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Fungal diversity notes 1512–1610: taxonomic and phylogenetic contributions on genera and species of fungal taxa

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Abstract

This article is the 14th in the Fungal Diversity Notes series, wherein we report 98 taxa distributed in two phyla, seven classes, 26 orders and 50 families which are described and illustrated. Taxa in this study were collected from Australia, Brazil, Burkina Faso, Chile, China, Cyprus, Egypt, France, French Guiana, India, Indonesia, Italy, Laos, Mexico, Russia, Sri Lanka, Thailand, and Vietnam. There are 59 new taxa, 39 new hosts and new geographical distributions with one new combination. The 59 new species comprise *Angustimassarina kunmingense*, *Asterina lopi*, *Asterina brigadeirensis*, *Bartalinia bidenticola*, *Bartalinia caryotae*, *Buellia pruinocalcarea*, *Coltricia insularis*, *Colletotrichum flexuosum*, *Colletotrichum thasutense*, *Coniochaeta caraganae*, *Coniothyrium yuccicola*, *Dematipyriforma aquatic*, *Dematipyriforma globispora*, *Dematipyriforma nilotica*, *Distoseptispora bambusicola*, *Fulvifomes jawadhuvensis*, *Fulvifomes malaiyanurensis*, *Fulvifomes thiruvannamalaiensis*, *Fusarium purpurea*, *Gerronema atrovirens*, *Gerronema flavum*, *Gerronema keralense*, *Gerronema kuruvense*, *Grammothele taiwanensis*, *Hongkongmyces changchunensis*, *Hypoxylon inaequale*, *Kirschsteiniothelia acutisporum*, *Kirschsteiniothelia crustaceum*, *Kirschsteiniothelia extensum*, *Kirschsteiniothelia septemseptatum*, *Kirschsteiniothelia spatiosum*, *Lecanora*

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immersocalcarea, *Lepiota subthailandica*, *Lindgomyces guizhouensis*, *Marthe asmius pallidoaurantiacus*, *Marasmius tangerinus*, *Neovaginatispora mangiferae*, *Pararamichloridium aquisubtropicum*, *Pestalotiopsis piraubensis*, *Phacidium chinaum*, *Phaeoisaria goiasensis*, *Phaeoseptum thailandicum*, *Pleurothecium aquisubtropicum*, *Pseudocercospora vernoniae*, *Pyrenophora verruculosa*, *Rhachomyces cruralis*, *Rhachomyces hyperommae*, *Rhachomyces magrinii*, *Rhachomyces platyprosophi*, *Rhizomarasmius cunninghamietorum*, *Skeletocutis cangshanensis*, *Skeletocutis subchrysella*, *Sporisorium anadelphiae-leptocomae*, *Tetraploa dashaoensis*, *Tomentella exiguelata*, *Tomentella fuscoaraneosa*, *Tricholomopsis lechatii*, *Vaginatispora flavispora* and *Wetmoreana blastidiocalcarea*. The new combination is *Torula sundara*. The 39 new records on hosts and geographical distribution comprise *Apiospora guiyangensis*, *Aplosporella artocarpi*, *Ascochyta medicaginicola*, *Astrocystis bambusicola*, *Athelia rolfsii*, *Bambusicola bambusae*, *Bipolaris luttrellii*, *Botryosphaeria dothidea*, *Chlorophyllum squamulosum*, *Colletotrichum aeschynomenes*, *Colletotrichum pandanicola*, *Coprinopsis cinerea*, *Corylicola italica*, *Curvularia alcornii*, *Curvularia senegalensis*, *Diaporthe foeniculina*, *Diaporthe longicolla*, *Diaporthe phaseolorum*, *Diatrypella quercina*, *Fusarium brachygibbosum*, *Helicoma aquaticum*, *Lepiota metulispora*, *Lepiota pongduadensis*, *Lepiota subvenenata*, *Melanconiella meridionalis*, *Monotosporella erecta*, *Nodulosphaeria digitalis*, *Palmiascoma gregariascomum*, *Periconia byssoides*, *Periconia cortaderiae*, *Pleopunctum ellipsoideum*, *Psilocybe keralensis*, *Scedosporium apiospermum*, *Scedosporium dehoogii*, *Scedosporium marina*, *Spegazzinia deightonii*, *Torula fici*, *Wiesneriomyces laurinus* and *Xylaria venosula*. All these taxa are supported by morphological and multigene phylogenetic analyses. This article allows the researchers to publish fungal collections which areimportant for future studies. An updated, accurate and timely report of fungus-host and fungus-geography is important. We also provide an updated list of fungal taxa published in the previous fungal diversity notes. In this list, erroneous taxa and synonyms are marked and corrected accordingly.

Keywords 59 New taxa · 39 New records · Ascomycota · Basidiomycota · Dothideomycetes · Lecanoromycetes · Leotiomycetes · Sordariomycetes · Ustilaginomycotina

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1601. ***Skeletocutis subchrysella*** B.K. Cui & Shun Liu, ***sp. nov.*** (contributed by B.K. Cui and Shun Liu)

Psathyrellaceae Vilgalys, Moncalvo & Redhead,
1602. ***Coprinopsis cinerea*** (Schaeff.) Redhead, Vilgalys & Moncalvo, ***new record from India*** (contributed by S. Mahadevakumar, Y.S. Deepika, N. Lakshmidevi and S.S.N. Maharachchikumbura)

Thelephorales Corner ex Oberw
Thelephoraceae Chevall
1603. ***Tomentella exiguelata*** Y.H. Mu & H.S. Yuan, ***sp. nov.*** (contributed Y.H. Mu, T. Cao and H.S. Yuan)
1604. ***Tomentella fuscoaraneosa*** Y.H. Mu & H.S. Yuan, ***sp. nov.*** (contributed Y.H. Mu, T. Cao and H.S. Yuan).

Agaricales genera incertae sedis
1605. ***Gerronema atrovirens*** Wannathes, N. Suwannarach, J. Kumla, Phonrob & S. Lumyong, ***sp. nov***. (contributed by N Wannathes, N Suwannarach J Kumla and S Lumyong)
1606. ***Gerronema flavum*** Wannathes, N. Suwannarach, J. Kumla, Phonrob & S. Lumyong, ***sp. nov.*** (contributed by N Wannathes, N Suwannarach J Kumla and S Lumyong)
1607. ***Gerronema keralense*** K. P. D. Latha & Manim, ***new record from Thailand*** (contributed by N Wannathes, N Suwannarach J Kumla, S Khuna, W Phonrob and S Tabtan)
1608. ***Gerronema kuruvense*** K. P. D. Latha & Manim, ***new record from Thailand*** (contributed by N Wannathes, N Suwannarach J Kumla, S Khuna, W Phonrob and S Tabtan)
1609. ***Tricholomopsis lechatii*** Courtec., S. Dumez, S. Welti & P.-A. Moreau, ***sp. nov.*** (contributed by Courtec., S. Dumez, S. Welti and P.-A. Moreau)

Subphylum Ustilaginomycotina Doweld
Class Ustilaginomycetes R. Bauer et al.
Ustilaginales G. Winter
Ustilaginaceae Tul & C. Tul
1610. ***Sporisorium anadelphiae-leptocomae*** T. Denchev, Denchev, Kemler, M.P. Martín & Begerow, ***sp. nov.*** (contributed by T. Denchev, Denchev, Kemler, M.P. Martín and Begerow)

Introduction

Fungi play a key role in many biological processes, influencing ecosystems (Schimann et al. 2017). They are saprobes, epiphytes, endophytes, animal and plant pathogens or symbionts (Chethana et al. 2021a, b). High species diversity in fungi exhibits a huge variation in morphology, lifestyles and the mode of dispersal (Hyde et al. 2018). Fungi are also important in biotechnological applications (Hyde et al. 2019).

The current estimate of fungal diversity is highly uncertain, ranging from 1.5 to 12 million species (Wu et al. 2019; Hyde et al. 2021; Bhunjun et al. 2022). Of this massive number, only around 150,000 species have been named and classified to date. With the introduction of DNA-based techniques in species delimitation, the newly described taxa per year have dramatically increased. Whether these newly introduced taxa are novel is another challenge the mycologists face. With only 10% of fungi being named and classified, many species remain to be discovered (Hyde et al. 2021). Some species are poorly described and lack molecular data. This can be overcome if we collect, isolate, sequence and provide new data on fungi from different hosts and habitats. Identification of new taxa, recollection of already known taxa, the establishment of reference specimens and epitypification or neo-typification of taxa with fresh material and cultures are necessary as they contribute to providing a stable taxonomy for fungi Chethana et al. (2021a) as well as for carrying out assays to identify any potential compounds that can be harnessed at the industrial level. Identification and documentation of the host and the geographical range of a fungus can be particularly important in disease management (Dugan et al. 2009).

In order to provide an outlet for the mycologists to publish their findings in mycology, different publication series such as AJOM new records and collections of fungi (Hyde et al. 2019; Chethana et al. 2021b), Fungal Diversity notes (Liu et al. 2015; Ariyawansa et al. 2015; Hyde et al. 2017, 2019, 2020; Tibpromma et al. 2018; Wanasinghe et al. 2018; Phookamsak et al. 2019; Boonmee et al. 2021), Fungal planet (Crous et al. 2015a, b, c, 2017, 2018) and Mycosphere notes (Thambugala et al. 2015; Hyde et al. 2018, 2021; Jayawardena et al. 2018; Manawasinghe et al. 2022), are now available. As a result, numerous new taxa, geographical and host records, new combinations, and reference data were introduced along with morphological and multigene analyses.

This is the 14th in the series of Fungal Diversity Notes with entries mainly collected from Australia, Brazil, Burkina Faso, Chile, China, Cyprus, Egypt, France, French Guiana, India, Indonesia, Italy, Laos, Mexico, Russia, Sri Lanka, Thailand, and Vietnam. We aim to provide new data including morphological, geographical and sequence data for a stable taxonomy and phylogeny, which become significantly important for the accurate identification of fungi as suggested by Cao et al. (2021), Chethana et al. (2021a), Manawasinghe et al. (2019), Maharachchikumbura et al. (2021), Jayawardena et al. (2021b) and Pem et al. (2021). We provide a detailed description and an updated tree for the genus or family of each entry. The 'notes' under each entry discuss how the new taxa are established, including the host and geographical ranges. The data compiled in this study can be used by future researchers for a better understanding of the taxonomy of each different group of fungi.

Materials and methods

Materials and methods follow the previous fungal diversity notes (Hyde et al. 2016, 2020a, b, c; Tibpromma et al. 2017; Wanasinghe et al. 2018; Phookamsak et al. 2019; Boonmee et al. 2021 and Senanayake et al. 2020). When specific details are available for material and methods they are given in the 'notes' section of each taxon. Taxa described in this study were collected from Australia, Brazil, Burkina Faso, Chile, China, Cyprus, Egypt, France, French Guiana, India, Indonesia, Italy, Laos, Mexico, Russia, Sri Lanka, Thailand, and Vietnam. Taxa were described and illustrated based on morphological features, coupled with phylogenetic analyses performed by maximum likelihood (ML), maximum parsimony (MP) and Bayesian posterior probability (BYPP) criteria. Colour codes followed the Methuen Handbook of Colour (Kornerup and Wanscher 1978). Phylogenetic analyses were performed based on details outlined by Dissanayake et al. (2020). Details of each analysis are given in Supplementary Table 1. The pairwise homoplasy index (PHI) test was carried out when necessary, using Split Trees as described by Quaedvlieg et al. (2014) to determine the recombination level within phylogenetically closely related species. The new taxa are justified based on the guidelines of Cao et al. (2021), Chethana et al. (2021a, b), Manawasinghe et al. (2021), Maharachchikumbura et al. (2021), Jayawardena et al. (2021b) and Pem et al. (2021).

Results

Ascomycota R.H. Whittaker
Notes: We follow the latest treatments and updated accounts of Ascomycota in Wijayawardene et al. (2020, 2022).
Subphylum Pezizomycotina O.E. Erikss. & Winka
Class Dothideomycetes O.E. Erikss. & Winka
Notes: We follow the latest treatments and updated accounts of Dothideomycetes in Hongsanan et al. (2020a, b) and Wijayawardene et al. (2020, 2022).

Subclass Dothideomycetidae P.M. Kirk, P.F. Cannon, J.C. David & Stalpers ex C.L. Schoch, Spatafora, Crous & Shoemaker

Mycosphaerellales (Nannf.) P.F. Cannon
Notes: Abollahzadeh et al. (2020) based on LSU, *tef1* and *rpb2* sequence data revalidated Mycosphaerellales as a separate order. Mycosphaerellales include species that are saprobes, ectophytes, plant pathogens and lichenised fungi. This order includes eight families *viz.* Cystocoleaceae, Dissoconiaceae, Extremaceae, Mycosphaerellaceae, Neodevriesiaceae, Phaeothecoidiellaceae, Schizothyriaceae and Teratosphaeriaceae (see Abdollahzadeh et al. 2020).

Mycosphaerellaceae Lindau, Nat. Pflanzenfamilien: 421(1897)
Notes: Mycosphaerellaceae was established by Lindau (1896) with *Mycosphaerella* as the type genus. This is one of the largest families including asexual morphs, asexual holomorphs or species with mycosphaerella-like sexual morphs. The majority of them are parasitic or saprobic on plants, fungi and lichens (Hyde et al. 2013). Wijayawardene

et al. (2022) accepted a total of 119 genera having molecular data under Mycosphaerellaceae.

