. Cai, in Wang, Liu, Crous & Cai, Persoonia 39: 127 (2017)

Index Fungorum number: IF820800; *Facesoffungi number*: FoF 14210, Fig. 122

Holotype: HMAS 246696

Saprobic, isolated from leaves of on twigs of *Bambusa multiplex* (Lour.) Raeusch. ex Schult. f. **Sexual morph**: Not observed. **Asexual morph**: Sporulate on PDA after four weeks, dark brown to black spore masses visible on cultures and host substrates. *Hyphae* 2–6 μm diam., initially hyaline, turn to olivaceous to pale brown with time, branched, thick-walled, septate. *Conidiophores* 18–25 × 2–4 μm ($\bar{x}$ = 20 × 3 μm, n = 25), straight, pale brown, aseptate, unbranched. *Conidiogenous cells* 5–10 × 1–2 μm ($\bar{x}$ = 8 × 1.5 μm, n = 25), holoblastic, monoblastic, hyaline, cylindrical, straight, discrete, aseptate, smooth-walled. *Conidia* 8–12 × 10–12 μm ($\bar{x}$ = 10 × 10 μm, n = 20), dark brown, globose to subglobose, smooth-walled, with one or more longitudinal germ slits.

Culture characteristics: Colonies on PDA reaching 5 cm diam. after 5 days in dark at 20 °C, floccose, edge entire, initially white, becoming black when sporulate, reverse off-white with black patches due to sporulation.

Material examined: Thailand, Chiang Mai Province, Chiang Dao Mountain, leaves of *Bambusa multiplex* (Poaceae), 17 Febuary 2019, I.C. Senanayake, 46 (MHZU 22-0069), living cultures ZHKUCC 22-0126, ZHKUCC 22-0144.

Hosts and distribution: on bamboo leaves in China (Guangdong Province, Jiangxi Province) (Wang et al. 2017); on leaves of *Bambusa multiplex* in Thailand (this study)

GenBank numbers: ITS: OR164908, OR164909; LSU: OR164955, OR164956; *tef*1-α: OR166287; *β-tubulin*: OR166319, OR166320.

Notes: The sequence data of ITS, LSU, *β-tubulin* and *tef*1-α of our collection (MHZU 22-0069) gives species in *Nigrospora* as the closest matches with NCBI. The phylogenetic analysis (Fig. 117) showed that our collection is grouped with *Nigrospora bambusae* forming a clade with MP/BI = 91%/0.95 statistical support. Our collection MHZU 22-0069 is morphologically similar to holotype of *Nigrospora bambusae* (Wang et al. 2017). Our collection obtained from Thailand on bamboo leaves. This is the first report of *Nigrospora bambusae* in Thailand.

Nigrospora ficuum Senan., ***sp. nov.***

Index Fungorum number: IF900458; *Facesoffungi number*: FoF 14211; Fig. 123

Etymology: based on the host genus *Ficus*.

Saprobic, isolated from dead twigs of *Ficus* sp. **Sexual morph**: Not observed. **Asexual morph**: Sporulate on PDA after four weeks, dark brown to black spore masses visible on cultures and host substrates. *Hyphae* 2–6 μm diam., initially hyaline, turn to olivaceous to pale brown with time, branched, thick-walled, septate. *Conidiophores* 18–25 × 2–4 μm ($\bar{x}$ = 20 × 3 μm, n = 25), straight, pale brown, aseptate, unbranched. *Conidiogenous cells*

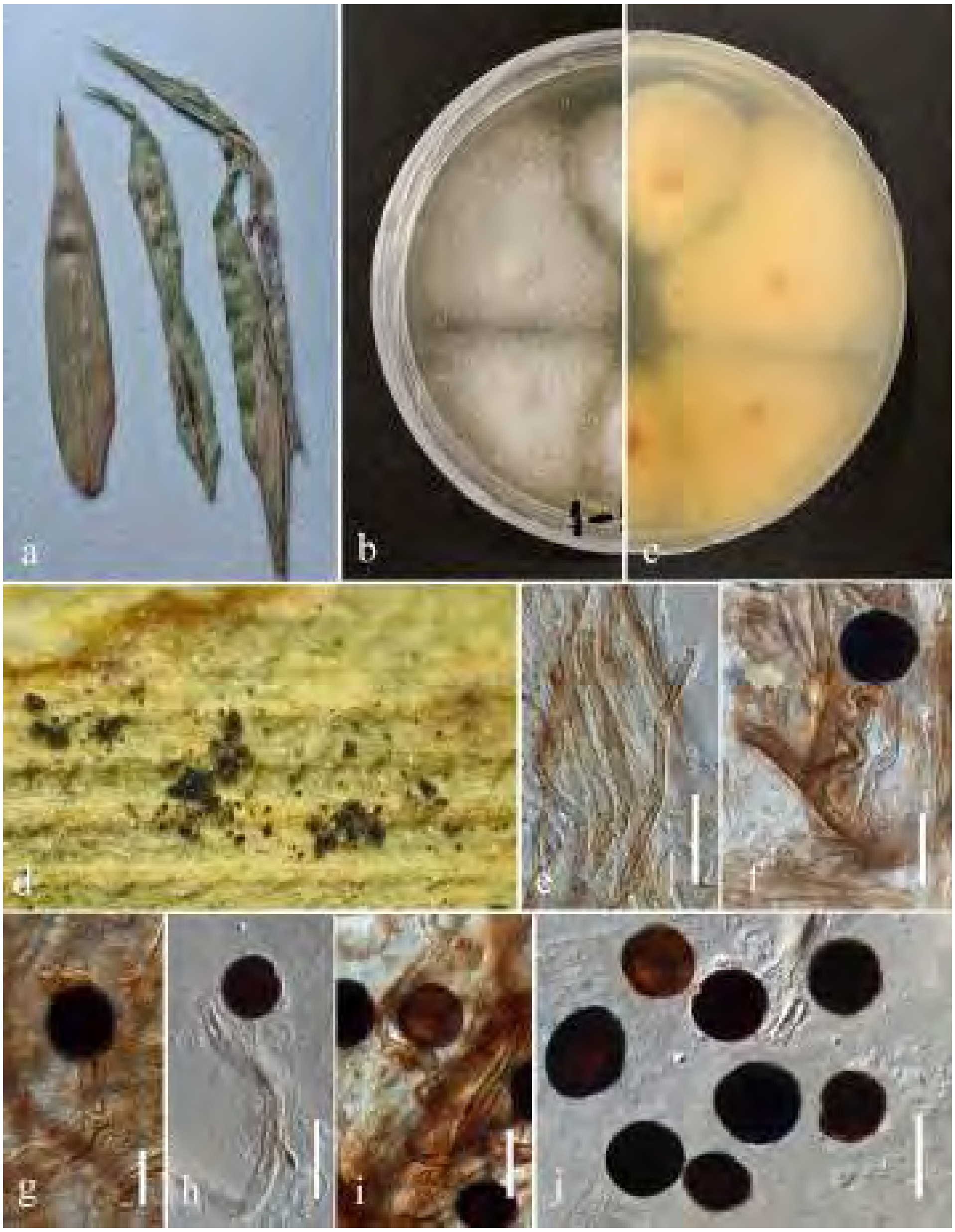


Fig. 122 ***Nigrospora bambusae*** (ZKUH 22-0069). **a** Herbarium specimen. **b** Upper view of culture on PDA. **c** Reverse view of culture on PDA. **d** Conidial mass on substrate. **e** Hyphae. **f–i** Conidiogenous cells attached to the conidia. **j** Conidia. Scale bars: e–j = 10 µm

5–10 × 1–2 µm ($\bar{x}$ = 8 × 1.5 µm, n = 25), holoblastic, monoblastic, hyaline, cylindrical, straight, discrete, aseptate, smooth-walled. *Conidia* 8–12 × 10–12 µm ($\bar{x}$ = 10 × 10 µm, n = 20), dark brown, globose to subglobose, smooth-walled, with a longitudinal germ slit.

Culture characteristics: Colonies on PDA reaching 5 cm diam. after 5 days in dark at 20 °C, floccose, edge entire, initially white, becoming black when sporulate, reverse off-white with black patches due to sporulation.

Material examined: China, Guangdong Province, Guangzhou City, Baiyun Mountain (23° 09′ 35″ N 113° 17′ 40″ E), dead twigs of *Ficus* sp., 23 September 2021, I.C. Senanayake, 14 (MHZU 22-0068, **holotype**), ex-type cultures ZHKUCC 22-0125, ZHKUCC 22-0143.

GenBank numbers: ITS: OR164910, OR164911; *β-tubulin*: OR166317, OR166318.

Notes: The sequence data of ITS, LSU, *β-tubulin* and *tef*1-α of our collection (MHZU 22-0068) gives species in *Nigrospora* as the closest matches with NCBI. The phylogenetic analysis (Fig. 117) showed that our collection is genetically close to *N. bambusae*, but genetically distinct forming a clade with MP/BI = 91%/0.90 statistical support. Morphologically, our collection is different from *N. bambusae* by cylindrical, solitary conidiogenous cells and small conidia while *N. bambusae* has globose to ampulliform conidiogenous cells aggregated in clusters on hyphae and large conidia (Wang et al. 2017). Therefore, we introduce our collection as a new species, *Nigrospora ficuum*.

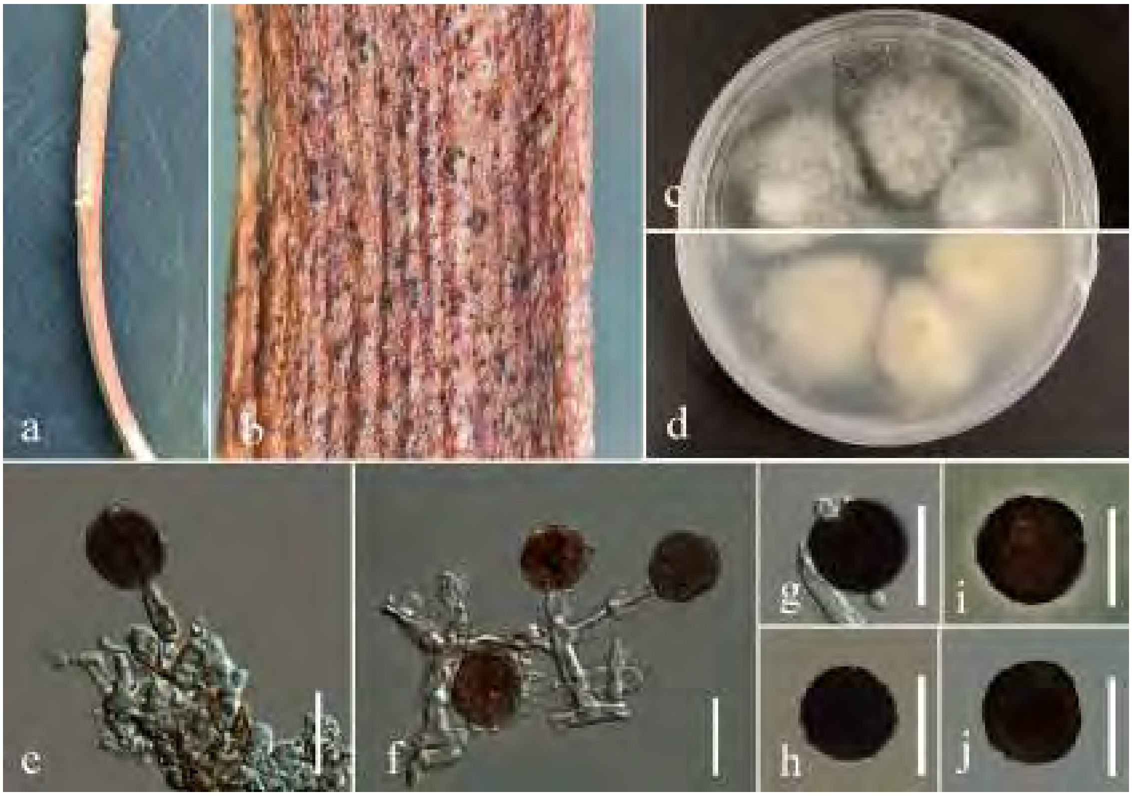


Fig. 123 ***Nigrospora ficuum*** (ZKUH 22-0068, **holotype**). **a** examined Specimen. **b** Conidial mass on substrate. **c** Upper view of culture on PDA. **d** Reverse view of culture on PDA. **e–f** Conidiogenous cells attached to the conidia. **g–j** Conidia. Scale bars: e–j = 10 µm

Nigrospora pyriformis Mei Wang & L. Cai, in Wang, Liu, Crous & Cai, Persoonia 39: 136 (2017)

Index Fungorum number: IF820737; *Facesoffungi number*: FoF 14212; Fig. 124

Holotype: HMAS 247067

Endophytic, isolated from leaves of *Clematis chinensis* Osbeck. **Sexual morph**: Not observed. **Asexual morph**: Sporulate on PDA, after 8 weeks of incubation in dark at 25 °C. *Hyphae* branched, septate, hyaline to pale brown, thick-walled. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–8 × 2–3 µm ($\overline{x}$ = 7.2 × 2.5 µm, n = 15), monoblastic, discrete, solitary, determinate, ampulliform or subcylindrical, olivaceous to pale brown. *Conidia* appear as brown to black clusters on PDA, 14–17 µm diam. ($\overline{x}$ = 15 µm, n = 30), initially pale brown, become black when mature, globose to subglobose, black, shiny, smooth, aseptate, 1–2-guttulate, with truncated basal scars, occasionally with a longitudinal germ slit.

Culture characteristics: Colonies on PDA reaching 6 cm diam. after 3 days in dark at 20 °C, circular, smooth, flat, woolly at the center, thinning towards the margin, floccose, white; reverse: white to off white, no pigments produced.

Material examined: China, Guangdong Province, Guangzhou City, Baiyun Mountain (23° 09′ 35″ N 113° 17′ 40″ E), from leaves of *Clematis chinensis* (Ranunculaceae), 16 August 2021, Li Hua, LH 60, (MHZU 23-0007), living cultures ZHKUCC 23-0026, ZHKUCC 23-0027.

Hosts and distribution: China, Jiangxi Province, on leaves of *Citrus reticulata* Blanco, on *Camellia sinensis* (L.) Kuntze, on *Lindera aggregate* (Sims) Kosterm., on *Rubus reflexus* Ker Gawl., on *Castanopsis* sp., on *Rosa* sp.; Hainan Province, on leaves of *Musa paradisiaca* (L.).

GenBank numbers: ITS: OQ971751, OQ971752; *tef*1-α: OR046689, OR046689.

Note: *Nigrospora pyriformis* was introduced by Wang et al. (2017) from Jiangxi Province, China on leaves of *Citrus reticulate*. The distinguish character of this species is dimorphic conidia viz. pyriform or globose to subglobose. The closest matches of our isolates (ZHKUCC 23-0026, ZHKUCC 23-0027) with NCBIs give *Nigrospora pyriformis* for ITS, *β-tubulin* and *tef1-α*. Combined gene analysis of ITS, LSU, *β-tubulin* and *tef1-α* (Fig. 117) shows that, our isolates (ZHKUCC 23-0026, ZHKUCC 23-0027) clusters with *Nigrospora pyriformis* strains with ML/BI = 98%/0.90 statistical support. Morphologically, our collection is similar to holotype of *Nigrospora pyriformis*. However, we could not observe pyriform conidia from our collection and it is suggested that pyriform conidia are occasionally formed. The hyphal thinning

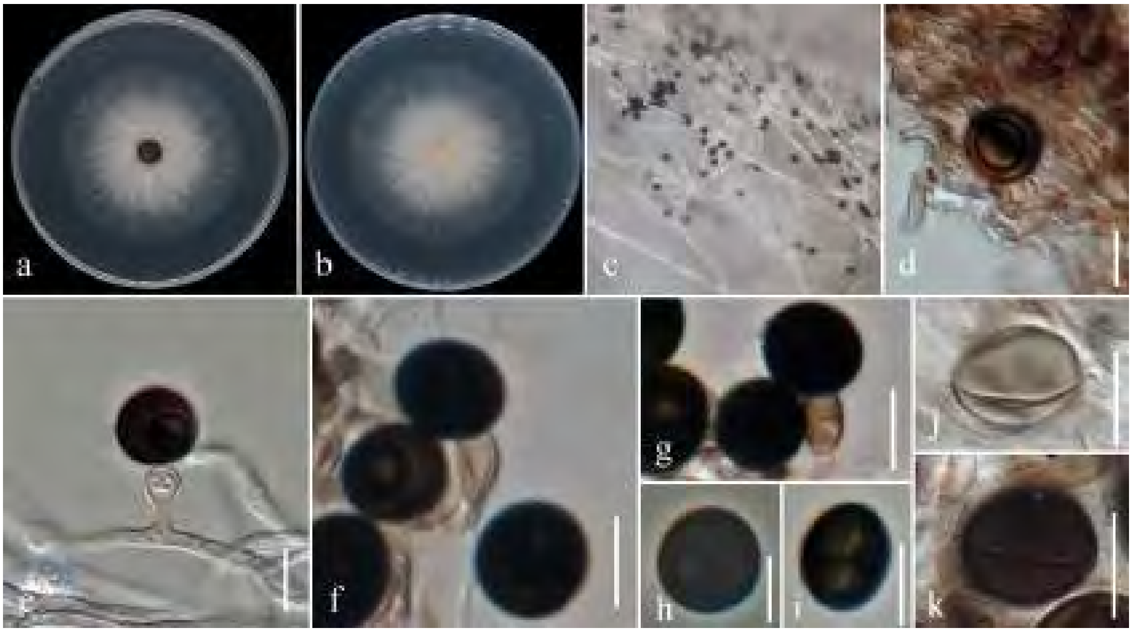


Fig. 124 ***Nigrospora pyriformis*** (ZHKUCC 23-0026). **a** Colonies from above on PDA. **b** Colonies from below on PDA. **c** Conidial mass forming on culture. **d**–**g** Conidia attached to conidiogenous cells. **h**–**k** Conidia. Scale bars: d–k = 10 µm

towards the margin can occur in our colonies which absent in ex-type cultures.

Xylariales Nannf.

Xylariales is a specious order in the class Sordariomycetes (Maharachchikumbura et al. 2016; Hyde et al. 2020b). Currently, 148 genera (Wijayawardene et al. 2020) are accepted in Xylariales, which are distributed in 22 families and 12 families incertae sedis. This order comprises morphologically diversified taxa and different studies have been revised this order providing monographs, checklists and keys along with detailed descriptions and illustrations (Miller 1961; Lowen 1991; Petrini 2013; Stadler et al. 2014; Shang et al. 2018; Niranjan and Sarma 2020; Hyde et al. 2020a).

Cainiaceae J.C. Krug

Cainiaceae was introduced by Krug (1978) to include *Cainia* and cainia-like species with a unique series of apical rings in the asci and ascospores with longitudinal germ slits (Senanayake et al. 2015). An asexual morph of Cainiaceae was coelomycetous with black, scattered, immersed pycnidial conidiomata; hyaline, denticulate, sympodially proliferating conidiophores; hyaline, filiform, branched or simple, septate conidiogenous cells with one to three phialides; and hyaline, elongate fusiform, falcate to lunate, unicellular or septate conidia, with pointed ends (Maharachchikumbura et al. 2016). There are eight genera in this family viz. *Alishanica*, *Amphibambusa*, *Arecophila*, *Atrotorquata*, *Cainia*, *Endocalyx Longiappendispora*, and *Seynesia* (Hyde et al. 2020a; Mapook et al. 2020). Most members in this family are found on monocotyledons, including grasses (Senanayake et al. 2015).

Endocalyx Berk. & Broome

Endocalyx was introduced and typified by *E. thwaitesii* Berk. & Broome (= *E. psilostoma* Berk. & Broome) which was described based on the dead leaves of *Oncosperma* sp. (Arecaceae) from Sri Lanka (Berkeley and Broome 1877). The genus *Endocalyx* is characterized by sporodochial or synnematous, funnel-shaped, cupulate, cylindrical to pancake-shaped conidiomata arising from an annulus and containing a mass of conidia that is enclosed by yellow or brown sterile peridial hyphae (Petch 1908; Hughes 1953; Morris 1963; Ellis 1971; Okada and Tubaki 1984; Seifert et al. 2011; Delgado et al. 2022). Konta et al. (2021) transferred *Endocalyx* to Cainiaceae (Xylariales) based on multigene phylogenetic analyses. There are 11 species listed under *Endocalyx* in Species Fungorum (2023). We introduced a new species in this study.

Endocalyx phoenicis Senan. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900459; *Facesofungi number*: FoF 14214; Fig. 125

Etymology: Refers to the name of the host genus, *Phoenix*.

Saprobic on dead petioles of *Phoenix roebelenii* O'Brien. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 230–250 µm diam., 250–270 µm high, scattered or aggregated, emerging from annulus-like, black, circular pustules, short, cylindrical or cup-shaped, reaching up to 100 mm high, well-developed, consisting of dark brown, conidial mass enclosed by greenish yellow, mass of sterile peridial hyphae. *Sterile peridial hyphae* grow upwards surrounding the conidial column, hyaline to olivaceous, ends bulbous with greenish yellow, globose bulbs. *Conidiomata wall* 60–70 µm wide, thick, comprising dark brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cell. *Conidiogenous cells* 15–20 × 1.5–2.5 µm long ($\bar{x}$ = 18 × 2 µm, n = 20), holoblastic, monoblastic, integrated, terminal, cylindrical, flexuous, hyaline, septate, smooth. *Conidia* 10–15 × 8–10 µm ($\bar{x}$ = 13 × 10 µm, n = 30), globose to subglobose, unicellular, dark brown, with a paler equatorial germ slit, thick-walled, smooth to finely roughened, often with a central attachment scar.

Culture characteristics: Colonies on PDA reaching 6 cm diam., after seven days at 25 °C, white at first, irregular, raised, undulate, rough, after maturity, smooth at the margin, white from above, pale-brown from below.

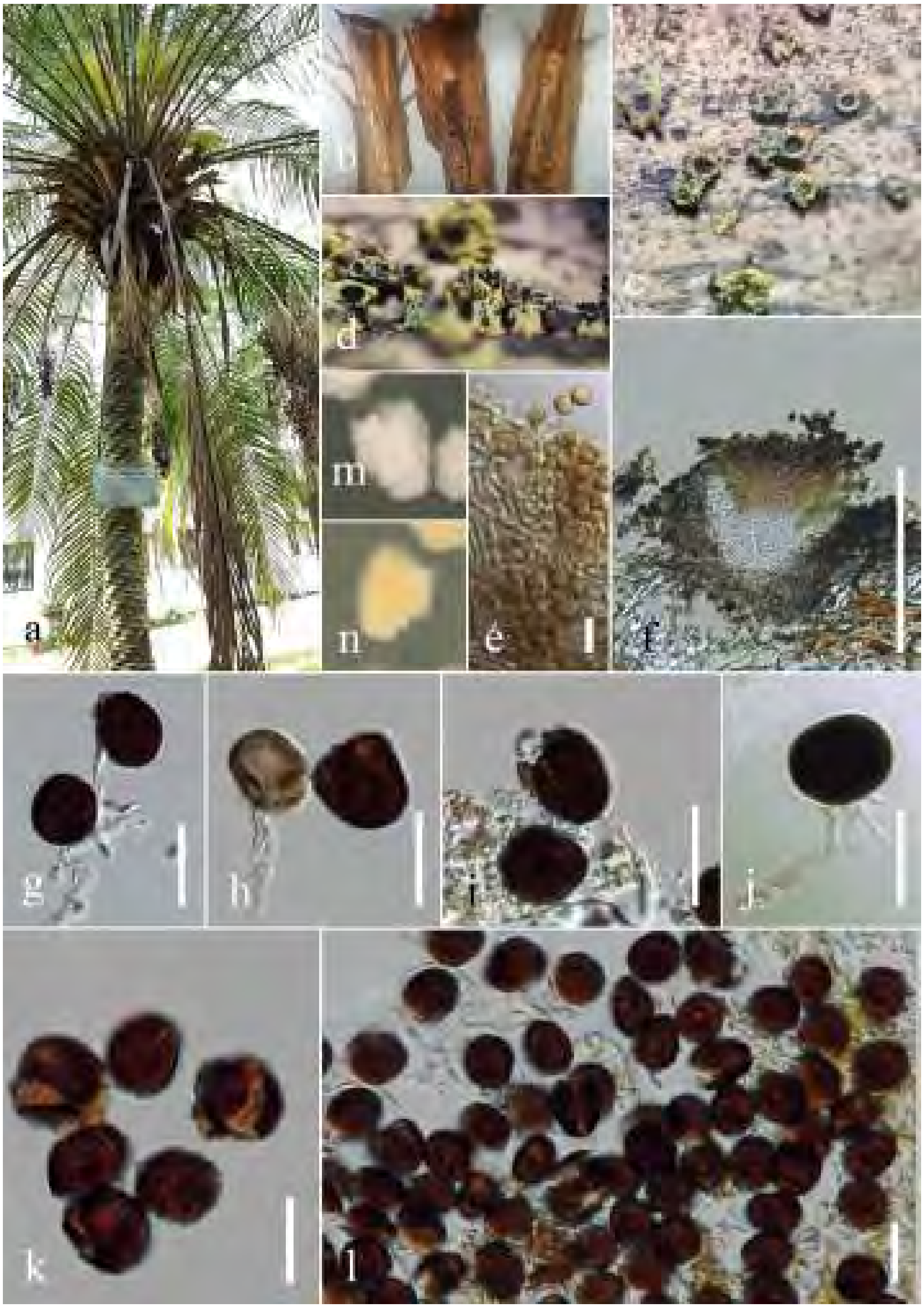


Fig. 125 ***Endocalyx phoenicis*** (MHZU 22-0078, **holotype**). **a** Host. **b** Examined material. **c** Lateral view of conidiomata. **d** Upper view of conidiomata on the natural substrate. **e** Cross section of conidioma. **f** Sterile peridial hyphae. **g–j** Conidiogenous cells attached to conidia. **k, l** Conidia. Scale bars: e = 300 µm, f–l = 15 µm

Material examined: China, Guangdong Province, Shenzhen City, Futian District, northwest of Futian, Bijiashan Park, on dead petioles of *Phoenix roebelenii* (Arecaceae), 8 June 2020, I.C. Senanayake, SI 2-2 (MHZU 22-0078, **holotype**), ex-type cultures ZHKUCC 22-0135, ZHKUCC 22-0128.

GenBank numbers: ITS: OR164914, OR164915.

Notes: The sequence data of ITS, and LSU of our isolate (ZHKUCC 22-0135) gives species in *Endocalyx* as the closest matches with NCBI. The phylogenetic analysis (Fig. 126) showed that our isolate grouped with *E. ptychospermatis* Y.R. Xiong, Manawas & K.D. Hyde and *E. melanoxanthus* (Berk. & Broome) Petch, but distinct from them forming a separate subclade with MP/BI = 93%/1.00 support. Comparison of the sequence of ITS, and LSU locus of our isolate (ZHKUCC 22-0135) with strains of *E. ptychospermatis* and *E. melanoxanthus* revealed the base pair differences of 1.02%, 5.66%, 0.34% and 2.51% respectively. Our collection (MHZU 22-0078) is morphologically different from *E. melanoxanthus* by absence of conidiophores, smooth-walled conidiogenous cells and only globose to sub-globose-shaped conidia while *E. melanoxanthus* comprises anastomosing, micronematous, filiform conidiophores, minutely denticulate conidiogenous cells with intercalary conidiogenesis, conidia with broadly ellipsoidal, slightly polygonal and fattened in front view and ellipsoidal, lenticular or rarely oblong in lateral view. *Endocalyx ptychospermatis* has wider (470–520 μm diam.) conidiomata and elliptical to closed polygonal conidia with verrucous inclusions and our collection has narrowed (230–250 μm diam.) conidiomata with globose to sub-globose conidia. Most species in *Endocalyx* are reported from Arecaceae plants as saprobes. Therefore, ecological and life mode data are uninformative for species identification. We introduce our collection as a new species, *Endocalyx phoenicis*.

Diatrypaceae Nitschke

Diatrypaceae was introduced by Nitschke (1869) with *Diatrype* as the type. The family comprises 22 genera which are included in more than 1500 species (Wijayawardene et al. 2022). The taxa occur worldwide in both aquatic and terrestrial habitats (Konta et al. 2020). Members of this family have been recorded mainly as saprobes also have been recorded as pathogens or endophytes (Shang et al. 2017; Thiyagaraja et al. 2019; Konta et al. 2020; Dissanayake et al. 2021). The sexual morph is characterized by erumpent to immersed, rarely superficial, eustromatic or pseudostromatic stromata, perithecial ascomata, 8 to polyspored asci with long pedicillate and allantoid ascospores (Shang et al. 2017; Dissanayake et al. 2021). The asexual morph is reported as coelomycetous or hyphomycetous states (Shang et al. 2017). The morphology provides less resolution for the taxonomy of Diatrypaceae due to overlapping phenotypic characters (Zhu et al. 2021). Combined ITS and *β-tubulin* sequences data have been commonly used in the classification. However, the placement of several genera remains unresolved and needs further studies (Shang et al. 2017; Konta et al. 2020).

Allocryptovalsa Senwanna, Phookamsak & K.D. Hyde

Allocryptovalsa (Valsaceae, Diaporthales) was introduced and typified by *A. polyspora* Senwanna, Phookamsak & K.D. Hyde (Senwanna et al. 2017). Meanwhile, Senwanna et al. (2017) accommodated *Eutypella cryptovalsoidea* and *Cryptovalsa rabenhorstii* in *Allocryptovalsa* based on morphological and phylogenetic analysis. This genus is distinct by immersed stromata, polysporous asci and allantoid ascospores and asexual morph having hyaline, elongate-allantoid conidia (Senwanna et al. 2017; Zhu et al. 2021). There are eight species in Index Fungorum (2023).

Most species in *Allocryptovalsa* are saprobes on dead wood, dead petiole or lignified canes of *Vitis vinifera* on the ground (Trouillas et al. 2011; Senwanna et al. 2017; Hyde et al. 2020a; Konta et al. 2020; Zhu et al. 2021). *Allocryptovalsa* occurs on *Castanea mollissima* Blume, *Elaeis guineensis* Jacq., *Ficus carica* L., *Hevea brasiliensis* (Willd. ex A. Juss.) Muell. Arg., *Sambuscus nigra* L. and *Vitis vinifera* L., from America, Australia, China, India and Thailand (Trouillas et al. 2011; Senwanna et al. 2017; Hyde et al. 2020a; Konta et al. 2020; Zhu et al. 2021). Phylogenetically, *Allocryptovalsa* and *Eutypella* are closely related but differ by having polysporous asci, while *Eutypella* has 8-spored asci (Senwanna et al. 2017). *Allocryptovalsa* species are major decomposers that degrade dead organic materials. We introduce a new species in this genus.

Allocryptovalsa aceris T.Y. Du & Tibpromma, ***sp. nov.***

Index Fungorum number: IF558765; *Facesoffungi number*: FoF 10261, Figs. 127, 128

Etymology: based on the host genus, *Acer*.

Saprobic on dead twigs of *Acer palmatum* Thunb. **Sexual morph**: *Ascostromata* gregarious, obviously, 3–11-ascomata, raised, immersed to semi-immersed, becoming erumpent through the host tissue, the surrounding host tissue obviously black. *Ascomata* (including neck) 500–660 μm high × 230–380 μm diam. ($\bar{x}$ = 558 × 310 μm, n = 10), perithecial, gregarious, immersed in the stroma, obovoid to ellipsoid, coriaceous, dark brown to black, wrapped in white entostroma, ostiolate, papillate. *Ostiolar canal* 160–260 μm high × 95–200 μm diam. ($\bar{x}$ = 224 × 172 μm, n = 10), central, not protruding or protruding a little from the substrate, cylindrical, straight, dark brown to black, periphysate. *Peridium* 18–45 μm wide, composed of two type layers, outer layer comprised of several layers of thick-walled, dark brown to black cells of *textura angularis*, which are not fully fused

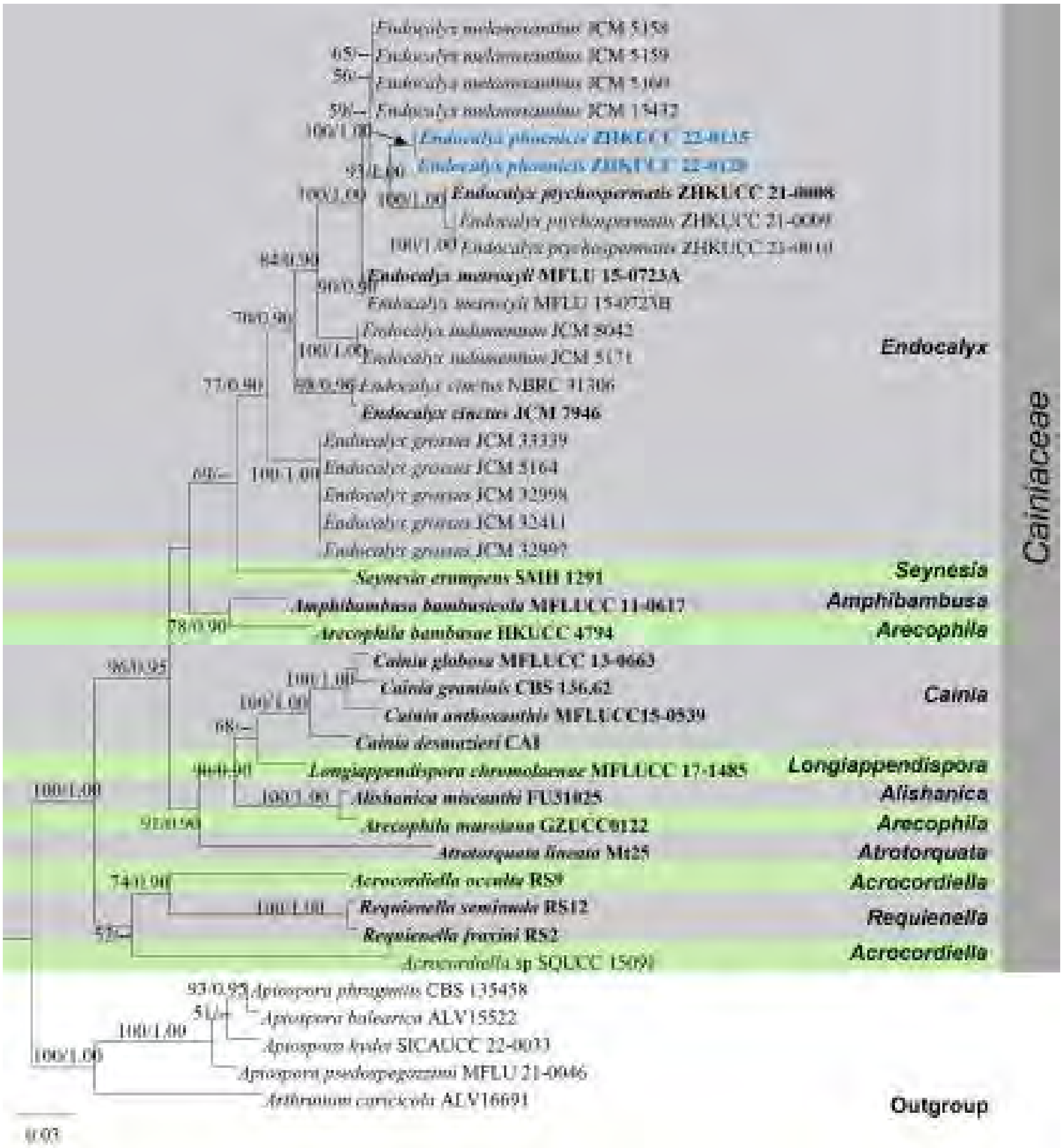


Fig. 126 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of 40 taxa, which comprised 1514 characters (ITS = 635 bp, LSU = 879 bp). The best scoring RAxML tree with a final likelihood value of − 8357.252007 is presented. The matrix had 582 distinct alignment patterns, with 14.19% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.250270, C = 0.238774, G = 0.272133, T = 0.238823; substitution rates: AC = 1.344249, AG = 1.787142, AT = 1.867513, CG = 1.324573, CT = 4.906484, GT = 1.0; gamma distribution shape parameter α = 0.225328. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (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 blue bold. The tree is rooted to *Arthrinium caricicola* (ALV16691)

with the host tissue; inner layer comprising 3–5 layers of thin-walled, hyaline cells of *textura angularis*. *Hamathecium* 2–4 µm wide, comprise few, granulate, filamentous, unbranched, septate, hyaline paraphyses, slightly constricted at the septa, tapering towards the apex. *Asci* (90–)100–145(–170) × (15–)16–24 µm ($\bar{x}$ = 116 × 18.6 µm, n = 10), spore-bearing part length (48–)55–100(− 121) µm ($\bar{x}$ = 75 µm, n = 20), polysporous, unitunicate, thin-walled, clavate, with long and fragile pedicellate, apically rounded, narrowing towards lower region. *Ascospores* 9–14 × 2–4 µm ($\bar{x}$ = 12 × 2.8 µm, n = 30), crowded, oblong to allantoid, pale yellowish at maturity, aseptate, slightly curved, smooth-walled, granules, without appendages and mucilaginous sheath. **Asexual morph**: Undetermined.