Pseudocercospora Speg., Anales del Museo Nacional de Historia Natural Buenos Aires 20 (13): 438 (1910)

Notes: *Pseudocercospora* was established by Spegazzini (1910) with *P. vitis* as the type genus. The genus is characterized by conidiophores solitary, fasciculate, synnematal or arranged in sporodochia, conidia coloured, scars unthickened or slightly thickened (Crous and Braun 2003; Crous et al. 2014). They are mostly plant pathogenic fungi associated with leaf and fruit spots and are widely distributed in a wide range of climatic conditions including cool temperate, sub-tropical and tropical regions (Crous et al. 2014).

Pseudocercospora vernoniae Archana Singh & N.K. Dubey, ***sp. nov***

Mycobank Number: *MB 834618, Facesoffungi number: FoF 07979, Figs. 1, 2*

Etymology: Based to the host genus from which the taxon was isolated

Holotype: AMH:10043

Asexual morph: *on leaf spots* of *Vernonia cineria*, hypophyllous later amphiphyllous, 2–5 mm, angular, vein limited,

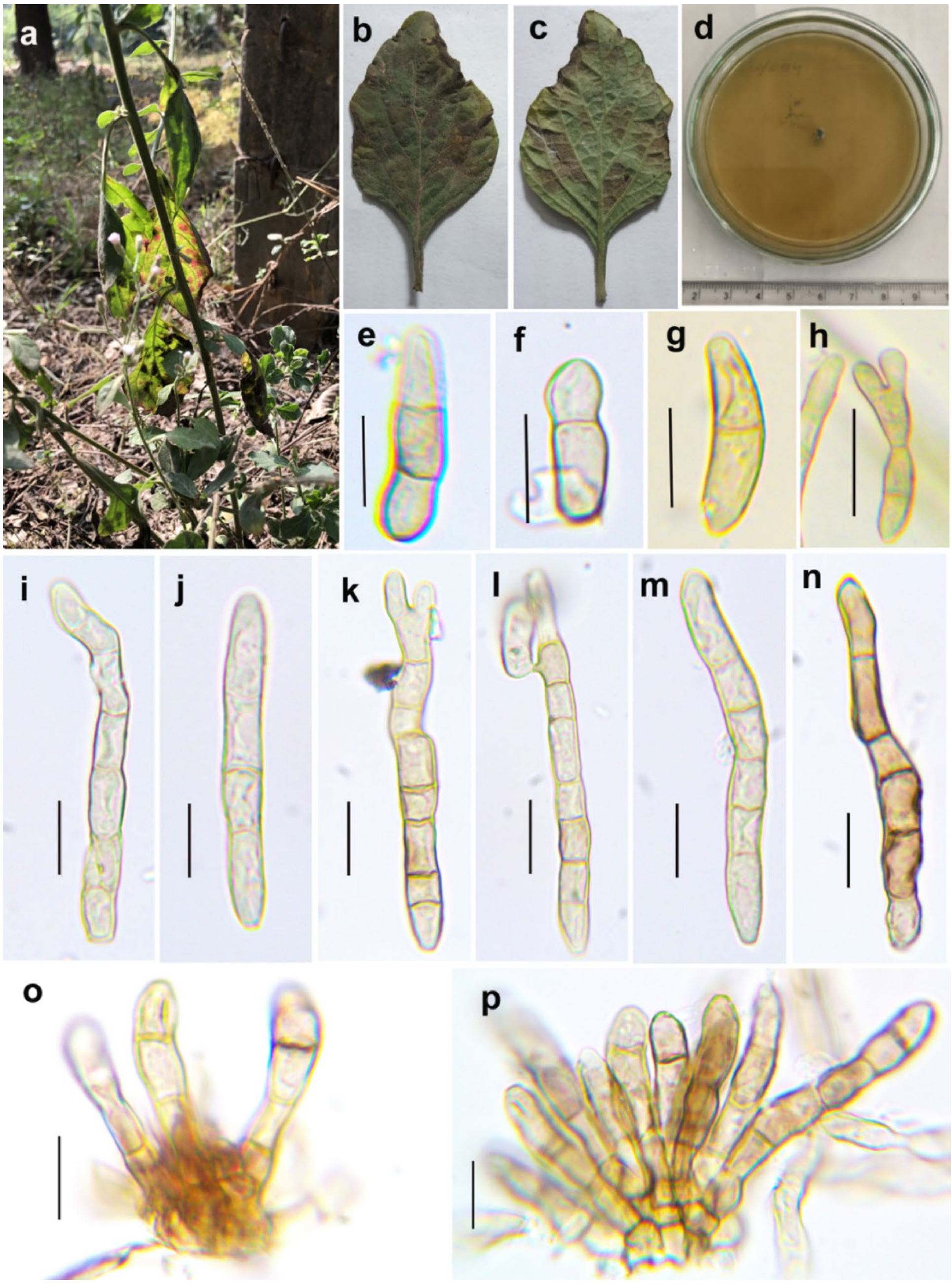


Fig. 1 *Pseudocercospora vernoniae* (AMH: 10043, **Holotype**) **a** Habit of infected plant *Vernonia cineria.* **b** Symptoms on the upper leaf surface. **c** Symptoms on the lower leaf surface. **d** Culture after 3 weeks. **e–o** Conidia. **k** Conjugating conidia. **p–q** Fascicle of conidiophores. Scale bars: **e–j** = 20 µm, **k–o** = 10 µm

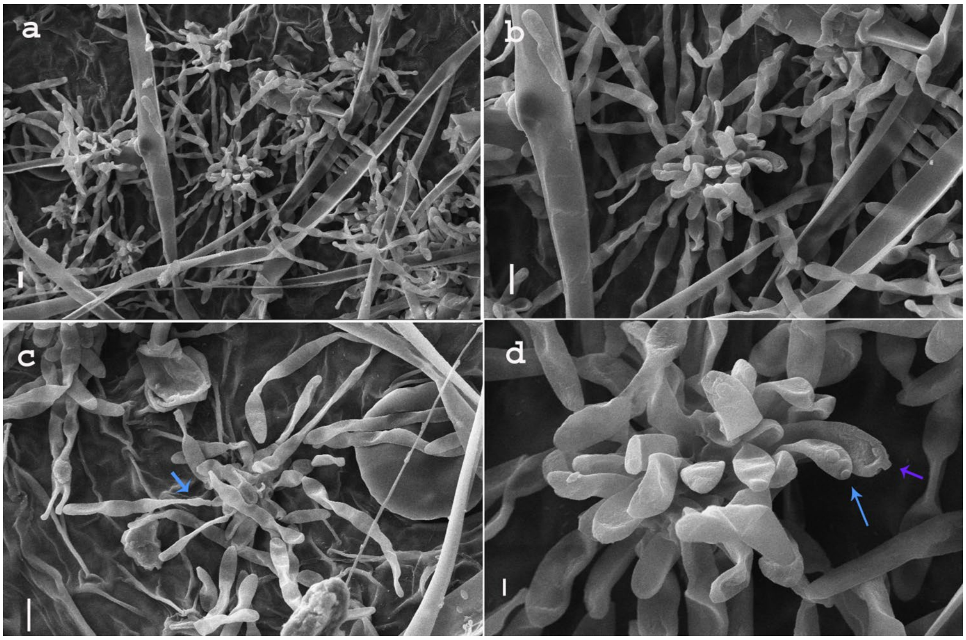


Fig. 2 Scanning Electron Micrographs of *Pseudocercospora vernoniae*. **a** Fascicles of conidiophores arising from stomata of the host plant. **b** Single fascicle of conidiophores. **c** Conidia attached to conidiophores. **d** Conidiogenous cells with scars. Scale bars: **a–c** = 10 µm, **d** = 2 µm

discrete and later forming irregular larger patches, grayish brown on lower surface and dark blackish- brown on upper surface. *Caespituli* hypophyllous later amphiphyllous, dark brown, erumpent. *Stromata* substomatal, few cells to well-developed, made up of oval to round 3–5 µm wide pseudoparenchymatous cells, median to dark brown. *Conidiophores* fasciculate, unbranched or rarely branched, geniculate, 1–8-septate, light brown 13.6–40.3 (50) × 3.5–5.5 µm. *Conidiogenous* cells integrated, polyblastic, cicaterised. *Conidia* septate (1–7), catenate in branched chains, straight to curved, cylindrical, constricted at septa, olivaceous brown, subcylindrical, base obclavate to obconico truncate, tip subacute to obtuse 21.7–44.8 (92) × 4.5–5.5 µm. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on Potato Dextrose Agar (PDA). Colonies very slow growing, velvety, greyish brown; reaching 2–5 mm diam., in 28 days at 27 °C, margin circular to irregular, reverse blackish brown raising centrally, of dense cottony mycelium and hard texture. Mycelium smooth, branched, asexual and sexual spores not formed within 60 days.

Material examined: India, Sonebhadra U.P., on living leaves of *Vernonia cineria* (L.) Less (Asteraceae), Dec 2017, AMH: 10043 (**Holotype**), culture ex type NFCCI: 4441.

GenBank numbers: MN691042 (LSU); MN691041 (ITS); MT106617 (*act*); MT106618 (*tef1*)

Notes: Pseudocercospora species are mostly host-specific (with few exceptions) related to a single host species, host genus or closely related host genera (Braun et al. 2013; Crous et al. 2013). Two species of *Pseudocercospora* has been reported earlier on *Vernonia*, *Pseudocercospora cinereae* (Deighton 1976) and *Pseudocercospora vernoniacearum* (Shukla et al. 1982). *Pseudocercospora cineriae* has dark brown circular, coalescing leaf spots and *P. vernoniacearum* has oval, effuse leaf spots whereas *P. vernoniae* has grayish brown, angular and vein limited leaf spots. Conidiophores are much smaller (14–40 µm) and more septate (1–8) in *P. vernoniae* compared to previously described species *P. cinereae* (1–3 septate, 40–150 × 3.5–5 µm) and *P. vernoniacearum* (44–133 × 3.5–5.4 µm). Conidia are simple and longer in *P. cinereae* (28.5–145 × 2.8–5.7 µm) and *P. vernoniacearum* (40–100 × 3.5–5.4 µm). The presence of catenate conidia in branched chains with smaller and variable in size 21.74– 44.76 × 4.5–5.5 µm) differentiate *P. vernoniae* from the previously described species. Molecular analysis based on combined gene analysis of LSU, ITS, *act* and *tef1* (Fig. 3) reveals that *P. vernoniae* clusters with *P. hakeae* (CBS 144520) with moderate support.

Subclass Pleosporomycetidae C.L. Schoch, Spatafora, Crous & Shoemaker

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

Kirschsteiniotheliales was introduced by (Hernandez-Restrepo et al. 2017) based on phylogenetic analysis. Kirschsteiniotheliales consists with Kirschsteiniotheliaceae, and two genera incertae sedis, *viz. Brachysporiella*, *Taeniolella* (Hongsanan et al. 2020a; Wijayawardene et al. 2020)

Kirschsteiniotheliaceae Boonmee & K.D. Hyde, in Boonmee et al., Mycologia 104(3): 705 (2012)

The monotypic family, Kirschsteiniotheliaceae, was introduced by Boonmee et al. (2012) to accommodate *Kirschsteiniothelia* species based on morphology and phylogenetic

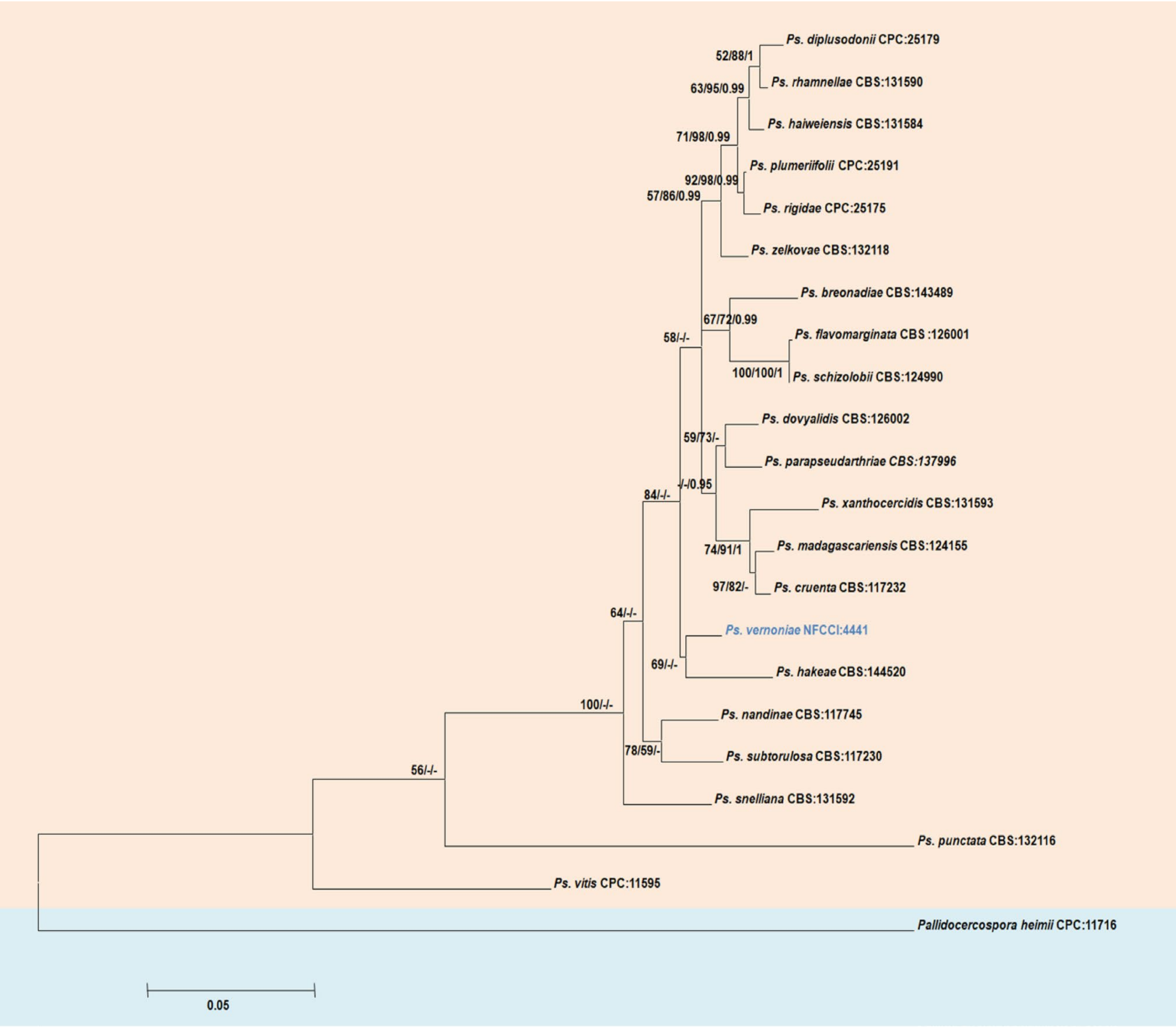


Fig. 3 Maximum likelihood tree illustrating the phylogeny of *Pseudocercospora vernoniae* with related species in *Pseudocercospora* based on LSU, ITS, *act* and *tef1* concatenated sequences. Branches are labelled with ML and MP values ≥ 50% and BYPP ≥ 0.95 are indicated above the node respectively. The ex-types/reference strains are in **bold**; the new species is in blue. The tree is rooted with *Pallidocercospora heimii* (CPC:11716)

analyses. Kirschsteiniotheliaceae species are mostly saprobes on dead wood from terrestrial and aquatic habitats in tropical and subtropical regions (Boonmee et al. 2012; Su et al. 2016; Mehrabi et al. 2017; Bao et al. 2018; Sun et al. 2021).

Kirschsteiniothelia D. Hawksw., Bot. J. Linn. Soc. 91: 182 (1985)

We follow the latest treatment and updated accounts of *Kirschsteiniothelia* in Sun et al. (2021)

Kirschsteiniothelia acutisporum S. Wang, Q. Zhao & K.D. Hyde, ***sp. nov.***

Index Fungorum number*: IF559759*; *Facesoffungi number: 1FoF1799*; *Fig. 4*

Etymology: Named after the acute conidia

Holotype: MFLU 21-0127

Saprobic on decaying plant substrates. **Sexual morph**: Not observed. **Asexual morph**: *Colonies* effuse, scattered, dark-brown to black, glistening, hairy, sparse. *Mycelium* partly superficial, partly immersed in the substratum,

Fig. 4 ***Kirschsteiniothelia acutisporum*** (MFLU 21–0127, **holotype**) **a**–**c** Colonies on dead wood. **d**, **e** Conidiophore with conidia. **f**, **g** Conidiogenous cells and conidia. **h** Conidiogenous cell. **i**–**m** Conidia. **n** Germinating conidium. Scale bars: **a** = 100 µm, **b** = 200 µm, **c**–**e** = 100 µm, **f**, **g** = 50 µm, **h** = 20 µm, **i**–**n** = 50 µm

composed of dark brown, septate, branched hyphae. *Conidiophores* macronematous, mononematous, solitary, cylindrical, straight or slightly flexuous, dark brown, slightly tapering towards the apex, 8–12 septate, truncate at the apex, 180–260 µm ($\bar{x}$ = 230 µm, *n* = 10) long, 7–12.5 µm ($\bar{x}$ = 9 µm, *n* = 10) wide. *Conidiogenous cells* integrated, terminal, monoblastic, cylindrical and brown, calyciform. *Conidia* acrogenous, solitary, obclavate to obspathulate, tapering to the apex, rostrate, 7–12-euseptate, mid to dark brown, becoming pale brown to pale towards the apex, truncate at the base, 75–120 µm ($\bar{x}$ = 92 µm, *n* = 15) long, 10.5–19.5 µm ($\bar{x}$ = 15 µm, *n* = 15) wide.

Material examined: Thailand, Chiang Mai Province, saprobic on decaying wood at the Mushroom Research Center (MRC), August 2020, Song Wang, SW231 (MFLU 21-0127, **holotype**).

GenBank numbers: ON980758 (LSU); ON980754 (SSU); OP120780 (ITS); OP009582 (*rpb2*)

Notes: *Kirschsteiniothelia acutisporum* shares similar characteristics with *K. fluminicola* in having macronematous, unbranched, cylindrical, septate, conidiophores and solitary, obclavate, septate, conidia. However, *Kirschsteiniothelia acutisporum* differs from *K. fluminicola* in having a gelatinous rounded sheath at the apex of shorter and thinner conidia (33–43 × 7.5–8.5 µm *vs* 47.5–86.5 × 8–10 µm). *Kirschsteiniothelia acutisporum* phylogenetically creates an independent branch with 100ML/100MP/1.00BYPP support (Fig. 5).

Kirschsteiniothelia crustaceum S. Wang, Q. Zhao & K.D. Hyde, ***sp. nov.***

Index Fungorum number: *IF559760*; *Facesoffungi number: FoF11802*; *Fig. 6*

Etymology: Referring to the conidial 'shell' shape.

Holotype: MFLU 21-0129

Saprobic on decaying bamboo culms. **Sexual morph**: Not observed. **Asexual morph**: *Colonies* effuse, scattered, dark brown to black, glistening, hairy, sparse. *Mycelium* partly superficial, partly immersed in the substratum, composed of dark brown, septate, branched hyphae. *Conidiophores* macronematous, mononematous, solitary, cylindrical, straight or slightly flexuous, brown to dark brown, slightly tapering towards the apex, 4–8 septate, truncate at the apex, 60–170 µm ($\bar{x}$ = 128 µm, *n* = 15) long, 6.5–10.5 µm ($\bar{x}$ = 8 µm, *n* = 15) wide. *Conidiogenous cells* integrated, terminal, monoblastic, cylindrical and calyciform, brown, 9–16 µm ($\bar{x}$ = 12 µm, *n* = 15) long, 5.5–8 µm ($\bar{x}$ = 6.5 µm, *n* = 15) wide. *Conidia* acrogenous, solitary, obclavate to obspathulate, globose to the apex and hyaline to light brown, rostrate, 5–6-euseptate, mid to dark brown, becoming pale brown to pale towards the apex, truncate at the base, 45–75 µm ($\bar{x}$ = 55 µm, *n* = 20) long, 10–18 µm ($\bar{x}$ = 14 µm, *n* = 20) wide.

Material examined: Thailand, Nang Lae, Mueang Chiang Rai, Chiang Rai Province, saprobic on decaying bamboo, submerged in a freshwater stream, July 2020, Rongju Xu, MD71 (MFLU 21–0129, **holotype**)

GenBank numbers: MW851854 (LSU); MW851849 (ITS)

Notes: *Kirschsteiniothelia crustaceum* shares similar morphology with *K. rostrata* in having macronematous, unbranched, cylindrical, septate, conidiophores and solitary, obclavate, septate, conidia. However, conidiophores of *Kirschsteiniothelia crustaceum* (60–170 × 6.5–10.5 µm) are much shorter than those of *K. rostrata* (up to 280 µm long, 12 µm wide). Conidia of *K. crustaceum* (45–75 × 10–18 µm) are much shorter than those of *K. rostrata* (up to 115 µm long, 15 µm wide) also. The combined LSU, SSU and ITS phylogenetic analysis show that *Kirschsteiniothelia crustaceum* represents a sister taxon to *K. rostrata* with good separation (89ML/1.00BYPP) (Fig. 5).

Kirschsteiniothelia extensum. S. Wang, Q. Zhao & K.D. Hyde, ***sp. nov.***

Index Fungorum number: *IF559761*; *Facesoffungi number: FoF11803*; *Fig. 7*

Etymology: Referring to the conidiophore extending characteristic

Holotype: MFLU 21-0130

Saprobic on decaying wood. **Sexual morph**: Not observed. **Asexual morph**: *Colonies* effuse, scattered, brown or black, hairy, glistening. *Mycelium* partly superficial, partly immersed in the substratum, composed of brown, septate, branched hyphae. *Conidiophores* macronematous, mononematous, solitary, cylindrical, straight or slightly flexuous, dark brown, unbranched, thick-walled, smooth, slightly tapering towards the apex, 4–9 septate, truncate at the apex, 80–230 µm ($\bar{x}$ = 140 µm, *n* = 15) long, 6.5–9.5 µm ($\bar{x}$ = 7.5 µm, *n* = 15) wide. *Conidiogenous cells* integrated, terminal, monoblastic, percurrent, pale brown, cylindrical, 11–19 µm ($\bar{x}$ = 15 µm, *n* = 15) long, 4–7.5 µm ($\bar{x}$ = 6 µm, *n* = 15) wide. *Conidia* acrogenous, solitary, smooth, obclavate, straight or slightly curved, tapering to the apex, 5–8-euseptate, becoming pale brown to pale towards the apex, truncate at the base, 45–120 µm ($\bar{x}$ = 60 µm, *n* = 30) long, 5–12 µm ($\bar{x}$ = 9 µm, *n* = 30) wide.

Material examined: Thailand, Nang Lae, Mueang Chiang Rai, Chiang Rai Province, saprobic on decaying wood, July 2020, Rongju Xu, MD73 (MFLU 21-0130, **holotype**).

GenBank numbers: MW851855 (LSU); MW851850 (ITS)

Notes: *Kirchsteiniothelia extensum* is introduced here based on both morphology and molecular data. *Kirchsteiniothelia extensum* forms a distinct clade within Kirschsteiniotheliaceae and is sister to *K. submersa* (Fig. 5). The difference between them is that conidiophores of *Kirschsteiniothelia extensum* (80–230 × 6.5–9.5 µm) are much shorter than those of *K. submersa* (220–280 × 6–7 µm)

Kirschsteiniothelia septemseptatum S. Wang, Q. Zhao & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF559762; *Facesoffungi number: FoF11800*; *Fig. 8*

Etymology: Referring to the number of septa mostly observed in conidia

Holotype: MFLU 21–0126

Saprobic on decaying wood. **Sexual morph**: Not oberved. **Asexual morph**: *Colonies* on natural substrate, scattered or fascicular, effuse, hairy, dark brown to black, glistening. *Mycelium* partly superficial, partly immersed in the host tissue, composed of smooth, light brown, branched, septate. *Conidiophores* macronematous, mononematous, single to loosely fasciculate, erect, straight to slightly flexuous, branched at the apex, dark brown, multiseptate, 9–16 septate, 250–580 µm ($\bar{x}$ = 415 µm, *n* = 20) long, 6.5–14.5 µm ($\bar{x}$ = 10 µm, *n* = 20) wide. *Conidiogenous cells* mostly