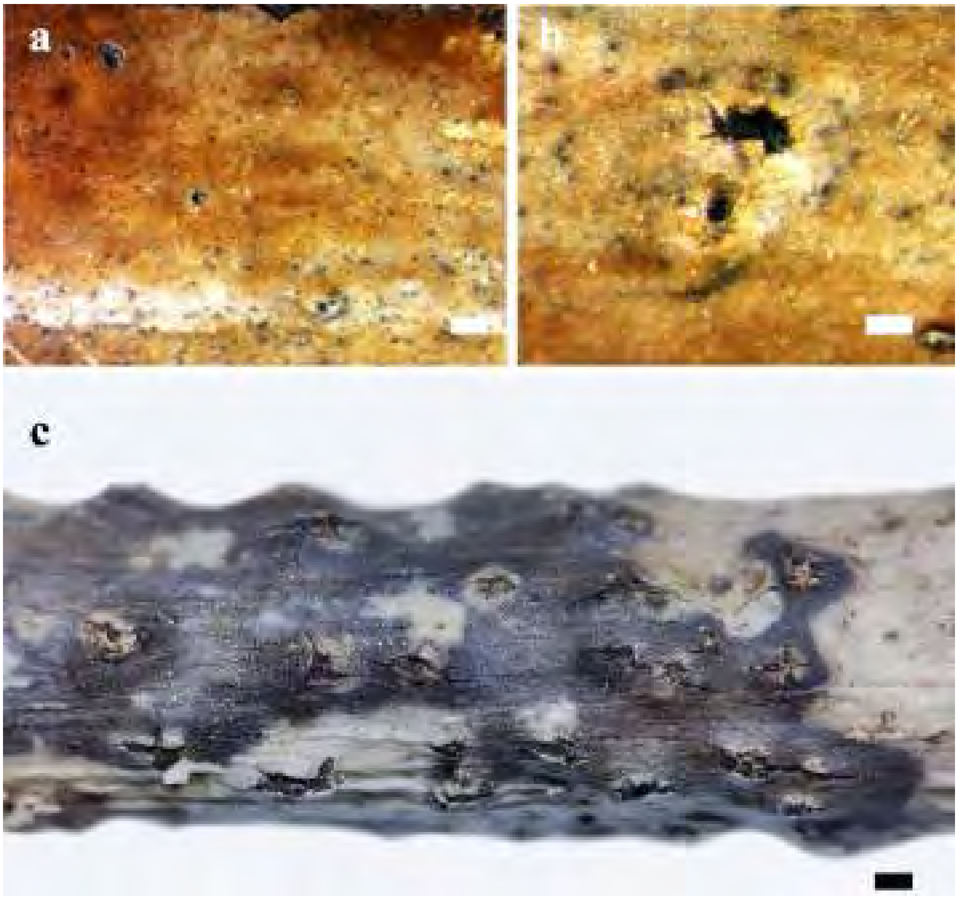


Fig. 127 Comparation of ascostromata on the host. **a, b** *Allocryptovalsa elaeidis* (MFLU 15-1438). **c** *Allocryptovalsa aceris* (HKAS 121126). Scale bars: a, c = 500 µm, b = 200 µm

Culture characteristics: Colonies on PDA reaching 4 cm diam., after 4 days at room temperature (20–25 ℃), flattened, filamentous, filiform margin, with white aerial mycelia; reverse white, smooth, not produced pigments in culture, not sporulate in the culture.

Material examined: China, Yunnan Province, Kunming City, Kunming Botanical Garden, 25° 8′ 30″ N 102° 44′ 16″ E, live on dead twigs of *Acer palmatum* (Aceraceae), 19 March 2021, S. Tibpromma, KMD20, (HKAS 121126, **holotype**), ex-type culture, KUMCC 21-0085.

GenBank numbers: ITS: MZ727001, *β-tubulin*: OK043823

Notes: Our collection (HKAS 121126) clusters with *Allocryptovalsa elaeidis* (MFLUCC 15-0707) in the combined ITS and *β-tubulin* gene analysis (Fig. 129). The nucleotide comparison of ITS region of our collection with *A. elaeidis* gives two base pair difference, and the *β-tubulin* fragments of our collection is identical to *A. elaeidis*. However, morphological characters showed that our collection differs from *A. elaeidis* by 3–11-gregarious ascomata in black ascostromata, the surrounding host tissue, while *A. elaeidis* has 1–2-ascomata in ascostromata mostly solitary, surrounded by black circle on host surface (Figs. 127, 128) (Konta et al. 2020). Therefore, we introduce our collection as a novel species, *Allocryptovalsa aceris* and it is the first *Allocryptovalsa* species collected from *Acer palmatum*.

Neoeutypella M. Raza, Q.J. Shang, Phookamsak & L. Cai

The monotypic genus *Neoeutypella* was introduced for a saprobic species *N. baoshanensis*. The taxon was recorded on dead wood of *Pinus armandii* from China (Phookamsak et al. 2019). The genus is characterized by immersed to semi-immersed perithecial ascostromata, multilayered inner and outer wall, spindle-shaped, long pedicellate with amyloid J+, subapical ring, allantoid ascospores. The asexual morph produces long, branched conidiophore, holoblastic, discrete, phialidic, doliiform conidiogenous cells with filiform, aseptate conidia (Phookamsak et al. 2019). We introduce a new host record of *N. baoshanensis*.

Neoeutypella baoshanensis M. Raza, Q.J. Shang, Phookamsak & L. Cai, in Phookamsak et al., Fungal Diversity: https://doi.org/10.1007/s13225-019-00421-w, [168] (2019)

Index Fungorum number: IF 555372; *Facesoffungi number*: FoF 04928; Fig. 130

Saprobic on dead wood of *Robinia pseudoacacia* L. **Sexual morph**: *Ascomstromata* 200–300 µm diam., carbonaceous, black, solitary to gregarious, globose to long

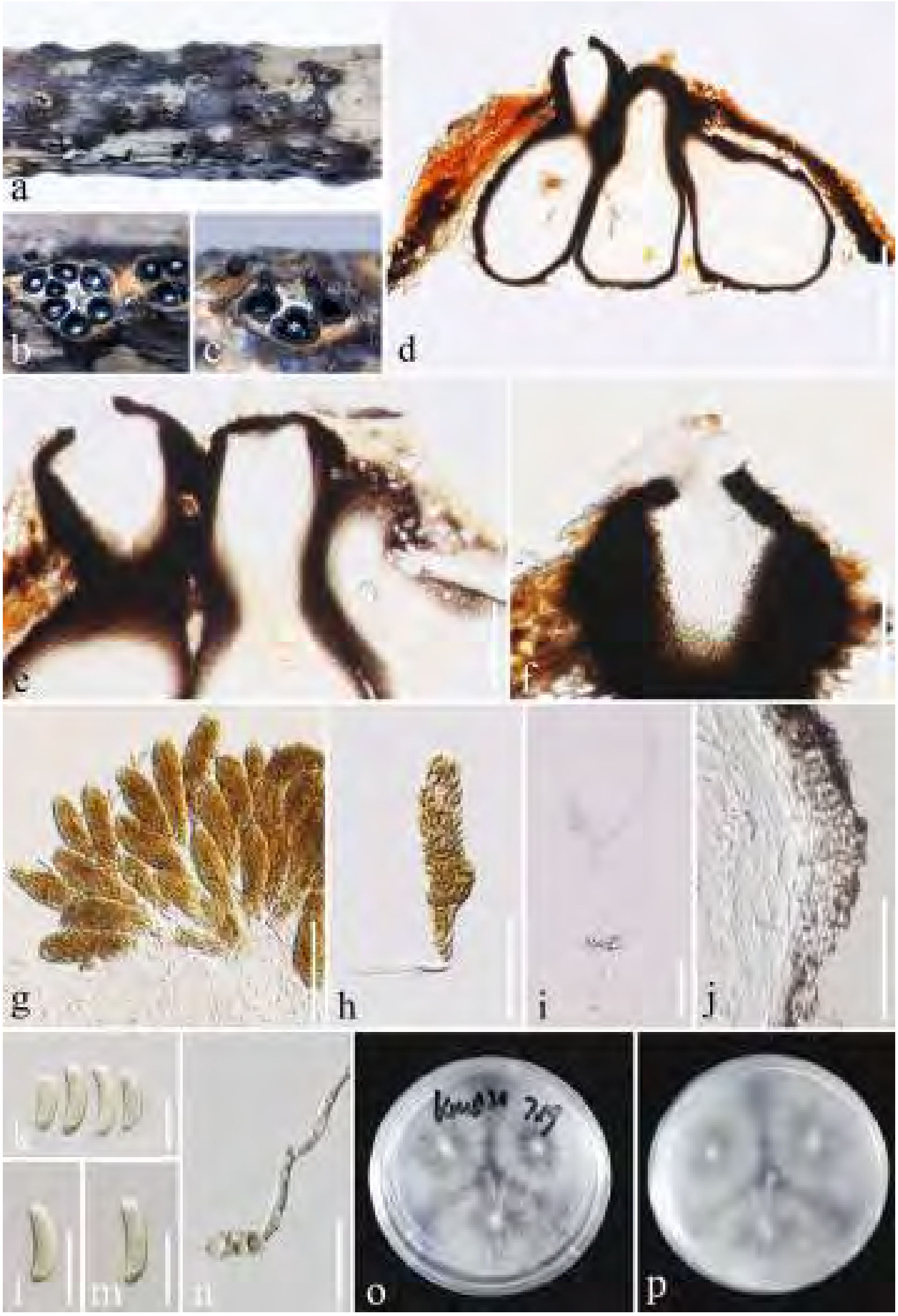


Fig. 128 ***Allocryptovalsa aceris*** (HKAS 121126, **holotype**). **a** Appearance of ascostromata on the host. **b** Transverse sections through ascostroma. **c, d** Section through the ascostroma. **e** Ostiolate. **f** Ostiolate with periphysate. **g, h** Asci. **i** Paraphyses. **j** Peridium. **k–m** Ascospores. **n** Germinated ascospore. **o, p** Culture characteristic on PDA after 4 days (o = colony in front, p = colony in reverse). Scale bars: d = 300 µm, e, f = 100 µm, g–j = 50 µm, k–m = 10 µm, n = 20 µm

irregular in shape on host surface, erumpent through host epidermis. *Ascomata* perithecial 500–770 µm high, 450–530 µm diam., black, immersed to semi-immersed, solitary to aggregated, globose or subglobose, ostiolate. *Ostiole* distinct, papillate, slightly conspicuous, filled with periphyses. *Peridium* 145–250 µm wide, thickened, composed of two layers; outer layer unequally thicken, brown to dark brown cells of *textura angularis*; inner layer thin-walled, hyaline to brown cells of *textura prismatica*. *Hamathecium* comprising filamentous paraphyses and asci. *Paraphyes* 0.6–2 µm thickness, numerous, anastomosing, not branched, aseptate, hyaline, filamentous, generally exceeding the length of asci. *Asci* 60–80 × 10–24 µm ($\bar{x} = 70 \times 17$ µm, n = 20), 8-spored,

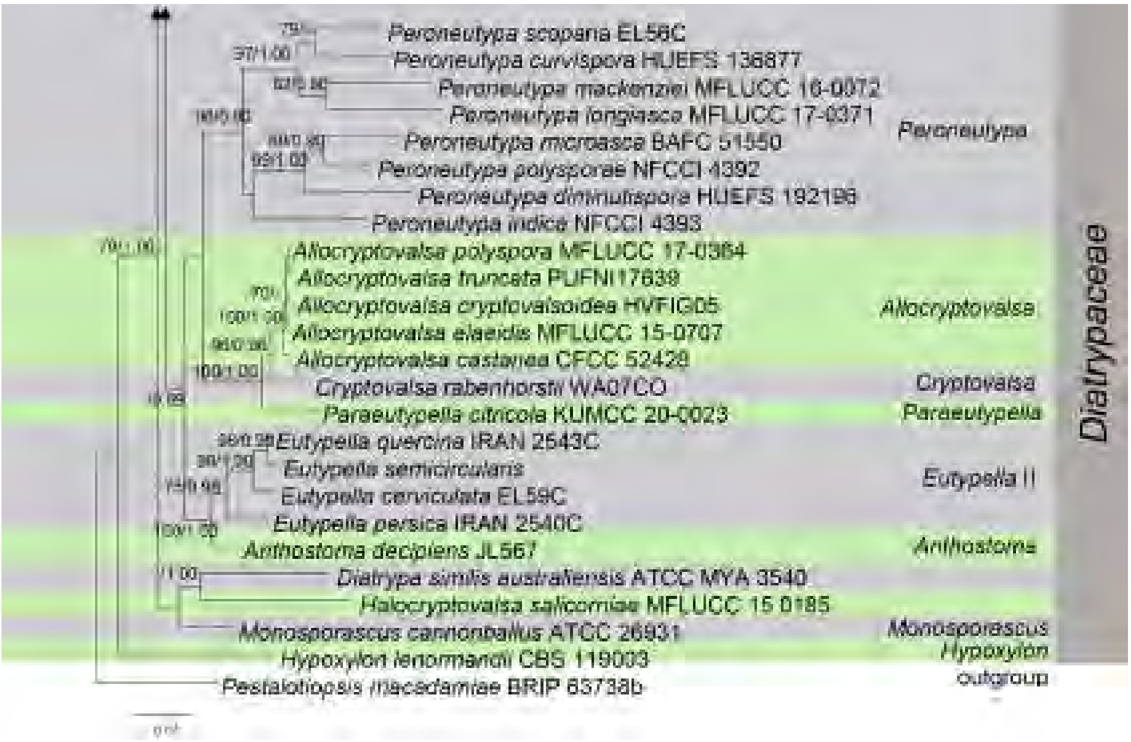


Fig. 129 Phylogram generated from maximum likelihood analysis based on combined ITS and β-tubulin sequence data of 26 taxa, which comprised 1200 characters (ITS = 471 bp, β-tubulin = 729 bp). The best scoring RAxML tree with a final likelihood value of − 5252.308511 is presented. The matrix had 432 distinct alignment patterns, with 39.91% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.232475, C = 0.260249, G = 0.230662, T = 0.276614; substitution rates: AC = 0.897989, AG = 3.062620, AT = 1.270241, CG = 1.001517, CT = 3.997945, GT = 1.0; gamma distribution shape parameter α = 0.713963. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (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 blue bold. The tree is rooted to *Cryptovalsa ampelina* (DRO101, A001)

unitunicate, spindle-shaped, tip blunted, long pedicellate, amyloid. *Ascospores* 10–17 × 6–9 µm ($\overline{x}$ = 13.5 × 7.5 µm, n = 40), 8-spored, ellipsoid, overlapping 1–3 seriate, initially hyaline, becoming pale brown at maturity, allantoid, slightly or moderately curved, aseptate, mostly with 1–2 small guttules. **Asexual morph**: Undetermined.

Culture characteristics: Colonies on PDA, 16–20 mm diam., after three weeks, colonies from above: medium dense, circular, flat, slightly raised, surface smooth with crenate edge, with smooth aspects, grey to dark brown at the margin, light brown in the center; reverse: dark brown to black at the margin, brown to grey in the center.

Material examined: Italy, *Robinia pseudoacacia* (Fabaceae), Erio Camporesi, 24 June 2021, D27 (MFLU 21-4687).

Hosts and distribution: China (*Pinus armandii*) (Phookamsak et al. 2019), Italy (*R. pseudoacacia*) (This study).

GenBank numbers: ITS: OR053733; *β-tubulin*: OR079742.

Notes: Our collection (MFLU 21-4687) grouped with *Neoeutypella baoshanensis* (HMAS 255436) with ML/BI = 100%/1.00 statistical support forming a sister clade to *Diatrype* (Fig. 133). Our collection obtained from a dead stem of *Robinia pseudoacacia* from Italy shares similar morphological characteristics with *N. baoshanensis* in the size and shape of ascomata, asci and pale brown ascospores. They also share similar morphological characteristics such as solitary to gregarious, globose to long irregular and carbonaceous ascomata, papillate ostiole, periphyses, a two-layered peridium and aseptate, filamentous paraphyses. However, our collection differs from the holotype material of *N. baoshanensis* in the absence of the yellow pigment and asexual structures. In the base pair comparison between our collection and *N. baoshanensis* (HMAS 255436) there are 1% and 1.3% differences for ITS and *β-tubulin* respectively. Based on the recommendation from Jeewon and Hyde (2016) with morphological characteristics, we provide our collection as new geographical record from Italy as well as a new host record from *Robinia pseudoacacia* (Fig. 131).

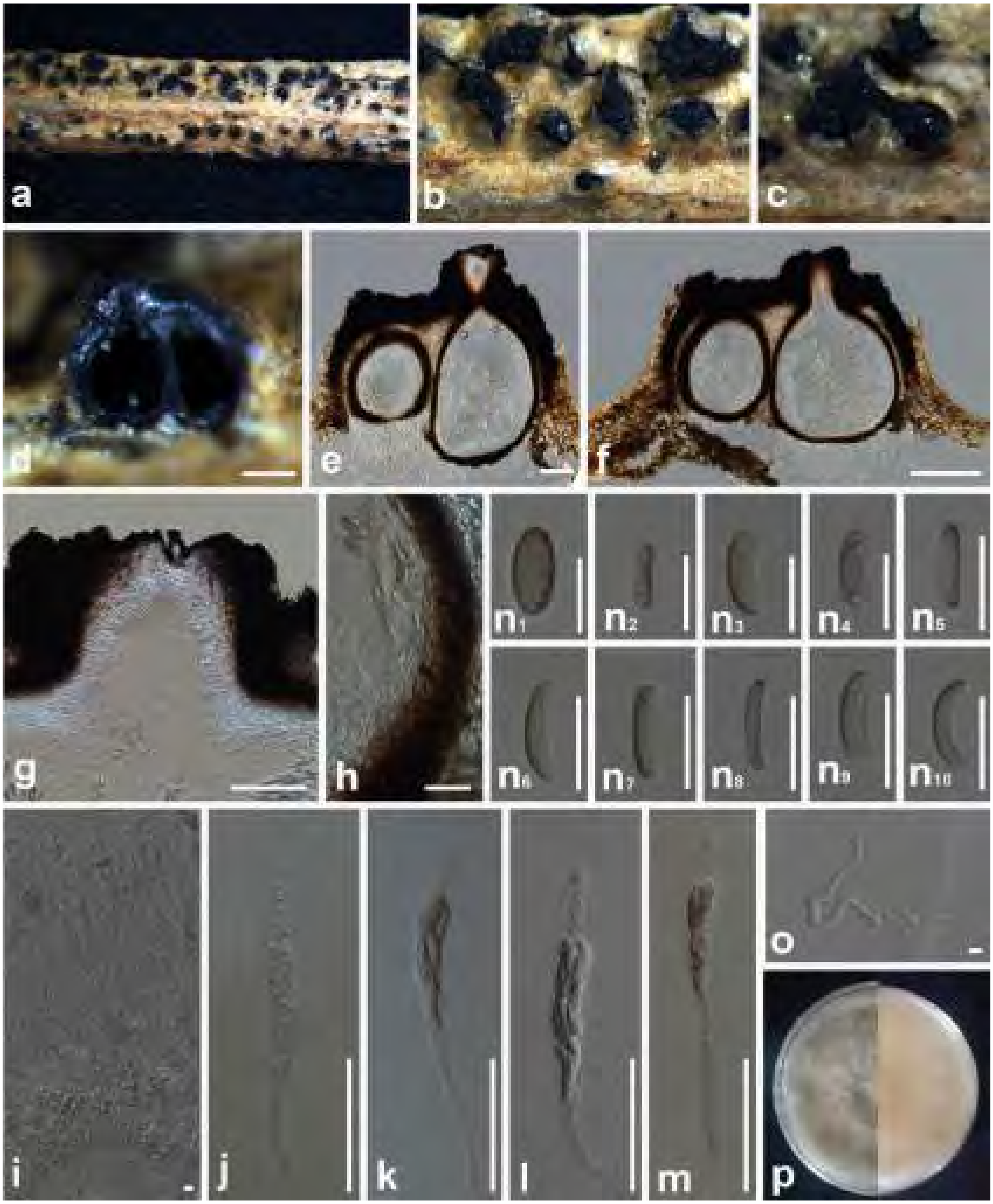


Fig. 130 ***Neoeutypella baoshanensis*** (MFLU 21-4687). **a–c** Appearance of ascomata on substrate. **d–f** Vertical cross-sections through ascomata. **g** Vertical cross-sections through ostiole. **h** Peridium. **i** Paraphyses. **j–m** Asci. **n1–n10** Ascospores. **o** A germinating ascospore. **p** Colony from above and below (on PDA). Scale bars: c–g = 100 µm, h = 20 µm, i = 10 µm, j–m = 30 µm, n1–n10, o = 10 µm

Oxydothidaceae S. Konta & K.D. Hyde

The monotypic family Oxydothidaceae was established to accommodate the genus *Oxydothis* (Konta et al. 2016). It is phylogenetically close, but distinct from Vialaeaceae and Iodosphaeriaceae in Xylariales (Samarakoon et al. 2021). Hyde et al. (2017a, b) provided a molecular clock to evaluate the ranking of taxa of Sordariomycetes, and proved that Oxydothidaceae is a well-supported family.

Oxydothis Penz. & Sacc.

Species in *Oxydothis* commonly occur in monocotyledonous hosts such as family Arecaceae, Pandanaceae and

Fig. 131 The best scoring RAxML tree with a final likelihood value of − 14,228.890517 for combined dataset of ITS and *β-tubulin* sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses. The tree is rooted with *Pestalotiopsis macadamiae* (BRIP 63738b). The matrix had 743 distinct alignment patterns with 31.15% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.228059, C = 0.263930, G = 0.237101, T = 0.270909; substitution rates AC = 0.991638, AG = 2.523032, AT = 0.315447, CG = 0.674576, CT = 3.904225, GT = 1.0; gamma distribution shape parameter α = 0.582489. Ex-type strains are in bold and newly generated sequences are in red. Bootstrap support for ML equal to or greater than 65% and BI equal to or greater than 0.90 are given above the nodes

Fig. 131 (continued)

Gramineae as saprobes (Hyde 1993b, c, 1994; Wang and Hyde 1999; Fröhlich and Hyde 2000; Wong and Hyde 2001; Taylor and Hyde 2003; Shenoy et al. 2005; Hidayat et al. 2006; Tibpromma et al. 2018). However, few species reported as phytopathogens (Fröhlich and Hyde 1994) and endophytes (Hyde 1994). Konta et al. (2016) suggested that *Oxydothis* species associated with healthy plants as endophytes and later become saprobes, based on their observations of appressoria (Taylor et al. 1999). *Oxydothis* species may use as biological control agents against plant pathogens (Hyde et al. 2020a). This study introduce two new *Oxydothis* species.

Oxydothis chinensis Senan. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900462; *Facesoffungi number*: FoF 14215; Fig. 132

Etymology: Species epithet based on the region where sample has been collected.

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph**: *Ascomata* 130–175 µm high, 80–110 µm diam. ($\bar{x} = 160 \times 100$ µm, n = 10), with black, circular clypeus, solitary, scattered or rarely in groups of two, immersed under clypeus, compressed globose, dark brown, coriaceous, axis parallel to the host surface, with central, indistinct papilla. *Peridium* 10–18 µm ($\bar{x} = 15$ µm, n = 10), outer cells merging with the host epidermal cells, comprising dark brown cells of *textura angularis*. *Hamathecium* comprises cellular, paraphyses. *Asci* 100–130 × 18–25 µm ($\bar{x} = 120 \times 20$ µm, n = 10), 8-spored, unitunicate, cylindrical to fusiform, pedicellate, with a J+, wedge-shaped, subapical ring. *Ascospores* 38–43 × 6–8 µm ($\bar{x} = 40 \times 7$ µm, n = 20), 1-seriate, upper cell longer than lower cell, fusiform, tapering gradually from the center to the ends, centrally 1-septate, not constricted at the septum, with pointed ends, hyaline, smooth-walled. *Appressoria* not observed. **Asexual morph**: Undetermined.

Culture characters: Colonies grew on PDA at 20 °C in the dark attenuated 3 cm diam., within 7 days, circular to irrigular, entire margin, flat, fluffy, with sparse wooly, aerial mycelia, surface white and reverse white to off-white.

Material examined: China, Guangdong Province, Guangzhou City, Nansha District, near BaiHui Tian reservoir, (22° 78′ 74.2″ N 113° 58.4′ 21″ E), on dead leaves of *Pandanus* sp. (Pandanaceae), 15 July 2021, I.C. Senanayake, GZ6 (MHZU 22-0134, **holotype**), ex-type culture ZHKUCC 22-0134.

GenBank numbers: ITS: OR164912, LSU: OR164957, *rpb*2: OR166292.

Notes: Combined ITS, LSU and *tef1-α* gene analysis (Fig. 134) showed that our isolate (ZHKUCC 22-0134) grouped with *Oxydothis inaequalis* and *O. fortunei*, forming a distinct clade with ML/BP = 91%/0.95 statistical support. Our collection differs from *Oxydothis inaequalis* by having astromatic ascomata with small asci and ascospores while *O. inaequalis* has stromatic ascomata, long (200–285 µm) asci and long (78–88 µm) ascospores (Hidayat et al. 2006). Our collection differs from *Oxydothis fortunei* by its wide asci with J+, apical ring and *O. fortunei* has large (200–315 µm diam.), solitary or aggregated ascomata, narrow asci (9–14 µm), J- subapical ring and long (56–72 µm) ascospores (Hu et al. 2022).

There are two *Oxydothis* species have been reported from *Pandanus* species viz. *O. pandani* and *O.*

Fig. 132 ***Oxydothis chinensis*** (MHZU 22-0134, **holotype**). **a** Host. **b** Examined material. **c** Ascoma on substrate. **d** Paraphyses. **e** Vertical cross section of ascomata. **f, g** Asci. **h–k** Ascospores. **l** Surface view of colonies. **m** Reverse view of colony. Scale bars: e = 50 μm, f–g = 40 μm, h–k = 20 μm

pandanicola. Sequence data of both these species are unavailable. Morphologically, *Oxydothis pandanicola* differs from our collection by large (470–620 × 340–400 μm), aggregated ascomata immersed in stromatic tissues, long asci (125–195 μm), 1–3-septate ascospores with filiform appendages at both ends (Huguenin 1964; Hyde 1994) and *O. pandani* differs by its long (56–60 μm), 1-median septate ascospores (Hyde 1994). *Oxydothis pandani* has been reported from Tubuai Island (South Pacific) and Hawaii (USA) while *O. pandanicola* was collected from Philippines and Indonesia. Our collection does not fit with any exist species and thus, we introduce this collection as a new species, *O. chinensis*.

Oxydothis yunnanensis Q.R. Li & J.C. Kang, ***sp. nov.***

Index Fungorum number: IF801978; *Facesoffungi number*: FoF05080; Fig. 133

Etymology: based on the collected location, Yunnan Province, China.

Saprobic on branches of palms. **Sexual morph**: *Ascomata* 223–363 μm diam., 74–85 μm high, forms slightly raised blistering areas on the host surface, clustered, immersed, subglobose, ostiole, coriaceous, black, eccentric, long axis horizontal to that of the host surface with neck at one end long axis parallel to plant surface. *Peridium* 28–40 μm thick, comprised of 2–3 layers outer layers of oblong, compressed, dark-brown cells of *textura angularis*. *Asci* 108–152 × 6.5–13.5 μm ($\bar{x}$ = 132 × 8.5 μm, n = 30), 8-spored, unitunicate, cylindrical, mostly bending, short pedicellate, apically rounded, with a J- subapical ring

Fig. 133 ***Oxydothis yunnanensis*** (GZUH 0127, **holotype**). **a** Examined material. **b**, **c** Ascomata on the surface of host. **d** Cross-section of ascomata. **e** Peridium. **f**, **g** Ascus apex with a J- subapical ring (stained in Melzer's reagent). **h**–**k** Asci. **l**–**n** Ascospores. Scale bars: b, c = 500 µm, d = 50 µm, e–g = 5 µm, h–n = 10 µm

not blue in Melzer's reagent. *Ascospores* 54–69 × 2.5–4 µm ($\bar{x}$ = 59.5 × 3.5 µm, n = 30), filiform, 2-seriate, uniseptate at the center, hyaline, tapering from center to end. **Asexual morph**: Undetermined.

Culture characters: The colony on PDA medium with a diameter of 5 cm after two weeks at 25 °C; white, circular, surface rough. Not sporulate on OA or PDA.

Material examined: China, Yunnan Province, Kunming City, Kunming Botanical Garden, on dead culms of palm, 15 August 2015, Q.R. Li, KIB 8 (GZUH 0127, **holotype**), ex-type culture GZUCC 0127.

GenBank numbers: ITS: ON176681, LSU: ON176684

Notes: ITS and LSU sequences of our collection (GZUH 0127) reveals *Oxydothis* species as the closest matches with NCBI and phylogenetically, it is related to *Oxydothis inaequalis* Hidayat, To-anun & K.D. Hyde with ML/BI = 100%/0.99 statistical support (Fig. 134). However, base pair differences of our collection (GZUH 0127) with *Oxydothis inaequalis* are 15.5% for ITS and 3% for LSU. Our collection (GZUH 0127) is morphologically similar to *O. livistonae* Syd. & P. Syd., *O. nonamyloidea* K. D. Hyde and *O. rhapidicola* Konta & K.D. Hyde. in the shape of its ascospores (Fröhlich and Hyde 1994; Hidayat et al. 2006; Konta et al. 2016). However, *O. nonamyloidea* and *O. livistonae* have larger ascospores than our collection viz. 94−115 × 3.5−4.5 µm and 150−170 × 4−5.5 µm respectively. *Oxydothis rhapidicola* differs from our collection by its smaller ascospores (47−50 × 3−5 µm) and the slit-like J + ascus subapical ring. Nevertheless, *O. yunnanensis* differs from *O. inaequalis* by its smaller ascospores (60 × 3.5 µm *vs.* 78–100 × 5–6 µm) and the J- ascus subapical ring. Therefore, we introduce our collection as a new species, *Oxydothis yunnanensis.*

Xylariaceae Tul. & C. Tul.

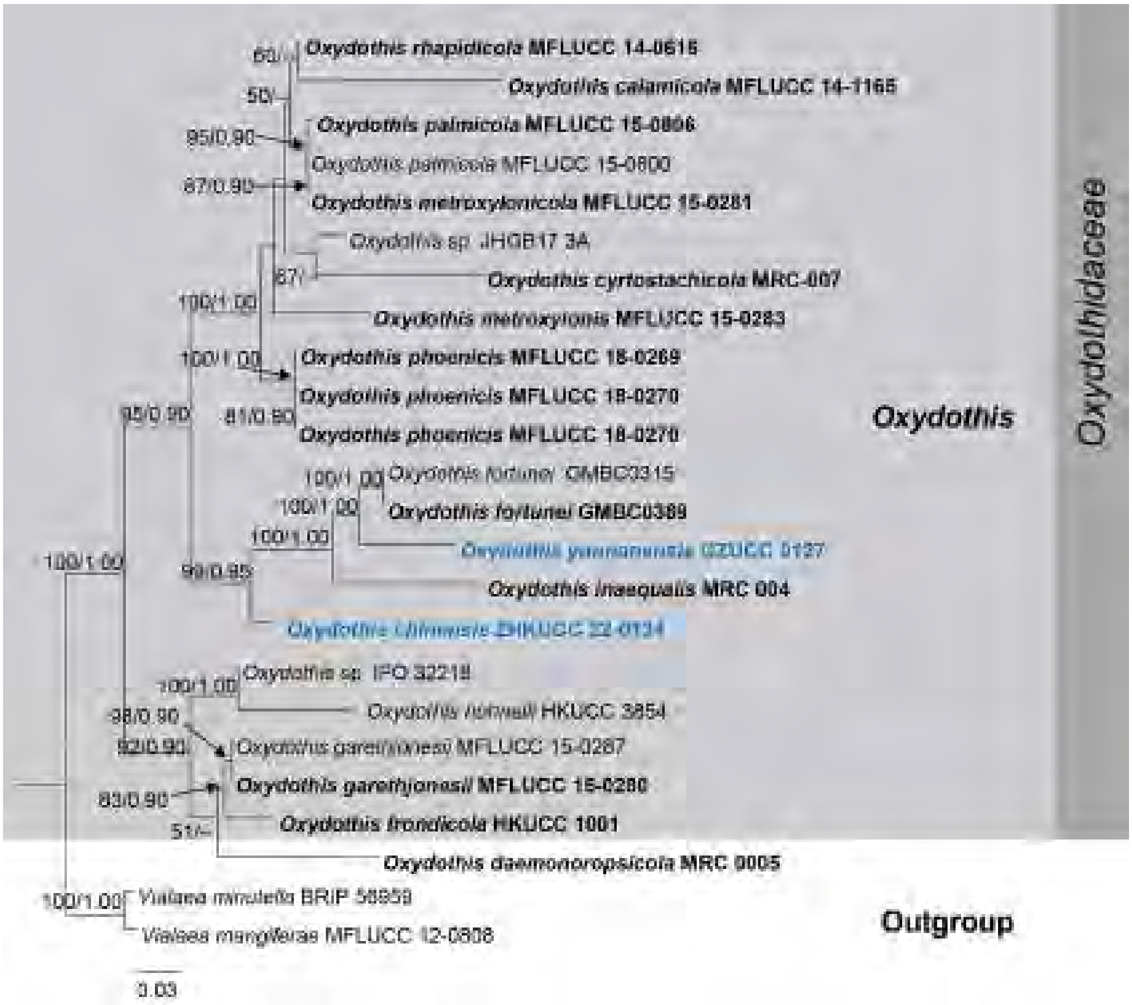


Fig. 134 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, and *tef1-α* sequence data of 23 taxa, which comprised 2549 characters (ITS = 697, LSU = 866, *tef1-α* = 984). The best scoring RAxML tree with a final likelihood value of − 9941.739756 is presented. The matrix had 752 distinct alignment patterns, with 36.07% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.234608, C = 0.258487, G = 0.267824, T = 0.239080; substitution rates: AC = 0.999075, AG = 1.873946, AT = 1.369435, CG = 1.130755, CT = 4.743944, GT = 1.0; gamma distribution shape parameter α = 0.272581. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (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 blue bold. The tree is rooted to *Vialaea minutella* (BRIP 56959) and *V. mangiferae* (MFLUCC 12-0808)

Species in Xylariaceae are distributed worldwide as saprobes, pathogens and endophytes in wood, leaves and fruits or associated with insect vectors (Maharachchikumbura et al. 2016). Hyde et al. (2020c) accepted 32 genera in Xylariaceae.

Nemania Gray

Nemania was introduced by Gray (1821) and typified by *N. serpens*. Species in this genus are endophytes, saprobes and pathogens from terrestrial or marine environments worldwide (U'Ren et al. 2016; Daranagama et al. 2018; Hyde et al. 2020a). This genus is distributed in Europe (Denmark, Sweden, and the United Kingdom), Australia, North America and Asia (China, Thailand), while only few specimens have been recorded from Africa and South America (Tibpromma et al. 2021). *Nemania* species are characterized by stromata not associated with bark rupturing structures, lacking KOH-extractable pigments and finely papillate ostioles, unitunicate, cylindrical asci, ascospores with a germ slit in their sexual morph, and geniculosporium-like asexual morph (Daranagama et al. 2018). Endophytic *Nemania* species have shown interesting applications associated with its bioactive compounds on many hosts (Kumarihamy et al. 2019; Medina et al. 2019). Currently, there are 78 species (Species Fungorum 2023).

Nemania guangdongensis Senan., ***sp. nov.***

Index Fungorum number: IF900463; *Facesoffungi number*: FoF 14216; Fig. 135

Etymology: in reference to the region where sample has been collected.

Saprobic on dead wood. **Sexual morph**: *Ascostromata* 750–1,100 × 750–1,450 µm ($\bar{x}$ = 950 × 1,200 µm, n = 15), superficial with immersed base, solitary or rarely aggregated, scattered, globose, black, carbonaceous. *Ascomata* 720–850 × 625–1,270 µm ($\bar{x}$ = 770 × 751 µm, n = 15), globose, covered with thin stromata, ostiolate, papillate. *Ostioles* centric, surrounding area slightly flattened, shiny, black, conspicuous. *Paraphyses* 1.2–2 µm ($\bar{x}$ = 1.6 µm, n = 25) wide, cellular, long, numerous, septate, smooth-walled. *Asci* 65–105 × 7–10 µm ($\bar{x}$ = 88.5 × 8.6 µm, n = 20), 8-spored, unitunicate, cylindrical, short pedicellate, with a 1.7–2.5 × 2.4–3.3 µm ($\bar{x}$ = 2 × 2.8 µm, n = 8), discoid-shaped, apical ring, J + in Melzer's reagent, apex rounded. *Ascospores* 9.5–14.5 × 5–7.5 µm ($\bar{x}$ = 12.5 × 6.2 µm, n = 35), uniseriate to overlapping uniseriate, hyaline, when immature, turning pale brown and dark brown when mature, 1–2-guttulate, oblong to ellipsoid, symmetrical to slightly inequilateral, aseptate, smooth-walled, with a straight germ slit along the entire spore length. **Asexual morph**: Undetermined.

Culture characteristics: Colonies on PDA reaching 4 cm diam., after seven days at 25 °C, circular, umbonate, entire, undulate, rough, wooly aerial mycelia, white from above, off-white from below.

Material examined: China, Guangdong Province, Guangzhou City, Xiaogang Park, dead bark of unidentified plant, 18 July 2021, I.C. Senanayake, S3-13 (MHZU 22-0079, **holotype**), ex-type cultures ZHKUCC 22-0136, ZHKUCC 22-0156.

GenBank numbers: ITS: OR164916, OR164917, *rpb2*: OR166293, OR166294.

Notes: The sequence data of ITS, LSU, *rpb2* and *β-tubulin* of our isolate (ZHKUCC 22-0136) gives species in *Nemania* as the closest matches with NCBI. The phylogenetic analysis (Fig. 137) showed that our isolate is phylogenetically close to *Nemania paraphysata* Samarak. & K.D. Hyde and *N. pouzarii* J.D. Rogers & Y.M. Ju, but distinct from them forming a subclade with MP/BI = 94%/0.90 support. Comparison of the sequence of ITS, LSU, and *rpb2* locus of our isolates (ZHKUCC 22-0136, ZHKUCC 22-0156) with *Nemania paraphysata* and *N. pouzarii* revealed the base pair differences of 1.02%, 5.66%, 1.5%, 0.3%, 2.5%, and N/A respectively. No *β-tubulin* sequences are available for both *Nemania paraphysata* and *N. pouzarii.* Our collection (MHZU 22-0079) is morphologically different from *Nemania paraphysata* by carbonaceous, superficial stromata with immersed base, and absence of mucilaginous sheath or knob-like structure at the base of ascospores while *N. paraphysata* has mammiform stromata with broad base, ascospores often with a knob at base and with a thick, mucilaginous sheath (Samarakoon et al. 2021). Therefore, we introduce our collection as *Nemania guangdongensis* sp. nov.

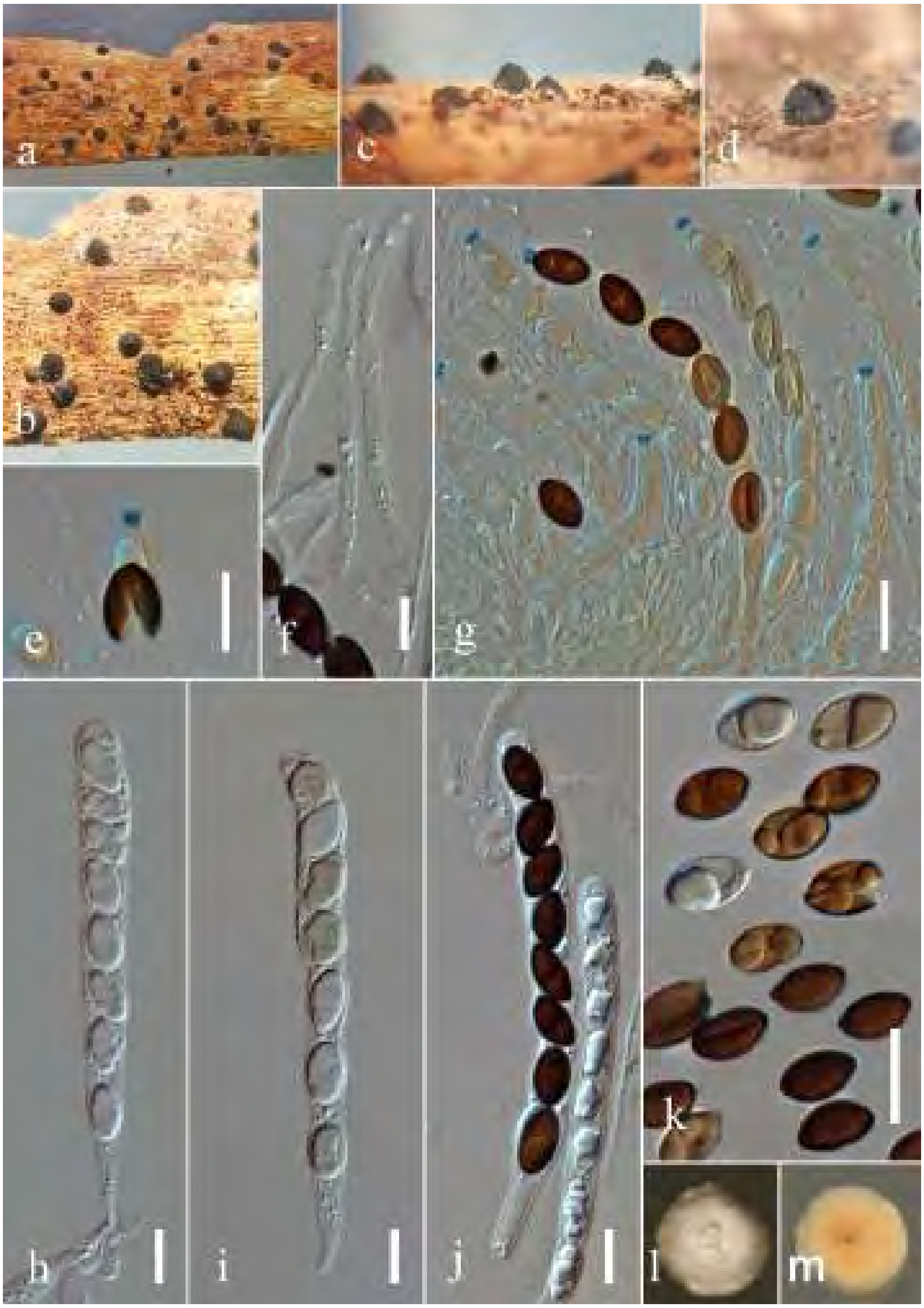
Nemania phetchaburiensis Dayar., E.B.G. Jones & K.D. Hyde, in Dayarathne et al., Mycosphere 11(1): 165 (2020)

Index Fungorum number: IF556602; *Facesoffungi number*: FoF 06195; Fig. 136

Holotype: MFLU 16-1185

Saprobic on decaying submerged wood in freshwater. **Sexual morph**: *Ascostromata* 1–1.6 × 1.3–2.2 mm ($\bar{x}$ = 1.3 × 1.9 mm, n = 10), semi-immersed or superficial with immersed base, pulvinate to hemispherical, in clusters of up to 20 shiny, black, carbonaceous, stromata comprising plant cells and fungal hyphae. *Ascomata* immersed in stroma, subglobose to hemispherical, black, ostiolate, papillate. *Peridium* 80–130 µm wide, two-layered, outer, brown, thick-walled cells of *textura angularis* fusing at the outside with the pseudostromata, inner, pale brown, small elongate cells. *Paraphyses* 2–3 µm wide, filamentous, hyaline, septate, flexuous, branched, numerous and embedded in a gelatinous matrix. *Asci* 90–150 × 12–15 µm ($\bar{x}$ = 120 × 13 µm, n = 20), 8-spored, unitunicate, cylindrical, short pedicellate, wedge-shaped, J + subapical ring. *Ascospores* 14–16 × 6–9 µm ($\bar{x}$ = 15 × 6.5 µm, n = 20) overlapping uniseriate, light brown at immature stage, dark to greenish brown when mature,

Fig. 135 ***Nemania guangdongensis*** (MHZU 22-0079, **holotype**). **a–c** Ascomata on substrate. **d** Vertical cross section through ascoma. **e** J + apical ring. **f** Paraphyses. **g–j** Asci. **k** Ascospores. **l** Cultures on PDA from above. **m** Cultures on PDA from below. Scale bars: c = 500 µm, d–f = 5 µm, g–i = 30 µm, j–p = 15 µm



inequilaterally ellipsoid, ventral side varying in degree of convex curvature, upper and lower ends slightly pointed, one-celled, 1–2 guttules, germination slit usually clearly seen on the ventral side, straight, conspicuous. **Asexual morph**: Undetermined.

Culture characteristics: Colonies on PDA at 25 °C reaching 2 cm in 7 days, flat, circular, diffuse margins, white, wooly, reverse white, turn yellowish to light brown with time.

Material examined: China, Guangdong Province, Guangzhou City, Baiyun Mountain, on submerged decaying wood, 16 August 2021, Jizhen Fu, WBHS 1 (MHZU 22-0080, **new geographical record**), living culture ZHKUCC 22-0137.

Hosts and distribution: On decaying wood of *Rhizophora* sp. (Thailand), submerged wood of unidentified plant in China (this study)

GenBank numbers: ITS: OR164947, LSU: OR164959.

Notes: The sequence data of ITS, and LSU of our isolate (ZHKUCC 22-0137) gives species in *Nemania* as the closest

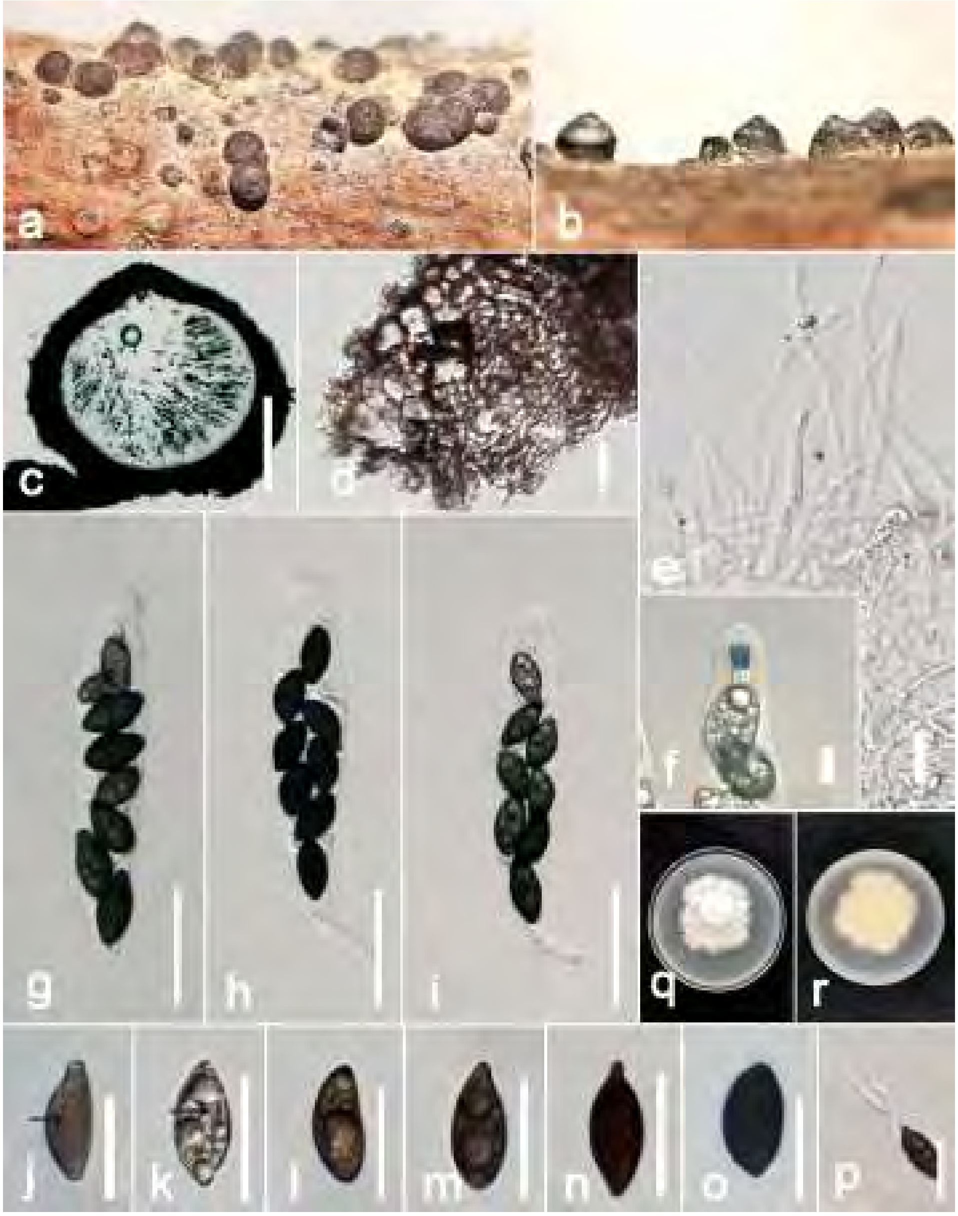


Fig. 136 ***Nemania phetchaburiensis*** (MHZU 22-0080). **a, b** Ascomata on substrate. **c** Vertical cross section through ascoma. **d** Peridium. **e** Paraphyses. **f** J+apical ring. **g–i** Asci. **j–o** Ascospores. **p** Germinating ascospore. **q** Cultures on PDA from above. **r** Cultures on PDA from below. Scale bars: c = 500 µm, d–f = 5 µm, g–i = 30 µm, j–p = 15 µm

matches with NCBI. Our isolate forms a well-supported clade (ML/BI = 100%/1.00) with the ex-type strain of *Nemania phetchaburiensis* (Fig. 137). ITS and LSU sequences of our isolate are identical to the sequences derived from ex-type strain and morphological characters of our collection same to the holotype (Dayarathne et al. 2020). Therefore, we identified our collection as *Nemania phetchaburiensis* and this is the first record of this species in China.

Basidiomycota R.T. Moore
Agaricomycetes Doweld
Agaricomycetidae Parmasto

Agaricales Underw.

Matheny et al. (2006) showed that Agaricales includes six subclades, viz. Agaricoid, Tricholomatoid, Marasmioid, Pluteoid, Hygrophoroid and Plicaturopsidoid. Some genera in this order are taxonomically uncertain and several genera are polyphyletic. He et al. (2019) listed 38 families, 508 genera and around 17,300 species in Agaricales. We follow the recommendations of He and Yang (2021) in introducing new taxa.

Agaricaceae Chevall.

The family Agaricaceae includes a monophyletic group of saprotrophic fungi with a wide range of spore colour and basidiocarp morphology. This family contains around 1340 species in 85 genera (Kirk et al. 2008; Sulastri and Basri 2021). The taxonomic arrangement of this family has

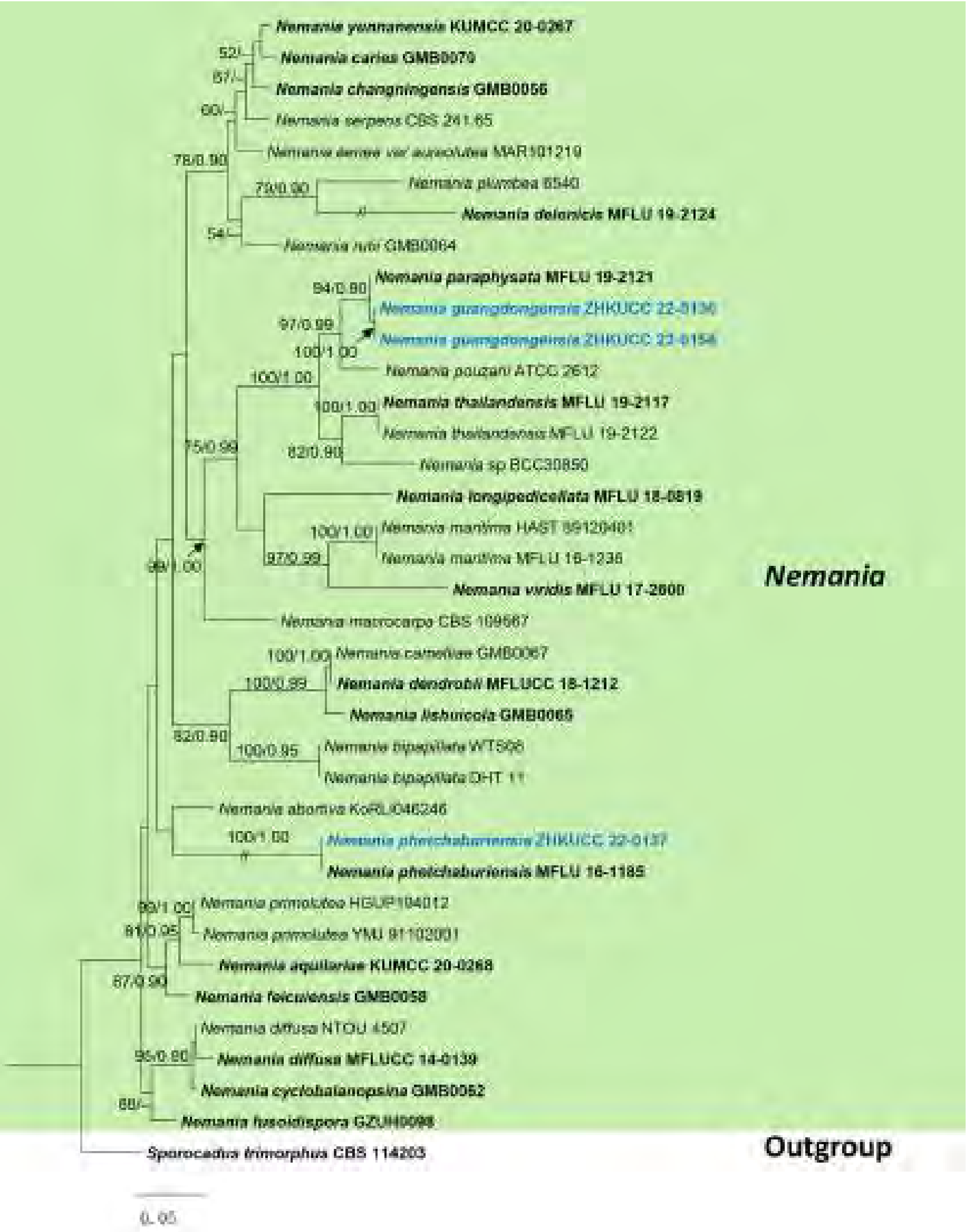


Fig. 137 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of 37 taxa, which comprised 1479 characters (ITS = 612 bp, LSU = 866 bp). The best scoring RAxML tree with a final likelihood value of − 8948.691975 is presented. The matrix had 590 distinct alignment patterns, with 10.36% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.233892, C = 0.254026, G = 0.301847, T = 0.210236; substitution rates: AC = 1.841685, AG = 3.640707, AT = 1.708445, CG = 1.248451, CT = 8.476357, GT = 1.0; gamma distribution shape parameter α = 0.583881. Bootstrap support for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (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 isolates are indicated in blue bold. The tree is rooted to *Sporocadus trimorphus* (CBS 114203)

significantly renovated with the application of molecular data (Moncalvo et al. 2000, 2002; Matheny et al. 2007). This is one of the few families that have seen a considerable influx of species (Vellinga et al. 2011).

Agaricus L.

The genus *Agaricus* was introduced with *A. campestris* L. as the type species (Donk 1962). Species of the genus *Agaricus* are saprobic and characterized by an annulate stipe, free lamellae and dark brown spore print. They commonly occur as solitary or gregarious on substrates and are found in a wide range of habitats viz., woodlands, gardens, roadsides, pastures, manure heaps, and decaying organic materials (Cappelli 1984). *Agaricus* species originated in the tropics approximately 66 million years ago and extends to all continents except Antarctica (Parra 2008; Zhao et al. 2011, 2016; He et al. 2017; He and Yang 2021).

Some species of *Agaricus* viz., *A. bisporus* (J.E. Lange) Imbach and *A. subrufescens* Peck are commercially important due to their culinary and medicinal values. Certain species in the sect. Xanthodermatei and sect. Hondenses contain toxic phenolic chemicals that cause gastrointestinal issues (Kerrigan et al. 2005; Petrova et al. 2007; Parra 2013; Mahdizadeh et al. 2016). This study introduces a new variety and provides descriptions, illustrations and notes for few noteworthy collections of *Agaricus* from India.

Agaricus duplocingulatoides *var*. ***brevisporus*** C.P. Arya & C.K. Pradeep, ***var. nov.***

Index Fungorum number: IF900408; *Facesoffungi number*: FoF 14217; Fig. 138

Etymology: Refers to the small basidiospores of the variety.

Diagnosis: Differs from the type variety *Agaricus duplocingulatoides* by larger basidiomata, smaller basidiospores and negative KOH reaction.

Macroscopic characters: *Pileus* 39–78 mm diam., convex to plano-convex, then applanate with an obtuse umbo at the disc; surface dry, dark brown (6F8/7F5/7F7/7F8) appressed squamules dense and smooth at disc, elsewhere almost in concentric rings, scarce towards margin on an off white background, develops reddish white (7A2) tinge here and there during heavy rain; margin straight, appendiculate, white, with remnants from the partial veil, entire, exceeding the lamellae. *Lamellae* free, crowded, up to 8 mm wide, greyish brown to dark brown (7D3/7F4/7F5/8D3/8E3) intercalated with lamellulae of different lengths; edge concolorous to the sides. *Stipe* 28–55 × 6–13 mm, central, cylindric, curved, stuffed to narrowly hollow, tapering slightly upwards from a broad base; surface dry, white to off white become brownish on handling, smooth and glabrous above the annulus, minutely squamulose below annulus, vanishing on handling. *Context* up to 5 mm thick at the pileus disc, fleshy, white, not discoloring when cut. *Annulus* superous, pendent, skirt like, white, upper side smooth, lower side floccose, evanescent. White mycelial codons present. *Odor* of anise.

Microscopic characters: *Basidiospores* 4.3–5.6 × 3.2–3.8 µm, (avL = 4.9 ± 0.37, avW = 3.53 ± 0.19), Q = 1.2–1.6, Qm = 1.41, broadly ellipsoid to ellipsoid, brown, thick-walled, without apical pore. *Basidia* 14–23 × 5–7 µm, clavate to broadly clavate, tetrasporic, thin-walled, hyaline. *Lamella edge* sterile with abundant cheilocystidia, 10–32 × 6–25 µm, simple or with one basal cell, pyriform, vesiculose, clavate, broadly clavate, thin-walled, hyaline. *Pleurocystidia* absent. *Hymenophoral trama* regular, hyphae 3–13.5 µm wide, thin-walled with constricted at the septa, hyaline. *Pileal trama* interwoven, branched,

Fig. 138 ***Agaricus duplocingulatoides var. brevisporus*** (TBGT17998). **a** Habit. **b** Gill view. **c** Sectional view. **d** Basidiospores. **e** Cheilocystidia. **f** Annulus. Scale bars: a–c = 10 mm, d–f = 10 µm

septate, hyphae 6–26 µm wide, cylindrical, thin-walled, hyaline. *Pileipellis* an interrupted cutis, composed of cylindrical hyphae with brownish contents, 4–6.5 µm, not or slightly constricted at the septa, thin-walled. *Stipitipellis* composed of parallel, hyaline hyphae, cylindrical, 4–16 µm wide, thin-walled, hyaline. Lower surface of the annulus composed of cylindrical hyphae, 4–7.5 µm wide not or hardly constricted at the septa with brownish contents in some hyphae. *Clamp connections* absent. *Oleiferous hyphae* present.

Macrochemical reactions: Schäffer's and KOH reactions negative on fresh basidiomata.

Holotype: India, Kerala State, Thiruvananthapuram District, Palode, JNTBGRI campus, 8.75° N, 77.02° E, elev. 150 m, 23 October 2019, TBGT(M)17998.

Habitat and distribution: solitary, scattered on soil, known only from the type collection in Kerala State, India (this study).

Other materials examined: India, Kerala State, Thiruvananthapuram District, Palode, JNTBGRI campus, 8.75° N, 77.02° E, elev. 150 m, 3 November 2017, TBGT(M)17239, *ibid.* 9 July 2020, TBGT(M)18157; 16 September 2021, TBGT(M)18689, **paratypes**.

GenBank numbers: ITS: OP520722, OP528741, OP528742, OP520724

Notes: This collection are morphologically very similar and phylogenetically closely affiliated to *Agaricus duplocingulatoides* Tarafder, A.K. Dutta & K. Acharya which was collected from India (Tarafder et al. 2018). However, *Agaricus duplocingulatoides* has smaller basidiomata (22–32 mm), a positive KOH reaction and larger basidiospores (6–) 6.5–7.5(–8) × 3.5–4.2 (–4.5) µm while our collection comprises medium-sized basidiomata, white to cream-coloured pileus with brownish squamules, negative Schäffer's and KOH reactions, fistulose stipe with a broad base, smaller basidiospores, pileipellis an interrupted cutis and presence of pyriform to broadly clavate cheilocystidia. Molecularly, there are five nucleotide differences in ITS locus of our collection with *Agaricus duplocingulatoides.*

Agaricus duplocingulatus Heinem. morphologically similar to our collection in its pileus size, shape, color of pileus and negative Schaeffer's reaction. However, it differs by larger basidiospores (4.8–5.4–6(–6.6) × 3.5–4.5 µm), presence of catenulate cheilocystidia, ochraceous to reddish discoloration when cut or bruised and poor DNA sequence similarity (97.12% identity) in ITS. Thus, we introduce our collection as a new variety *viz., Agaricus duplocingulatoides* var. *brevisporus* (Fig. 138).

Agaricus duplocingulatoides Tarafder, A.K. Dutta & K. Acharya, in Tarafder et al., Phytotaxa 374(2): 142 (2018)

Index Fungorum number: IF826889; *Facesoffungi number*: FoF 14217; Fig. 139

Holotype: CUH AM537

Macroscopic characters: *Basidiomata* medium. *Pileus* 47 mm diam., broadly convex with a low umbo; surface orange white (6A2) with brown (6E5) disc, which is smooth, with pale brown (6E5) appressed squamules, dry; margin straight, uneven, exceeding the lamellae. *Lamellae* free, dull

Fig. 139 *Agaricus duplocingulatoides* (TBGT17885). **a** Habit. **b** Gill view. **c** Sectional view. **d** Basidia. **e** Basidiospores. **f** Cheilocystidia. Scale bars: a–c = 10 mm, d–f = 10 µm

red to maiden's blush (8B3/8B4) up to 6 mm wide, crowded with lamellulae of 2–5 mm length; edge concolorous with the sides, entire. *Stipe* 55 × 6 mm, central, cylindric, hollow, tapering downward with a small bulbous base; surface orange white (5A2) with white pruinae, vanishing on handling and become brownish. *Annulus* superior, white, membranous, pendant, flaring with white floccose squamules on lower side, double edged, evanescent. *Context* white, up to 5 mm, thick, soft, fleshy. White mycelial codons present. *Odor* pleasant.

Microscopic characters: *Basidiospores* 6–6.8(8) × 4–4.8 µm diam. (avL = 6.24 ± 0.38 µm, avW = 4.18 ± 0.28), Q = 1.3–1.8 µm, (avQ = 1.45 ± 0.1), ellipsoid, smooth, brown, thick-walled. *Basidia* 18–28 × 6–8 µm, clavate, tetrasporic, thin-walled, hyaline. *Lamellae edge* sterile with crowded cheilocystidia. *Cheilocystidia* abundant, 12–30 × 6–22 µm, pyriform, clavate, broadly clavate, globose, vesiculose, thin-walled, hyaline. *Pleurocystidia* absent. *Hymenophoral trama* regular, 2.4–8 µm diam., composed of cylindrical to inflated hyphae, constricted at the septa, thin-walled, hyaline. *Subhymenium* pseudoparenchymatous. *Pileal trama* composed of multiseptate, cylindrical to inflated hyphae, 6.4–40 µm diam., thin-walled, hyaline. *Pileipellis* a cutis interrupted at places with bundles of hyphae, 3.2–7.2 µm wide with yellowish brown contents. *Stipitipellis* composed of parallel, multiseptate cylindrical hyphae, 4–15 µm wide, pale yellowish in KOH, thin-walled. *Oleiferous hyphae* present. *Clamp connections* absent.

Macrochemical reactions: Schäffer's and KOH reactions negative.

Habitat and distribution: solitary on soil in grass land, known only from the type collection in West Bengal, India (Tarafder et al. 2018) and Kerala State, India (this study).

Material examined: India, Kerala State, Thiruvananthapuram district, Palode, JNTBGRI campus (8.75° N, 77.02° E, elev. 150 m), soil in grass land, 24 July 2019, TBGT(M)17885.

GenBank number: ITS: OP503497.

Notes: *Agaricus duplocingulatoides* Tarafder, A.K. Dutta & K. Acharya was described from West Bengal, India (Tarafder et al. 2018). The species is characterized by a negative Schäffer's test, presence of small brownish squamules on the pileus, fistulose stipe with rounded bulbous base, considerably shorter pileipellis hyphae, and presence of pyriform to broadly clavate cheilocystidia. Our collection is morphologically and molecularly similar to the holotype collection of *A. duplocingulatoides* however, our collection has larger basidiomata than the holotype collection (22–32 mm diam.). Therefore, we identified our collection as *A. duplocingulatoides.*

Agaricus bingensis Heinem., Bull. Jard. Bot. État Bruxelles 26: 72 (1956)

Index Fungorum number: IF292245; *Facesoffungi number*: FoF 14218; Fig. 140

Holotype: BR3052

Macroscopic characters: *Pileus* 67–92 mm diam., convex when young, later plano-convex to applanate on maturing with or without an umbo; surface dry, chalky white when young with concolorous punctiform squamules, washed off during rain to appear smooth and

Fig. 140 ***Agaricus bingensis*** (TBGT13568). **a, b** Habit. **c** Gill view. **d** Basidiospores. **e** Cheilocystidia. **f** Annulus. Scale bars: a–c = 20 mm, d–f = 10 µm

glabrous, developing a brownish tinge towards margin during heavy rain in old basidiomata; margin appendiculate with remnants of the partial veil, entire to variously incised, exceeding the lamellae. *Lamellae* free, crowded, up to 7 mm wide, with lamellulae of different lengths, pale red (7A3/8A3) to dark brown (7F7/8F8/9F5); edge concolorous with the sides, entire. *Stipe* 55–90 × 10–15 mm, central, cylindrical, hollow, brittle, tapering upwards from a bulbous base; surface chalky white, smooth and glabrous above the annulus, punctiform squamules below the annulus, vanishing on handling or during heavy rain. White mycelial strands present at the base. *Annulus* superior, white, pendant, easily evanescent, upper surface smooth, lower side floccose squamulose. *Context* white become brownish on bruising, up to 9 mm thick at the pileal disc, fleshy, white. *Odor* strong of anise.

Microscopic characters: *Basidiospores* 7.6–10.2 × 4.9–6 µm, (avL = 8.6 ± 0.7, avW = 5.47 ± 0.31), Q = 1.5–2 (avQ = 1.58 ± 0.09), ellipsoid to oblong, smooth, brown, thick-walled, without apical pore. *Basidia* 22–28 × 7–9 µm, 4-spored, rarely 2-spored, clavate, thin-walled, hyaline. *Lamella edge* sterile with abundant cheilocystidia. *Cheilocystidia* 14–46.5 × 6–21 µm, simple, cylindrical, cylindro-clavate, pyriform, clavate, globose, thin-walled, hyaline. *Pleurocystidia* absent. *Hymenophoral trama* regular, hyphae 3–7 µm wide, thin-walled, hyaline. *Subhymenium* pseudoparenchymatous. *Pileal trama* interwoven, 8–13 µm, cylindrical to inflated, thin-walled, hyaline. *Pileipellis* a cutis, composed of parallel, cylindrical hyphae 3–9 µm, not or slightly constricted at the septa, thin-walled, hyaline. *Stipitipellis* a cutis composed of parallel, hyaline hyphae 4.3–10 µm wide, thin-walled, hyaline. *Annulus* composed of parallelly arranged cylindrical septate hyphae, not or slightly constricted at the septa, 4–7.6 µm wide, thin-walled, hyaline and some broad elements up to 21.3 µm wide. *Clamp connections* absent.

Macrochemical reactions: Schäffer's and KOH reactions negative on dried basidiomata.

Habitat* and *distribution: solitary on soil in grassland, known from Africa: Bénin, Democratic Republic of the Congo, Togo, Uganda (Chen et al. 2015a) and Kerala State, India (this study)

Materials examined: India, Kerala State, Thiruvananthapuram district, Eanikkara, 8.56° N, 76.97° E, elev. 18 m, 26 April 2011, TBGT(M)13568; *ibid*. Varkala 8.76° N, 76.72° E, elev. 30 m, 18 May 2021, TBGT(M)18562; 18 May 2021, TBGT(M)18563; 19 May 2021, TBGT(M)18564; 20 May 2021, TBGT(M)18568; Govt. College for Women Campus 8.49° N, 76.95° E, elev. 10 m, 1 July 2022, TBGT(M)18888.

GenBank number: ITS: OP518683.