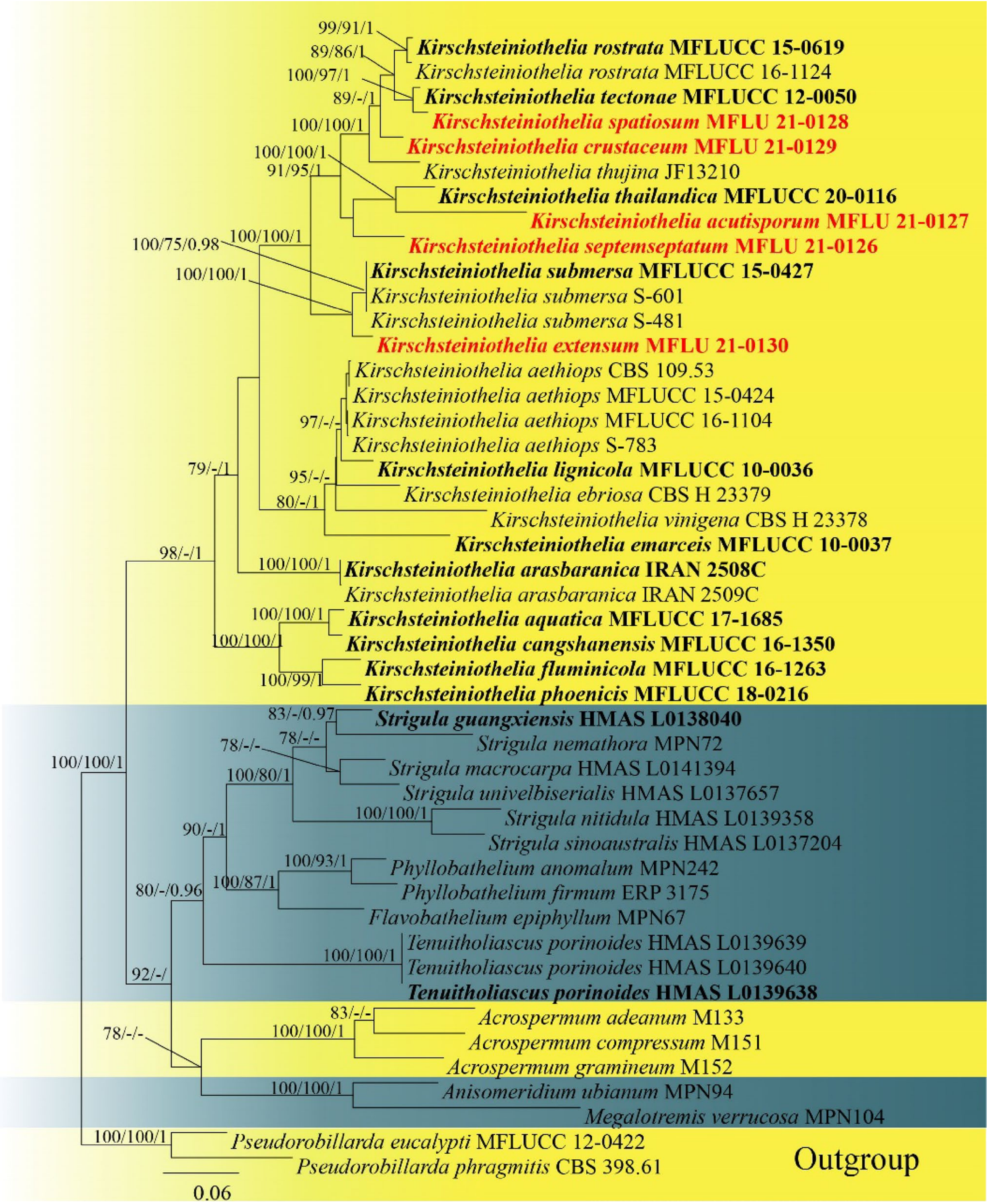


Fig. 5 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS sequence data. Forty-six taxa were included in the combined analyses, which comprised 2,104 characters (LSU = 1–788 bp, SSU = 789–1,632 bp, ITS = 1,633–2,104 bp), including alignment gaps. Among them, 1,191 characters were constant, 239 characters were singleton sites, and 674 characters were parsimony informative. The best scoring RA×ML tree is presented. Bootstrap support values for ML and MP ≥ 75% and BYPP ≥ 0.95 are given above the nodes. *Pseudorobillarda eucalypti (*MFLUCC 12–0422*)* and *P. phragmitis (*CBS 398.61*)* were used as the outgroup taxa. The newly generated sequences are indicated in red. The ex-type strains are indicated in **bold**

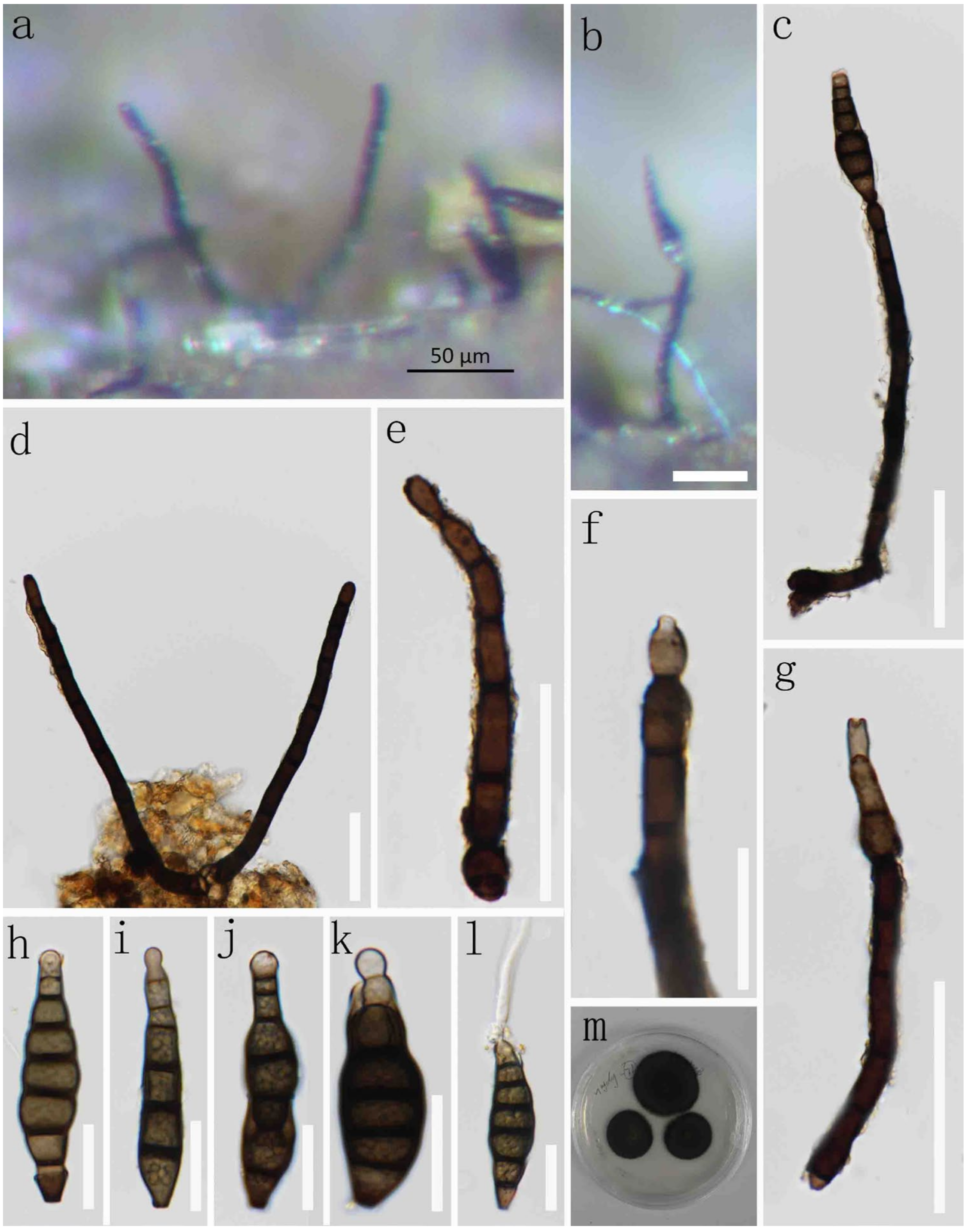


Fig. 6 ***Kirschsteiniothelia crustaceum*** (MFLU 21–0129, **holotype**) **a**, **b** Colonies on dead wood. **c** Conidiophore with conidia. **d**–**g** Conidiogenous cells and conidia. **h**–**k** Conidia. **l** Germinating conidium. **m** Culture on MEA. Scale bars: b–e = 50 µm, f = 20 µm, g = 50 µm, h–l = 20 µm

polytretic, sometimes monotretic, integrated, discrete, terminal and lateral, calyciform, 2 septate, 9.5–21 µm ($\bar{x}$ = 16 µm, *n* = 20) long, 4–8 µm ($\bar{x}$ = 6 µm, *n* = 20) wide. *Conidia* acrogenous, solitary, dry, olivaceous brown to brown, pale at apex, obclavate, rostrate, smooth, straight or curved, truncate at base, 5–8– euseptate, 25–55 µm ($\bar{x}$ = 41 µm, *n* = 20) long, 6.5–12.5 µm ($\bar{x}$ = 10.5 µm, *n* = 20) wide.

Material examined: Thailand, ChiangMai Province, saprobic on decaying wood at MRC, July 2020, Song Wang, SW212, (MFLU 21–0126, **holotype**)

GenBank numbers: ON980757 (LSU); ON980752 (SSU); OP120779 (ITS); OP009581 (*rpb2*)

Notes: *Kirschsteiniothelia septemseptatm* shares similar characteristics with *K. fluminicola* in having macronematous, unbranched, cylindrical, septate, conidiophores and solitary, obclavate, septate, conidia. However, *K. cangshanensis* differs from *K. fluminicola* in having a gelatinous rounded sheath at the apex of shorter and thinner conidia (33–43 × 7.5–8.5 µm *vs* 47.5–86.5 × 8–10 µm). In our phylogetic analyses, *K. septemseptatum* forms an independent branch with 91ML/95MP/1.00BYPP support (Fig. 5)

Kirschsteiniothelia spatiosum. S. Wang, Q. Zhao & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF559763; *Facesoffungi number: FoF11801*; *Fig. 9*

Etymology: Referring to the long conidia

Holotype: MFLU 21-0128

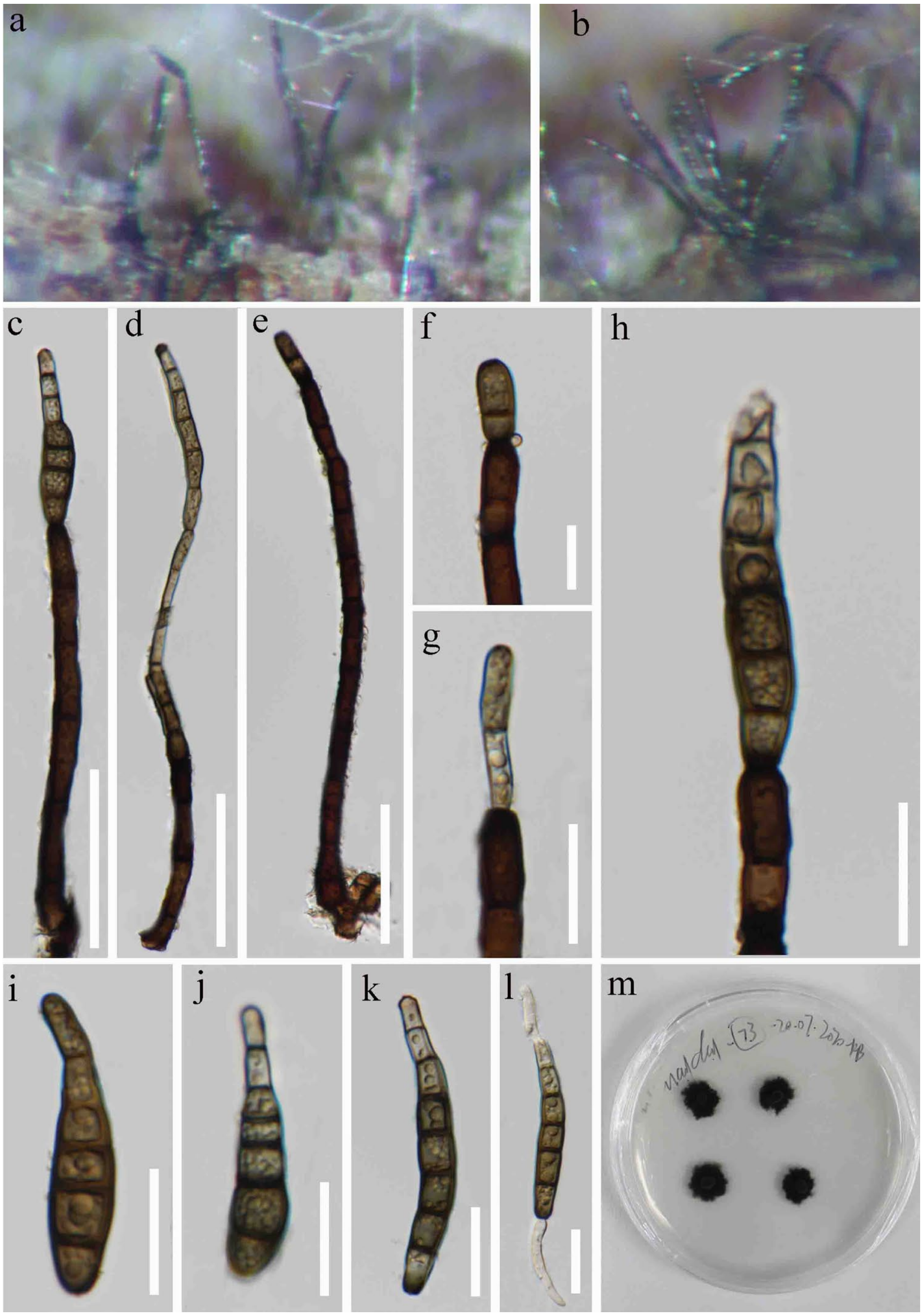


Fig. 7 ***Kirschsteiniothelia extensum*** (MFLU 21–0130, **holotype**) **a**, **b** Colonies on dead wood. **c**, **d** Conidiophore with conidia. **e** Conidiophore. **f**–**h** Conidiogenous cells and conidia. **i**–**k** Conidia. **l** Germinating conidium. **m** Culture on MEA. Scale bars: **c**–**e** = 50 µm, **f**–**l** = 20 µm

Saprobic on decaying wood. **Sexual morph**: Not oberved. **Asexual morph**: *Colonies* effuse on natural substrate, scattered or fascicular, hairy, black, glistening. *Mycelium* partly immersed, partly superficial in the substrate, composed of pale brown, ranched hyphae. *Conidiophores* macronematous, mononematous, solitary or sometimes caespitose, cylindrical, wide at base, tapering towards apex, straight or slightly flexuous, smooth, light brown to dark brown, unbranched, 6–12 septate, 70–128 µm ($\bar{x}$ = 100 µm, n = 15) long, 7.5–12.5 µm ($\bar{x}$ = 9 µm, n = 15) wide. *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, determinate, cylindrical, smooth, mid to dark brown. *Conidia* acrogenous, solitary, dry, olivaceous brown to brown, pale at apex, obclavate, rostrate, smooth, straight or curved, truncate at base, 8–23– euseptate, sometimes with a mucilaginous sheath, 90–139 µm ($\bar{x}$ = 113 µm, n = 15) long, 9.5–16.5 µm ($\bar{x}$ = 14 µm, n = 15) wide.