Notes: *Agaricus bingensis* Heinem., was introduced and described by Heinemann (1956) from Binga, Democratic Republic of the Congo and placed in the section *Brunneopicti* based on morphology and negative Schäffer's reaction. This species is characterized by medium to large basidiomata with punctiform squamules on the pileus, large basidiospores (8.3–10 × 5.1–5.7 µm), simple, pyriform, clavate, globose cheilocystidia and pileipellis a cutis. The ITS sequence of our collection is identical to the Benin collection of *Agaricus bingensis* (KJ540954). Apart from the slightly smaller basidiomata (67–92 mm diam.) and larger cheilocystidia (14–46.5 × 6–21 µm) of our collection, no significant morphological differences were observed with the type collection.

Agaricus brunneosquamulosus Linda J. Chen, R.L. Zhao, K.D. Hyde & Callac, in Chen et al., Phytotaxa 192:154 (2015)

Index Fungorum number: IF808173; *Facesoffungi number*: FoF 14219; Fig. 141

Holotype: MFLU 12-0881

Macroscopic characters: *Basidiomata* small to medium, thick and fleshy. *Pileus* 43–84 mm diam., convex to plano-convex when young, later applanate with a flat disc; surface white to off white with brownish orange to brown (5F7/6C3/6D3/7E4) appressed squamules arranged in a more or less concentric fashion expect at the disc which is entire; scales may be washed off during heavy rain especially near margin to expose the greyish red (9B4) context below, dry; margin straight, wavy, variously incised, appendiculate with remnants of the partial veil. *Lamellae* free, reddish grey to dull red (7B2/7B3/7C2/8B3/8C3) when young becoming eye brown (7F6) when mature, up to 6 mm wide, crowded with lamellulae of different lengths; edge concolorous to the sides, entire. *Stipe* 39–93 × 4–7 mm, central, cylindric, stuffed to hollow, equal with a subclavate to clavate base; surface white becoming brown on handling; white fine squamules present below the annulus and glabrous above the annulus; squamules easily vanishing on handling to appear smooth. White mycelial rhizoids present. *Annulus* superior, double, white, membranous, pendant, flaring, with floccose squamulose on lower side. *Context* white, turn brownish on exposure, up to 6 mm, thick, soft, fleshy. *Odor* aniseed like. *Taste* mild.

Microscopic characters: *Basidiospores* 4.8–6 × 3.2–4 µm diam., (avL = 5.28 ± 0.38 µm, avW = 3.54 ± 0.28), Q = 1.3–1.6 µm, (avQ = 1.44 ± 0.084), ellipsoid, smooth, brown, thick-walled. *Basidia* 15–24 × 6–10 µm, clavate, hyaline, tetrasporic, thin-walled, hyaline. Lamella edge sterile with crowded cheilocystidia. *Cheilocystidia* 12–40 × 4.8–20 µm, clavate, broadly clavate, vesiculose, subglobose with one to two basal septa in some, thin-walled, hyaline. *Pleurocystidia* absent. *Hymenophoral trama* regular composed of cylindrical hyphae, 4–16 µm diam., thin-walled, hyaline. *Subhymenium* pseudoparenchymatous.

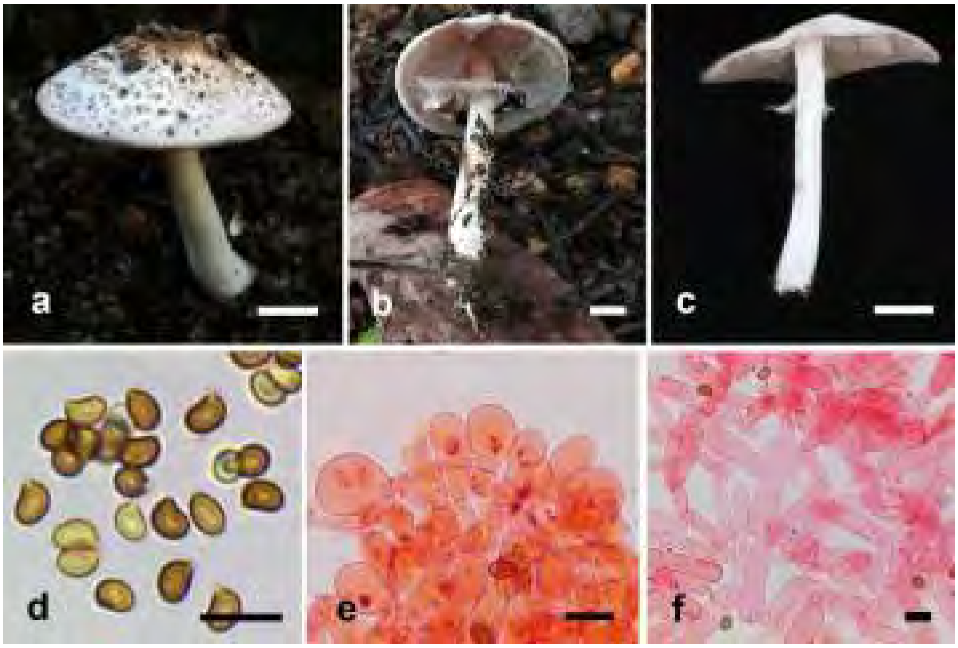


Fig. 141 ***Agaricus brunneosquamulosus*** (TBGT17828). **a** Habit. **b** Gill view. **c** Sectional view. **d** Basidiospores. **e** Cheilocystidia. **f** Annulus. Scale bars: a–c = 10 mm; d–f = 10 µm

Pileal trama composed of multiseptate, inflated hyphae, 4–28 µm diam., thin-walled, hyaline. *Pileipellis* an interrupted epicutis with erect to suberect hyphae, 4–14 µm diam., with brown vacuolar contents, slightly constricted at the septa. *Stipitipellis* a cutis, composed of multiseptate cylindrical hyphae, 4–16 µm, thin-walled, hyaline. *Annulus* lower surface composed of branched cylindrical interconnected hyphae 4–12 µm wide, mixed with easily disarticulating shorter, wider hyphae up to 16 µm wide, thin-walled, hyaline. *Oleiferous hyphae* present. *Clamp connections* absent.

Macrochemical reactions: Schäffer's and KOH reactions negative.

Habitats and distribution: solitary to scattered on soil, known from Thailand (type collection) and Kerala State, India (this study).

Materials examined: India, Kerala State, Thiruvananthapuram District, Palode, JNTBGRI campus, 8.75° N, 77.02° E, elev. 150 m, 13 May 2019, TBGT(M)17808; *ibid*. 17 June 2019, TBGT(M)17822; 18 June 2019, TBGT(M)17828; 3 September 2019, TBGT(M)17954; 13 May 2020, TBGT(M)18054; 26 November 2020 TBGT(M)18440; Kottayam District, Chittadi, 9.54° N, 76.86° E, elev. 67 m, 1 June 2022, TBGT(M)18847.

GenBank numbers: ITS: OP518433, OP518480, OP518603.

Notes: *Agaricus brunneosquamulosus* Linda J. Chen, R.L. Zhao, K.D. Hyde & Callac, is characterized by a set of features such as medium-sized basidiomata, white pileus with concentrically arranged brownish squamules, double annulus with floccose squamules on lower surface, clavate to pyriform cheilocystidia and negative KOH and Schaffer's reaction. The species was originally described from Thailand (Chen et al. 2015a), and the Indian collection is similar to the type description both morphologically and molecularly. ITS sequence (692 bp) of Indian collection shows 99% sequence identity with *A. brunneosquamulosus* (KJ540968) with only three nucleotide differences. Slightly larger basidiomata, smaller basidiospores and abundant cheilocystidia are the changes observed in the present collection from the type description. As no major differences were noticed in the Indian material, we confirm the Indian collection as *A. brunneosquamulosus* (Fig. 142).

Hydnangiaceae Gäum. & C.W. Dodge

Hydnangiaceae was described by Gäumann and Dodge (1928) in Agaricales based on type genus *Hydnangium.* This family is composed four genera viz. *Hydnangium*, *Laccaria*, *Maccagnia* and *Podohydnangium* (He et al. 2019).

Laccaria Berk. & Broome

Laccaria is characterized by globose to oblong, echinulate, multinucleate and red, orange, brown, white or purple-colored basidiomata (Berkeley and Broome 1883; Singer 1986; Mueller 1991). The type species, *L. laccata* was described from Slovenia (Europe), approximately 110 species have been described from all over the world (Cui et al. 2021). Species of *Laccaria* are known to form ectomycorrhizal associations with a broad range of gymno- and angiosperm trees (Mueller 1992).

Laccaria rubriporus S. M. Tang, ***sp. nov.***

Index Fungorum number: IF900128; *facesoffungi number*: FoF 13869; Figs. 143, 144

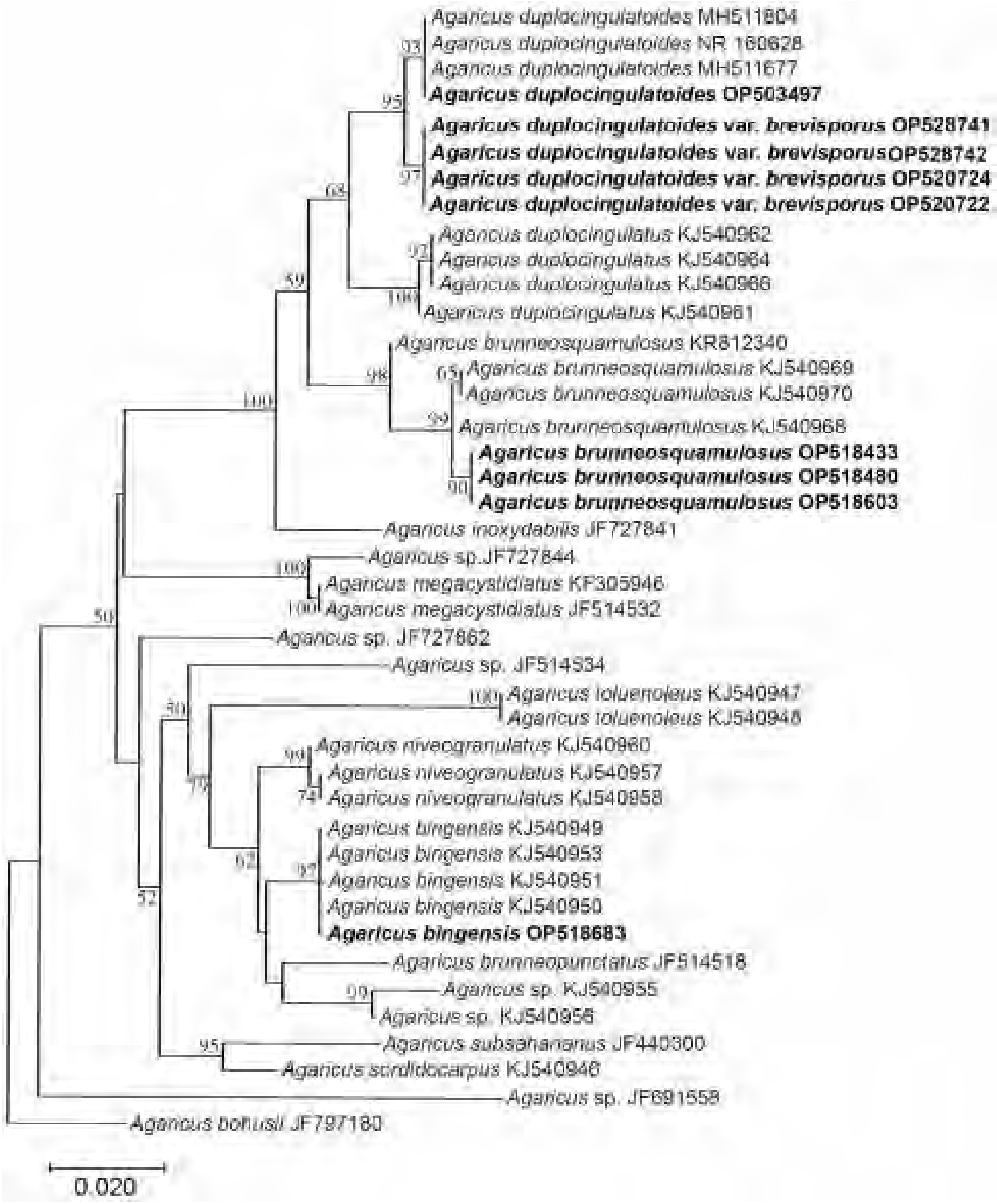


Fig. 142 Phylogeny of species of *Agaricus* section *Brunneopicti* generated from ML analysis of ITS sequence data rooted with *Agaricus bohusii.* Bootstrap values (ML, ˃50%) are indicated above/below branches. Taxa from Kerala, India used in the present study are in bold

Fig. 143 ***Laccaria rubriporus*** (HKAS107552, **holotype**). **a** Basidioma. **b** OM basidiospores. **c**–**d** SEM basidiospores. Scale bars: a = 1 cm, b = 10 μm, c–d = 5 μm

Etymology: The epithet 'rubriporus' refers to the red basidioma of this species.

Diagnosis: Laccaria rubriporus is distinguished by its brownish red to deep orange pileus, small basidioma, and fasciation or scattered, a pastel red to greyish red context, a reddish brown stipe, broadly ellipsoid to basidiospores (6.6–9.3 × 7.4–10 μm), and the presence of clamps.

Macromorphology: Fasciation or scattered on ground in temperate forests of *Pinus*. *Basidioma* small, fasciation or scattered. *Pileus* 5–15 mm diam., hemispherical to paraboloid, brownish red (8C6-8) at centre, but becoming orange (6A6-7) to dark orange (6A8) towards the margin; margin plicate striate, decurved; trama white (1A1), unchanging. *Lamellae* pastel red (10A4-5) to greyish red (10D4-5). *Lamellulae* emarginated with decurrent tooth, regular, close. *Stipe* 17–22 × 1–2.2 mm, reddish brown (9E5-8), cylindrical, solid, broadly fistulose, fibrillose-striate. *Context* thin, pastel red (10A4-5) to greyish red (10D4-5).

Micromorphology: Basidia 34–42 × 4–11 μm, clavate, 2-spored, rarely 1-spored, sterigmata 5–7 μm long. *Basidiospores* [113/9/1] (5.9–) 6.6–9.3 (–9.8) × (5.9–) 7.4–10.0 (–10.4) μm, Q = (1.00–) 1.02–1.09 (–1.11), $Q_m = 1.05 \pm 0.02$, globose, hyaline, echinulate; echinulate 0.7–2.2 μm in length, 0.4–1.0 μm wide at base. *Cheilocystidia* 14–48 × 2–4 μm, subclavate, sometimes irregular, thin-walled, hyaline. *Pleurocystidia* 16–22 × 3–5 μm, subclavate, thin-walled, hyaline hyphae. *Lamella* edge appearing as a sterile strip composed of clavate, cylindrical inflated cells 23–34 × 5–9 μm, thin-walled, colourless, similar to basidioles in shape. *Subhymenium* 16–24 μm thick, with 2–3-layered, with ovoid, subglobose to ellipsoid or irregular cells of 3–10 × 3–5 μm. *Pileipellis* 140–210 μm thick composed of parallelly, thin-walled, cylindrical, greyish-red to reddish-orange, filamentous hyphae 9–16 μm thick. *Stipe trama* composed of longitudinally arranged, clavate terminal cells, light brown, 16–53 × 3–6 μm. *Stipitipellis* a cutis, of closely packed, predominantly longitudinally arranged hyphae, with grey pigmentation; hyphae 4–6 μm broad. *Clamp* present.

Material examined: China, Yunnan Province, Chuxiong Prefecture, Wuding County, 24° 58.289′ N, 100° 48.153′ E, 2078 m a.s.l., 24 July 2019, Song-Ming Tang, T89 (HKAS107552, **holotype**).

GenBank numbers: ITS: MT500503; LSU: MT500543.

Notes: Our laccaria-like collection is grouped with *L. canaliculata*, *L. glabripes* and *L. ohiensis* (Figs. 143, 144). The ITS locus of our collection compared with these three

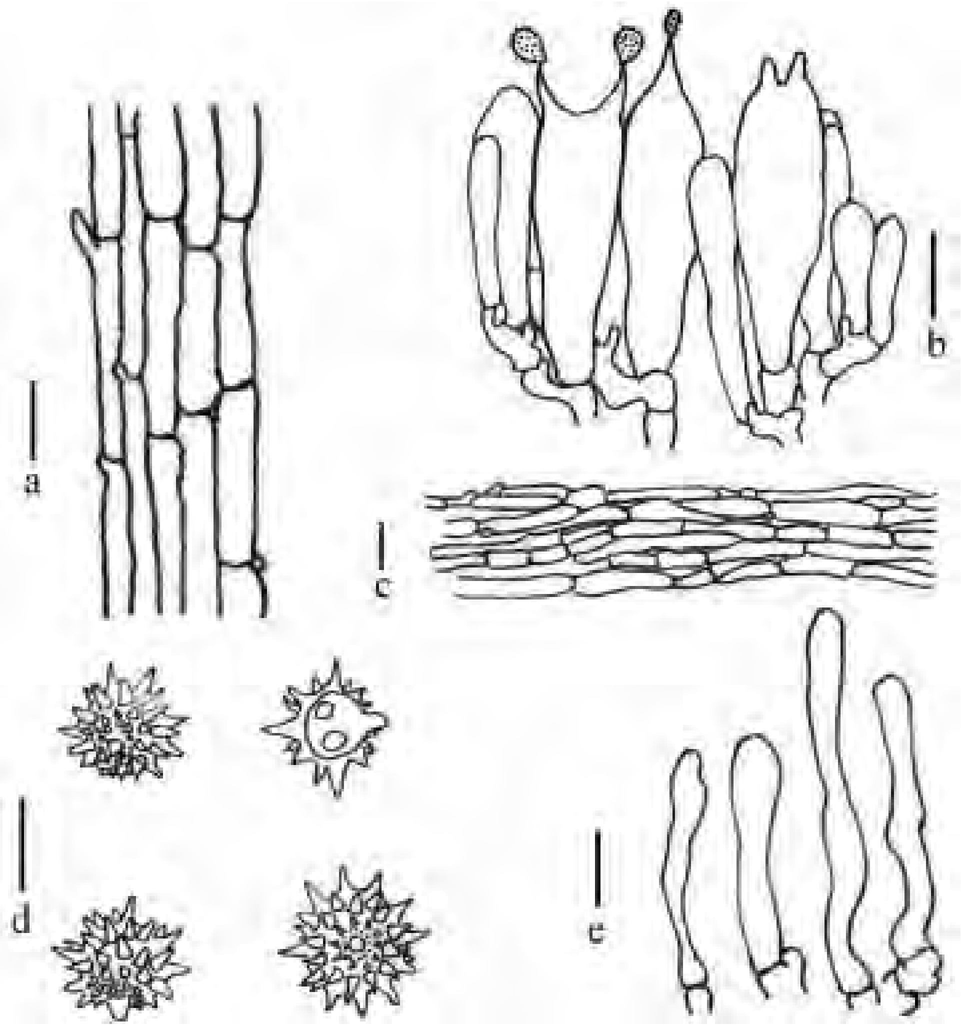


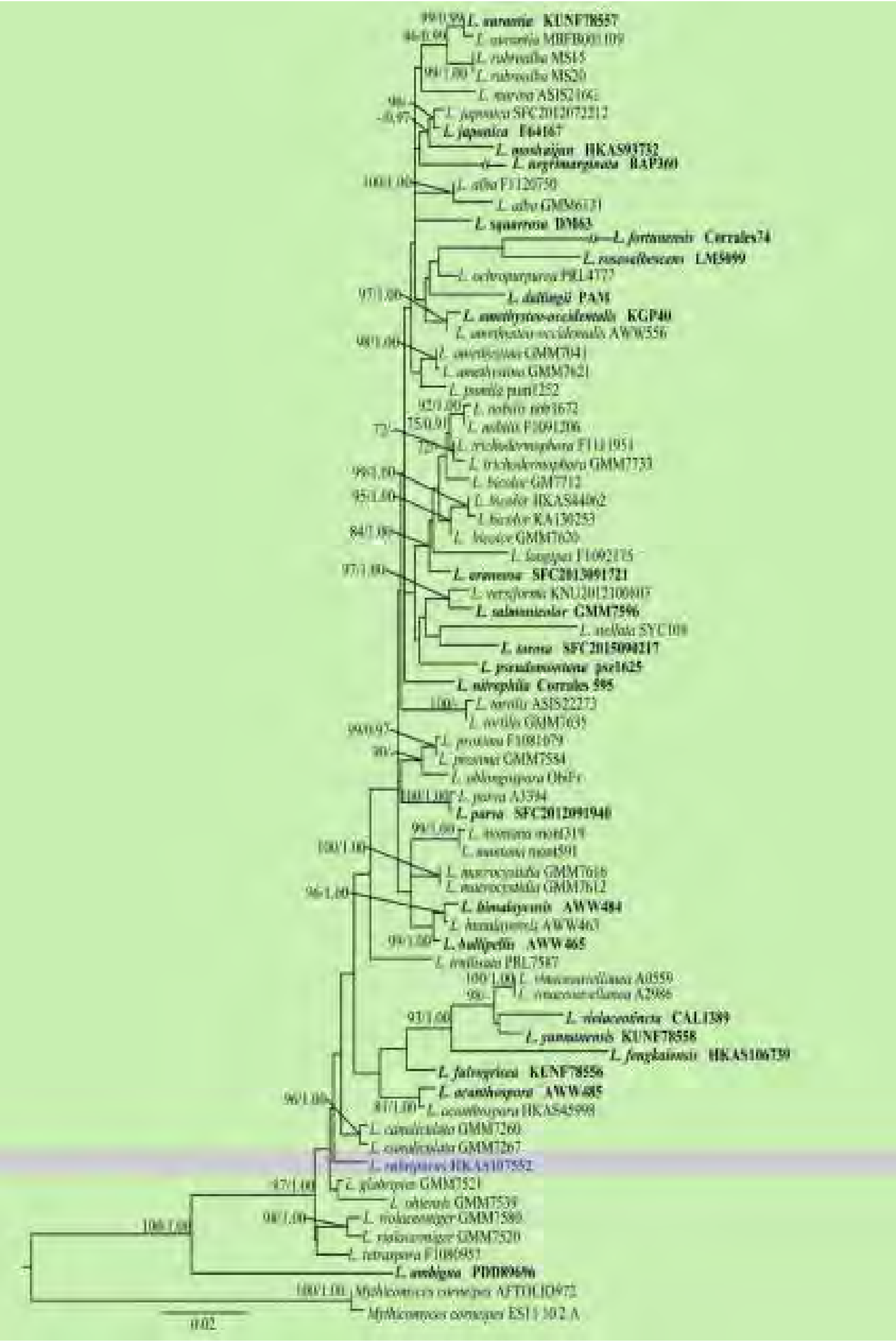
Fig. 144 ***Laccaria rubriporus***. **a** Stipitipellis. **b** Hymenium. **c** Pileipellis. **d** Basidiospores. **e** Cheilocystidia. Scale bars: a–c = 20 µm, b, d–e = 10 µm

species and *L. canaliculata*, *L. glabripes* and *L. ohiensis* have 1.95%, 1.3%, and 3.25% nucleotides difference respectively. Further, our collection morphologically differs from these phylogenetically related species (Table 5).

Our collection is morphologically similar to *L. acanthospora* A.W. Wilson & G.M. Muell., *L. ambigua* K. Hosaka, A. W. Wilson, & G. M. Mueller, *L. aurantia* Popa, Rexer, Donges, Zhu L. Yang & G. Kost, *L. indohimalayana* K. Das, I. Bera & Vizzini, *L. pseudomontana* Osmundson, C.L. Cripps & G.M. Muell. and *L. trichodermophora* G.M. Muell. in their brownish red to orange basidioma (Mueller 1984; Osmundson et al. 2005; Wilson et al. 2013, 2017; Popa et al. 2014; Wang et al. 2019a, b). However, *L. acanthospora* has relatively larger (40–56 × 10–14 µm) basidia (Wilson et al. 2013), while cheilocystidia and pleurocystidia are absent in *L. indohimalayana*, *L. pseudomontana* and *L. trichodermophora* (Mueller 1984; Osmundson et al. 2005; Wang et al. 2019b). *Laccaria ambigua* has 2–4-spored sterigmata (Wilson et al. 2017) and *L. aurantia*

Table 5 Morphological comparison of phylogenetically closely related *Laccaria* species with our collection

Species	Pileus colour	Basidiospores Shape, size µm	Locality	References
L. canaliculata	Bright tawny-brown	Globose, 9–10 × 9–10	Australia	Saccardo (1891), Massee (1899)
L. glabripes	Flesh pink to reddish brown	Globose, 7–7.7 × 8–8.5	New Zealand	Aguirre-Acosta and Pérez-Silva (1978)
L. ohiensis	Reddish brown to dark reddish brown	Oblong, 9.5–12.5	USA	McNabb (1972)
L. rubriporus	Brownish red to deep orange	Globose, 6.6–9.3 × 7.4–10	China	This study


99/0.99 L. aurantia KUNF78557
96/0.99 L. aurantia MBFB001109
L. rubroalba MS15
99/1.00 L. rubroalba MS20
L. murina ASIS21661
96/-
-/0.97 L. japonica SFC20120722l2
L. japonica F64167
L. moshuijun HKAS93732
L. negrimarginata BAP360
100/1.00 L. alba F1120750
L. alba GMM6131
L. squarrosa DM63
L. fortunensis Corrales74
L. roseoalbescens LM5099
L. ochropurpurea PRL4777
L. dallingii PAM
97/1.00 L. amethysteo-occidentalis KGP40
L. amethysteo-occidentalis AWW556
98/1.00 L. amethystina GMM7041
L. amethystina GMM7621
L. pumila pum1252
92/1.00 L. nobilis nob1672
75/0.91 L. nobilis F1091206
72/-
72/- L. trichodermophora F1111951
L. trichodermophora GMM7733
L. bicolor GM7712
99/1.00 L. bicolor HKAS84062
95/1.00 L. bicolor KA130253
84/1.00 L. bicolor GMM7620
L. longipes F1092175
L. araneosa SFC20130917 21
97/1.00 L. versiformis KNU20121008 07
L. salmonicolor GMM7596
L. stellata SYC108
L. torosa SFC20150902 17
L. pseudomontana pse1625
L. nitrophila Corrales 595
100/- L. tortilis ASIS22273
L. tortilis GMM7635
99/0.97 L. proxima F1081679
90/- L. proxima GMM7584
L. oblongospora ObFr
100/1.00 L. parva A3594
L. parva SFC20120919 40
99/1.00 L. montana mont319
L. montana mont591
100/1.00 L. macrocystidia GMM7616
L. macrocystidia GMM7612
96/1.00 L. himalayensis AWW484
L. himalayensis AWW463
99/1.00 L. bullipellis AWW465
L. trullisata PRL7587
100/1.00 L. vinaceoavellanea A0559
98/- L. vinaceoavellanea A2986
93/1.00 L. violaceotincta CAL1389
L. yunnanensis KUNF78558
L. fengkaiensis HKAS106739
L. fulvogrisea KUNF78556
L. acanthospora AWW485
81/1.00 L. acanthospora HKAS45998
96/1.00 L. canaliculata GMM7260
L. canaliculata GMM7267
L. rubripora HKAS107552
97/1.00 L. glabripes GMM7521
L. ohiensis GMM7539
98/1.00 L. violaceonigra GMM7580
L. violaceonigra GMM7520
L. tetraspora F1080957
100/1.00 L. ambigua PDD89696
100/1.00 Mythicomyces corneipes AFTOL ID972
Mythicomyces corneipes ES11 30 2 A
0.02

◂**Fig. 145** Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data which comprised 1496 characters (ITS = 616, LSU = 880). The best scoring RAxML tree with a final likelihood value of − 6720.166487 is presented. The matrix had 438 distinct alignment patterns, with 22.36% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.257506, C = 0.197810, G = 0.252372, T = 0.292312; substitution rates: AC = 1.960957, AG = 6.783927, AT = 2.184484, CG = 0.370410, CT = 7.815524, GT = 1.0; gamma distribution shape parameter α = 0.191204. Bootstrap support for maximum likelihood (ML) equal to or greater than 70% and clade credibility values greater than 0.90 (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 strain is indicated in blue bold. The tree is rooted to *Mythicomyces corneipes* (AFTOLID 972; ES11102A)

has a relatively larger basidiomata (35–40 mm) and basidia (40–50 × 10–12 µm) (Popa et al. 2014).

Laccaria araneosa H.J. Cho & Y.W. Lim, *L. bullulifera* Contu & Ballero, *L. negrimarginata* A.W. Wilson & G.M. Mueller and *L. tetraspora* Singer are also similar to our collection in their small basidiomata (≤ 20 mm) (Singer 1946; Aguirre-Acosta and Pérez-Silva 1978; Wilson et al. 2013; Cho et al. 2018). However, *L. araneosa* has an orange brown to light brown pileus, relatively large basidia (42–52 × 11–14 µm) and lack of cheilocystidia and pleurocystidia (Cho et al. 2018). *Laccaria bullulifera* has a rufous to pink basidioma with a pileus ca. 7–14 mm, and has relatively broad (7.5–8.5 µm) basidia (Aguirre-Acosta and Pérez-Silva 1978). *Laccaria negrimarginata* has a dark blackish brown to dark brown basidioma, a relatively broad (5–10 µm) pileipellis hyphae (Wilson et al. 2013). *Laccaria tetraspora* has relatively larger (40–50 × 11 µm) basidia (Singer 1946). Even though, statistical support in the phylogeny is not supported, we introduce our collection as *Laccaria rubriporus* sp. nov. based on morphological significance (Fig. 145).

Inocybaceae Jülich

Inocybaceae is a monophyletic family within the Agaricales, with a worldwide distribution and contains approximately 1050 species characterized by a dirty- to tobacco-brown spore print. The majority of species form ectomycorrhiza and associated with 23 vascular plant families (Matheny et al. 2006, 2020). Currently, the family includes seven genera viz. *Auritella* Matheny & Bougher, *Inocybe* (Fr.) Fr., *Inosperma* (Kühner) Matheny & Esteve-Rav., *Mallocybe* (Kuyper) Matheny, Vizzini & Esteve-Rav., *Nothocybe* Matheny & K.P.D. Latha, *Pseudosperma* Matheny & Esteve-Rav. and *Tubariomyces* Esteve-Rav. & Matheny, according to the phylogenetic studies presented by Matheny et al. (2020).

Inocybe (Fr.) Fr.

According to Matheny et al. (2020), *Inocybe* (Type species *Agaricus relicinus* Fr.) comprises approximately 850 species worldwide, representing the largest genus in the family Inocybaceae. They are characterized by the presence of metuloid cystidia (with calcium oxalate microcrystals at the apex and more or less thickened walls), spores that are both smooth and angular or with nodules or spines on their surface. All of them form ectomycorrhizal associations with a wide range of vascular plant families.

Inocybe avellaneorosea Esteve-Rav., E. Larss. & Pancorbo, ***sp. nov.***

Index Fungorum number: IF900464; *Facesoffungi number*: FoF 14220; Fig. 146

Etymology: Referring to the colour of the pileus (from Latin “avellaneus” which refers to the hazelnut colour of the pileus) and the stipe (from Latin “roseus” which refers to the pink or rosy tone of the stipe).

Diagnosis: *Inocybe avellaneorosea* is close to *I. oblectabilis* (Britzelm.) Sacc. in morphological and ecological characters. It differs macroscopically by the conspicuous and persistent pink to rosy tone along the entire length of the stipe of fresh and young basidiomes (except bulb), the slightly shorter pleurocystidia on average (Lm = 47 µm *vs.* 52.5 µm) and the spores with a slightly higher Qm (1.3 µm *vs.* 1.25 µm), provided with a lower number of nodules (11–15 µm *vs.* 14–18 µm), these being slightly higher and gently tapered towards their apex. Both species also differ in their molecular characters in the ITS sequence (90% similarity).

Macromorphology*: Basidiomata* agaricoid and stipitate. *Pileus* 15–25(–30) mm, at first conical-campanulate, then convex to plano- convex, broadly obtuse umbonate to subumbonate, matt, not or hardly hygrophanous; margin straight, regular to wavy with age, fissurate at times; velipellis present at the umbo, usually poorly developed and persistent, at least in young specimens; colour uniformly brownish, rarely slightly lighter towards the margin, from chestnut brown to hazelnut brown (Mu 7.5YR 5/6-8, 4/4-6); surface radially fibrous, smooth, tending to become slightly rimose towards the margin, in older specimens sometimes broken into shreds and longitudinally frayed, greasy in appearance when moist. *Lamellae* crowded (L = 48–60; l = 1), free to almost free, ventricose, initially white, becoming ochraceous to pale brown, then tobacco brown, edge concolourous to slightly paler in adult specimens, finely crenulate. *Stipe* 25–40 × 3–5 mm, straight, abruptly bulbous, bulb clearly marginate [6–8(-10) mm broad]; colour typically pinkish (rosé) over its entire length when young and fresh (Mu 5YR 7/2-4), only slightly paler towards the base, then brownish-pink with age or when dry, white in the bulb; surface densely pruinose along the entire surface, pruina sparser towards the

Fig. 146 ***Inocybe avellaneorosea*** (AH 51879, **holotype**). **a** Basidiomata in situ. **b** Basidiospores. **c** Pleurocystidia. **d** Cheilocystidia. **e** Caulocystidia at the base of stipe (mounting media: NH_4OH). Scale bar: b = 10 µm, c–e = 50 µm, a = 20 mm

base in some specimens. *Cortina* absent. *Context* fibrose, dirty whitish at the pileus, uniformly pinkish along the stipe, white in the bulb. *Smell* not significant when cut, *taste* not recorded. Colour of exsiccatum uniformly tobacco brown (pileus and stipe), not blackening.

Micromorphology: *Spores* (7.7–)8–*9.2*–10.6(–11.5) × (5.6–)6–*7*–8(–8.7) µm, Q = (1.02–)1.12–*1.3*–1.53(–1.63) (n = 232 from 3 coll.), mostly subisodiametric to sometimes subheterodiametric, nodulose under the optical microscope, provided with 11–15 distinct knobs variable in height (≈1 µm high), yellowish, apicula distinct. *Basidia* (23.7–)24–*27.1*–31(–32.1) × (8.2–)8.5–*9.9*–11.2(–11.3) µm; Q = (2.27–)2.3–*2.7*–3.01(–3.06), 4-spored, rarely 2-spored, clavate. *Pleurocystidia* abundant, (30.5–)38.2–*47*–55.2(–69.2) × (11.7–)14.3–*18.1*–20.8(–27.3) µm. Q = (1.56–)2.04–*2.6*–3.18(–3.52), (n = 100 from 3 coll.), broadly fusiform, hyaline, base often attenuate but not pedicellate, rather crystalliferous at the apex, walls (0.99–)1.07–*1.4*–1.85(–2.03) µm thick, reaching – 2.8 µm at the apex, hyaline in 10% NH_4OH. *Lamella edge* practically sterile, composed by numerous protruding hyaline cheilocystidia mixed with abundant hyaline clavate paracystidia. *Cheilocystidia* numerous, (28.7–)31–*42.4*–52.3(–55.3) × (10.8–)12.2–*16.8*–20.9(–24.8) µm, Q = (1.23–)1.64–*2.5*–3.42(–4.23), from globose-pyriform to fusiform to subcylindrical, some with brownish intracellular contents. *Hymenophoral trama* regular to subregular, consisting of parallel hyphae, 4.9–11.2 µm wide, cylindrical to subfusiform in shape, often constricted at the septa, hyaline. *Subhymenium* poorly developed, consisting of 2–3 layers of small, sub-isodiametric, irregular cells, (5.6–)6.0–*7.7*–9.7(–10.1) µm diam. *Pileipellis* a cutis consisting of parallel cylindrical cells, 5–11 µm wide, with finely encrusting brown- yellowish pigment; subcutis with paler and wider elements, 10–25 µm diam., often constricted at the septa. *Stipitipellis* a cutis of parallel hyphae (3.6–)3.9–*5.0*–6.5(–6.9) µm, bearing numerous caulocystidia along the entire length of the stipe, a towards the base, (20.6–)23.8–*38.9*–55.3(–58.2) × (8.4–)9.2–*14.5*–18.7(–22.8) µm, Q = (1.42–)1.5–*2.7*–3.88(–4.51) (n = 100 from 3 coll.), somewhat smaller but similar in shape to hymenial cystidia, mixed with numerous clavate to subclavate hyaline cauloparacystidia. *Clamp connections* abundant.

Habitat: in temperate and humid continental forests, on preferably acidic soils, under Fagaceae (*Quercus*, *Fagus*). The two studied collections from Sweden were collected in deciduous forest with *Fagus*, *Quercus* and *Tilia* on calcareous soil.

Geographical distribution: in continental and Mediterranean Europe, known from France, Spain, Sweden and Romania, and also Eurasia (Turkey).

Material examined: France, Corsica, Moltifao, Capannace, on the banks of the river Asco, 42.481388, 9.153611, 257 msl, in acidic soil in holm oak forest (*Quercus ilex* subsp. *ilex*), 7 November 2019, A. Altés, G. Moreno, F. Pancorbo, F. Esteve-Raventós, E. Larssson, P.A. Moreau & N. Subervielle, (AH 51879, **holotype**), (EL346-19, GB, **isotype**). Spain, Madrid province, El Escorial, Prado del Molino, Arroyo del Batán, 40.576944, − 4.134166, 915 msl, in acidic soil in oak forest (*Quercus pyrenaica*), 1 June 1988, M. Heykoop & F. Esteve-Raventós, (AH 23468). Navarra Foral Community, Señorío de Bértiz Natural Park, 200 msl, in acidic soil in beech-oak forest (*Fagus sylvatica*-*Quercus robur*), 26 May 2012, A. & P. Arrillaga, (Aranzadi Zientzia Elkartea/Sociedad de Ciencias Aranzadi herbarium ARAN-Fungi, A5058255). Sweden, Västergötland, Medelplana, Råbäcks Munkängar, in soil of deciduous woods in calcareous ground, 8 August 1978, S. Jacobsson, (GB-0125617). Ibidem, in soil in deciduous woods under oaks and lime trees (*Quercus robur* and *Tilia* sp.), 8 September 2008, E. Larsson, (EL 74-08).

GenBank numbers: ITS-LSU: (AH 51879, ON994216); ITS: (EL346-19, OP002030); ITS-LSU: (AH 23468, ON994217); ITS-LSU: (A5058255, ON994218); ITS: (GB-0125617, AM882898); ITS-LSU: (EL 74-08, OP002031).

Notes: The macroscopic description is based on the holotype (Fig. 146). Phylogenetically, *I. avellaneorosea* belongs to the clade Oblectabilis. This group is represented by *I. oblectabilis* (Stangl and Schwöbel 1985; Stangl 1989; Marchetti et al. 2014), with two new species, *I. avellaneorosea* and *I. lucida* which are introduced in this study (Fig. 149). These three species share many similarities in the macromorphology, such as a slender habit, pinkish tones on the stipe, the presence of a distinct marginal bulb and the hygrophanous appearance in wet condition of the pileus, which is smooth and radially fibrous, often subrimose at the margin. They also show similar preferences for the type of habitat as temperate and/or mediterranean forests of Fagaceae (*Quercus* sp., *Fagus* sp.). According to our data, *I. oblectabilis* is most often encountered in basic to neutral soils, whereas *I. avellaneorosea* and *I. lucida* seem to prefer acidic soils.

There are also macromorphological similarities with other European species such as *I. brunneorufa* Stangl & J. Veselský (= *I. calida* Velen. *s*. Kuyper 1985) and *I. asterospora* Quél., which differ in the darker chestnut brown colours of both the stipe and pileus in young basidiomes. Also the larger cystidia and asteriform to (sub-) isodiametric spores are different in these species (Stangl 1989). Besides, the phylogenetic analysis (Fig. 149) shows that the group or clade Brunneorufa (= Calida *s*. Kuyper) does not support with the clade Oblectabilis, but there is a significant bootstrap support with the clade Asterospora. *Inocybe avellaneorosea* shows a very characteristic and conspicuous pinkish (rosy, salmon) colour throughout the stipe, especially when young, which contrasts sharply with the chestnut-brown colour of the pileus (Fig. 146). It has sometimes been confused in Europe with *I. calida* or *I. brunneorufa* (KY496805, AM882898, cited as *I. calida* and *I. calida* var. *brunneorufa* respectively) (Table 6). The size of the cystidia of *I. avellaneorosea* are similar to those of *I. oblectabilis*, although the spores are a distinguishing feature between the two, when analyzing the appearance, number and size of the nodules (Fig. 146, 148).

Inocybe lucida Esteve-Rav., Pancorbo & E. Larss., ***sp. nov.***

Mycobank number: MB844183; *Facesoffungi number*: FoF 14221; Fig. 147

Etymology: from latin "lucidum", referring to the shiny and smooth appearance of the pileus.

Diagnosis: *Inocybe lucida* is close in morphological characters and habitat to *I. oblectabilis* and *I. avellaneorosea*. It differs from both by the greater average length of the pleurocystidia (Lm = 57.3 µm) and the smaller spores (Sp_{avg} = 8.3 × 6.3 µm), provided with 11–14 nodules of non-uniform height and width (from 1 to 1.8 µm). Similar to *I. oblectabilis* in the greasy appearance of the pileus in humid environment and the pale pinkish tones of the stipe, characters that separate both at first sight from *I. avellaneorosea*. In ITS sequence the similarity is 92% from *I. oblectabilis* and 89.5% from *I. avellaneorosea.*

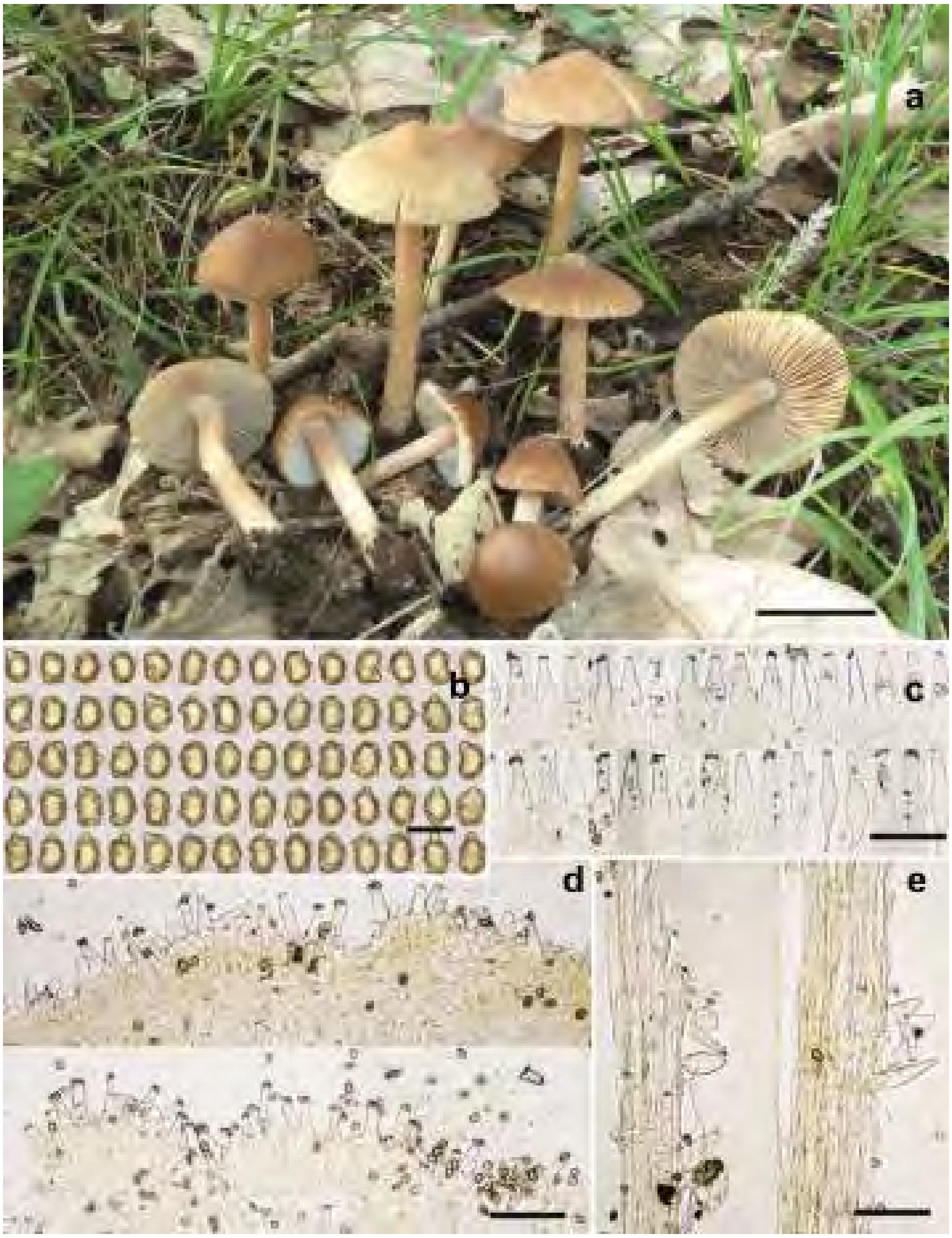
Macromorphology: *Basidiomata* agaricoid and stipitate. *Pileus* (12–)15–35(–45) mm, at first conical-campanulate, then convex to plano-convex, with distinct obtuse umbo when expanded, hygrophanous in wet weather; margin straight, regular to wavy or cracked with age, fissurate at

Table 6 Data of sequenced collection of *Inocybe avellaneorosea*, *I. lucida* and *I. oblectabilis*

Species	Voucher	Country	Habitat	ITS	LSU
I. avellaneorosea	A5058255	ESP	(1), (2)	ON994218	ON994218
I. avellaneorosea	AH 23468	ESP	(3)	ON994217	ON994217
I. avellaneorosea (as *Inocybe calida* var. *brunneorufa*)	GB-0125617	SWE	N/A	AM882898*	N/A
I. avellaneorosea (as *Inocybe calida*)	4211	TUR	N/A	KY496805*	N/A
I. avellaneorosea (as *Inocybe* sp.)	LM2714	ROU	(2)	KM576430*	N/A
***I. avellaneorosea* (holotype)**	AH 51879	FRA	(4)	ON994216	ON994216
I. lucida	AH 25011	ESP	(4)	ON994210	ON994210
I. lucida	AH 36259	ESP	(5), (14)	ON994214	N/A
I. lucida	AH 36385	ESP	(14)	ON994206	ON994206
I. lucida	AH 40423	ESP	(2)	ON994207	ON994207
I. lucida	AH 46863	ESP	(5)	ON994211	ON994211
I. lucida	AH 50982	ESP	(5), (6)	ON994213	ON994213
I. lucida	AH 51854	FRA	(7), (5), (8), (9), (10), (11)	ON994209	ON994209
I. lucida	AH 51866	FRA	(7), (5), (8), (9), (10), (11)	ON994215	ON994215
I. lucida	AH 51880	FRA	(4), (5), (8), (7), (12)	ON994204	ON994204
I. lucida	AH 51881	FRA	(4), (5), (8), (7), (12)	ON994208	ON994208
I. lucida	AH 51895	FRA	(4), (5), (8), (7), (12)	ON994212	ON994212
I. lucida (as *Inocybe* sp. clone)	Plot2-48-M3	SVN	(8)	MW028042*	N/A
***I. lucida* (holotype)**	AH 50955	ESP	(3)	ON994205	ON994205
I. oblectabilis	AH 24538	ESP	(13), (4)	ON994234	ON994234
I. oblectabilis	AH 25455	ESP	(14)	ON994232	ON994232
I. oblectabilis	AH 30691	ESP	(4), (15)	ON994226	ON994226
I. oblectabilis	AH 30692	ESP	(4), (16)	ON994221	ON994221
I. oblectabilis	AH 36268	ESP	(14)	ON994220	ON994220
I. oblectabilis	AH 36269	ESP	(14)	ON994228	ON994228
I. oblectabilis	AH 36343	ESP	(4)	ON994224	ON994224
I. oblectabilis	AH 40307	ESP	(14), (17)	ON994230	ON994230
I. oblectabilis	AH 40406	ESP	(2), (18)	ON994223	N/A
I. oblectabilis	AH 40407	ESP	(2), (18)	ON994231	ON994231
I. oblectabilis	AH 40408	ESP	(2), (18)	ON994225	ON994225
I. oblectabilis	AH 40424	ESP	(2), (18)	ON994233	ON994233
I. oblectabilis	AH 40475	ESP	(4)	ON994219	ON994219
I. oblectabilis	AH 45228	ITA	(4)	ON994229	ON994229
I. oblectabilis	AH 48211	ESP	(13)	ON994227	ON994227
I. oblectabilis	AH 56436	ESP	(3), (19)	ON994222	ON994222
I. oblectabilis	MCVE8458	ITA	(4)	JF908129*	N/A
***I. oblectabilis* (epitype)**	M 0222614	DEU	(2), (20), (21), (22)	KM873365*	N/A
I. oblectabilis (as *Inocybe* sp.)	LMKR794	GBR	(19)	MF352728*	N/A
I. oblectabilis (as uncultured ectomycorrhyza)	Isolate 1	ITA	(2)	AJ879660*	N/A
Pseudosperma spurium	SJ92017	SWE	N/A	AM882784*	N/A
I. brunneorufa	GB-0125615	EST	(2), (23), (24), (19)	AM882760*	AM882760*
***I. brunneorufa* (holotype)**	M-0151589	DEU	(1), (25), (20), (21)	OP035649	N/A
I. asterospora	EL372	FRA	(4), (5), (8), (7), (12)	OP001731	OP001731
I. asterospora	TF01-038	DNK	(1)	AJ889951*	N/A

All sequences have been generated for this study except those marked with * which have been retrieved from GenBank. Type species are marked in bold. Legend to Habitat: *Fagus sylvatica* (1), *Quercus robur* (2), *Quercus pyrenaica* (3), *Quercus ilex* (4), *Quercus suber* (5), *Olea europaea* v. *sylvestris* (6), *Pinus pinaster* (7), *Quercus pubescens* (8), *Arbutus unedo* (9), *Cistus* (10), *Erica arborea* (11), *Cistus monspelliensis* (12), *Quercus faginea* (13), *Quercus rotundifolia* (14), *Pinus halepensis* (15), *Cistus albidus* (16), *Cistus salvifolius* (17), *Salix atrocinerea* (18), *Pinus sylvestris* (19), *Ulmus* (20), *Acer* (21), *Salix* (22), *Tilia cordata* (23), *Betula pubescens* (24), *Alnus* (25). N/A = Not available. The country of origin of each collection is abbreviated by ISO 3166-1 alpha-3 codes

Fig. 147 ***Inocybe lucida*** (AH 50955, **holotype**). **a** Basidiomata in situ. **b** Basidiospores mounting in NH_4OH. **c** Pleurocystidia. **d** Cheilocystidia. **e** Caulocystidia at the base of stipe. Scale bar: a = 20 mm, b = 10 µm, c–e = 50 µm



times; velipellis absent or very fleeting, observed only in a few very young specimens; colour initially uniformly brownish to chestnut brown (Mu 7.5YR 5/6-8, 4/6 to Mu 5YR 4/4-6) when wet, paling to brown ochraceous to tawny (Mu 10YR 5/6-8, 6/6-8) when dehydrating, especially from the umbo towards the margin; surface radially fibrous, smooth, shiny, often with a greasy aspect in wet condition, sometimes sticky and adhering earth particles, at first with uniform appearance, then becoming subrimose or distinctly rimose towards the margin. *Lamellae* crowded (L = 52–60; l = 1), free to almost free, ventricose, initially white, becoming ochraceous or yellow ochraceous, then pale brown, finally tobacco brown; edge concolourous to slightly paler in adult specimens, finely crenulate. *Stipe* 25–50(−60) × 3–7 mm, straight or sometimes sinuose or curved towards the base, abruptly bulbous, bulb clearly marginate, 7–10 mm broad; colour initially very pale pinkish or pinkish grey (Mu 5YR 7/3-4), especially in the upper half of the stipe, soon fading with age, especially in the lower half, and practically whitish to ochraceous with, sometimes, a pinkish reflection (in AH 51880 the pinkish shade being absent); surface densely pruinose over the entire length. *Cortina* absent. *Context* fibrose, dirty whitish at the pileus, at the stipe sometimes with a faint pinkish reflection or white along the entire length, including the bulb. *Smell* not significant when cut, *taste* not recorded. *Colour of exsiccatum* brown at the pileus, somewhat paler at the stipe (tawny to light ochraceous), not blackening.

Fig. 148 SEM spores of *Inocybe oblectabilis* epitype: **a** Basidiomata. **b** Basidiospores. *Inocybe avellaneorosea* holotype: **c** Basidiomata. **d** Basidiospores. *Inocybe lucida* holotype: **e** Basidiomata. **f** Basidiospores. Scale bar: b, d, f = 2 µm

Micromorpholology: *Spores* (6.5–)7.1–*8.3*–10(–11.5) × (5.0)5.3–*6.3*–7.5(–8.3) µm, Q = (1.02–)1.16–*1.3*–1.51(–1.63) (n = 257 from 5 coll.), mostly subisodiametric to sometimes subheterodiametric, distinctly nodulose under the optical microscope, provided with 11–17 distinct knobs variable in height (0.9–1.8 µm high), yellowish, apicula distinct. *Basidia* (22.8–)23.2–*25.9*–28.3(–29.3) × (8–)8.3–*9.6*–10.7(–11.1) µm; Q = (2.17–)2.35–*2.7*–3.04(–3.12), 4-spored, rarely 2-spored, clavate. *Pleurocystidia* abundant, (37.3–)48.4–*57.3*–67.2(–70) × (11.6–)12.6–*15.7*–20.5(–23.8) µm, Q = (2.36–)2.71–*3.6*–4.76(–5.29), (n = 132 from 5 coll.), fusiform to rarely lageniform, hyaline, base attenuate even pedicellate, weakly crystalline apex, walls (0.7–)0.85–*1.6*–2.58(–2.75) µm thick, slightly thicker at the apex, hyaline to hardly yellowish in 10% NH_4OH. *Lamella edge* practically sterile, composed by numerous protruding hyaline cheilocystidia mixed with abundant mostly hyaline, clavate, paracystidia. *Cheilocystidia* numerous, (30.5–)36–*47.8*–59.7(–65) × (11–)12.2–*15.3*–20(–21.9) µm, Q = (1.87–)2.29–*3.1*–4.07(–4.36), somewhat shorter and wider than pleurocystidia. *Hymenophoral trama* regular to subregular, consisting of parallel hyphae, 3.3–7.3 µm wide, cylindrical to subfusiform in shape, often constricted at the septa, hyaline. *Subhymenium* poorly developed, consisting of 2–3 layers of small, subisodiametric, irregular cells, (5.8–)6.7–*8.2*–9.8(–10.7) µm diam. *Pileipellis* a cutis consisting of parallel cylindrical cells, 4.8–9.4 µm wide, somewhat constricted at the septa, with finely encrusting yellowish pigment, mixed with oleiferous, aseptate, flexuous hyphae of variable width, with yellowish ochraceous content; subcutis with wider and paler elements. *Stipitipellis* a cutis of parallel hyphae (2.8–)3.5–*4.5*–5.6(–5.8) µm, mixed with some oleiferous hyphae, bearing numerous caulocystidia along the entire length of the stipe, (33–)36.5–*58.1*–86.8(–93.5) × (6.8–)11–*15*–19.1(–22.3) µm, Q = (2.13–)2.39–*3.9*–5.94(–7.07) (n = 102 from 5 coll.), lageniform, fusiform, mixed with numerous clavate to subglobose hyaline paracaulocystidia. *Clamp connections* abundant.

Habitat: In mediterranean and warm continental forests in Europe, on acid or decalcified soils under *Quercus* (*Q. ilex* subsp. *ilex*, *Q. ilex* subsp. *rotundifolia*, *Q. suber*, *Q. pyrenaica* and *Q. humilis*).

Distribution: found in mediterranean Europe, known from France, Spain and Slovenia.

Material examined: France, Corsica, Ghisonaccia, Domaine de Pinia, 42.012777, 9.459444, 4–12 msl, in acidic sandy soil of mixed mediterranean forest [*Quercus suber*, *Q. humilis* (= *Q. pubescens*), *Cistus sp.*, *Pinus pinaster*, *Arbutus unedo*], 6 November 2019, A. Altés, G. Moreno, F. Pancorbo, F. Esteve-Raventós, E. Larsson, P.A. Moreau & N. Suberbielle, (AH 51854). Idem, (AH 51866). Corte, Domaine Saint Jean (San Giovanni), 42.295277, 9.172222, 400 msl, in acidic soil in mixed forest [*Quercus suber*, *Q. humilis* (= *Q. pubescens*), *Cistus sp*., *Pinus pinaster*, *Arbutus unedo*], 7 November 2019, A. Altés, G. Moreno, F. Pancorbo, F. Esteve-Raventós, E. Larsson, P.A. Moreau & N. Suberbielle, (AH 51880). Ibidem, (AH 50881). Ibidem, (EL 351-19, GB). Ibidem, 8 November 2019, A. Altés, G. Moreno, F. Pancorbo & F. Esteve-Raventós, (AH 51895). Spain, Andalucía, Cádiz, road from Los Barrios to Facinas (CA-221), Puerto de Ojén, 220 msl, in acidic soil of cork oak wood (*Quercus suber*), 20 December 1993, A. Ortega, (GDA 31866; AH 46863). Andalucía, Cádiz, Tarifa, Parque Natural del Estrecho, Sierra de la Plata, Monte Silla del Papa, 36.126732, -5.763624, 360 msl, in acidic cork oak wood (*Quercus suber*), 18 May 2016, F. Sánchez, (FP16051801, AH 50982). Andalucía, Córdoba, road of Las Ermitas, El Bañuelo, 37.934166, -4.848611, 516 msl, in acidic mixed cork oak and holm oak wood (*Quercus suber* and *Q. ilex* subsp. *rotundifolia*), 13 December 2005, G. Moreno, J. Llistosella, P. Pérez-Daniels & F. Esteve-Raventós, (AH 36259). Castilla-León, Avila, Candeleda, Fuente del Roble, 40.172425, -5.234914, 594 msl, in acidic soil in oak wood (*Quercus pyrenaica*), 1 May 2011, M.A. Ribes, (AH 50955, **holotype**), (FP11050102 **isotype**). Cataluña (Catalonia), Barcelona, road from Vallgorguina to Collsacreu (C-61), in acidic soil of holm oak wood (*Quercus ilex* subsp. *ilex*), 15 October 1991, G. Moreno & F. Esteve-Raventós, (AH 25011). La Rioja, Ocón, Santa Lucía, 42.301666, -2.263333, 800 msl, in decalcified sandy soil of holm oak wood (*Quercus ilex* subsp. *rotundifolia*), 15 June 2008, A. Caballero, (AC3858, AH 36385). Pais Vasco (Euskadi), Vizcaya (Bizkaia), Musques (Muskiz), La Campa Auzoa, 43.321388, -3.133333, 70 msl, under oaks (*Quercus robur*), 1 June 2013, R. Fernández-Sasia, (RFS 130601-02, AH 40423).

GenBank numbers: ITS-LSU: (AH 51854, ON994209; AH 51866, ON994215; AH 51880, ON994204; AH 50881, ON994208; EL 351-19, OP002056; AH 50955, ON994205; AH 36385, ON994206; AH 40423, ON994207), ITS: (AH 36259, ON994214; AH 25011, ON994210)

Notes: *Inocybe lucida* is similar to *I. oblectabilis* in their macroscopic characters viz, a slender habit, colours of the pileus and stipe with a marked hygrophaneity, being the pileus very smooth and acquiring in wet weather a shiny and glossy appearance. However, the two species differ markedly in the spore size (clearly smaller in *I. lucida*), in the appearance of the knobs (higher in *I. lucida*), and also in the much larger cystidia in *I. lucida*, with a clear tendency to be narrowly fusiform and pedicellate (Fig. 147). Although the spores are similar in ornamentation (Fig. 148), *I. lucida* can be distinguished from *I. avellaneorosea* by the longer cystidia, differently coloured stipe and the shiny and very smooth appearance of the pileus in wet weather. According to the data from the numerous collections studied, it seems to behave as a southern species on the European continent, with a marked preference for acid soils, fruiting in mediterranean and subcontinental *Quercus* sp. (Fagaceae) forests, both evergreen (*Q. ilex*, *Q. suber*) and deciduous (*Q. faginea*, *Q. pyrenaica*, *Q. robur*) (Table 6) (Figs. 148, 149).

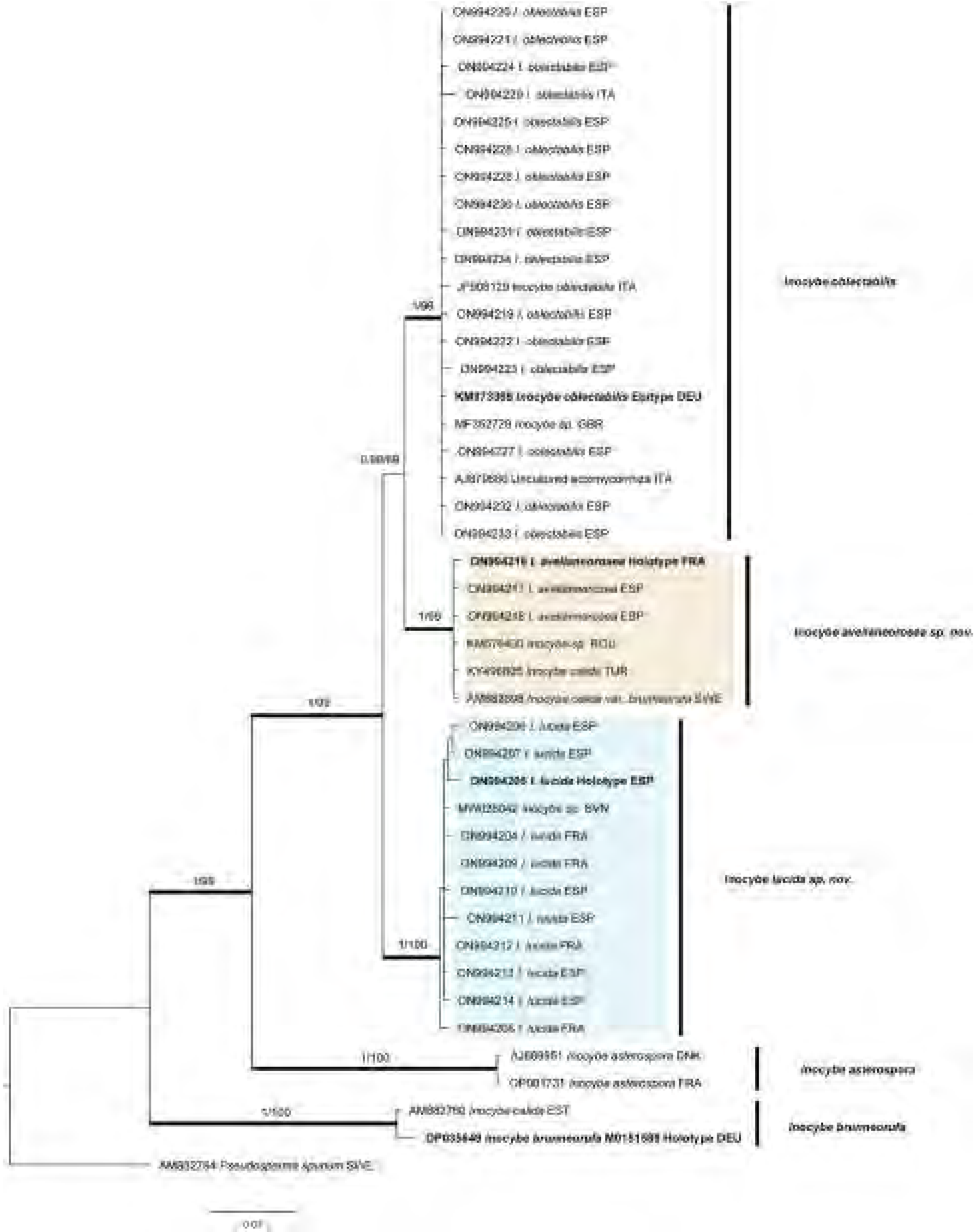
Lyophyllaceae Jülich

The family Lyophyllaceae was established by Jülich (1981). The members of the family are found all over the world. However, the majority of species are found in the northern temperate and arctic regions. The presence of clamp connections on all hyphae and the presence of siderophilous granules in basidia, detected by aceto-carmine treatment, are the most important characteristics of the family (Kühner 1938; Jülich 1981; Kalamees 2004). Singer (1986) classified this group as the Lyophylleae tribe of the Tricholomataceae. Recent multigene phylogenetic analyses established the monophyly of Lyophyllaceae (Sánchez-García et al. 2014; Bellanger et al. 2015).

Lyophyllum P. Karst.

The genus *Lyophyllum* represents one of the well-known agaric genera with about 116 species names (including synonyms) listed in the Index Fungorum (2023). The genus is widespread in the boreal, temperate, and arid regions, but only a few species are reported from the tropics (Pegler 1986; Singer 1986). The genus has an inconsistent taxonomic history. Traditionally, species of *Lyophyllum* are characterized by dull-coloured, collybioid, clitocyboid or tricholomatoid basidiocarps and basidia with siderophilous granules (Pegler 1983; Singer 1986; Kalamees 2004). In their phylogenetic analysis of the Lyophyllaceae, Hofstetter et al. (2002) demonstrated that *Lyophyllum* species fell into three separate groups and the type species of the genus, *Lyophyllum leucophaeatum,* nested in a clade containing *Calocybe*. To retain the genus name for the many commonly encountered dull-coloured species of *Lyophyllum*, conservation of the genus name with the new type *L. semitale* was proposed (Redhead et al. 2006). Subsequently, Hofstetter et al. (2014) identified a monophyletic lineage, the lyophylloid clade or *Lyophyllum* sensu stricto, which is composed of species characterized by basidiocarps with brown or dusky pigments and basidia containing siderophilous granules of the macro-type (Clémençon 1986). Some species of *Lyophyllum* (e.g., *L. ambustum*, and *L. atratum*) are reported to be carbonicolous.

So far, only four species of *Lyophyllum* (*L. ulmarium*, *L. leucocephalum*, *L. ambustum*, and *L. subnigricans*) have been reported from India (Manjula 1983). Of these, *L.*


ON994220 I. oblectabilis ESP
ON994221 I. oblectabilis ESP
ON994224 I. oblectabilis ESP
ON994229 I. oblectabilis ITA
ON994225 I. oblectabilis ESP
ON994226 I. oblectabilis ESP
ON994228 I. oblectabilis ESP
ON994230 I. oblectabilis ESP
ON994231 I. oblectabilis ESP
ON994234 I. oblectabilis ESP
JF908129 Inocybe oblectabilis ITA
1/98
ON994219 I. oblectabilis ESP
ON994222 I. oblectabilis ESP
ON994223 I. oblectabilis ESP
KM873368 Inocybe oblectabilis Epitype DEU
MF352729 Inocybe sp. GBR
0.98/69
ON994227 I. oblectabilis ESP
AJ879666 Uncultured ectomycorrhiza ITA
ON994232 I. oblectabilis ESP
ON994233 I. oblectabilis ESP
Inocybe oblectabilis
ON994215 I. avellaneorosea Holotype FRA
ON994217 I. avellaneorosea ESP
ON994218 I. avellaneorosea ESP
1/99
KM678460 Inocybe sp. ROU
KY496835 Inocybe calida TUR
AM882898 Inocybe calida var. brunneorufa SWE
Inocybe avellaneorosea sp. nov.
1/99
ON994206 I. lucida ESP
ON994207 I. lucida ESP
ON994205 I. lucida Holotype ESP
MW025042 Inocybe sp. SVN
ON994204 I. lucida FRA
ON994209 I. lucida FRA
1/99
ON994210 I. lucida ESP
ON994211 I. lucida ESP
1/100
ON994212 I. lucida FRA
ON994213 I. lucida ESP
ON994214 I. lucida ESP
ON994208 I. lucida FRA
Inocybe lucida sp. nov.
1/100
AJ889951 Inocybe asterospora DNK
OP001731 Inocybe asterospora FRA
Inocybe asterospora
1/100
AM882792 Inocybe calida EST
OP035649 Inocybe brunneorufa M0151688 Holotype DEU
Inocybe brunneorufa
AM882764 Pseudosperma spurium SWE
0.01

◀**Fig. 149** Most probable tree inferred by Bayesian inference in species of *Inocybe oblectabilis* group based on ITS and LSU sequences. Posterior probability from Bayesian analysis/Bootstrap-ML values are shown at the branches. Thick branches indicate nodes with phylogenetic support in both analysis (posterior probability ≥ 0.95 and bootstrap values ≥ 95%). The tree is rooted with *Pseudosperma spurium* (AM882784). The country of origin of each collection is abbreviated by ISO codes, with the species types marked in bold

ulmarium and *L. leucocephalum* have now been transferred to *Hypsizygus* (as *H. ulmarius*) and *Tricholomella* (as *T. constricta*) respectively of the family Lyophyllaceae. *Lyophyllum* species have not been described so far in Kerala State of India (Sathe and Daniel 1980; Farook et al. 2013). During the course of our studies on the agarics of Kerala State, we came across an undescribed carbonicolous species of *Lyophyllum*. It is formally described, illustrated, and discussed here based on both morphology and molecular phylogeny.

Lyophyllum agnijum K.N.A. Raj, K.P.D. Latha & Manim., ***sp. nov.***

Index Fungorum number: IF559692; *Facesoffungi number*: FoF10842; Fig. 150

Etymology: "agnijum" means born in fire in Sanskrit, referring to the occurrence of the basidiocarps on a burned substratum.

Macromorphology*: Basidiocarps* small, omphalinoid. *Pileus* 3–8 mm diam., convex or hemispherical with a small, distinct umbo; surface greyish brown (6F3/OAC640) all over when young, becoming greyish brown at the centre (6F3/OAC640) and dark brown (6F5/OAC734) elsewhere, hygrophanous and becoming paler, finely striate, appressed-fibrillose all over; margin initially incurved, becoming decurved, crenate. *Lamellae* emarginate with a small decurrent tooth, close, greyish brown (6D2/OAC723) when young, becoming brownish grey (6C2/OAC669) at maturity, up to 3 mm wide, with lamellulae of 3 lengths; edge finely torn, concolourous with the sides. *Stipe* 9–40 × 1–2 mm, central, terete, equal or slightly tapering towards the base, fistulose; surface greyish brown (6F3/OAC640) when young, becoming light brown (6D4/OAC646), longitudinally fibrillose, white-furfuraceous at the apex; base slightly enlarged, whitish. *Context* up to 1 mm thick. *Odour* and *taste* not distinctive. *Spore print* not obtained.