Material examined: Thailand, Chiang Mai Province, saprobic on decaying wood at MRC, August 2020, Song Wang, SW280 (MFLU 21–0128, **holotype**)

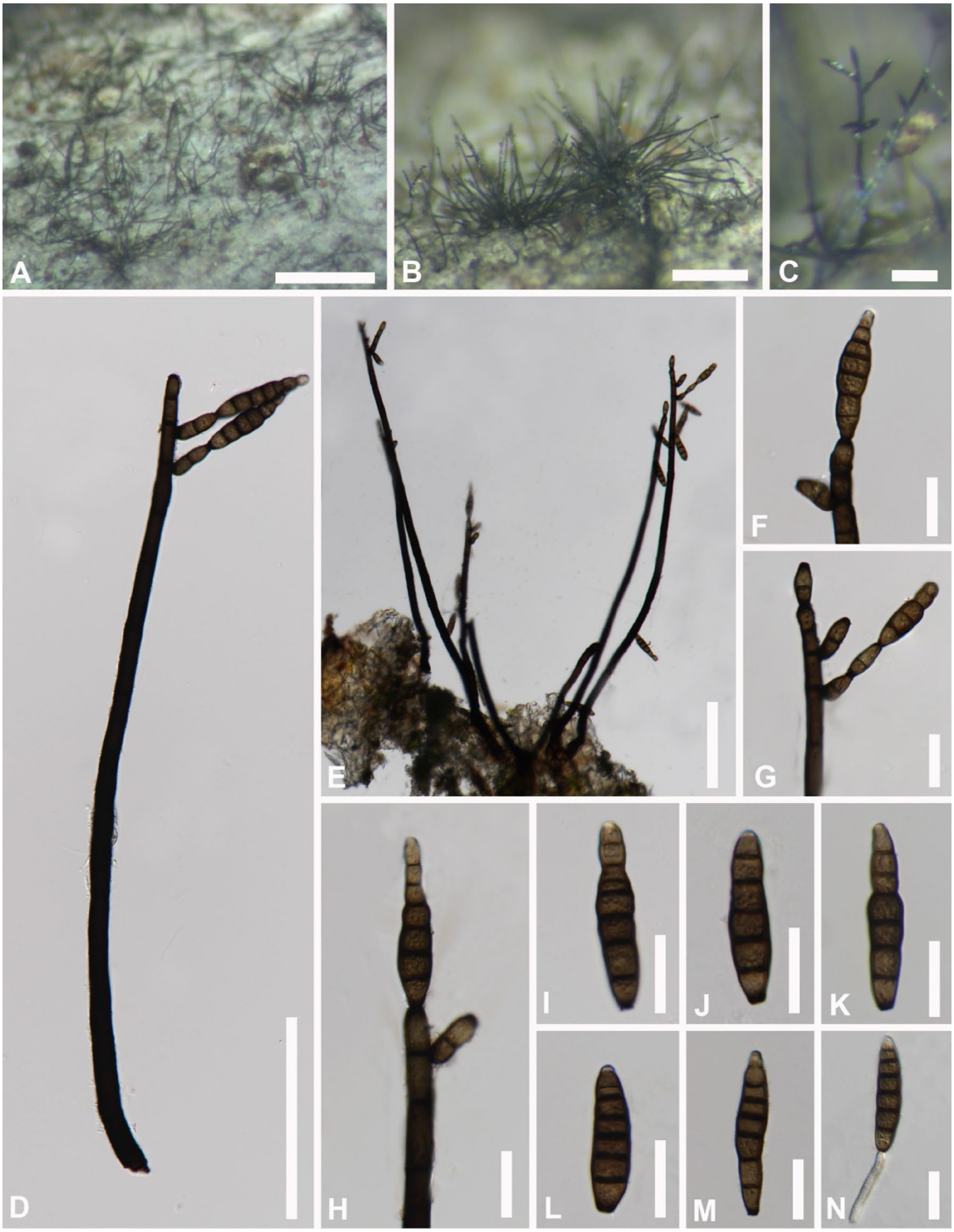


Fig. 8 ***Kirschsteiniothelia septemseptatum*** (MFLU 21–0126, **holotype**) **a**–**c** Colonies on dead wood. **d**, **e** Conidiophore with conidia. **f**–**h** Conidiogenous cells and conidia. **i**–**m** Conidia. **n** Germinating conidium. Scale bars: **a** = 500 µm, **b** = 200 µm, **c** = 50 µm, **d**, **e** = 100 µm, **f**–**n** = 20 µm

GenBank numbers: OP077294 (LSU); ON980753 (SSU)

Notes: In the phylogenetic analyses our strain is closely realted with *K. tectonae* (Fig. 5). *Kirschsteiniothelia spatiosum* shares similar characteristics with *Kirschsteiniothelia tectonae* in having macronematous, unbranched, cylindrical, septate, conidiophores and solitary, obclavate, septate, conidia. However, *K. spatiosum* differs from *K. tectonae* in having a gelatinous rounded sheath at the apex of shorter and thinner conidia and in having shorter and thinner conidia (90–139 × 9.5–16.5 µm

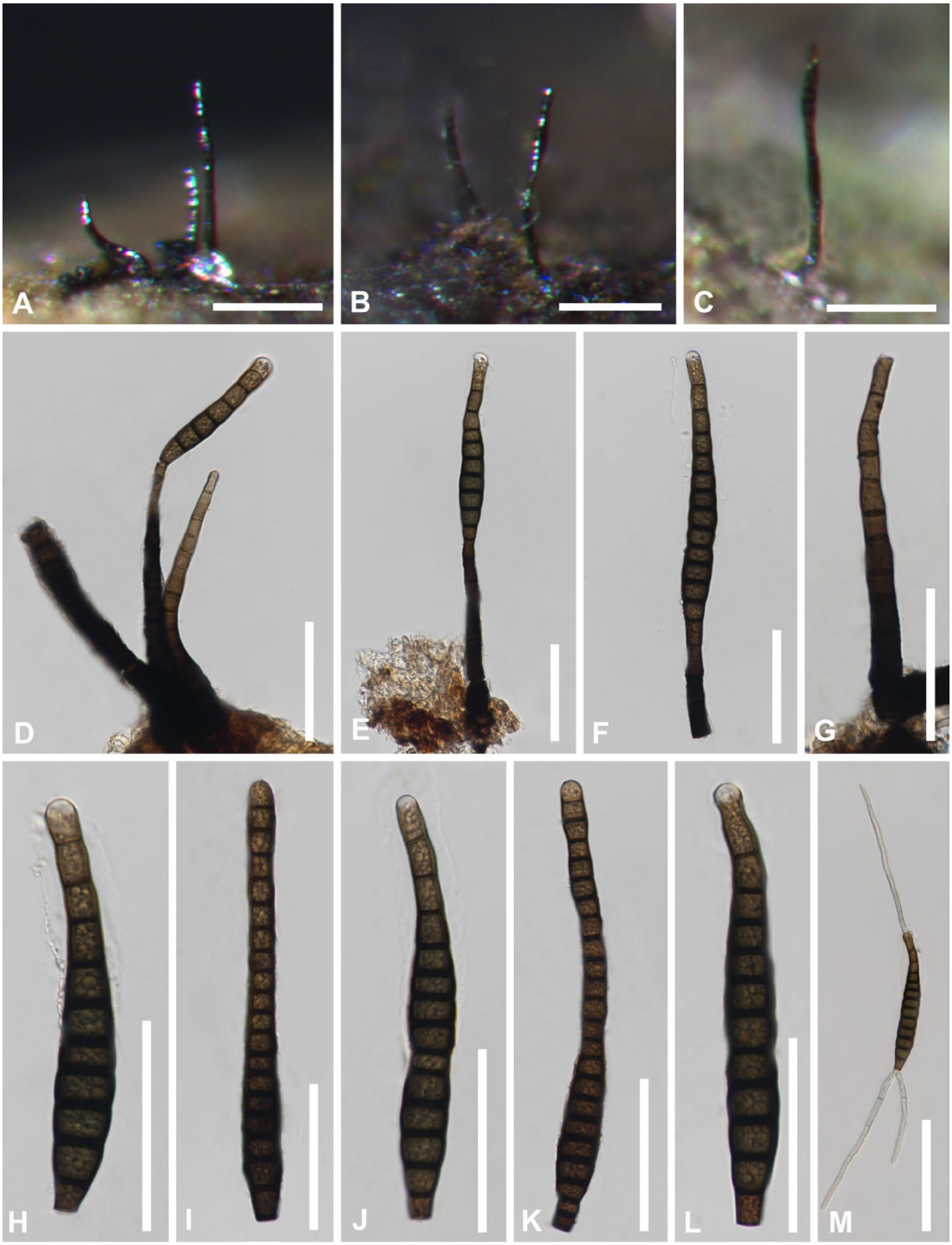


Fig. 9 ***Kirschsteiniothelia spatiosum*** (MFLU 21–0128, **holotype**) **a**–**c** Colonies on dead wood. **d**, **e** Conidiophore with conidia. **f** Conidiogenous cells and conidia. **g** Conidiophore. **h**–**l** Conidia. **m** Germinating conidium. Scale bars: **a**–**c** = 100 µm, **d**–**g** = 50 µm, **m** = 100 µm

vs 135–150 × 16–19 µm). *Kirschsteiniothelia spatiosum* differs from *K. tectonae* in having shorter conidiophores (70–128 × 7.5–12.5 µm *vs* 200 × 4–8 µm).

Pleosporales Luttrell ex M.E. Barr.

Notes: We follow the latest treatments and updated accounts of Pleoporales in Hongsanan et al. (2020b) and Wijayawardene et al. (2022).

Amorosiaceae Thambug. & K.D. Hyde

Thambugala et al. (2015) introduced this family to accommodate *Amorosia* Mantle & D. Hawksw. and *Angustimassarina* Thambug., Kaz. Tanaka & K.D. Hyde. The family is characterized by immersed or semi-immersed ascomata with a short, crest-like papilla, and hyaline ascospores with a mucilaginous sheath (Thambugala et al. 2015). Wijayawardene et al. (2022) accepted five genera in this family.

Angustimassarina Thambug., Kaz. Tanaka & K.D. Hyde

Thambugala et al. (2015) introduced this genus to accommodate fungi that have ascospores resembling *Massarina*, while being narrowly fusiform. There are 12 species listed in the Index Fungorum (accessed on 30 August 2022). In this study, we introduce a new species from China based on molecular phylogeny and morphology.