Micromorphology*: Basidiospores* 5–6(6.5) × 5–5.5(6.5) (5.47 ± 0.44 × 5.12 ± 0.27) µm, Q = 1–1.2, Qm = 1.06, subglobose to globose, smooth, cyanophilous, thin- to slightly thick-walled, inamyloid. *Basidia* 24–34 × 6.5–8 µm, clavate, hyaline, thin-walled, siderophilous, 1-, 2-, 4-spored; sterigmata up to 9 µm long. *Pleurocystidia* absent. *Lamella-edge* heterogeneous, fertile basidia intermixed with scarce, hard-to-detect cystidia. *Marginal cells* (*Cheilocystidia*) 10–28 × 3–7 µm, versiform: clavate, flexuose, narrowly utriform, filiform or sometimes septate, hyaline, thin-walled. *Lamellar trama* with a broad mediostratum composed of subregular compactly arranged hyphae, slightly but distinctly gelatinized towards the subhymenium; hyphae 3.5–11 µm wide, hyaline, thin-walled, inamyloid. *Pileus trama* subregular; hyphae 2–10 µm wide, hyaline, hyaline or with a pale-yellow wall pigment, thin- to slightly thick-walled, inamyloid. *Pileipellis* a cutis; hyphae 3.5–17 µm wide, with yellowish brown wall pigment and yellowish-brown spiral encrustations, thin- to slightly thick-walled. *Stipitipellis* a cutis disrupted by short trichodermial patches towards the apex; hyphae 3–8 µm wide, with a pale yellowish brown wall pigment. Terminal elements 22.5–44 × 4–7 µm, hyaline, thin- to slightly thick-walled. *Caulocystidia* absent. *Clamp connections* observed on all hyphae.

Habitat and distribution: gregarious, often as small clusters, on charred bamboo clumps, in tropical broad-leaved forests.

Materials examined: India, Kerala State, Wayanad District, Kuruva islets on the river Kabani, 6 July 2015, K.P. Deepna Latha and K.N. Anil Raj DKP356 (CAL 1388, **holotype**).

GenBank numbers: ITS: MK860709.

Notes: In the traditional infra-generic classification of *Lyophyllum*, the dull-coloured, caespitose basidiocarps and the smooth, globose basidiospores of our collection *L. agnijum* places it in the subsection *Difformia* of section *Difformia* (Kalamees 2004; Knudsen and Vesterholt 2008; Sesli et al. 2015). *Lyophyllum atratum* (Fr.) Singer, a widespread carbonicolous species described from different parts of Europe, North America, Australia and New Zealand (Singer 1943; Cooper 2014), shares a few features such as brownish basidiocarps with a fibrillose pileus, a cylindrical stipe that is tapered towards the base, inamyloid and somewhat similar-sized basidiospores (5.5–7.5 × 3.5–5.5 µm) and clamped hyphae, with *L. agnijum*. However, *L. atratum* differs from *L. agnijum* in having larger basidiocarps (pileus 20 mm diam., and stipe 10–20 × 1–3 mm), a pileus with striations that are confined to the margin, adnate lamellae, a hollow stipe, a strong, rancid odour, ellipsoid basidiospores, lamellae devoid of cystidia and consistently 4-spored basidia.

Lyophyllum ambustum (Fr.) Singer, another carbonicolous species distributed in Europe and India, seems to be closely related to *L. agnijum* in having brownish basidiocarps with an umbonate, hygrophanous pileus, rather similar-sized basidiospores (5.5–8 × 5–6.5 µm), hyphae of pileipellis with brown encrustations and a gregarious habit. However, *L. ambustum* has larger basidiocarps (pileus up to 20 mm diam., stipe 25–45 × 1.5–2.5 mm), translucent-striate pileus, dry, almost whitish grey when mature and with a denticulate margin, broadly adnate lamellae with smooth edges, a stipe with white fibrous flakes which is hollow when mature, a flour-like odour, tuberculate-verrucose

Fig. 150. ***Lyophyllum agnijum*** (CAL 1388, **holotype**). **a** Basidiocarps in their natural habitat. **b** Basidiospores. **c** Basidia. **d** Marginal cells. **e** Pileipellis. **f** Stipitipellis towards the apex of the stipe. Scale bars: a = 10 mm, b–d = 10 µm, e–f = 20 µm

basidiospores, a lamella-edge without cystidia and the absence of clamp connections (Moser 1983; Breitenbach and Kränzlin 1991a). *Lyophyllum anthracophilum* (Lasch) M. Lange & Sivertsen, a carbonicolous species reported from Europe, North America, Africa and Asia, is similar to *L. agnijum* in having brown-tinted basidiocarps with a striate, hygrophanous pileus, a longitudinally fibrillose stipe which is furfuraceous at the apex, globose to subglobose basidiospores, a pileipellis composed of parallel hyphae, the presence of clamp connections and a gregarious habit. *Lyophyllum anthracophilum*, however, is distinguished from *L. agnijum* by its larger basidiocarps (pileus up to 30 mm diam., stipe 30–50 × 1.5–2 mm) with black-brown pileus and stipe, a non-umbonate pileus which becomes applanate with age, broadly adnate to subdecurrent, grey-white lamellae with a smooth edge, smaller basidiospores (4.8–5.7 × 4.5–5.5 µm) and lamellae devoid of cystidia (Moser 1983; Breitenbach and Kränzlin 1991b).

The closest hit of our collection in the Blastn search was *Lyophyllum decastes*. *Lyophyllum decastes* is a species complex that includes several lineages and this has caused considerable taxonomic confusion in the past (Larsson and Sundberg 2011). Therefore, a morphology-based comparison of *L. decastes* is not useful. In our ML analyses (Fig. 151), our collection was grouped with *L. littorale* (ML = 66%) representing a well-differentiated clade from *L. decastes* species complex with ML = 98% bootstrap support. *Lyophyllum littorale* (Ballero & Contu) Contu, a species described from Sardinia in Italy, shares some characters such as close, decurrent lamellae, a fibrillose stipe with pruina restricted to the apex, globose to subglobose basidiospores (4.5–6.3 × 4.5–5.7 µm), clamped hyphae and a gregarious habitat. However, *L. littorale* is distinguished from our collection in having large (pileus 15–65 mm diam., stipe 20–60 × 4–8 mm), grayish basidiocarps fruiting on calcareous soil, a non-hygrophanous pileus with a depressed centre and pruinose surface devoid of striations, a stipe which is tapered towards the apex and an orange-yellow base, 4-spored basidia and slightly gelatinized pileipellis (Ballero and Contu 1990). *Lyophyllum atratum*, *L. anthracophilum, L. ambustum,* and the other carbonicolous species treated in the present phylogenetic analyses, seem to be phylogenetically unrelated with our collection and hence we introduce our collection as *L. agnijum*.

Porotheleaceae Murrill

The family Porotheleaceae was phylogenetically revised and 14 genera were accepted (Antonín et al. 2019; He et al. 2019; Vizzini et al. 2019; Kalichman et al. 2020; Matheny et al. 2020). These studies indicated that taxonomic placements of some genera are still doubtful. Consiglio et al. (2022) mentioned that there are no obvious morphological or ecological synapomorphies shared by all members of the pale-spored Porotheleaceae *s. stricto*, with the exception of their lignicolous habit and the presence of clamp connections. Unfortunately, the same situation within the genus *Porotheleum* is amended by Consiglio et al. (2022). Moreover, their phylogenetic trees (Consiglio et al. 2022, p. 104, 106 and 107), as well as our tree (Fig. 152) support that *Porotheleum* sensu Consiglio et al. contains more genera. All specimens classified by Consiglio et al. (2022) under the genus *Porotheleum* formed a clade with ML/BI = 72%/0.95 statistical support (Fig. 152). We identified several well-separated lineages as, (1) *Clitocybula albida* (*P. albidum*), (2) *P. dominingense* and *P. nigripes* (3) *P. fimbriatum* and *Porotheleum* sp. G0006 (4) *P. parvulum,* (5) *Porotheleum* sp. PBM4282, and a lineage of (6) *Marasmiellomycena pseudoomphaliiformis* and *M. omphaliiformis*.

Porotheleum fimbriatum (Pers.) Fr. is the type species of *Porotheleum* Fr. Thus, lineage 3) *P. fimbriatum* and *Porotheleum* sp. G0006 represents *Porotheleum* sensu *stricto*. *Clitocybula albida* A.K. Dutta, K. Acharya & Antonín clustered with *Porotheleum* in the phylogenetic analysis of Consiglio et al. (2022). Phylogenetic analysis in this study

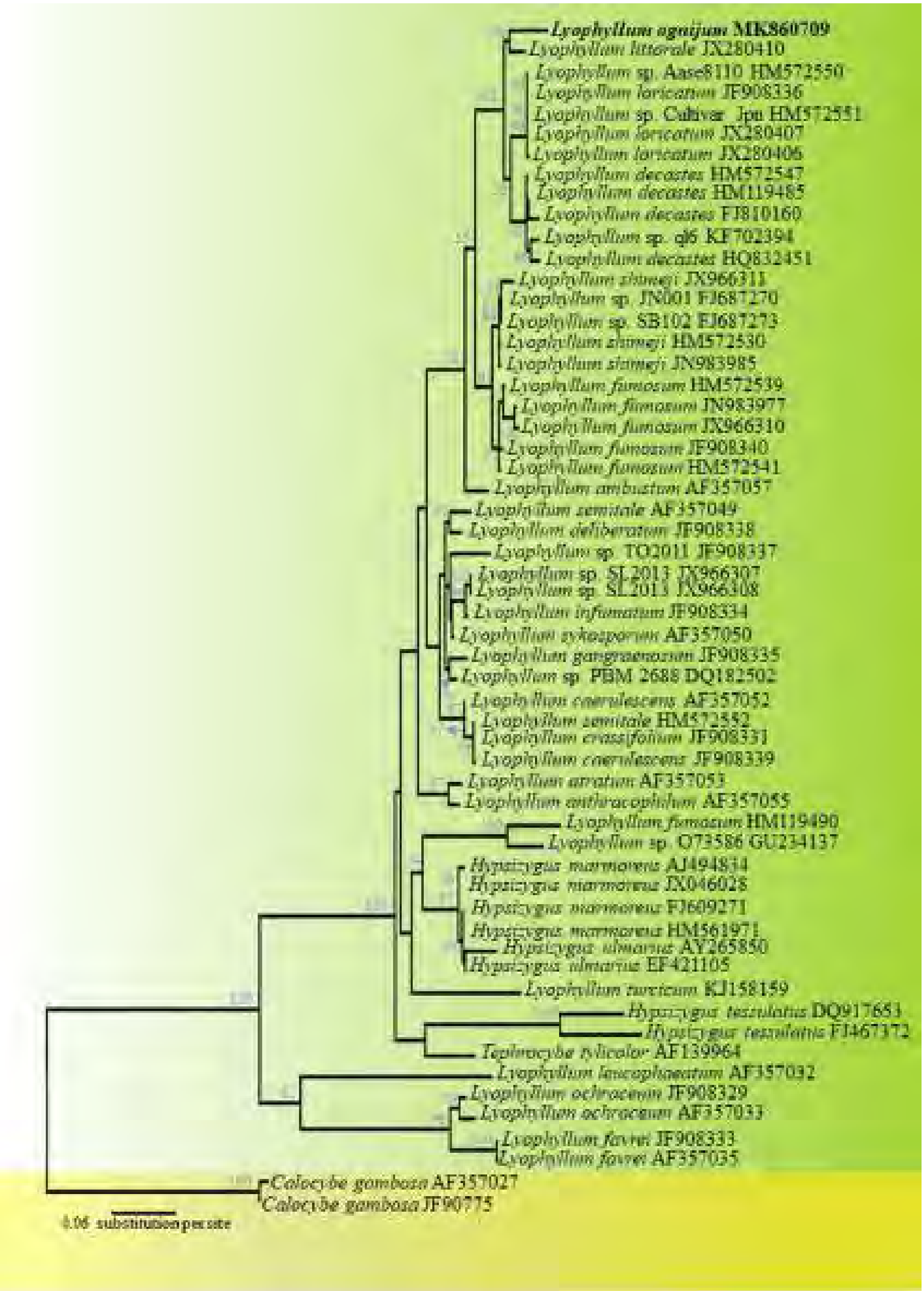
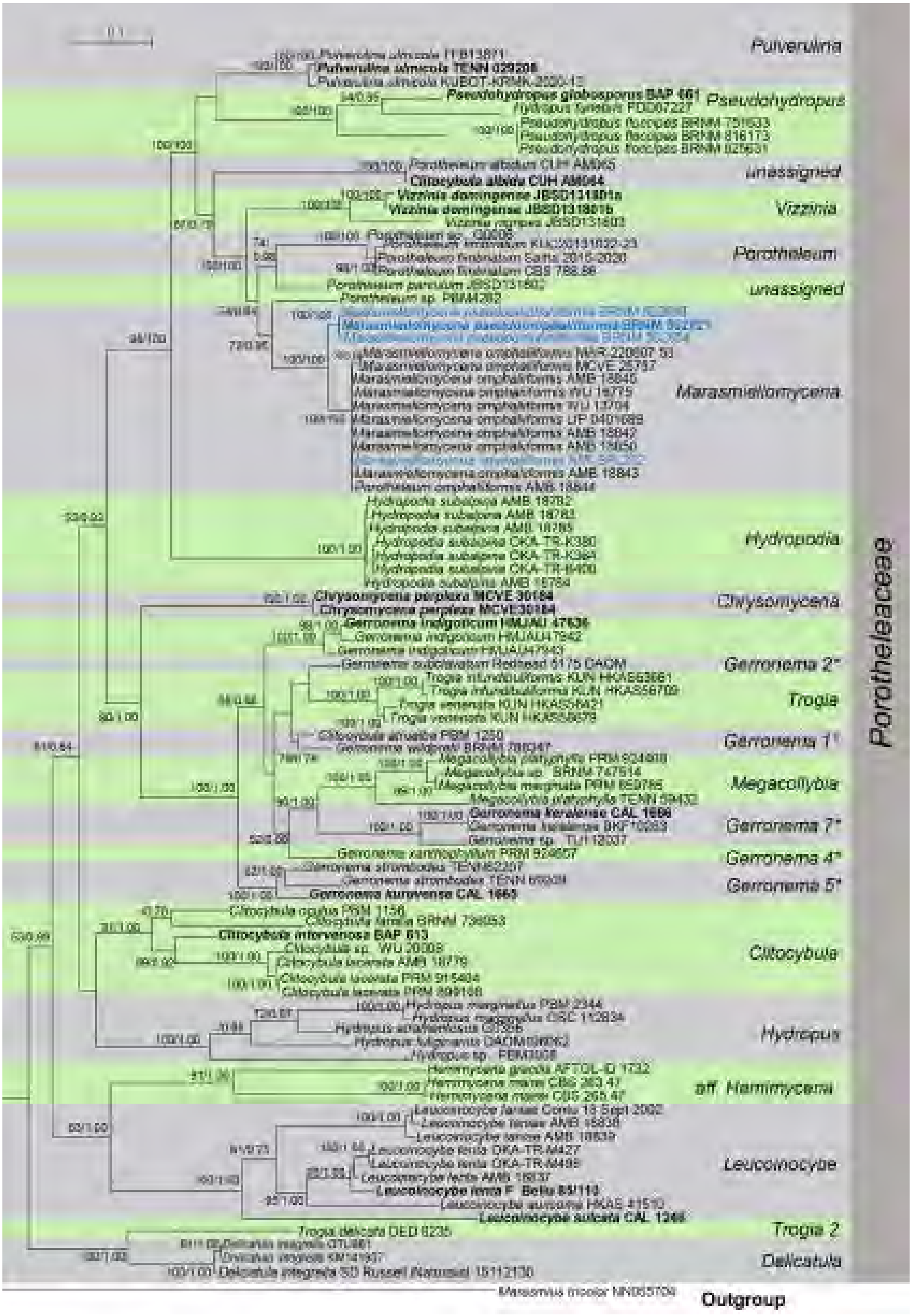


Fig. 151. ML phylogeny based on ITS sequence dataset depicting the placement of *Lyophyllum agnijum*. The newly sequenced species is displayed in black bold. ML bootstrap values ≥ 50% are shown. The scale bar indicates the number of substitutions per site. *Calocybe gambosa* (AF357027, JF90775) were selected as the outgroup taxon


0.1
Pulverulina
Pulverulina ulmicola TENN 029208
Pulverulina ulmicola KUBOT-KRMK-2020-13
Pseudohydropus
Pseudohydropus globosporus BAP 661
Hydropus funebris PDD87227
Pseudohydropus floccipes BRNM 751633
Pseudohydropus floccipes BRNM 816173
Pseudohydropus floccipes BRNM 825631
unassigned
Porotheleum albidum CUH AM065
Clitocybula albida CUH AM064
Vizzinia
Vizzinia domingense JBSD131801a
Vizzinia domingense JBSD131801b
Vizzinia nigripes JBSD131803
Porotheleum
Porotheleum sp. G0606
Porotheleum fimbriatum KUC20131022-23
Porotheleum fimbriatum Saftu 2015-2020
Porotheleum fimbriatum CBS 788.88
unassigned
Porotheleum parvulum JBSD131802
Porotheleum sp. PBM4262
Marasmiellomycena
Marasmiellomycena omphaliiformis MAR 220607 53
Marasmiellomycena omphaliiformis MCVE 25757
Marasmiellomycena omphaliiformis AMB 18846
Marasmiellomycena omphaliiformis WU 16775
Marasmiellomycena omphaliiformis WU 13704
Marasmiellomycena omphaliiformis LIP 0401089
Marasmiellomycena omphaliiformis AMB 18842
Marasmiellomycena omphaliiformis AMB 18850
Marasmiellomycena omphaliiformis AMB 18843
Porotheleum omphaliiforme AMB 18844
Hydropodia
Hydropodia subalpina AMB 18782
Hydropodia subalpina AMB 18783
Hydropodia subalpina AMB 18785
Hydropodia subalpina OKA-TR-K380
Hydropodia subalpina OKA-TR-K384
Hydropodia subalpina OKA-TR-B409
Hydropodia subalpina AMB 15784
Chrysomycena
Chrysomycena perplexa MCVE 30184
Chrysomycena perplexa MCVE30184
Gerronema indigoticum HMJAU 47636
Gerronema indigoticum HMJAU47942
Gerronema indigoticum HMJAU47943
Gerronema 2*
Gerronema subclavatum Redhead 5175 DAOM
Trogia
Trogia infundibuliformis KUN HKAS53861
Trogia infundibuliformis KUN HKAS56709
Trogia venenata KUN HKAS58421
Trogia venenata KUN HKAS58679
Gerronema 1†
Clitocybula atrialba PRM 1250
Gerronema waldpoeti BRNM 788047
Megacollybia
Megacollybia platyphylla PRM 924918
Megacollybia sp. BRNM 747514
Megacollybia marginata PRM 859765
Megacollybia platyphylla TENN 59432
Gerronema 7*
Gerronema keralense CAL 1666
Gerronema keralense BKF10063
Gerronema sp. TU112037
Gerronema 4*
Gerronema xanthophyllum PRM 924667
Gerronema 5*
Gerronema strombodes TENN62207
Gerronema strombodes TENN 69009
Gerronema kuruvense CAL 1665
Clitocybula
Clitocybula oculus PRM 1156
Clitocybula familia BRNM 736053
Clitocybula intervenosa BAP 613
Clitocybula sp. WU 20008
Clitocybula lacerata AMB 18776
Clitocybula lacerata PRM 915404
Clitocybula lacerata PRM 899168
Hydropus
Hydropus marginellus PBM 2344
Hydropus marginellus OSC 112834
Hydropus atramentosus G0356
Hydropus fuliginarius DAOM196062
Hydropus sp. PBM3008
aff. Hemimycena
Hemimycena gracilis AFTOL-ID 1732
Hemimycena mairei CBS 263.47
Hemimycena mairei CBS 265.47
Leucoinocybe
Leucoinocybe lanae Conte 18 Sept 2002
Leucoinocybe lanae AMB 18838
Leucoinocybe lanae AMB 18839
Leucoinocybe lenta OKA-TR-M427
Leucoinocybe lenta OKA-TR-M498
Leucoinocybe lenta AMB 18837
Leucoinocybe lenta F. Bellù 89/118
Leucoinocybe auricoma HKAS 41510
Leucoinocybe sulcata CAL 1246
Trogia 2
Trogia delicata DED 8235
Delicatula
Delicatula integrella OTU861
Delicatula integrella KM141607
Delicatula integrella SD Russell iNaturalist 15112130
Marasmius tricolor NN053704
Outgroup
Porotheleaceae

◂**Fig. 152** Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Maximum likelihood bootstrap supports (≥ 60%) followed by Bayesian posterior probabilities (≥ 0.70) followed by supports are indicated. The dataset was compiled using data from previous studies of *Clitocybula*, *Gerronema, Hydropus* and *Megacollybia* (Matheny et al. 2006; Antonín et al. 2019; Kaygusuz et al. 2020; Consiglio et al. 2022) and the most similar sequences (> 91% sequence similarity in LSU rDNA) were selected from GenBank using BlastN similarity search tool. The ITS and LSU sequences originating from the single voucher or strain were concatenated (93 sequence pairs). Sequence alignment generated in MAFFT 6 (Katoh and Toh 2008) was curated manually to remove hypervariable regions. Bayesian searches were conducted in MrBayes 3.0 (MB) with 10 million replicates. Maximum likelihood searches were conducted in IQ-TREE multicore version 1.4.1. in IQ-TREE including standard automated model selection ("-m TEST") as well as FreeRate (+R) model, and standard nonparametric bootstrap approximation ("-b 1000"). The dataset had 1872 columns, 1225 distinct patterns, 735 parsimony-informative characters, 249 singleton sites, 888 constant sites. The substation models for MB (TPM2+F+I+G4 for both partitions) were estimated in jModeltest 0.1.1. Two data partitions (one for each subunit) were recognized in the rDNA concatenated dataset. For each terminal, the species name and the voucher/herbarium code are indicated, and the type strains are in bold and new isolates are in blue bold. **Gerronema* genera sensu (Vizzini et al. 2019)

(Fig. 152) also showed that, *Clitocybula albida* (=*Porotheleum albidum*) forms a separate clade and however, further studies are required to confirm its generic position using additional materials and more genes, since only ITS data for *C. albida* are available (Dutta et al. 2018). *Porotheleum dominingense* and *P. nigripes* form well-separated lineage and clearly represent a new genus, described here as *Vizzinia*.

Marasmiellomycena De la Peña-Lastra, Mateos, Kolařík, Ševčíková & Antonín, ***gen. nov.***

MycoBank number: MB839731; *Facesoffungi number*: FoF 14222

Etymology: Epithet reflects its similarity to *Marasmiellus* and (Hemi) mycenoid genera.

Diagnosis: *Basidiomata* omphaloid or marasmioid, non-fragile. *Pileus* thin-fleshed, minutely tomentose, pubescent, granulose to subsquamulose. *Lamellae* well-developed, frequently forked, anastomose, adnate, sub-decurrent or decurrent, triangular or arcuate. *Stipe* central, filiform, entirely pruinose or pruinose-floccose, flesh thin. *Basal tomentum* present. *Spores* smooth, inamyloid. *Basidia* mostly tetrasporic. *Cheilocystidia* less distinct. *Pleurocystidia* absent. *Pileipellis* a cutis or with transitions to a trichoderm, terminal elements cylindrical, fusiform, lageniform or mucronate with or without excrescences or long rostrum (pileocystidioid structures). *Clamp connections* present. *Chemical reactions* metachromatic in cresyl blue or not, no other part of basidiomata dextrinoid or amyloid. *Ecology* saprotrophic, on dead wood and decayin leaves.

Type species: Marasmiellomycena pseudoomphaliiformis Antonín & Ševčíková.

Notes: Our three new collections (BRNM 552658, BRNM 552721, BRNM 552654) are morphologically identical and they shares many similar characters with *Porotheleum omphaliiforme*. Therefore, this well-supported clade herein introduce as *Marasmiellomycena* gen. nov. Vu et al. (2018) predicted that optimal thresholds for fungi (at least for filamentous) at the genus level of 98.2% based on LSU barcodes and 94.3% based on ITS barcodes. The genetic similarity of the genus *Marasmiellomycena* to neighboring genera, expressed by the similarity of *M. pseudoomphaliiformis* (type collection) to *P. parvulum* and (sequences identified as) *P. fimbriatum*, is 97.8% for LSU, and 88.9% for ITS. *Marasmiellomycena* has morphological affinities with *Marasmiellus*, *Hemimycena*, *Pulverulina*, and several mycenoid genera in Mycenaceae (Redhead and Singer 1981; Moncalvo et al. 2002; Matheny et al. 2006, 2020; Redhead 2012; See discussion under *M. pseudoomphaliiformis* for detailed comparison with the most similar species).

The phylogenetically closely related genus, *Pseudohydropus* Vizzini & Consiglio differs from *Marasmiellomycena* by a mycenoid habit, sinuate, adnexed to adnate lamellae, globose to broadly ellipsoid basidiospores and the presence of pileocystidia (Consiglio et al. 2022). *Vizzinia* (see below) differs by basidiomata turning brown on handling, a distinctly squamulose pileus, a floccose or floccose-fibrillose stipe, weakly amyloid spores, and the absence of cheilocystidia (Consiglio et al. 2022). *Pulverulina ulmicola* (H.E. Bigelow) Matheny & K.W. Hughes, the only species of the genus *Pulverulina* Matheny & K.W. Hughes, differs by clitocyboid basidiomata, a white stipe, a pileipellis in the form of a regular cutis and constantly cylindrical caulocystidia (Matheny et al. 2020).

Marasmiellomycena pseudoomphaliiformis Antonín & Ševčíková, ***sp. nov.***

Index Fungorum number: IF900584; *Facesoffungi number*: FoF 14223; Fig. 153

Etymology: species epithet refers to the close resemblance of this species to *M. omphaliiformis*.

Diagnosis: differs from *M. omphaliiformis* by distinct ITS and LSU sequences and by the geographic distribution in North America.

Macromorphology: *Pileus* 4–16 mm, convex with plane, slightly papillate or slightly depressed centre when young, then ± applanate and omphalioid, funnel-shaped at the end, with small central umbilicus, with involute to straight, finally uplifted, slightly undulate margin, entirely finely tomentose to pubescent when young, partly glabrescent when old, but with constantly pubescent margin, hygrophanous, slightly translucently striate in older basidiomata, distinctly radially grooved at margin when old, with small brown radial

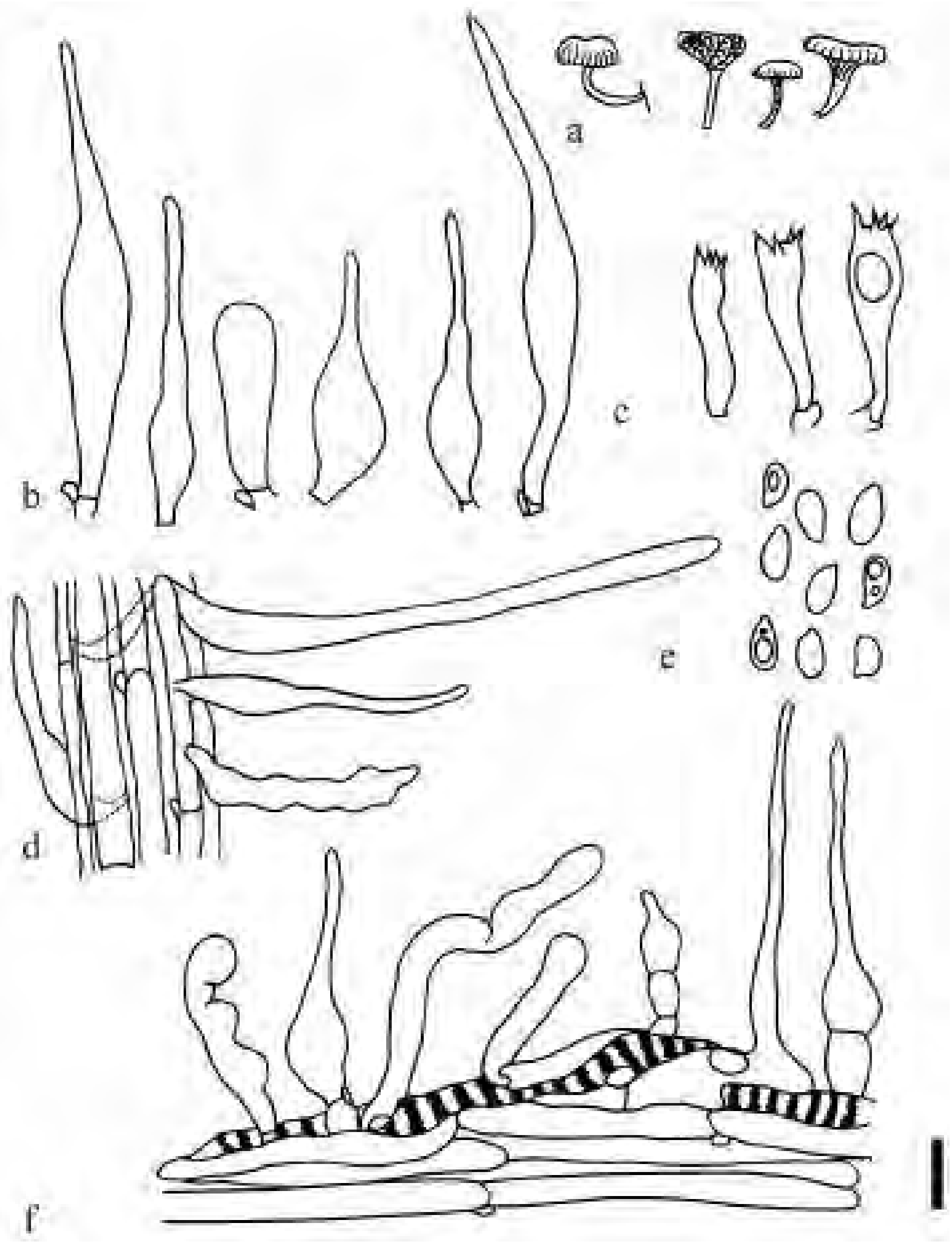


Fig. 153 ***Marasmiellomycena pseudoomphaliiformis*** (Drawing based on BRNM 552721). **a** Basidiomata. **b** Cheilocystidia. **c** Basidia. **d** Stipitipellis with caulocystidia. **e** Basidiospores. **f** Pileipellis with pileocystidia. Scale bar = 10 µm

fibrils, most close and suberect at centre, less frequent and adpressed at margin, dark watery brown (up to 8E7) when moist and very young then whitish to pale beige (c. 5B2−3) with darker centre, in mature basidiomata watery beige to greyish (slightly paler than 5B2−4), or greyish (between 6B3 and 6C3), sometimes brownish or brown (c. 7D6, 7E8) when moist, drying-up to whitish. *Lamellae* distant, L = 14–17, l = 1–2(−3), broadly adnexed when young, almost triangular and shortly decurrent when old, intervenose and sometimes forked especially when old, white to cream-white or beige (c. 6B3), with concolorous, finely pubescent edge. *Stipe* 5−11 × 0.6−1.3 mm, central to slightly eccentric, subinsititious, cylindrical when very young, then tapering towards base, broadened into a small disc at base, entirely white pubescent, finely longitudinally fibrillose in lower part, basal hairs brown, slightly carneous tinged (paler than 8B2) when very young, then whitish to pale brownish at apex and dark brown to black-brown (7F6−7, 9F5, 9F8) at base and sometimes entirely dark brown when old. *Context* without distinct smell and taste, very thin, in pileus whitish and greyish under pileipellis, in stipe hollow, cortex concolorous with the colour of stipe surface.

Micromorphology: *Basidiospores* (6.5−)7.0–9.0(−9.5) × 4.0–5.5 µm, average 7.93 × 4.64 µm, E = 1.55–1.88(−2.0), Q = 1.69−1.75, ellipsoid, ellipsoid-fusiform, smooth, inamyloid, non-dextrinoid. *Basidia* (21.5−)29–33 × 6.1–9.0 µm, 4-spored. *Basidioles* 15–34 × 3.5–8.0 µm, clavate, subfusiform or cylindrical. Cheilocystidia 25–87 × 9.0–18 µm, sometimes indistinct, (irregularly) clavate, fusiform to lageniform, sometimes with up to 40 µm long, tapering neck. Trama hyphae ± cylindrical, colourless, thin-walled, up to 17 µm wide. *Pileipellis* a cutis composed of cylindrical, smooth or incrusted, sometimes with brown walls, 3.0−9.2(−14) µm wide hyphae; terminal cells in groups (especially towards margin), (7.2−)20−88 × (3.2−)4.8−12. 3 µm, irregularly cylindrical to narrowly clavate or clavate, often with coloured walls; awl-shaped cells (pileocystidia) present especially towards centre. *Stipitipellis* a cutis of cylindrical, ± slightly thick-walled, 2.5−8.5 µm wide hyphae. *Caulocystidia* (17.8−)20–50 × 5.2–12 µm, fusiform, clavate, sometimes rostrate, thin- to slightly thick-walled. Trama and cystidia metachromatic in Cresyl blue. *Clamps* present in all studied tissues.

Hosts and geographical distribution: On decaying wood of a broad-leaved tree and leaves veins in amixed forest (*Acer*, *Carya*, *Pinus*, *Quercus*, *Rhododenron*, *Tsuga*); USA, Tennessee and North Carolina.

Holotype: USA, Tennessee, Blount Co., Great Smoky Mts. Nat. Park, Parsons Branch Road, Gregory Ridge Trail, 29 July 1991 leg. V. Antonín 91/277 (BRNM 552721).

Additional material examined: USA, Tennessee, Blount Co., Great Smoky Mts. Nat. Park, Parsons Branch Road, 31 July 1991 leg. et det. V. Antonín 91/297 (BRNM 552653). USA, Tennessee, Blount Co., Great Smoky Mts. Nat. Park, Cades Cove, Crib Gap, 22 July 1991 leg. et det. V. Antonín 91/242 (BRNM 552654). USA, North Carolina, Swain Co., Great Smoky Mts. Nat. Park, Kephart Prong Trail, 25 July 1991 leg. et det. V. Antonín 91/258 (BRNM 552658).

Notes: Our collections (BRNM 552721, BRNM 552653, BRNM 552654, BRNM 552658) are morphologically identical and they are characterized by an omphalinoid habit, a small, mostly pale coloured pileus, broadly adnexed to (shortly) decurrent, white, cream-white, or beige lamellae, a short, central to slightly eccentric, subinsititious, entirely white pubescent stipe, ellipsoid, ellipsoid-fusiform Basidiospores, (irregularly) clavate, fusiform to lageniform cheilocystidia, a pileipellis a cutis with irregularly cylindrical to narrowly clavate, clavate or awl-shaped terminal cells, and fusiform, clavate, sometimes rostrate caulocystidia. Our collections formed a well-supported clade with strains of *Porotheleum omphaliiforme* (Fig. 152). The blastn searches with NCBI revealed most similar species to our collection as *P. omphaliiforme* (OM422782) with 97.1% (ITS) respective *P. omphaliiforme* (OM423656) with 99.5% sequence similarity (LSU). However, our collections are morphologically different from *P. omphaliiforme.* Consiglio et al. (2022) mentioned that *Hydropus omphaliiformis* (PBM4282, ITS: MT196987), collected in the USA is phylogenetically distant from *Hydropus* sensu stricto. representing an undescribed species. Therefore, our collections together with *P. omphaliiforme* represent a generic lineage and herein introduce as *Marasmiellomycena*. Our collections represent a distinct lineage which is sister to *P. omphaliiforme* and we introduce this clade as *Marasmiellomycena pseudoomphaliiformis.*

Hemimycena mairei belongs to the undescribed "hemimycenoid genus 1" in the Dima´s tree (Lehmann and Lüderitz 2018), while sequences of *H. gracilis* (Quél.) Singer (DQ457671) and (DQ490623) probably represent the "hemimycenoid genus 2" together with *H. ochrogaleata* (J. Favre) M.M. Moser. Both of these genera are distinct from *Marasmiellomycena*.

Marasmiellomycena pseudoomphaliiformis is macro- and micromorphologically very similar to *M. omphaliiformis*. The description of *Porotheleum omphaliiforme* by Antonín and Noordeloos (2010) is based on both European and North-American collections, and therefore, represents a mixed description of these vicariants. The morphological comparison of *Marasmiellomycena pseudoomphaliiformis* with similar taxa listed in Table 7.

Marasmiellomycena omphaliiformis (Kühner) Mateos, Kolařík, De la Peña-Lastra, Ševčíková & Antonín, ***comb. nov.***

Index Fungorum number: IF900585; *Facesoffungi number*: FoF 14224; Figs. 154, 155.

Basionym: *Marasmius omphaliiformis* Kühner, in Kühner & Romagnesi, Bull. Soc. nat. Oyonnax 8: 75, 1954

Synonym: *Porotheleum omphaliiforme* (Kühner) Vizzini, Consiglio & M. Marchetti, Rivista di Micologia 64: 110. (2021) 2022;

Marasmiellus omphaliiformis (Kühner) Noordel., [as '*omphaliformis*'], Persoonia 12 (1): 35. 1983;

Hydropus omphaliiformis (Kühner) Honrubia, [as '*omphaliformis*'], Cryptog. Mycol. 5 (1): 57. 1984;

Mycena lapalmaensis Dähncke & Robich, Bol. Soc. Micol. Madrid 34: 99. 2010

Holotype: France, Charente Maritime, Corniche de Nauzan pres Royan, 2 September 1935, R. Kühner (fragm. in PC).

Macromorphology: *Pileus* 1–5 mm, hemispherical, convex, plano-convex and/or with umbilicate, sometimes somewhat depressed centre when mature, with involute, not translucently striate, not hygrophanous, not radially grooved margin, Pileipellis distinctly pruinose, whitish pubescent, with innate conglomerated fibrils and also granulate appearance; cream-coloured in the background and reddish-brown fibres when young (Ség. 250), turning greyish or sordid with age (Ség. 694), especially in the center. *Lamellae* distant, L = 14–16, 1 = 0–1, arcuate-decurrent, sometimes forked, and somewhat intervened in the background, larger, cream-white to pale ochre with a slightly darker edge, with whitish abundant hairs on the lamellar edge. *Stipe* 5–10 × 0.6–1 mm, cylindrical, sometimes broadened towards the base, sometimes bulbous, pale ochre at the top, ochre in the middle part

Table 7 Differences between *Marasmiellomycena pseudoomphaliiformis* and morphologically similar species

Species	Difference	References
Marasmiellus candidus (Bolton) Singer	Distinctly larger basidiospores	Antonín and Noordeloos (2010)
Marasmiellus celebanticus Pérez-De-Greg., Vizzini, Contu & Roqué	A constantly darker, light brown, caramel then brown, dark brown pileus, distinctly larger basidiospores, smaller and differently shaped cheilocystidia and caulocystidia and pileipellis terminal cells (pileocystidia) without flabelliform elements	Pérez-De-Gregorio et al. (2011)
Porotheleum albodescendens J.A. Cooper	A constantly pale pileus, slightly narrower basidiospores, absence of cheilocystidia and pleurocystidia, and longer, differently shaped pleurocystidia	Consiglio et al. (2022)
Porotheleum parvulum Angelini, Vizzini, Consiglio & M. Marchetti	A sparse, minutely darkly squamulate pileus, ochre-brown in the center, fading to pale ochre-yellow outside, slightly smaller basidiospores, absence of cheilocystidia and pileocystidia and different pileipellis	Consiglio et al. (2022)
Clitocybula albida A.K. Dutta, K. Acharya & Antonín	A pileus with a brownish orange to light brown, later pale orange to light orange or light brown center, slightly larger weakly amyloid basidiospores, 2-spored basidia, cheilocystidia and pileocystidia without a flabelliform tapering neck	Dutta et al. (2018)
Marasmiellus tricolor (Alb. & Schwein.) Singer	A pileus with a conical papilla, larger spores (except f. *americanum* Singer), Rameales-structure of pileipellis and cystidia and occurs in Herbaceae and grasses	Antonín and Noordeloos (2010)
Hemimycena mairei (E.-J. Gilbert) Singer	smell resembles Clitopilus prunulus, smaller cheilocystidia, the absence of pileocystidia, only cylindrical to clavate caulocystidia and growing among mosses and grasses	Singer (1943); Antonín and Noordeloos (2004)
Hemimycena sordida Noordel. & Antonín	Clavate or irregular corraloid cheilocystidia and a pileipellis without pileocystidia and growing on soil together with mosses and grass	Antonín and Noordeloos (2004)
Atheniella delectabilis (Peck) Lüderitz & H. Lehmann	A hygrophanous pileus, cheilocystidia usually with subcapitate apex and a different pileipellis	Peck (1875); Antonín and Noordeloos (2004); Lehmann and Lüderitz (2018)

(Ség. 250) and turning dark brown (Ség. 701) to blackish in the lower part (Ség. 706), pubescent, formed by whitish hairs distributed along its entire length, non-insititious, with basal hairs. Species thin-fleshed, often with elastic, cartilaginous or leathery flesh and which generally dry out without rotting, reviviscent appearance.

***Micromorphology**:* *Spores* (6.3–)7.5–8.6–9.9(–10.3) × (3.7–)3.8–4.1–4.6(–4.9) µm; Q = (1.5–)1.8–2.1–2.3(–2.6); n = 32; Vm = 78 µm^3, smooth, narrowly ellipsoid or subcylindrical, ellipsoid, sublacrymoid or sometimes fusiform, with thick apiculum, usually with one, two or more oily guttules. *Basidia* 20–37 × 4–7 µm, claviform, with sterigmata 3–3.5 µm high, tetrasporic. *Basidioles* claviform or subcylindrical, 18–35 × 4–6.5 µm. *Lamellar edge* low fertile and heterogeneous, *cheilocystidia* numerous, 37–58 × 5.7–7.6 µm, sublageniform, with slightly broadened base and flagelliform neck (1.7–3.5 µm). *Pleurocystidia* absent. *Hymenophoral trama* subregular, 2.5–6.0 µm wide hyphae, *trama elements* 99–120 × 15–31 µm, abundant, fusiform, sometimes thick-walled. *Pileipellis* an irregular cutis with transitions to a trichoderm, made up of 3–10 µm wide cylindrical hyphae, with scattered suberect or erect fusiform, sublageniform or flagelliform, thin-walled, weakly diverticulate terminal elements, very polymorphous, 30–56 × 6–10.3 µm; with brown intracellular pigment. *Stipitipellis* a cutis of parallel, cylindrical, smooth, 2–6.0 µm

Fig. 154 ***Marasmiellomycena omphaliiformis*** (AMI-SPL252). **a** Habitat. **b** Basidiomata (RC,MLZ). **c** Basidiospores (RC, MLZ). **d** Cheilocystidia (RC). **e** Hymenophoral trama elements (RC). **f** Chemical reactions: 1–2, trama of lamellae (MLZ, KOH); 3–4, trama subpellis (MLZ, KOH); 5–6, trama stipitipellis (MLZ, KOH); 7 trama subpellis (BC); 8, trama stipitipellis (BC). **g** Hymenium (RC). **h** Pileipellis (RC). **i** Caulocystidia and stipitipellis. Scale bars: c–i = 10 µm

wide hyphae, with dark brown intracellular pigment. *Caulocystidia* numerous along the entire length of the stipe, (15.1–)30.8–62.6(–65.8) × (2–)2.4–11, 6(–15.5) µm, fusiform, subclavate, sublageniform, sometimes with digital projections, usually narrowed at the apex or large rostrum. *Clamps* present in all tissues. *Chemical reactions* no part of the basidiocarp dextrinoid or amyloid, except the spores which are slightly amyloid. Cresyl blue negative in all tissues. KOH 10% slightly yellowish in the subpellis.

Material examined: Spain, Galicia, Pontevedra, Vilagarcía de Arousa, Parque Nacional das Illas Atlánticas de Galicia, Illa de Cortegada, N42° 37′ 1.29″ W8° 47′ 10.97″, 10 m a.s.l., growing on the lower part of a living trunk of *Quercus robur* L., 22 August 2020, S. De la Peña-Lastra, AMI-SPL252.

GenBank numbers: ITS: MZ542542, LSU: MZ542546.

Hosts and geographical distribution: Saprobic on a woody trunk of *Quercus robur*; northwestern Spain.

Notes: Our collection (AMI-SPL252) and another unpublished collection (AMI-SPL250) were consistently showed negative Cresyl blue reaction in all tissues, in many preparations at various temperatures (up to 70 °C). Noordeloos (1983) mentioned the metachromatic reaction of the trama in Cresyl blue as one of the crucial features of this species

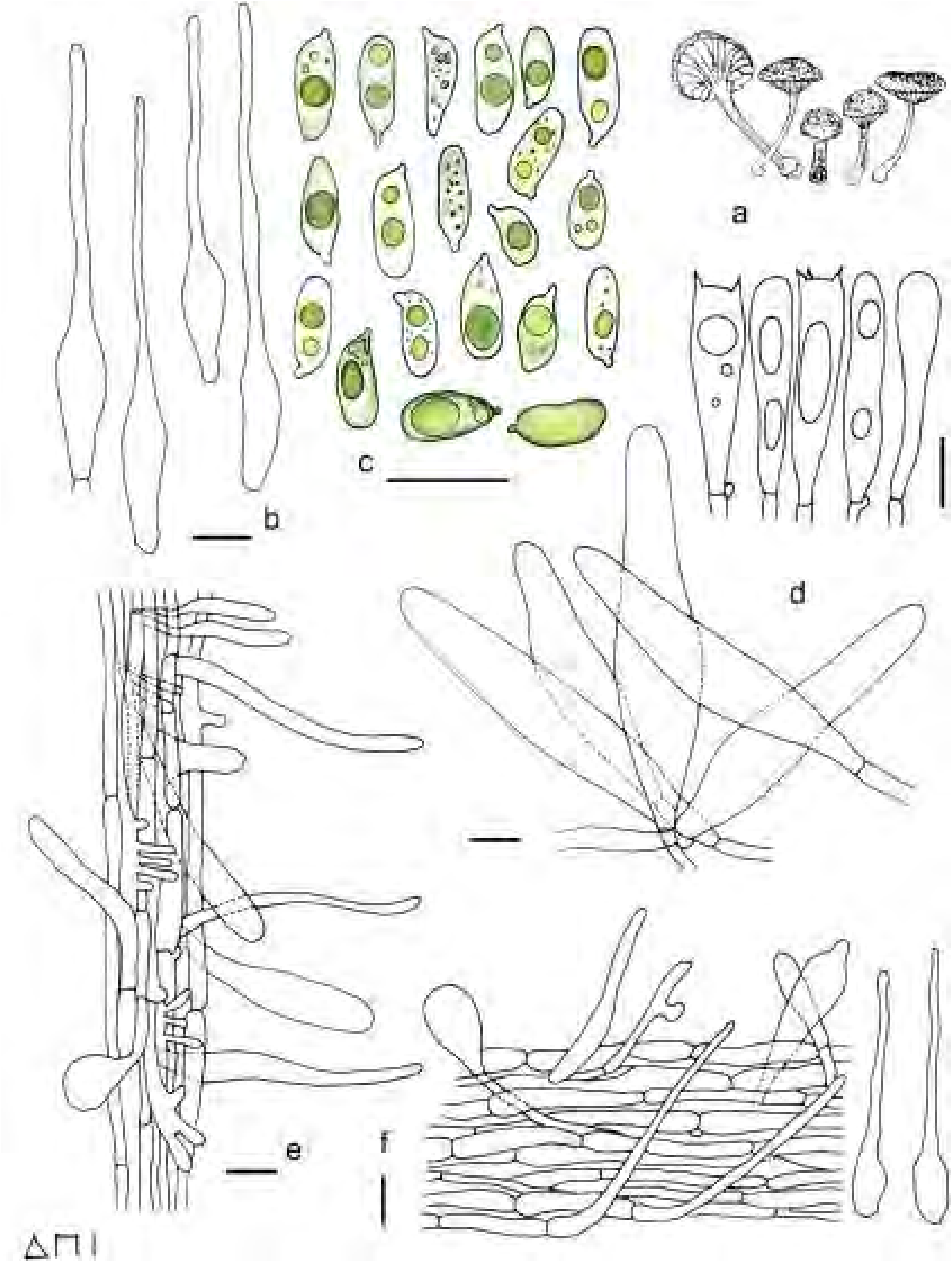


Fig. 155 Line drawing of ***Marasmiellomycena omphaliiformis*** (AMI-SPL252). **a** Basidiomata. **b** Cheilocystidia. **c** Basidiospores. **d** Hymenophore with basidia, basidioles and trama elements. **e** Stipitipellis and caulocystidia. **f** Pileipellis. Scale bars: b–f = 10 µm

together with its trichodermal pileipellis and almost setiform/flagelliform elements. Consiglio et al. (2022) also emphasized this feature as stable within this very variable species. Also caulocystidia with digital projections are atypical for *Marasmiellomycena omphaliiformis*. However, collection AMI-SPL252 clustered and is identical to

M. omphaliiformis. Thus, its variability is larger than these authors expected. *Marasmiellomycena omphaliiformis* is a morphologically variable species (Antonín and Noordeloos 1993, 2010; Consiglio et al. 2022) (Figs. 154, 155).

Vizzinia Ševčíková & Kolařík, ***gen. nov.***

Index Fungorum number: IF900586; *Facesoffungi number*: FoF 14225

Etymology: in honor of the mycologist Alfredo Vizzini for his excellent contribution to mycology.

Diagnosis: Genus *Vizzinia* (see below) differs from *Marasmiellomycena* by basidiomata turning brownish on handling, distinctly squamulose pileus, floccose or floccose-fibrillose stipe, weakly amyloid spores, and absence of cheilocystidia (Consiglio et al. 2022).

Basidiomata strongly omphalinoid to omphalinoid-clitocyboid-marasmioid. *Pileus* small, squamulose, translucently radially striate-furrowed. *Lamellae* often whitish, thick, distant, intervenose, adnate-decurrent to long-decurrent, with lamellulae of various length. *Stipe* cylindrical, fistulous, covered with floccose fibrils, often darker on the lower part, strigose at the lowest part of the base. *Context* thin, turning brownish on handling. *Odour* non-distinctive. *Basidiospores* colourless, thin-walled, smooth, congophilic, cyanophilic, weakly amyloid. *Basidia* slightly amyloid at apex. *Hymenial cystidia* absent. Subhymenium filamentous, consisting of intertwined short elements. *Hymenophoral trama* metachromatic. *Pileipellis* a cutis with frequent or rare pileocystidiod elements. *Caulocystidia* present. Thromboplerous hyphae and clamp connections present.

Type species: *Vizzinia nigripes* (Angelini, Vizzini, Consiglio & M. Marchetti) Ševčíková & Kolařík

Notes: The genus *Vizzinia* contains two species viz. *V. dominingense* and *V. nigripes* and it forms a well-supported lineage clearly represents a new genus. This genus matches optimal thresholds at the genus level according to Vu et al. (2018); which is 98.2% based on LSU barcodes and 94.3% based on ITS barcodes. The closest matches with NCBI were *P. fimbriatum* with 96.64–96.37% (*Vizzinia nigripes* type) and 97.59%–97.36% (*V. domingense* type) based on LSU; *P. omphaliiforme* reference species with 84.28% (*V. nigripes* type) and 90.19% (*V. domingense* type) based on ITS. Consiglio et al. (2022) mentioned that "these groups of species will probably be considered as independent genera, especially the *P. albodescendens*/*P. omphaliiforme* and *P. domingense*/*P. nigripes* pairs". In spite of these claims, they preferred to describe these species as *Porotheleum domingense* and *P. nigripes*. We could not avoid solving this new genus, if we want to justify the existence of the genus *Marasmiellomycena* and we believe that our new species *M. pseudoomphaliiformis* makes clear enough the relationship between *P. omphaliiforme* and *P. domingense*/*P. nigripes lineages*.

Vizzinia nigripes (Angelini, Vizzini, Consiglio & M. Marchetti) Ševčíková & Kolařík ***comb. nov.***

Index Fungorum number: IF900587; *Facesoffungi number*: FoF 14226

Basionym: *Porotheleum nigripes* Angelini, Vizzini, Consiglio & M. Marchetti, in Consiglio et al., Micologia 64 (2): 165, 2022.

Holotype: Dominican Republic, Sosúa (Puerto Plata Province), Puerto Chiquito, 20. December 2016, leg. C. Angelini (JBSD 131803).

Vizzinia domingense (Angelini, Vizzini, Consiglio & M. Marchetti) Kolařík & Ševčíková ***comb. nov***.

Index Fungorum number: IF900588; *Facesoffungi number*: FoF 14227

Basionym: *Porotheleum domingense* Angelini, Vizzini, Consiglio & M. Marchetti, in Consiglio et al., Micologia 64 (2): 163, 2022.

Holotype: Dominican Republic, Sosúa (Puerto Plata Province), Puerto Chiquito, 8 December 2013, leg. C. Angelini (JBSD 131801).

Notes: Both species share a lot of similarities to identical morphological features. However, *Vizzinia domingense* seems to possesses a strictly omphalinoid shape of basidiomata, while appearance of *V. nigripes* was described as omphalinoid-clitocyboid-marasmioid (Consiglio et al. 2022). Phylogenetically, *V. nigripes* is relatively distant from *V. domingense*. More collections need to explain the taxonomical position and limitation of the genus *Vizzinia*.

Pleurella E. Horak

Members of *Pleurella* are commonly characterized by smooth, strongly amyloid, elliptical or subcylindrical spores, conspicuous cheilocystidia, form of the carpophores and habitat (Horak 1971). Currently, this genus includes two species, viz. *Pleurella ardesiaca* and *P. microspora* (Alessio & Nonis) Vizzini, Consiglio & E. Campo (Horak 1971; Vizzini et al. 2022). In this study, we provide a new geographical record for *Pleurella ardesiaca* from China.

Pleurella ardesiaca (G. Stev. & G.M. Taylor) E. Horak, N.Z. Jl Bot. 9(3): 477 (1971)

Index Fungorum number: IF320667; *Facesofungi number:* FoF 14228; Fig. 156

Macromorphology: On rotten wood and bark of unidentified host. *Pileus* 13–40 mm diam., convex to plano-convex at first, then becoming umbellate to plane, margin smooth; white (5A1), grayish orange (5B4–7), brownish orange (5C5–6), brown (5E6–7); *Lamellae* adnate, emarginated or subdecurrent, regular, very crowded, white (1A1) at the beginning, later turning cream coloured (18B1), pale orange (5A5) when maturity or after bruising; gill edge even. *Stipe*

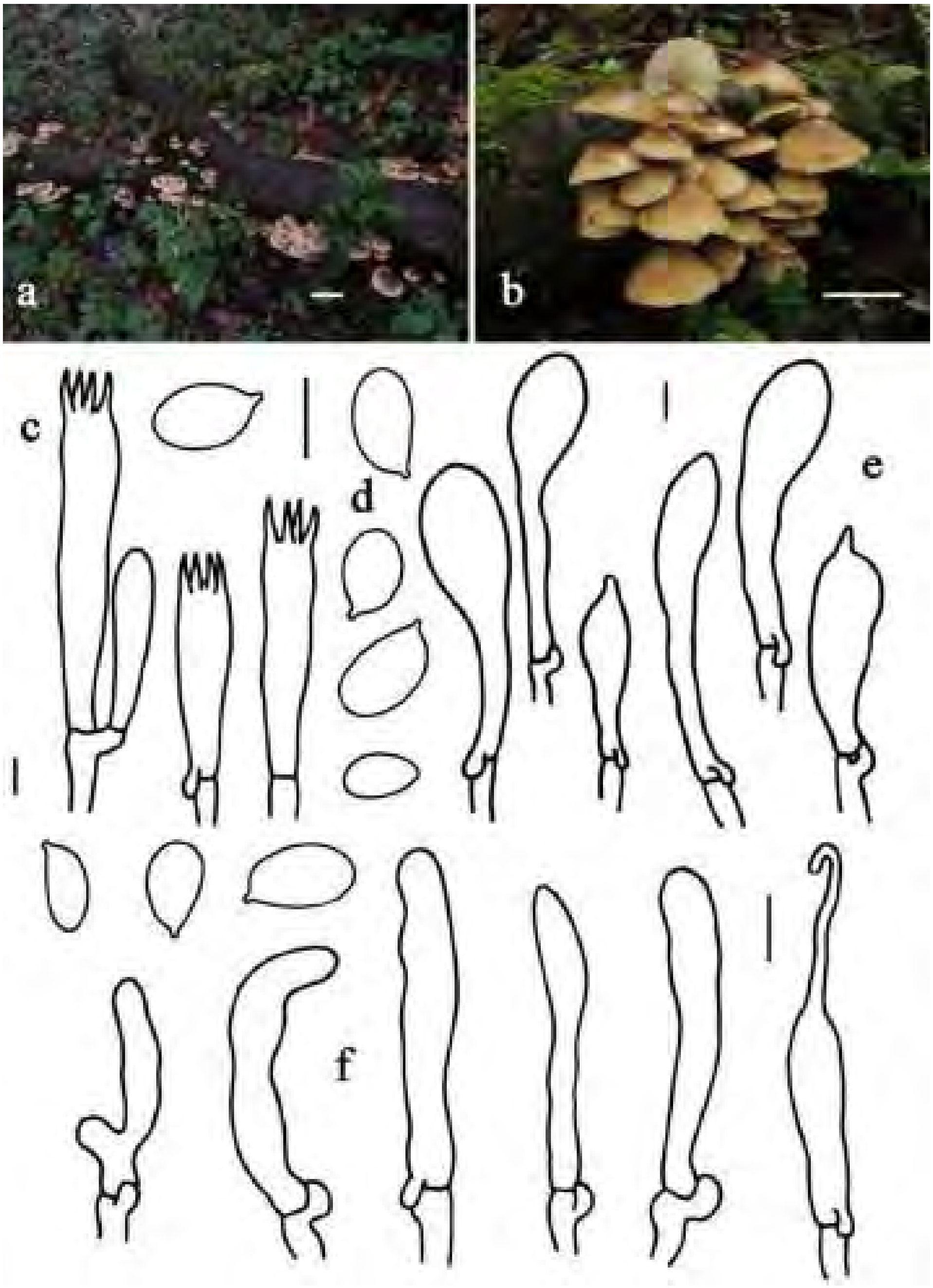


Fig. 156 ***Pleurella ardesiaca*** (HKAS 125916). **a, b** Fruiting bodies on host substrate. **c** Basidia. **d** Basidiospores. **e** Cheilocystidia. **f** Caulocystidia. Scale bars: a, b = 4 cm, c = 0.5 cm, d = 4 µm, e–f = 1 µm

30–50 × 3–5 mm, subcylindrical to cylindrical, excentric or lateral, rarely central, curved, solid; concolorous with pileus or paler on the upper part, with darker dots near the base. Context white (1A1). Taste and odour not observed.

Micromorphology: *Basidiospores* [40/1/2] 4–5 × 2–3 µm, elliptical or subcylindrical, smooth, thin-walled, strongly amyloid, germ pore absent. *Basidia* 15–20 × 4–5 µm. *Cheilocystidia* 22–50 × 4–11 µm, clavate or cylindrical, occasionally with a short projection at the apex, hyaline. thin-walled. forming a sterile zone at the edge. *Caulocystidia* 35–55 × 6–9 µm, cylindrical, thin-walled, with brown membranal or epicellular pigment. Clamp connections present.

Material examined: China, Yunnan Province, Jingdong County, Ailaoshan National Nature Reserve, 24° 30′ 56.875248″ N, 101° 1′ 8.445936″ E, alt 2409 m, 28 July 2018, Jianwei Liu, LJW1122 (HKAS 125916, **new geographical record**).

Hosts and distribution: on rotten wood and bark of (infrequently on living trees) of *Phyllocladus alpinus*, rarely on *Dacrydium cupressinum* or *Nothofagus* spp.

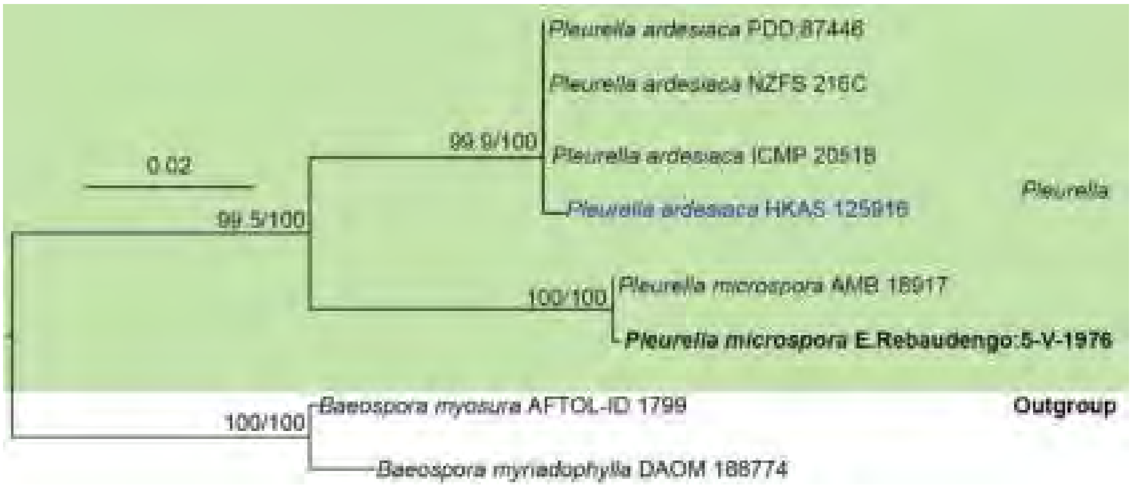


Fig. 157 Phylogram generated from maximum likelihood analysis based on combined ITS and nrLSU sequence data representing the species of *Pleurella*. *Baeospora myosura* AFTOL-ID 1799 and *B. myriadophylla* DAOM 188774 are selected as the outgroup taxa. Statistical supports are indicated next to each node, non-parametric maximum likelihood ultrafast-bootstrap (UFBS) values and SH-aLRT obtained from 1000 replicates using IQ-TREE and the TIM2 + F + G4 model. Bootstrap support for maximum likelihood with Shimodaira Hasegawa-like approximate likelihood ratio test (SH-aLRT) (left), ultrafast bootstrap (right). Only one of SH-aLRT > 80 or UFB > 95 for ML are indicated along branches (SH-aLRT/UFB). Eight collections are included in the combined analyses which comprise 1546 sites of which 1375 were found to be conserved, 164 were the variable sites and included nearly 152 parsimony-informative sites. The optimized log-likelihood value is − 3041.750. Estimated base frequencies are as follows: A = 0.249, C = 0.198, G = 0.262, T = 0.290; substitution rates AC = 2.46489, AG = 4.95937, AT = 2.46489, CG = 1.0, CT = 13.63798, GT = 1.0; gamma distribution shape parameter α = 0.168. New sequence data of *Pleurella ardesiaca* (HKAS 125916) is highlighted in blue bold

(Horak 1971). Currently, this species only known from New Zealand and China.

GenBank numbers: ITS: OP876783, LSU: OP866793.

Notes: The combined ITS and LSU sequence analyses of our collection (Fig. 157) revealed that our collection grouped with *Pleurella ardesiaca* (SH-aLRT/UFB) forming a monophyletic, clade with ML/BI = 100%/95.5 statistical support. The morphology of our collection also fits with the prologue of *P. ardesiaca*. The holotype of *P. ardesiaca* was collected from New Zealand (Southern Hemisphere) (Horak 1971), and has not been reported in other regions of the world. However, our collection was occurred Yunnan Province, China (Northern Hemisphere) that 6000 km away from New Zealand. This collection of *P. ardesiaca* indicates the geographical distribution of the species and here, we report this as a new geographical record.

Hymenochaetales Oberw.

Oberwinkler (1977) proposed the order Hymenochaetales. Currently, there are six families in this order viz. Hymenochaetaceae, Neoantrodiellaceae, Nigrofomitaceae, Oxyporaceae, Rickenellaceae, and Schizoporaceae.

Hymenochaetaceae Donk

Donk (1948) was described the family Hymenochaetaceae, which comprises of xanthochroid polypores (taxa showing xanthochroic reaction) in the order Aphyllophorales. Members of this family comprise resuspinate basidiomata, effused reflexed, pileate, imbricate to substipitate or stipitate with distinct hymenial structure (smooth, hydnoid or poroid). Microscopically monomitic, mono-dimitic or dimitic hyphal system with simple septate, clampless hyphae and presence or absence of cystidioles and setae, in the hymenium are distinct characteristics.

Kirk et al. (2008) was reported Hymenochaetaceae as one of the largest families in Basidiomycota which includes more than 500 species. Dai (2010) mentioned *Phellinus*, *Hymenochaete*, and *Inonotus* as the three largest genera under this family. Earlier, majority of dimitic polypores were grouped under *Phellinus* s.l., whereas monomitic xanthochoroid polypores in *Inonotus* s.l. Later Fiasson and Niemelä (1984), revised the taxas viz., *Fomitiporia*, *Fulvifomes*, *Fuscoporia*, *Ochroporus*, *Phellinidium*, *Phellinus* s.s. and *Porodaedalea* from *Phellinus* s.l.; *Inonotus* s.s., *Inocutis* and *Inonotopsis* from *Inonotus* s.l by studying the morphological, cultural, chemical, and nuclear behavioural characteristics. Wu et al. (2022) analyzed the systematics of Hymenochaetoid fungi from 37 countries and introduced seven new genera *Meganotus*, *Neophellinus*, *Nothonotus*, *Pachynotus*, *Perenninotus*, *Pseudophylloporia* and *Rigidonotus* and 37 new species along with key to the family Hymenochaetaceae.

Fulvifomes Murrill

Fulvifomes comprises annual to perennial, resupinate, effused-reflexed, imbricate to pileate, sessile, applanate to ungulate basidiomata with homogenous or duplex context and poroid hymenial layer, bearing round to angular pores (Hattori et al. 2022). Microscopically mono-dimitic to dimitic hyphal system, with or without sterile elements such as setae and cystidioles in hymenium and smooth, thick-walled, coloured, cyanopilic or acyanophilic, inamyloid, globose to ellipsoidal basidiospores are the characteristics in this genus (Murrill 1914; Wagner and Fischer 2002; Dai 2010; Zhou 2014; Hattori et al. 2014; Salvador-Montoya et al. 2018).

Earlier, *Fulvifomes* was treated as synonym of *Phellinus* Quél. (Ryvarden and Johansen 1980; Ryvarden 1991; Núñez and Ryvarden 2000). Nevertheless, studies on nuclear behaviour and molecular data are supported the generic rank of *Fulvifomes* from *Phellinus* s.l. in Hymenochaetaceae (Fiasson and Niemelä 1984; Wagner and Fischer 2002; Larsson et al. 2006; Baltazar and Gibertoni 2010; Dai 2010; Hattori et al. 2014; Zhou 2014). Wagner and Fischer (2002) was placed basidiomes with coloured spores without setal elements under *Fulvifomes*. Dai (2010) was included few resupinate basidiomes and species with hymenial setae in *Fulvifomes*. Approximately 87 associated records of *Fulvifomes* were documented in MycoBank and 50 related taxa were recorded in NCBI.

Fulvifomes karaiensis M. Kaliyaperumal, S. Gunaseelan & K. Kezo ***sp. nov.***

Index Fungorum number: IF559691; *Facesoffungi number*: FoF 12670; Fig. 158

Etymology: The species epithet "*karaiensis*" referring to the region of basidiomata collected

Macromorphology*: Basidiocarp* perennial, solitary, pileate, sessile, light in weight, hard when dry. *Pileus* applanate, triquetrous, projecting up to 6.1 cm, 11.5 cm wide and 5.8 cm thick near the attachment. *Pilear surface* meagrely warted near margin, weakly zonate, brown (6E5), on maturity pilei becoming rough, with few cracks, brownish grey (6F8). *Margin* entire, obtuse, velutinate, yellowish brown (5E8). *Pore surface* yellowish brown (5E7). *Pores* regular, round to angular, 4–5 per mm. *Dissepiments* entire, thick. *Context* up to 1 cm near the margin and up to 5 cm near the attachment, homogeneous, golden brown (5D7). *Tubes* brown (6E6), tubes layers not stratified, up to 1.1 cm.

Micromorphology*: Hyphal system* strictly dimitic, Generative hyphae dominant, both generative and skeletal hyphae acyanophilous, tissue darkening with KOH without swelling. *Context* generative hyphae, thin to thick-walled, hyaline to yellow, frequently simple septate, branched, 2–5.2 µm diameter; skeletal hyphae, thick-walled with narrow lumen, yellowish brown, aseptate, unbranched, 2–5 µm diameter. *Trama* generative hyphae, thin to thick walled, yellow to brown, infrequently septate, rarely branched, 2–5 µm diameter; skeletal hyphae, thick-walled with narrow to wide lumen, yellowish brown, aseptate, unbranched, 2–5.2 µm diameter. *Setae* absent. *Cystidioles* hyaline, ventricose to fusoid with elongated apical portion, 8.1–22.1 × 2.6–4.2 µm. *Basidioles* dominant, clavate, 6.5–14 × 2.6–6.9 µm. *Basidia* clavate to broadly clavate, with four sterigmata, 6.5–15.2 × 2.6–7.2 µm. *Basidiospores* globose to subglobose, thick–walled, smooth, golden yellow in water, turning rust brown in KOH, (5.2–) 5.5–6 (– 6.2) × (4.7–) 5.2–5.5 (– 5.7) µm, Q = 1.07 (Q range 1–1.15) (n = 50/2), CB^{-}, IKI^{-}.

Material examined: India, Tamil Nadu, Sivagangai District, Karaikudi, 10º04′ 45″ N 78º47′ 71″ E, on *Peltophorum pterocarpum*, 9 Febraury 2018, Malarvizhi Kaliyaperumal (MUBL4016, **holotype**; CRKK2/2A, **isotype**).

GenBank numbers: ITS: ON333609, OP028976; LSU: ON326580, OP028972.

Notes: Our collection (MUBL4016) shares similarity with *Fulvifomes azonatus*, *F. jouzaii*, *F. nakasoneae* (Wu et al. 2022), *F. nonggangensis, F. tubogeneratus* (Zheng et al. 2021), *F. thailandicus* (Zhou 2015), *F. submerrillii* (Liu et al. 2020) and *F. yoroui* (Olou et al. 2019) by having dimitic hyphal system and cystidioles alone. However, our collection shows significantly different, distinct morphological characters viz., numbers of pores/mm, size and shape of basidiospores with other *Fulvifomes* having dimitic hyphal system and cystidioles.

Fulvifomes thailandicus, and *F. submerrillii* are reported with broadly ellipsoid spores with 6–7 pores/mm whereas, *F. karaiensis* has globose to subglobose basidiospores with 4–5 pores/mm. *Fulvifomes jouzaii* has smaller pores (9–10/mm), black lines in context, stratified trama and subglobose to broadly ellipsoid basidiospores (Wu et al. 2022), while larger pores (4–5/mm), globose to subglobose spores and tubes without stratification was observed in our collection.

Our collection shows similarity with *F. azonatus* in having obtuse margin, dimitic hyphal system and cystidioles with 4–5 pores/mm, globose to subglobose basidiospores, but *F. azonatus* comprises smaller pores (7–9/mm) and smaller basidiospores (subglobose to ovoid spores; 4–5 × 3.2–4 µm) (Wu et al. 2022). Further, our collection shares few similar characters such as dimitic hyphal system, and presences of cystidiole with *F. tubogeneratus* and however, differs from our collection by duplex context and subglobose to ovoid spores (5– 6.4 × 4.1–5.8 µm).