Angustimassarina kunmingense H.D. Yang & K.D. Hyde, ***sp. nov.***

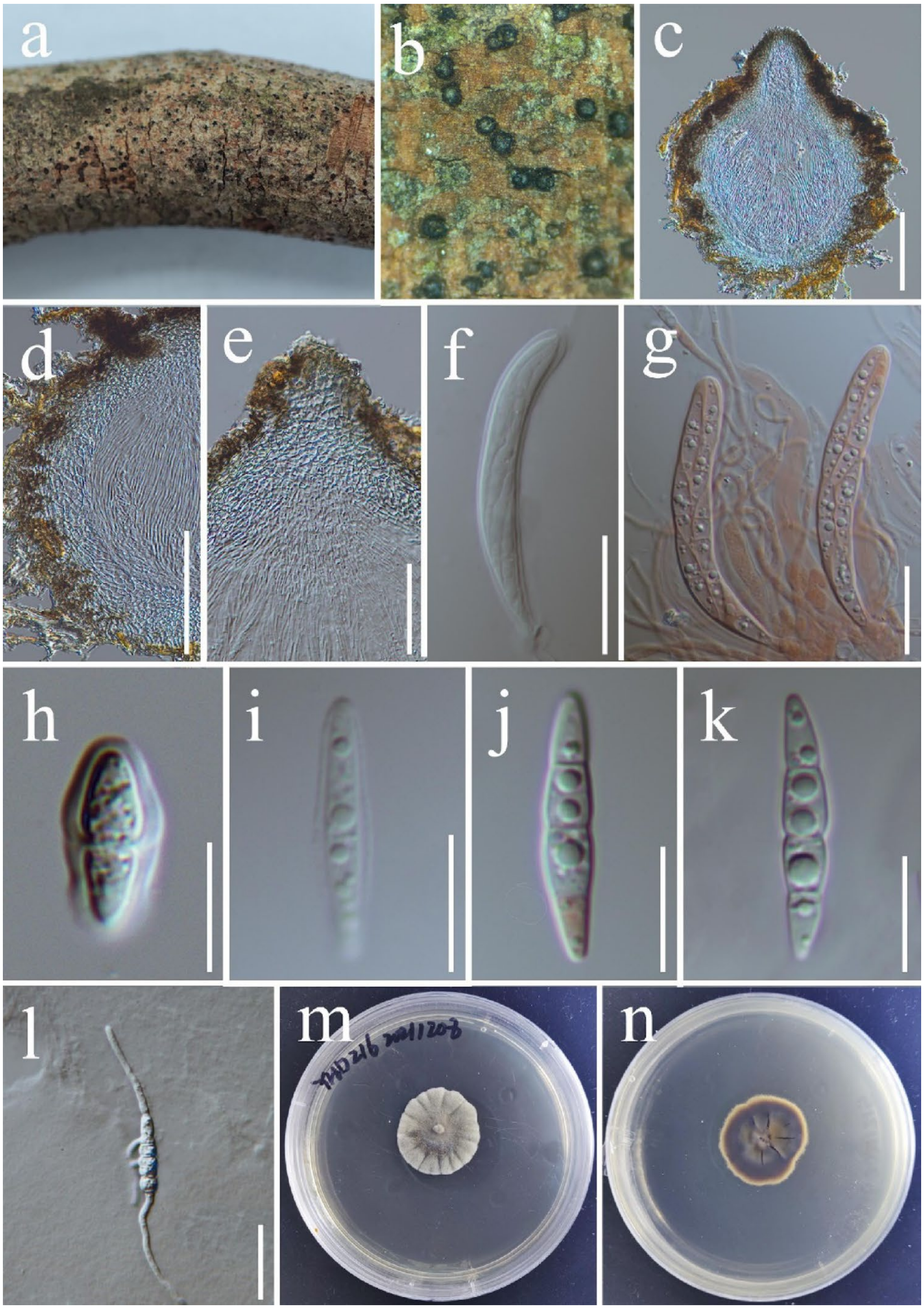


Fig. 10 ***Angustimassarina kunmingense*** (YHD216, **holotype**). **a, b** Ascomata immersed on host surface. **c** Section through ascoma. **d, e** Peridium. **f, g** Mature bitunicate asci (g. asci stained with Congo red). **h–k** Ascospores. **l** Gemmating ascospores. **m, n** Colonies on PDA. Scale bars: **c–d** = 100 µm, **e** = 50 µm, **l** = 30 µm, **f–g** = 20 µm, **i–k** = 10 µm, **h** = 5 µm

Index Fungorum number: IF559764; *Facesoffungi number: FoF11804*; *Fig. 10*

Etymology: Referring to the collecting site, Kunming City, Yunnan, China.

Holotype: HKAS123210

Saprobic on dead aerial stem of *Camellia semiserrata*. **Sexual morph**: *Ascomata (*162–*)*190–332(–333) × (119–)142–289(–300) µm ($\bar{x}$ = 261 × 221 µm, *n* = *5*), scattered, gregarious, immersed to semi-immersed in the host tissue, black, globose to subglobose, ostiolate. *Ostiole* in the centre, crest-like, rounded, papillate, with a pore-like opening. *Peridium* 27–56 µm thick, comprised of 5–10 layers of cells of *textura angularis*, cells smaller at the base and the apex, and larger at the side, brown to hyaline. *Hamathecium* composed of 1.2–2 µm ($\bar{x}$ = 1.6 µm, *n* = *30*) wide, numerous, septate, clamped, unbranched, hyaline, pseudoparaphyses, embedded in a gelatinous matrix, longer than asci. *Asci* (56–) 60–74(–77) × (7.2–)7.5–8.7(–9.3) µm ($\bar{x}$ = 68 × 8.1 µm, *n* = *20*), 8-spored, bitunicate, fissitunicate, cylindric-clavate, with short pedicel at the base, rounded at the apex with a minute ocular chamber. *Ascospores* (18–)20–22(–23) × (3.1)3.3–3.8(–4.1) µm ($\bar{x}$ = 20 × 3.5 µm, *n* = 30), 1–2 overlapping seriate, hyaline, fusiform, dimidiate, widest at the centre and tapering toward the ends, with 1–3 constricted septate septum, filled with 1–2 guttules per cell, smooth-walled and surrounded by a mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h and producing germ tubes from both ends and sides. Colonies on PDA reaching 28 mm diam. after 33 days at 20 °C, nearly circular, flat, dense, radial sulcate, edge entire, smoke grey to grey-white on the surface, dark brown on the reverse and becoming grey-white at the margin.

Material examined: China, Yunnan Province, Kunming City, Panlong District, on *Camellia semiserrata* C.W. Chi (Theaceae), 25° 8′ 29.27″ N, 102° 44′ 16.03″, 17 Dec 2021, Hongde Yang, (HKAS123210, **holotype**); ex-type living culture, KUNCC22-10799.

GenBank numbers: ON352672 (ITS); ON352671 (LSU); ON352675 (SSU); ON364144 (*tef1*); ON791602 (*act*); ON791682 (*tub2*)

Notes: Species of *Angustimassarina* are broadly distributed in Belgium, Germany and Italy (Hyde et al. 2020a, b, c; Phukhamsakda et al. 2020), but, have never been reported from China. Our collections from China are morphologically and phylogenetically related to *Angustimassarina*. Our new species *Angustimassarina kunmingense* resembles other

Table 1 Synopsis of mainly morphological characteristics of *Angustimassarina* species

Taxa	Host	Ascomata (µm)	Peridium (µm)	Asci (µm)	Ascospores (µm)	Locality	References
Angustimassarina acerina MFLUCC 14–0505	*Acer platanoides*	200–350 × 164–183	15–26	92–105 × 7.5–8.6	21–23 × 4.1–4.6	Germany	Thambugala et al. (2015)
A. alni MFLUCC 15–0184	*Alnus glutinosa*	160–250 × 130–200	28–44	71–89 × 8–10	19–22 × 3–4	Germany	Tibpromma et al. (2017)
A. arezzoensis MFLUCC 13–0578	*Salvia* sp.	169–234 × 166–245	22–41	67–95 × 10–15	19–21 × 5–6	Italy	Tibpromma et al. (2017)
A. camporesii MFLU 18–0057	*Galium* sp.	130–240 × 130–190	15–21	62–88 × 10–13	15–18 × 4–5	Italy	Hyde et al. (2020a, b, c)
A. coryli MFLU 15–2603	*Corylus avellana*	150–250 × 500–750	8–12	95–110 × 8– 12	21–25 × 4–5	Italy	Hyde et al. (2017)
A. italica MFLUCC 15–0082	*Ilex aquifolium*	127–159 × 97–131	23–40	78–103 × 10–12	15–22 × 3–6	Italy	Tibpromma et al. (2017)
A. kunmingense YHD216	*Camellia japonica*	162–333 × 119–300	27–56	56–77 × 7.2– 9.3	18–23 × 3.1– 4.1	China	This study
A. lonicerae MFLUCC 15–0087	*Lonicera* sp.	193–203 × 170–220	10–18	55–81 × 9–13	19–25 × 4–7	Italy	Tibpromma et al. (2017)
A. populi MFLUCC 13–0034	*Populus* sp.	125–175 × 100–120	14–32	80–95 × 9.5–13	19–22 × 3.2–5.5	Italy	Thambugala et al. (2015)
A. premilcurensis MFLUCC 15–0074	*Carpinus betulus*	231–238 × 290–311	20–30	64–93 × 11–15	19–23 × 4–7	Italy	Tibpromma et al. (2017)
A. quercicola MFLUCC 14–0506	*Quercus robur*	200–250 × 150–265	14–27	60–94 × 8.8–13	17–21 × 4–6	Germany	Thambugala et al. (2015)
A. rosarum MFLU 17–1513	*Clematis viticella, Rosa canina*	221–306 × 267–400	14–40	77–85 × 10–16	17–23 × 4–4.5	Italy	Wanasinghe et al. (2018)
A. sylvatica MFLU 15–2603	*Fagus sylvatica*	180–260 × 150–200	8–12	95–110 × 8– 12	21–25 × 4–5	Italy	Hyde et al. (2019)

Angustimassarina species in terms of ascomata, asci and ascospores (Table 1) and the new species was isolated from similar habitat to other *Angustimassarina* species (Thambugala et al. 2015). However, the taxon is charactered by slender asci and ascospores. The megablast search of the ITS and *tef1* sequences show the highest similarity with *Angustimassarina* populi (457/463, 98%) and *Angustimassarina populi* (827/830, 99%), respectively. In the phylogenetic analysis, *Angustimassarina kunmingense* formed a well-supported monophyletic clade basal to *Angustimassarina* species (97ML/1.00BYPP). Our phylogenetic tree was constructed using multi gene loci (ITS, SSU, LSU and *tef1*, Fig. 11). However, most taxa were not strongly supported. This could suggest that additional markers are required to achieve a

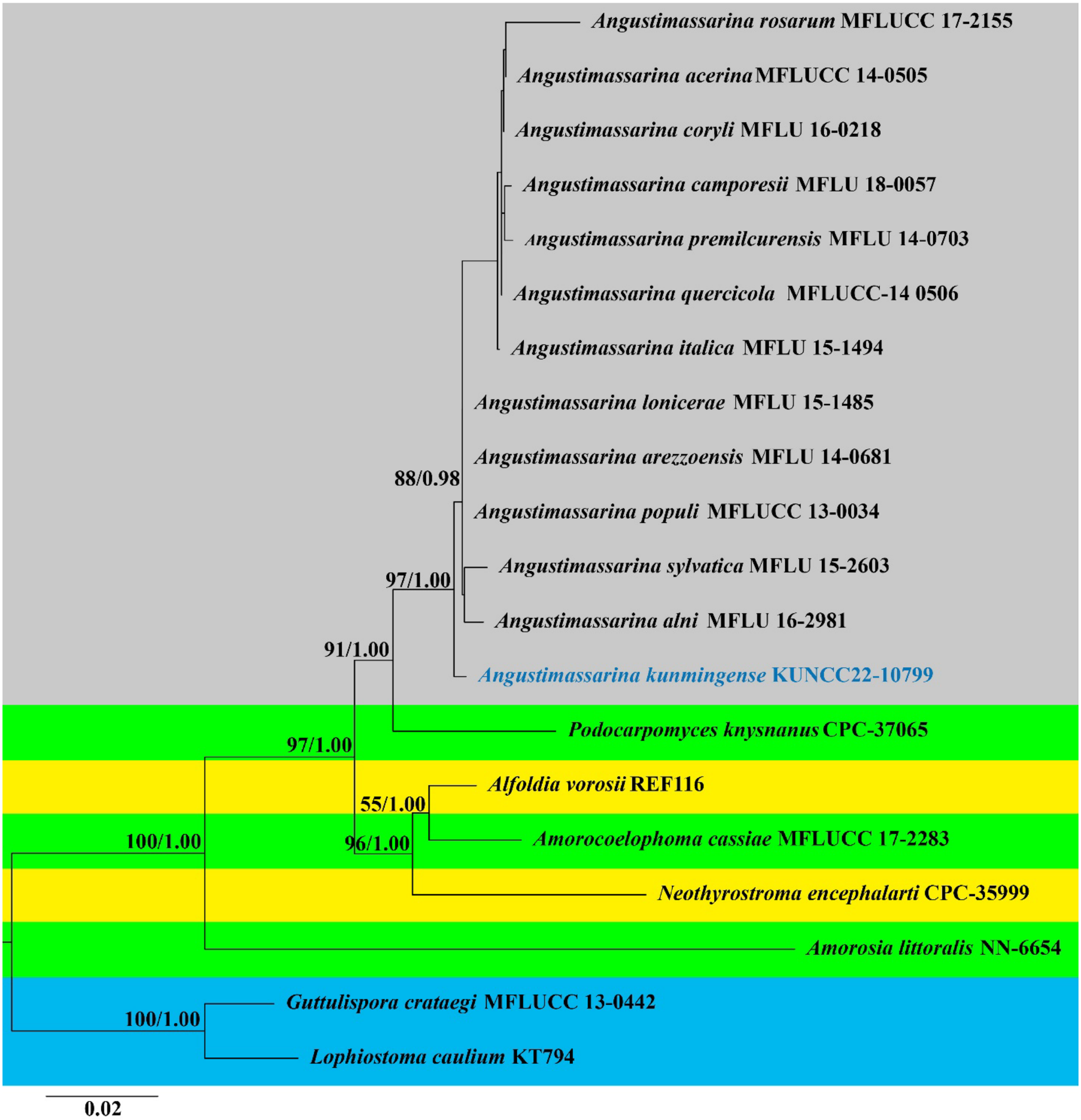


Fig. 11 Phylogram generated from maximum likelihood analysis based on combined ITS, SSU, LSU and *tef1* sequence data of *Angustimassarina*. Twenty strains were included in the analysis of the combined loci which comprised 2700 characters. The tree is rooted with *Guttulispora crataegi* (MFLUCC 13–0442) and *Lophiostoma caulium* (KT794). Bootstrap support values ≥ 50% in ML and BYPP ≥ 0.95 are given at the nodes. The ex-types and reference strains are in **bold**; the new isolate is in blue

more accurate identity, thus we also provide protein gene *act* and *tub2* herein.