The macro-and micro-morphological characters of *F. yoroui* highly varies with our collection. *Fulvifomes yoroui* has rimose pileus with deeply cracked, stratified tubes, andpores 6–7/mm. Further, the size of basidiospores varies between *F. yoroui* (5–6.6 × 4.3–6.3 µm) and our collection (5.2–6.2) × (4.7–5.7 µm). *Fulvifomes centroamericanus*, *F. combodiensis*, *F. costaricense*, *F. elaeodendri*, *F. hainanensis*, *F. imazekii*, *F. imbricatus* and *F. krugiodendri* are

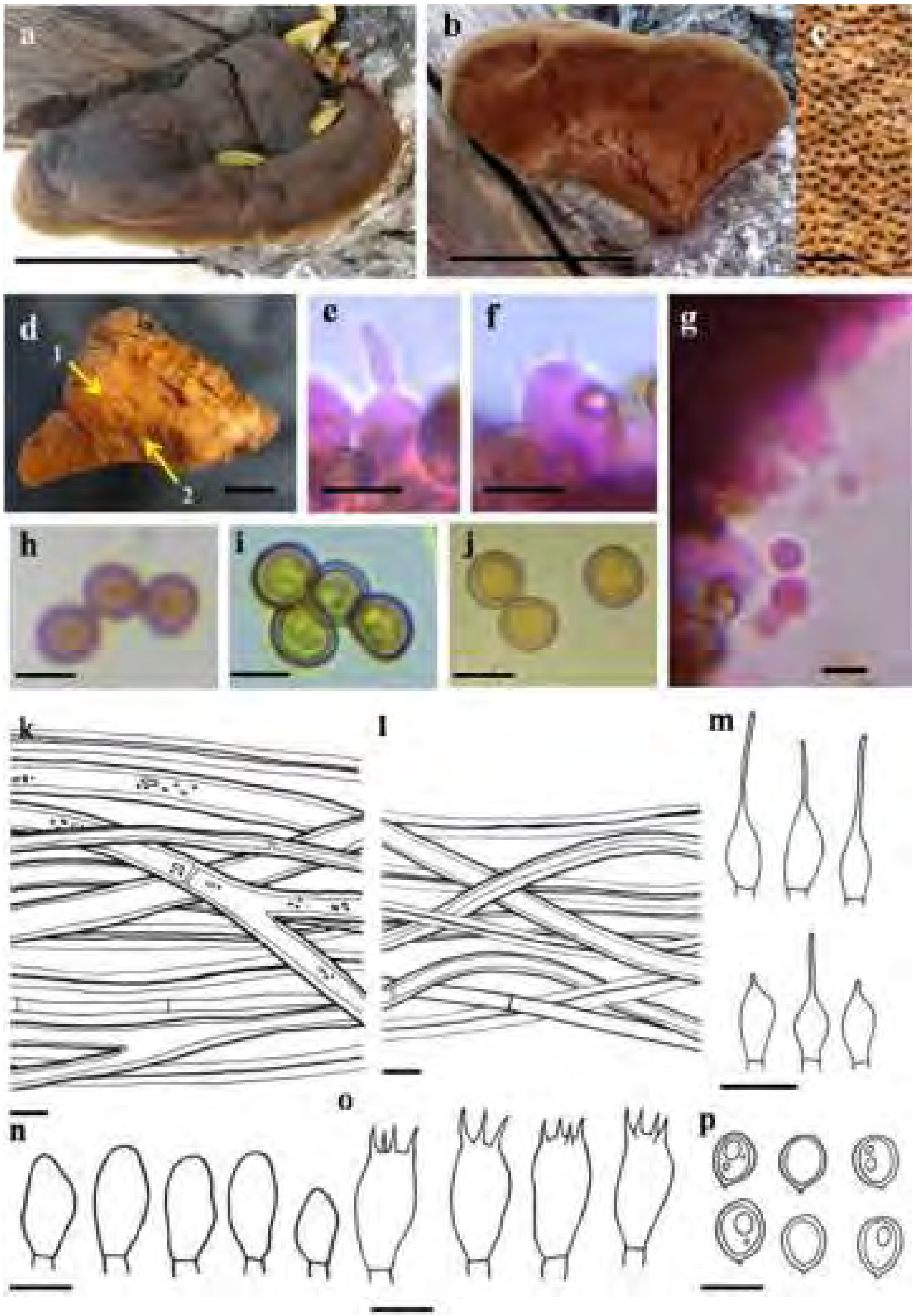


Fig. 158 ***Fulvifomes karaiensis*** (MUBL4016, **halotype**). **a, b** Basidiocarp. **c** Pore surface. **d** CS of basidiomata (d1. Context. d2. Tube layer.). **e** Cystidiole. **f** Basidioles. **g** Basidia. **h** Basidiospores in KOH. **i** Basidiospores in cotton blue. **j** Basidiospores in melzer's reagent. **k** Contextual hyphae. **l** Tramal hyphae. **m** Cystidioles. **n** Basidioles. **o** Basidia. **p** Basidiospores. Scale bars: a, b = 5 cm, c = 1 mm, d = 1 cm, e–p = 5 μm

reported with dimitic hyphal system and absence of cyctidioles, hence they are distinct from our collection (Zhou and Zhang 2012; Zhou 2014, 2015; Ji et al. 2017; Tchoumi et al. 2020; Hattori et al. 2022; Wu et al. 2022).

Fulvifomes cedrelae, *F. dracaenicola*, *F. floridanus*, *F. grenadensis*, *F. rimosus, F. robinae*, *F. squamosus*, and *F. subindicus* are having dimitic hypahe in trama, monomitic in context. However, our collection is strictly dimitic, besides shows distinct variation in morphological and microscopic illustrations. (Hattori et al. 2014; Salvador-Montoya et al. 2018; Du et al. 2021; Wu et al. 2022). Further, *F. boninensis* (Hattori et al. 2022) has subdimitic hyphal system with skeletoid hyphae, deeply rimose pileus, irregular cracks, and ellipsoid to broadly ellipsoid basidiospore (5–6.5 × 3.5–5 μm) without cystidioles, whereas our collection has dimitic with weakly rimose, presence of cystidiole and globose to subglobose basidiospores (5.2–6.2) × (4.7–5.7 μm). *Fulvifomes indicus* (Zhou

2014) and *F. caligoporus* (Wu et al. 2022) are reported to be having monomitic hyphal system. Therefore, we introduce our collection as *F. karaiensis* based on its morphological significance.

Fulvifomes pannaensis S. Gunaseelan, M. Kaliyaperumal & K. Kezo ***sp. nov.***

Index Fungorum number: IF559690; *Facesoffungi number*: FoF 12671; Fig. 159

Etymology: The species epithet "*pannaensis*" referring to the region of basidiomata collected

Macromorphology: *Basidiocarp* perennial, solitary, pileate, sessile, light in weight, hard when dry. *Pileus* dimidiate, semi–circular, with no distinct crust, projecting up to 5.4 cm, 6.6 cm wide and 3.6 cm thick near the attachment. *Pilear surface* smooth to glabrous, weakly zonate, golden brown (5D7) to yellowish brown (5E8), pilei on maturation becoming rough, weakly cracked near attachment, greyish brown (6F3). *Margin* entire, round, velutinate, golden brown (5D7). *Pore surface* yellowish brown (5E7). *Pores* round to angular, regular, 4–5 per mm. *Dissepiments* entire, thick. *Context* up to 3.6 cm, homogeneous, golden brown (5D7). *Tubes* yellowish brown (5D8), up to 4 mm, not stratified.

Micromorphology: *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,

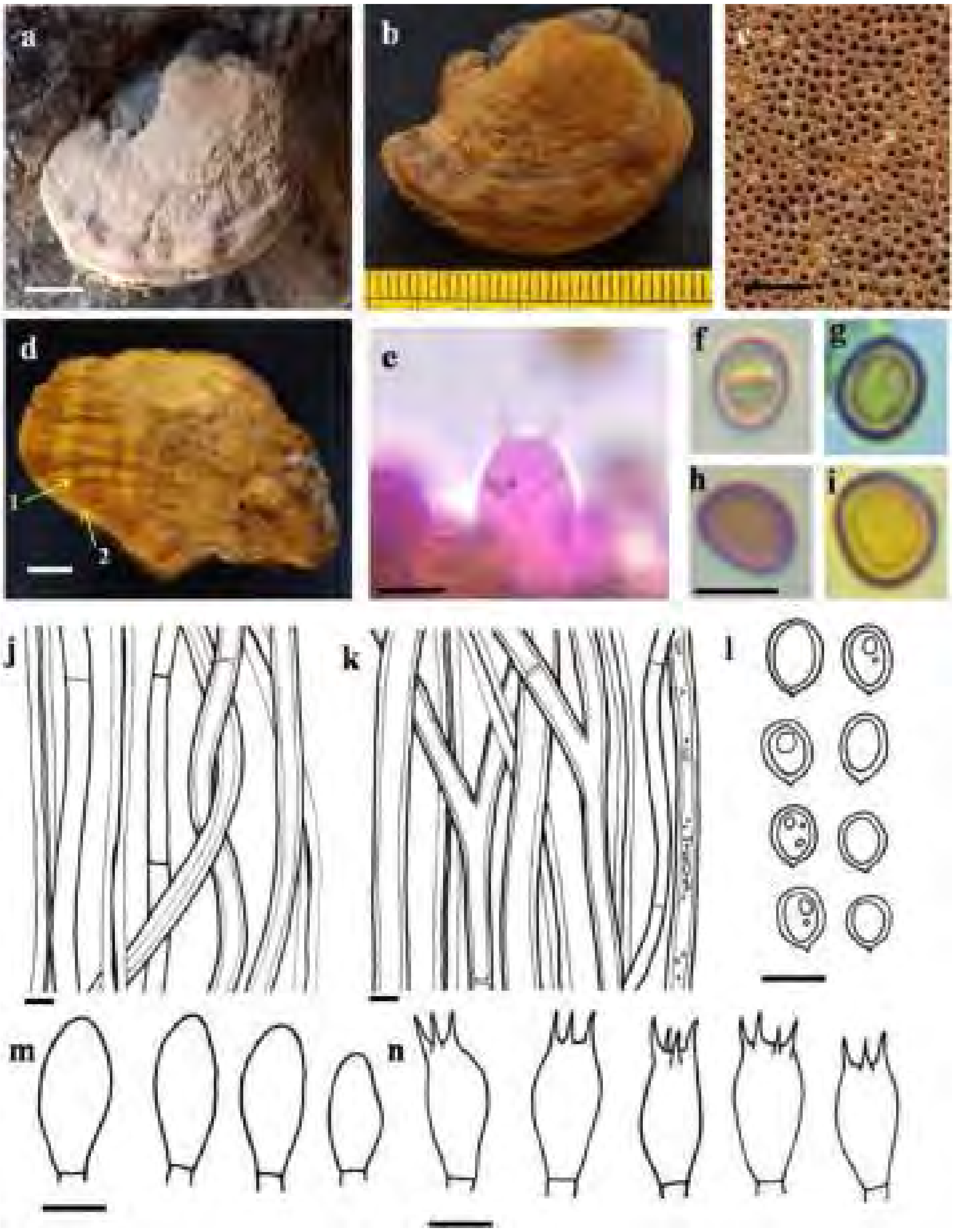


Fig. 159 ***Fulvifomes pannaensis*** (MUBL4017, **halotype**). **a, b** Basidiocarp. **c** Pore surface. **d** CS of basidiomata (d1. Context. d2. Tube layer.). **e** Basidia. **f** Basidiospores in water. **g** Basidiospores in cotton blue. **h** Basidiospores in KOH. **i** Basidiospores in melzer's reagent. **j** Tramal hyphae. **k** Contextual hyphae. **l** Basidiospores. **m** Basidioles. **n** Basidia. Scale bars: a, b, d = 1 cm, c = 1 mm, e–n = 5 µm

2–6.2 µm diameter; skeletal hyphae, thick–walled with narrow lumen, unbranched, yellowish brown, aseptate, 2–5 µm diameter. *Trama* Generative hyphae, thin to thick walled, yellow to brown, septate, rarely branched, 2–5 µm diameter; skeletal hyphae, thick walled with narrow to wide lumen, yellowish brown, aseptate, unbranched, 2–5 µm diameter. Setae and cystidioles absent. *Basidioles* dominant, clavate to broadly clavate, 8.7–15 × 5–8.7 µm. *Basidia* clavate to broadly clavate, with four sterigmata, 9.2–16.2 × 5–8 µm. *Basidiospores* subglobose to broadly ellipsoid, thick–walled, smooth, yellow in water, turning rust brown in KOH, (5.2–) 5.5–6.2 (–6.5) × (4.4–) 4.6–4.9 (–5.2) µm (n = 50/2), Q = 1.2 (Q range 1.1–1.3), CB^{-}, IKI^{-}. *Chlamydospores* globose to subglobose, thick walled rust brown to reddish brown, 4.2–7.8 × 3.5–7.8 µm, CB^{-}, IKI^{-}.

Material examined: India, Tamil Nadu, Thiruvannamalai District, Sathanur, Pennaiyar river, 12° 08′ 00.34″ N 78° 56′ 48.65″ E, on living *Albizzia amara* (Fabaceae), 3 Febraury 2018, Sugantha Gunaseelan (MUBL4017, **holotype**); *ibid*. Kezhocuyi Kezo (PRF32/2, paratype).

GenBank numbers: ITS: MW040080, OP028975; LSU: MW048890, OP028971

Notes: Our collection shares similar microscopical features such as dimitic hyphal system and absence of cystidioles with *Fulvifomes centroamericanus* (Ji et al. 2017), *F. combodiensis* (Zhou and Zhang 2012), *F. costaricense* (Wu et al. 2022), *F. elaeodendri* (Tchoumi et al. 2020), *F. hainanensis* (Zhou 2014), *F. imbricatus* (Zhou 2015) and *F. krugiodendri* (Ji et al. 2017), but significantly distinct from them in macro- and micromorphological characters.

Our collection lacks apilear crust, larger pores (4–5/mm), unstratified tubes with subglobose to broadly ellipsoid spores whereas *F. centroamericanus* (Ji et al. 2017) and *F. costaricense* (Wu et al. 2022) have crust in pileus, smaller pores (> 8/mm) and stratified trama with subglobose spores. Our collection similar to *F. imbricatus* (Zhou 2015), in having uncracked pilear surface, dimitic hyphal system and absence of cystidioles, but *F. imbricatus* has solitary and dimidiate basidiome, however, in the later basidiomata is dimidiate/imbricate. Besides, our collection differs in pores (4–5/mm) and basidiospores (5.2–6.5 × 4.4–5.2 µm) from *F. imbricatus* (8–9/mm; 4.4–5.3 × 3.5–4.5 µm). *Fulvifomes cambodiensis* (Zhou and Zhang 2012) and *F. imazekii* (Hattori et al. 2022) shares similarities having in dimitic hyphal system and absence of cystidoles with our collection but significantly varies with cracked to rimose pileal surface, smaller pores (5–6/mm) and presences of setae.

Fulvifomes hainanensis (Zhou 2014) similar to our collection from its uncracked pilear surface, absence of cystidioles and dimitic hyphal system. However, *F. hainanensis* has duplex context, stratified tubes with larger pores (3–4/mm), however, our collection has homogenous context, unstratified tubes with pores 4–5/mm.

Our collection has glabrous pilei with round margin, tube layer without stratification, larger pores (4–5/mm) and subglobose to broadly ellipsoid spores while *F. elaeodendri* and *F. krugiodendri* pilei have cracks or deeply sulcate with wide furrows, (near margin) with smaller pores (> 5/mm), stratified tubes and basidiospores shape. *F. azonatus* (Wu et al. 2022), *F. thailandicus* (Zhou 2015), *F. nakasoneae* (Wu et al. 2022), *F. nonggangensis* (Zheng et al. 2021) *F. tubogeneratus*, and *F. yoroui* (Olou et al. 2019) shares dimitic hyphal system but varies in other morpho-microscopical traits such as distinct pileal character, presence of cystidioles, shape and size of basidiospores.

Our collection is strictly dimitic while *F. cedrelae*, *F. dracaenicola*, *F. floridanus*, *F. grenadensis*, *F. rimosus*, *F. robinae*, *F. squamosus*, and *F. subindicus* comprise dimitic trama and monomitic in context. *F. boninensis* (Hattori et al. 2022) shows high variations both macro- and micro-morphological characters from our collection. Similarly, subdimitic hyphal system, deeply rimose pileus, irregular cracks, ellipsoid to broadly ellipsoid basidiospore (5–6.5 × 3.5–5 µm) were reported in *F. boninensis* (Hattori et al. 2022) while our collection varies in hyphal system with weakly rimose pileus and basidiospores shape (5.2–6.2 × 4.7–5.7 µm). Monomitic hyphal system was reported in *F. indicus* (Zhou 2014) and *F. caligoporus* (Wu et al. 2022). Therefore, based on distinct morphological differences, we introduce our collection as *Fulvifomes pannaensis.*

Polyporales Gäum.

Polyporales was proposed by Gäumann (1926) with ten families, based on their morphological characters. This order includes variety of basidiocarp types and lacks morphological synapomorphy that unites its associate taxon. Basidiomata varies from bracket-shaped (eg. *Ganoderma*, *Trametes*), effused to resupinate (*Wolfiporia*, *Phlebia*) or stipitate (*Microporus*, *Polyporus*), flabellate to imbricate (*Laetiporus*, *Sparassis*) and hymenophore differs from daedaloid to hydnoid (*Daedaliopsis*, *Flavodon*), poroid to lamellate (*Coriolopsis*, *Lentinus*) or smooth (*Podoscypha*) (Binder et al. 2005). Hyphal system includes monomitic, dimitic to trimitic (Gilbertson and Ryvarden 1986) with basidiospores shape ranging from globose, subglobose, ellipsoid, oblong to cylindrical. The phylogenetic inference from multigene data set resolved 40 valid legitimate families of Polyporales, which also reveal many genera and families to be poly- and/or paraphyletic (Justo et al. 2017). This may be due to the hyphal system and dynamic nature of phenetic characters, acquired adaption of spore dispersal against the diverse habitat and physical environment.

Ganodermataceae Donk

Ganodermataceae was derived by Donk (1948) from previously established Ganodermoideae. Members of this family includes perennial to annual, stipitate to pileate basidiocarps, with or without a cuticle or cuticle, white to greyish pore surface, di-trimitic hyphal system with arboriform skeleto-binding hyphae and saprophytes or parasites causing white rot decomposition (Corner 1983; Zhao 1989; Ryvarden 2004; Costa-Rezende et al. 2017). Basidiospores are distinct from other families of polypores by bearing an apical, often shrunk umbo, non-truncate to truncate apex basidiospore, double-walled with coloured inner wall and ornamented outer wall (Donk 1964; Moncalvo and Ryvarden 1997; Núñez and Ryvarden 2000; Ryvarden 2004; Costa-Rezende et al. 2017; Sun et al. 2020). Ganodermataceae is polyphyletic with 10 genera, of which, *Amauroderma* s. str., *Foraminispora*, *Furtadoa*, *Haddowia*, *Magoderna* and *Sanguinoderma* have non-truncate basidiospores whereas *Ganoderma*, *Humphreya*, *Tomophagus*, and *Trachyderma* have basidiospores with truncate apex (Karsten 1881; Steyaert 1972; Corner 1983; Moncalvo and Ryvarden 1997; Costa-Rezende et al. 2017, 2020; Sun et al. 2020).

Ganoderma P. Karst.

Ganoderma represents the largest genus of Ganodermataceae with most of the species belonging to *G. lucidum* species complex. *Ganoderma* was established by Karsten (1881) based on a single species, *Boletus lucidus* Leyss. Members of this genus vary from annual or perennial, stipitate to sessile, distinctive laccate or non-laccate basidiomata (Moncalvo and Ryvarden 1997). *Ganoderma* is characterized by, double-walled basidiospores, and interwall pillars with non-truncate, globose to subglobose, verrucose to asperulate (smooth in only one species) basidiospores (Moncalvo and Ryvarden 1997; Ryvarden 2004; Hapuarachchi et al. 2019). Approximately, 200 species have been described under *Ganoderma*, of which 167 could fall under so-called subgenus *Ganoderma* (Moncalvo and Ryvarden 1997). While, it is difficult to determine the actual number of species, NCBI has recorded 495 associated taxa and in MycoBank, there are 423 taxa recorded.

Ganoderma ghatensis K. Kezo, S. Gunaseelan & M. Kaliyaperumal ***sp. nov.***

Index Fungorum number: IF557014; *Facesoffungi number*: FoF10728; Fig. 160

Etymology: "*ghatensis*" refers to the place of collection.

Macromorphology*: Basidiocarps* annual, solitary to cluster, sessile, applanate, leathery when fresh and woody to corky when dry. *Pileus* semicircular, convex, projecting up to 10 cm, 9 cm wide and 4 cm thick near the base. *Pilear surface* reddish brown (9E8) when fresh, liver brown (7D6) when dry, covered by a laccate layer, hard and irregular surface towards the attachment becoming concentrically zonate near the margin. *Margin* acute, concolorous with the pilear surface. *Pore surface* orange white (6A2) to brownish orange (6C7). *Pores* round regular, 4–8 per mm. *Context* up to 1.5 cm, homogeneous, light brown (6D6) to brown (7E8). *Tubes* brown (6D6) to light brown (6D6), up to 3 cm thick.

Micromorphology*: Hyphal system* trimitic, skeletal hyphae dominant in the basidiomata. *Context* Generative hyphae, thin to thick walled, hyaline, clamped septate, branched, 2.5–6 µm diameter; skeletal hyphae, thick-walled with narrow lumen, unbranched, rust brown, aseptate, 3.7–8 µm diameter; binding hyphae, thick-walled with narrow lumen, branched, aseptate, 2.5–4 µm diameter. *Trama* Generative hyphae, thin to thick walled, hyaline, rarely clamped septate, frequently branched, 2–5 µm diameter; skeletal hyphae, thick walled with narrow lumen, rust brown, aseptate, unbranched, 3.7–7.5 µm diameter; binding hyphae, thick-walled with narrow lumen, branched, aseptate, 2.5–4.7 µm diameter. *Cutis* cell broadly clavate, rarely umbonate, 27.5–60 × 10–18.7 µm. *Cystidioles* absent. *Basidioles* clavate, 15.5–25 × 5–6.2 µm. *Basidia* clavate, with four sterigmata, 17–30 × 5–8.5 µm. *Basidiospores* ellipsoid, brown, thick-walled, truncate at the apex, bitunicate, exospore thin, subhyaline, smooth, endospore thick, brown, echinulate; (11.2-) 11.5–14.7 (–15) × (7.5–) 7.7–9 (–9.5) µm (n = 50/2), Q = 1.3–1.5; CB$^-$, IKI$^-$.

Material examined: India, Tamil Nadu, Thiruvannamalai District, Jawadhu hills, Nallapathur Reserve Forest, 12° 32′ 49.9″ N 78° 54′ 05.9″ E, on dead wood, 14 January 2020, Kezhocuyi Kezo, (MUBL4014, **Holotype**).

Additional material examined: India, Tamil Nadu, Salem District, Yercaud, 11° 48′ 12.4″ N 78° 16′ 03.0″ E, on dead wood, 26 February 2020, Kezhocuyi Kezo (Isotype, KSM-AR1). India, Tamil Nadu, Salem District, Yercaud, 11° 48′ 15.1″ N 78° 16′ 13.6″ E on dead wood, 26 February 2020, Kezhocuyi Kezo (Isotype, KSM-AR4). India, Tamil Nadu, Salem District, Yercaud, 11° 49′ 01.8″ N 78° 15′ 37.4″ E, on dead wood, 26 February 2020, Kezhocuyi Kezo (Isotype, KSM-VR6). India, Tamil Nadu, Salem District, Kolli Hills, 11° 19′ 46.0″ N 78° 21′ 22.8″ E, on dead wood, 26 February 2020, Kezhocuyi Kezo (Isotype, KSM-KV3). India, Tamil Nadu, Thiruvannamalai District, Jawadhu hills, 12° 28′ 58.0″ N 78° 49′ 26.7″ E, on dead wood, 14 January 2020, Kezhocuyi Kezo (Isotype, KSM-TM61).

GenBank numbers: ITS: MZ203592, LSU: OM432453, *β-tubulin*: MZ229331, RPB2: ON297669

Notes: *Ganoderma ghatensis* shares similarity with *G. mizoramense* by having semicircular and convex pileus, presence of laccate pilear layer, acute margin, absences of cystidioles and reddish-brown basidiocarp, but the former differs by having sessile, smaller basidiocarp size and concolorous pilear and margin; smaller pores (4–8/mm) and basidiospore size (11.2–) 11.5–14.7 (–15) × (7.5–) 7.7–9 (–9.5) µm (Crous et al. 2017; Mangaiha et al. 2019). *Ganoderma ghatensis* differs in having larger pores and basidiospores with other

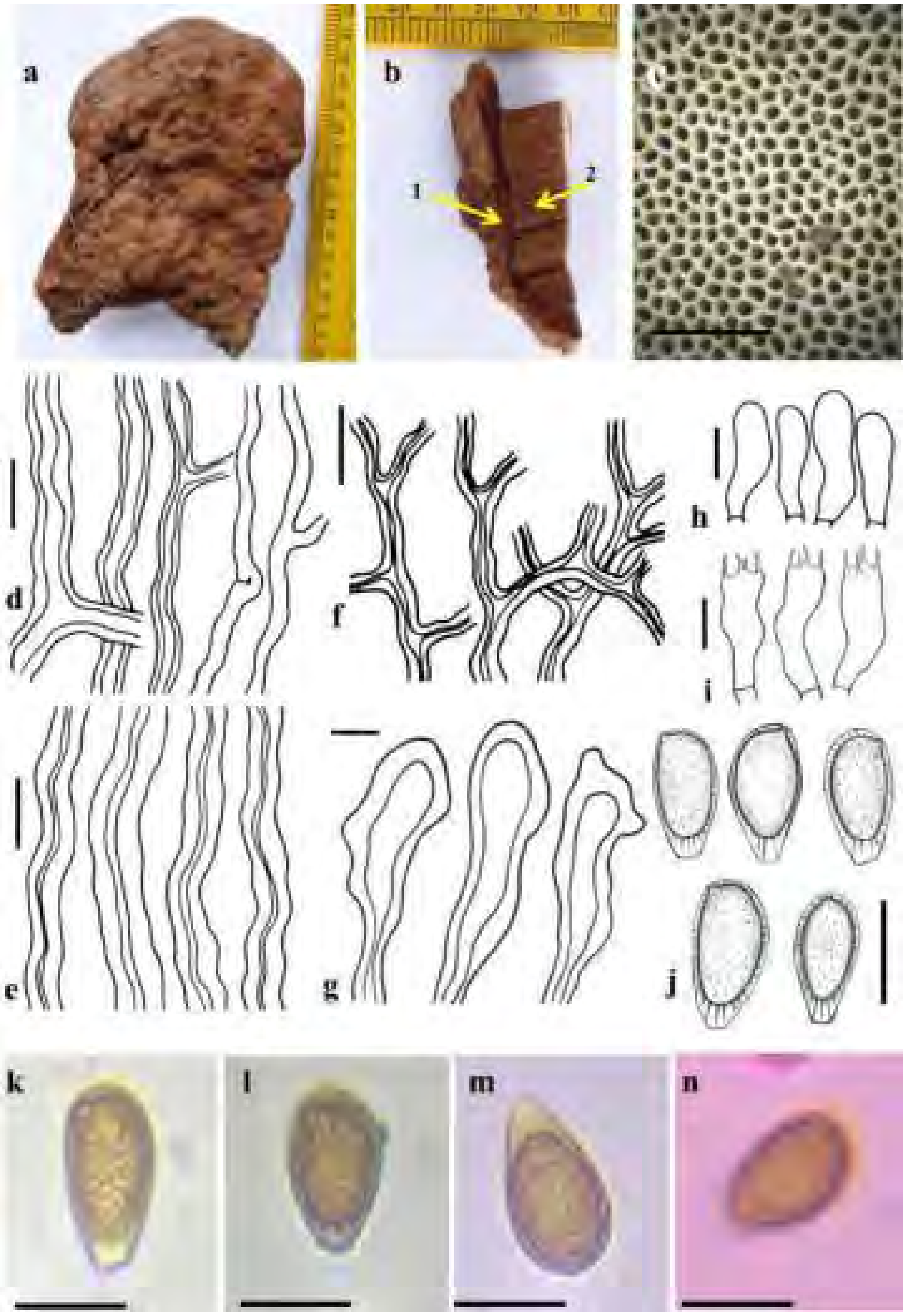


Fig. 160 ***Ganoderma ghatensis*** (MUBL4014, **holotype**). **a** Basidiocarp. **b**1 Context. **b**2 tube layer. **c** Pore surface. **d** Generative hyphae. **e** Skeletal hyphae. **f** Binding hyphae. **g** Cutis cell. **h** Basidioles **i** Basidia. **j** Basidiospores. **k** Basidiospore in H_2O. **l** Basidiospore in cotton. **m** Basidiospore Melzer's reagent. **n** Basidiospore in phloxine. Scale bars: c = 1 mm, d–n = 10 µm

closely-related species namely *G. dunense*, *G. destructans*, *G. martinicense*, *G. mizoramense*, *G. multiplicatum*, *G. multipileum* and *G. steyaertanum* (Hapuarachchi et al. 2015; Cabarroi-Hernández et al. 2019; Tchoumi et al. 2019) found in Cluster A.3 of Clade A, *Ganoderma* spp. meta-analysis as represented by Fryssouli et al. (2020).

Kingdom: **Chromista** Caval.-Sm.
Phylum: **Oomycota** Arx
Class: **Peronosporea**

Peronosporales Bek.

The Peronosporales are by far the largest order of the oomycetes and comprise more than 1000 species (Thines 2014). Members of the Peronosporales are found in both marine and terrestrial ecosystems and include saprotrophic, necrotrophic, hemibiotrophic and obligate biotrophic species (Judelson 2012).

Peronosporaceae de Bary

Peronosporaceae is a large complex family that contains a number of devastating plant-pathogenic oomycete species (Thines and Choi 2016). A broad circumscription of Peronosporaceae, encompassing *Phytophthora*, *Phytopythium*, *Halophytophthora*, *Nothophytophthora* and all downy mildew genera is currently accepted.

Phytophthora de Bary

The genus *Phytophthora* was established by de Bary (1876) and currently includes about 220 formally described species (Bregant et al. 2023). The genus has been divided into twelve monophyletic major clades (Fig. 161). The morphological characteristics and species composition of these monophyletic groups were reviewed by Yang et al. (2017b). In this study, we introduce a new *Phytophthora* species.

Phytophthora debattistii Bregant, Montecchio & Linaldeddu, ***sp. nov.***

Index Fungorum number: IF900191; *Facesoffungi number*: FoF13941; Fig. 161

Etymology: in honour and memory of Dr. Renzo De Battisti for his outstanding work on Alpine ecosystems.

Pathogenic on stems and roots of *Alnus incana* (L.) Moench forming cankers. **Sexual morph**: Homothallic. *Gametangia* produced abundantly on carrot agar (CA) after 7–10 days at 20 °C. *Oogonia* 40–55 µm diam. ($\bar{x} = 48.8 \pm 3.7$ µm, n = 50) smooth-walled, terminal. *Antheridia* 16.5–30 × 15–28 µm ($\bar{x} = 24.4 \pm 4.2 \times 20.9 \pm 3.9$ µm, n = 50), mostly amphigynous (around 70%), sometimes paragynous (around 30%), hyaline, rounded, club-shaped, attached near the oogonial stalk, one per oogonium. *Oospores* 37.8 ± 2.6 µm diam., spherical, aplerotic. **Asexual morph**: *Sporangia* 47–112 × 27–60 µm ($\bar{x} = 78.3 \pm 14.9 \times 43.4 \pm 7.4$ µm, n = 50), with a length/breadth ratio of 1.8 ± 0.1 (n = 50) persistent, non-papillate, mostly ovoid (around 60%) to ellipsoid (around 30%), sometimes elongate (around 8%) rarely distorted (around 2%) abundantly produced on CA plugs flooded in unsterile pond water after 24–36 h of incubation at 20 °C on simple or rarely compound sympodial sporangiophores. *Zoospores* abundantly produced in liquid cultures after 48 h at 20 °C. *Sporangial proliferation* mostly external emerging just below the mature sporangium and less frequently internal, both nested and extended. *Hyphal swellings* globose and catenulate, rarely

Fig. 161 ***Phytophthora debattistii*** (CBS 147721, **ex-holotype**). **a–c** Colony morphology after 7 days growth at 20 °C on **a** potato dextrose agar (PDA), **b** malt extract agar (MEA), **c** carrot agar (CA). **d–f** Non-papillate persistent sporangia on CA after 24–36 h flooding in nonsterile pond water: ovoid, ellipsoid and distorted respectively. **g, h** Releasing zoospores. **i** External proliferation. **j** Internal nested proliferation. **k** Intercalary globose catenulated hyphal swellings. **l** Mature oogonia with amphigynous. **m** Paragynous antheridia and slight aplerotic oospores. Scale bars: d–m = 20 µm

Fig. 162 Phylogram generated from maximum likelihood analysis based on combined ITS, *β-tubulin* and *cox*1 sequence dataset. Seventy-eight *Phytophthora* strains were included in the combined sequence analysis, which comprise 2261 characters. *Nothophytophthora* sp. (BD268) was used as the outgroup taxon. Sequences were aligned with ClustalX v. 1.83, using the default parameters. The evolutionary history was inferred by using the Maximum Likelihood method and General Time Reversible model (Nei and Kumar 2000). The tree with the highest log likelihood (− 21,877.77) is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.2597)). The rate variation model allowed for some sites to be evolutionarily invariable ([+I], 30.10% sites). Bootstrap support equal or greater than 50% are given at the nodes. Ex-type strains are in black bold and newly generated sequences are indicated in blue bold. Alignments and trees are available in TreeBase (TB2:S29999)

produced in unsterile pond water and absent in solid culture. *Chlamydospores* not observed.

Culture characteristics: colony growth pattern cottony on potato dextrose agar (PDA) with an irregular border, stellate on malt extract agar (MEA) and rosaceous to stellate on carrot agar (CA). On PDA and MEA colony growth was slow, whereas on CA colony reached 62 ± 3 mm (n = 5) diameter in 7 days at 23 °C.

Cardinal temperature for growth: Minimum < 2 °C, maximum 33 °C and optimum 23 °C. Isolates failed to grow at 35 °C and mycelium did not resume growth when plates were moved to 23 °C or below.

Material examined: Italy, Vigo di Cadore, the centre of the Dolomites, from aerial bark lesions and bleeding cankers on *Alnus incana* (Betulaceae), 17 December 2019, Carlo Bregant, (CBS H-24767 **holotype**, a dried culture on CA), ex-holotype culture CB83 = CBS 147721.

GenBank numbers: ITS: OP999674, *β-tubulin*: OQ067250, *cox1:* OQ067254.

Notes: Our phytophthora-like isolates phylogenetically close to the species in the sub-clade 6b (Fig. 162) and they grouped with *Phytophthora megasperma* forming a sister clade with ML = 100 statistical support. However, nucleotide differences in ITS, *β-tubulin* and *cox*1 loci of our isolates and *P. megasperma* revealed 0.12%, 0.61%, and 0.18% respectively. Our collection morphologically differs from *P. megasperma* by sporangia shape and sizes, colony growth and formation, a lower minimum temperature for growth, aplerotic oospores and antheridia mostly amphigynous. Further, our collection is phylogenetically closed to *P. crassamura* that have 0.49%, 0.73%, and 2.97% nucleotide differences in ITS, *β-tubulin* and *cox*1 loci respectively. *Phytophthora crassamura* produces sporangia similar in shape to our collection, but significantly smaller in size ($\overline{x} = 60.3 \pm 6.0 \times 37.4 \pm 3.6$ µm, with a length/breadth ratio of 1.6). Therefore, we introduce our collection as *P. debattistii* sp. nov.

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Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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