Bambusicolaceae D.Q. Dai & K.D. Hyde, in Hyde et al., Fungal Diversity 63: 49 (2013)

Notes: Bambusicolaceae was placed in Dothideomycetes by Hyde et al. (2013) to accommodate *Bambusicola* (Dai et al. 2012; Liu et al. 2015; Jayasiri et al. 2019; Yang et al. 2019; Bhunjun et al. 2021; Calabon et al. 2022). Four genera *viz. Bambusicola*, *Corylicola*, *Leucaenicola* and *Palmiascoma* are accepted in this family (Wijayawardene et al. 2022). Bambusicolaceae are characterized by solitary, scattered, immersed, semi-immersed to erumpent and conical or globose to subglobose ascomata, anastomosing, branching interascal filaments, cylindrical to clavate asci with a short furcate or rounded to obtuse pedicel and slightly broad-fusiform or clavate to ellipsoidal, hyaline or yellowish to brown, single-septate ascospores with a gelatinous sheath (Dai et al. 2012; Hyde et al. 2013; Liu et al. 2015; Dai et al. 2017).

Bambusicola D.Q. Dai & K.D. Hyde, in Dai, Bhat, Liu, Chukeatirote, Zhao & Hyde, Cryptog. Mycol. 33(3): 367 (2012)

Notes: *Bambusicola* is a well-studied genus, established by Dai et al. (2012). There are 15 species accepted in the genus and all species have sequence data in GenBank (Dai et al. 2012, 2015, 2017; Thambugala et al. 2015; Yang et al. 2018; Dong et al. 2020; Monkai et al. 2021). Both sexual and asexual morphs of *Bambusicola* are reported (Dai et al. 2012, 2015, 2017; Thambugala et al. 2015; Yang et al. 2018; Dong et al. 2020; Monkai et al. 2021). The sexual morph of *Bambusicola* is characterized by gregarious, immersed or semi-immersed, globose to subglobose, uni- to multi-loculate, coriaceous ascomata, bitunicate, cylindrical or cylindric-clavate, short pedicellate asci with a shallow or well-developed chamber and fusiform, septate, hyaline to pale brown ascospores mostly surrounded by a gelatinous sheath. The asexual morph of *Bambusicola* is characterized by pycnothyrial, immersed to semi-immersed, acerose or subglobose, pyriform or irregular, uni- to multi-loculate conidiomata, holoblastic, annellidic, discrete, cylindrical conidiogenous cells and cylindrical to ellipsoidal, pale brown to brown, septate conidia (Dai et al. 2012, 2017; Thambugala et al. 2015; Dong et al. 2020; Monkai et al. 2021).

Bambusicola species have been reported from both terrestrial and freshwater habitats in China and Thailand (Dai et al. 2012, 2015, 2017; Thambugala et al. 2015; Yang et al. 2018; Dong et al. 2020). Most *Bambusicola* species are reported as saprobes on bamboo. In this study, we report a new record of *Bambusicola bambusae* on submerged decaying wood from freshwater habitats for the first time.

Bambusicola bambusae D.Q. Dai & K.D. Hyde, Cryptog. Mycol. 33(3): 372 (2012)

Index Fungorum number: IF 801046; Facesofungi number: FoF11797; *Fig. 12*

Saprobic on decaying wood in a freshwater stream. *Ascomata* 135–175 µm high × 190–245 µm diam. ($\bar{x} = 155 \times 216$ µm, $n = 10$), solitary, scattered to gregarious, immersed under the host tissue, conical in section, brown to dark brown, coriaceous, subglobose, ostiolate. Ostiole crest-like, central, elongated to papillate, with a pore-like opening, plugged by hyaline, filamentous hyphae. *Peridium* comprising host and fungal tissues, 17–31 µm thick, composed of brown to dark brown cells of *textura angularis* intermingled with host cells. *Hamathecium* composed of numerous, filamentous, hyaline, septate, branched, 1.0–1.5 µm, pseudoparaphyses. Asci 55–75 × 7.5–9.5 µm ($\bar{x} = 66.3 \times 8.5$ µm, $n = 20$), 8-spored, bitunicate, fissitunicate, cylindrical, with a shallow apical chamber and a short furcate pedicel. *Ascospores* 19–21 × 4.0–4.5 µm ($\bar{x} = 20 \times 4.5$ µm, $n = 30$), 2–3-seriate, 1-septate, constricted at the septum, slightly broad fusiform, tapering towards the ends, occasionally with large upper cell, with narrowly rounded ends, hyaline, guttulate, smooth-walled.

Culture characteristics: Ascospores germinating on PDA within 24 h and germ tubes produced from both ends. Colonies growing on PDA, reaching a diam. of 20–25 mm after 20 d at 25 °C, surface smooth to velvety, with entire to slightly undulate edge, greenish in the centre, white at the edge; reverse dark greenish to black in the centre, white at the edge.

Material examined: Thailand, Tao Ngoi, Sakon Nakhon, on decaying wood submerged in a river, 12 November 2017, D.F. Bao, B110 (MFLU 22–0080), living culture, MFLUCC 22–0021.

Host/Substrate: Bamboo (Poaceae) (Dai et al. 2012); decaying wood submerged in a river (this study)

Distribution: Thailand (Dai et al. 2012; this study)

GenBank numbers: ON764309 (ITS); ON764310 (LSU); ON764313(SSU); ON788004 (*rpb2*)

Notes: In the phylogenetic analysis, our new isolate B110 clustered with the ex-type strain of *Bambusicola bambusae* (MFLUCC 11–0614) with 98% ML/1.00 BYPP support (Fig. 13). The morphology of our collection is almost identical to the holotype of *Bambusicola bambusae* except for the size of ascomata and the sheath of the ascospores. The ascomata of our collection are smaller than the holotype (190–245 *vs.* 450–70 µm diam) and the holotype of *B. bambusae* has ascospores with a thick sheath (Dai et al. 2012), whereas, the sheath of ascospores were not observed in our collection. A comparison of the ITS and *rpb2* gene regions of MFLUCC 11–0614 and B110 revealed 0 and 3 base pair differences and therefore we identified our new collection as

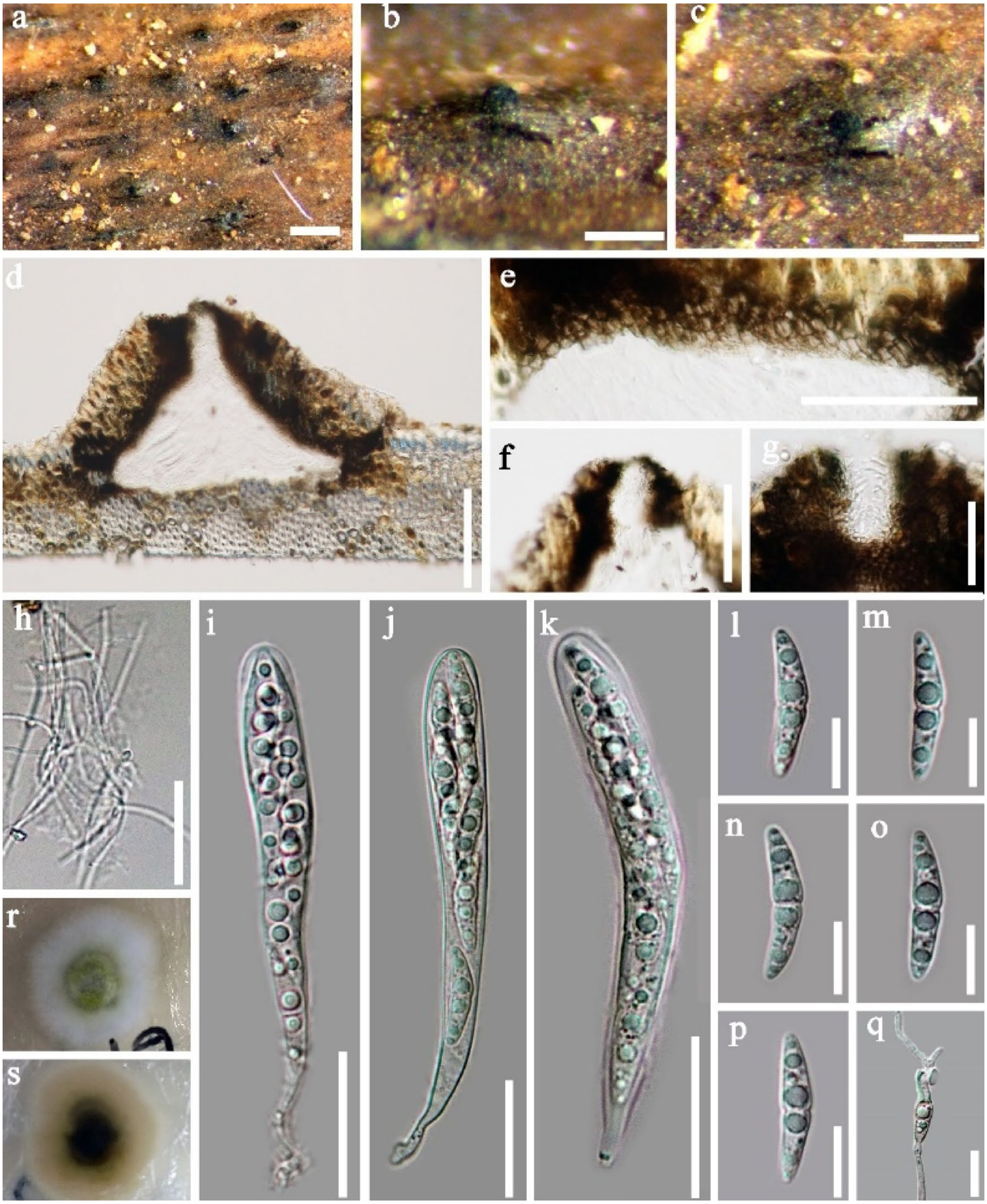


Fig. 12 ***Bambusicola bambusae*** (MFLU 22–0080, **new record**). **a–c** ascomata on wood **d** section of ascoma **e** peridium, **f, g** ostiole. **h** pseudoparaphyses. **i–k** asci. **l–p** ascospores. **q** Germinating ascospore. **r, s** culture on PDA from surface and reverse. Scale bars: **b, f** = 100 µm, **e** = 50 µm, **g** = 30 µm, **h–k** = 20 µm, **l–q** = 10 µm

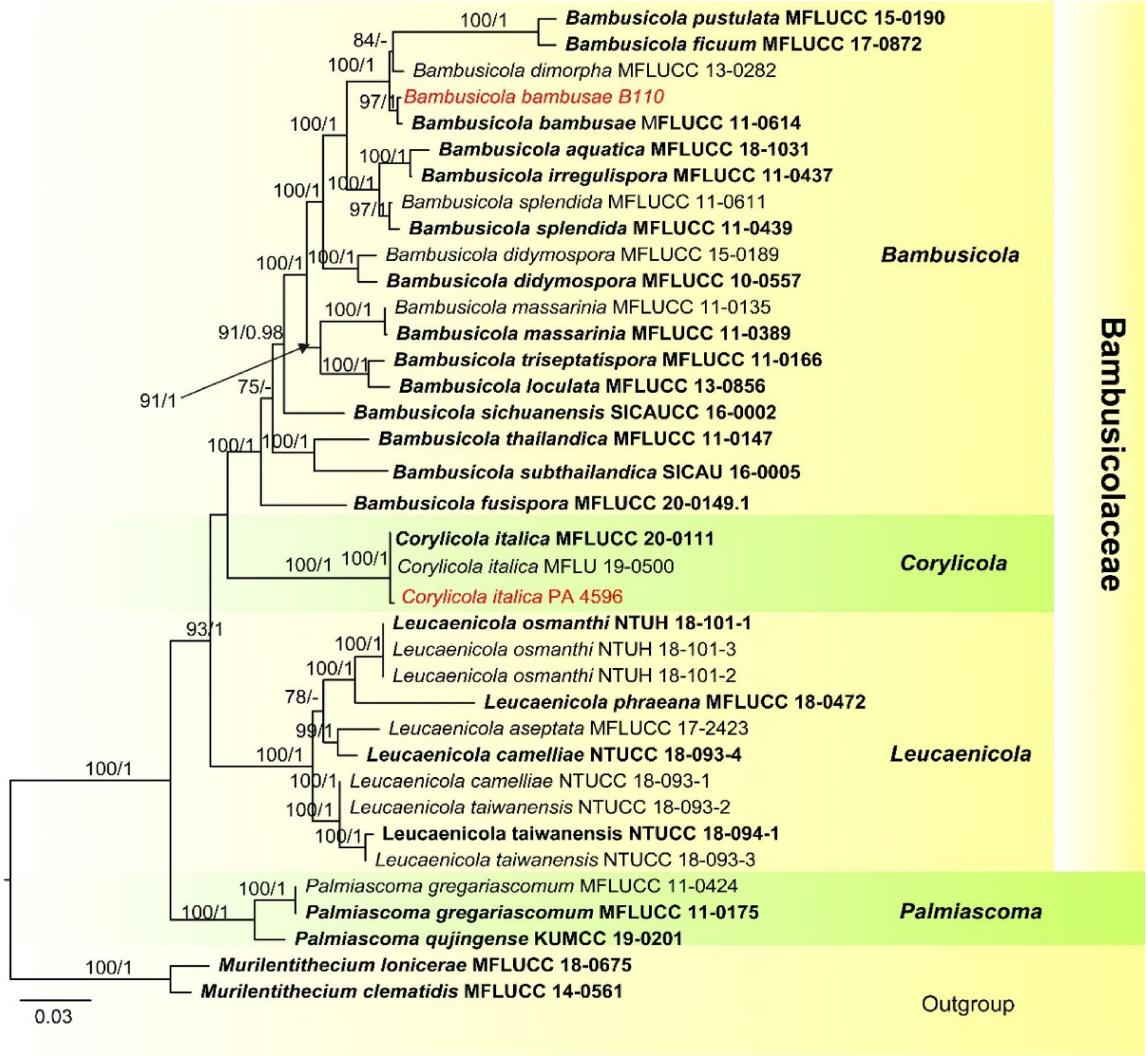


Fig. 13 Phylogram generated from ML analysis, based on combined ITS, LSU, SSU, *tef1* and *rpb2* sequence data for Bambusicolaceae. The combined dataset comprises 37 strains with 4617 characters including gaps (LSU: 854 bp, SSU: 1016 bp, ITS: 805 bp, *tef1*: 950 bp, *rpb2*: 992 bp). The tree is rooted with *Murilentithecium lonicerae* (MFLUCC 18–0675) and *M. clematidis* (MFLUCC 14–0561). Maximum likelihood bootstrap values ≥ 75% and baysian BYPP ≥ 0.95 are displayed on the nodes, respectively. Newly introduced taxa are indicated in red. Ex-type and representative strains are in **bold**

Bambusicola bambusae as recommended by Pem et al. (2021). *Bambusicola bambusae* was described by Dai et al. (2012), it was collected on bamboo from terrestrial habitats in Thailand. Our collection was from freshwater habitats and this is the first time this species reported from freshwater habitats.

Corylicola Wijesinghe, Camporesi, Yong Wang bis & K.D. Hyde, in Wijesinghe et al., Biodiversity Data Journal 8(e55957): 8 (2020)

Corylicola was introduced by Wijesinghe et al. (2020). This genus is characterized by uniseriate, fusiform to ellipsoidal, yellowish to pale brown, single-septate, echinulate ascospores, accumulating as yellowish-brown masses at the apices of ascomatal neck (Wijesinghe et al. 2020). We provide a new host record of *Corylicola italica* from *Rubus* sp. in Italy.

Corylicola italica Wijesinghe, Camporesi, Yong Wang bis & K.D. Hyde, in Wijesinghe et al., Biodiversity Data Journal 8(e55957): 8 (2020).

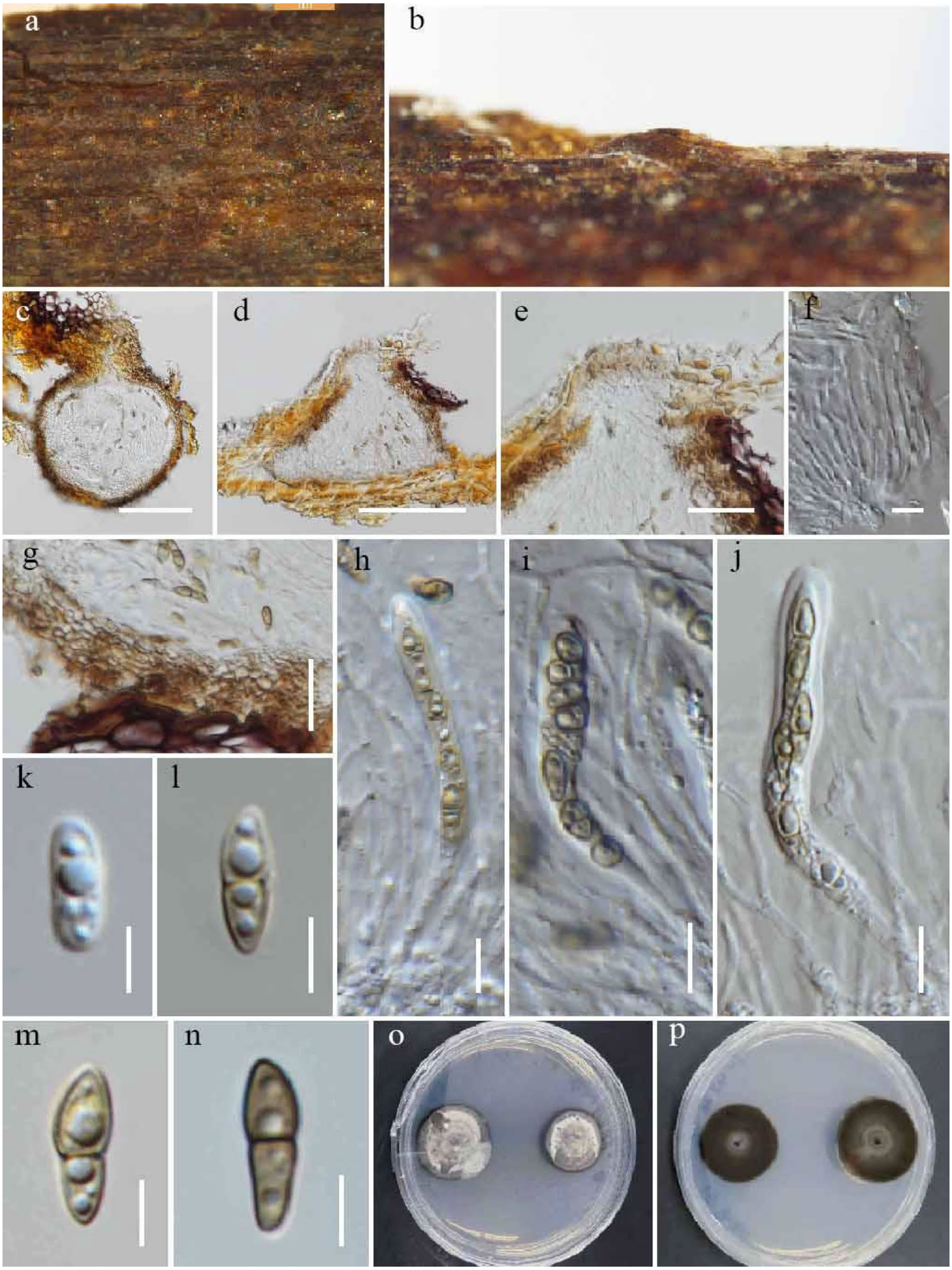


Fig. 14 ***Corylicola italica*** (MFLU 20–0251, new host record). **a–b** Appearance of ascomata on a twig of *Rubus* sp. **c–d** Section through ascomata. **e** Close-up of ostiole. **f** Pseudoparaphyses. **g** Peridium. **h–j** Asci. **k–n.** Ascospores. **o.** Culture characteristics on PDA after 20 days from above. **p** Culture characteristics on PDA after 20 days from below. Scale bars: **c–d** = 50 µm, **e–g** = 20 µm, **h–j** = 10 µm, **k–n** = 5 µm

Index Fungorum number: *IF557768; Facesofungi number: FoF08684; Fig. 14*

Saprobic on a dead branch of *Rubus* sp. **Sexual morph:** *Ascomata* 109–141 high, 91.5–106 µm diam. ($\bar{x}$ = 128.5 × 101.5 µm; *n* = 4), solitary, scattered, immersed, erumpent at maturity, raised as brown to dark spots on the substrate, globose to subglobose, coriaceous, uni-loculate with an ostiole. *Ostiole* 46–68 µm wide, central, papillate, lined with hyaline periphyses. *Peridium* composed of two layers, unequally thickened, 15–29 µm wide comprising brown, blackish to dark brown cells of *textura angularis* fused with host tissues, inner layer comprising hyaline cells of *textura prismatica*. *Hamathecium* comprising numerous pseudoparaphyses 1–2 µm wide ($\bar{x}$ = 1.6 µm, *n* = 6), filamentous, cellular, with distinct septa, not constricted at the septa, branching and anastomosing above the asci. *Asci* 52–74 × 4–6 µm ($\bar{x}$ = 61 × 5 µm, *n* = 5), 8-spored, bitunicate, fissitunicate, cylindrical, short distinct pedicel with furcate ends, apically rounded, well-developed ocular chamber. *Ascospores* 10–12 × 3–4 µm ($\bar{x}$ = 10 × 3.6 µm, *n* = 11), overlapping, uni-seriate, fusiform to ellipsoidal, 1-septate straight, hyaline and yellowish when young, becoming pale brown at maturity. **Asexual morph**: Not observed.

Culture characteristics: Spore germinating on PDA within 24 h from singles pore isolation. Colonies on PDA reaching 10 mm diam. after 20 days at 20 °C, circular, submerged, crenated edge, flat with dense, brown to whitish in the middle, grey at the edges from upper and reverse brownish-black in the lower surface of the colony.

Material examined: Italy, Forlì-Cesena Province near Meldola, on dead aerial branches of *Rubus* sp. (Rosaceae), 4 February 2020, Erio Camporesi IT-4596C (MFLU 20–0251); living culture MFLUCC 21-0118.

Host/Substrate: *Corylus avellana* (Betulaceae) (Wijesinghe et al. 2020); *Rubus* sp. (Rosaceae) (this study)

Distribution: Italy (Wijesinghe et al. 2020; this study).

GenBank numbers: OM471788 (ITS), OM630433 (*tef1*).

Notes: Wijesinghe et al. (2020) reported this species from *Corylus avellana*. Morphologically our collection resembles the ex-type strain of this species. Based on our phylogenetic analyses, our strain MFLUCC 21-0118 clustered together with MFLU 19–0500 and MFLUCC 20–0111 (Fig. 13) with 100/ML and1.00/BYPP support. Therefore, we introduce our collection as a new host record.

Palmiascoma Phook. & K.D. Hyde, in Liu et al., Fungal Diversity: https://doi.org/10.1007/s13225-015-0324-y, [65] (2015).

Notes: *Palmiascoma* was introduced by Liu et al. (2015) and is typified by *P. gregariascomum* collected from a dead frond of a palm. *Palmiascoma* is similar to *Didymosphaeria* in having didymosporous, brown, and echinulate ascospores, but differs in phylogeny. Monkai et al. (2021) introduced the second species into the genus as *P. qujingense* isolated from dead twigs of Fagaceae sp. in Yunnan, China.

Palmiascoma gregariascomum Phookamsak & K.D. Hyde, in Liu et al., Fungal Diversity: https://doi.org/10.1007/s13225-015-0324-y, [65] (2015).

Index Fungorum number: IF550927; Facesoffungi number: FoF00429; Fig. 15

Saprobic on dead twigs of *Rosa* sp. **Sexual morph:** See Liu et al. (2015). **Asexual morph:** *Conidiomata* 140–200 µm high, 130–220 µm diam. ($\bar{x}$ = 172 × 165 µm, *n* = 5), pycnidial, solitary or aggregated, immersed, erumpent neck, visible as black, uni- to multi-loculate, globose to subglobose, rarely irregular, glabrous, ostiole central, with minute papilla. *Conidiomata walls* 14–38 µm ($\bar{x}$ = 27 µm, *n* = 8), wide, thick-walled, of equal thickness, composed of several layers of hyaline to dark brown, pseudoparenchymatous cells, outer layers comprising 4–5 cell layers of 6–12 × 2–5 µm ($\bar{x}$ = 8.7 × 3.4 µm, *n* = 15), thick-walled, dark brown to black, organized in a *textura angularis* to *textura prismatica* cells, inner layers comprising 2–3 layers of 3–8 × 2–4 µm ($\bar{x}$ = 5.3 × 3.2 µm, *n* = 15), thin-walled, hyaline, organized in a *textura angularis*. *Conidiophores* arising from basal cavity of conidiomata mostly reduced to conidiogenous cells. *Conidiogenous cells* 5–7 × 1–2 µm ($\bar{x}$ = 5.8 × 1.6 µm, *n* = 25), holoblastic, phialidic, discrete, ampulliform to cylindrical, hyaline, aseptate, smooth-walled, guttulate. *Conidia* 3.2–4.5 × 1.7–2.4 µm ($\bar{x}$ = 3.7 × 2.1 µm, *n* = 35), in culture *Conidia* 3.4–4.7 × 1.6–2.5 µm ($\bar{x}$ = 4.1 × 2.1 µm, *n* = 35), solitary, one-celled, oblong to ellipsoidal, with rounded or obtuse ends, initially hyaline, becoming brown at maturity, smooth-walled.

Culture characteristics: Colonies on PDA fast growing, 33–37 mm diam. after 2 weeks at 25–30 °C, greenish-grey to grey, forming white tufts on surface, slightly radiating; reverse brown to dark brown at the margin, dark brown to black in the centre; medium dense, circular, flattened to slightly raised, dull to rough with entire edge, fairy fluffy to velvety, slightly radially furrowed.

Material examined: Thailand, Mueang, Chiang Rai District, Chiang Rai 57100, (20° 03′ 24.7″ N, 99° 52′ 23.5″ E), dead twigs of *Rosa* sp. (Rosaceae), 20 August 2017, MC. Samarakoon, SAMC070 (MFLU 18–0845, HKAS 102350), living culture MFLUCC 18-0505.

Hosts: on dead frond of palm (Liu et al. 2015), *Rosa* sp. (this study)

Distribution: Thailand (Liu et al. 2015; this study)

GenBank numbers: OM293742 (LSU), OM293753 (SSU), OM305060 (*tef1*), OM305066 (*tub2*)

Notes: Our new collection of *Palmiascoma gregariascomum* is described on dead twigs of *Rosa* species from Thailand. We found the asexual morph of the taxon with a similar range of conidiogenous cells (5–7 × 1–2 µm

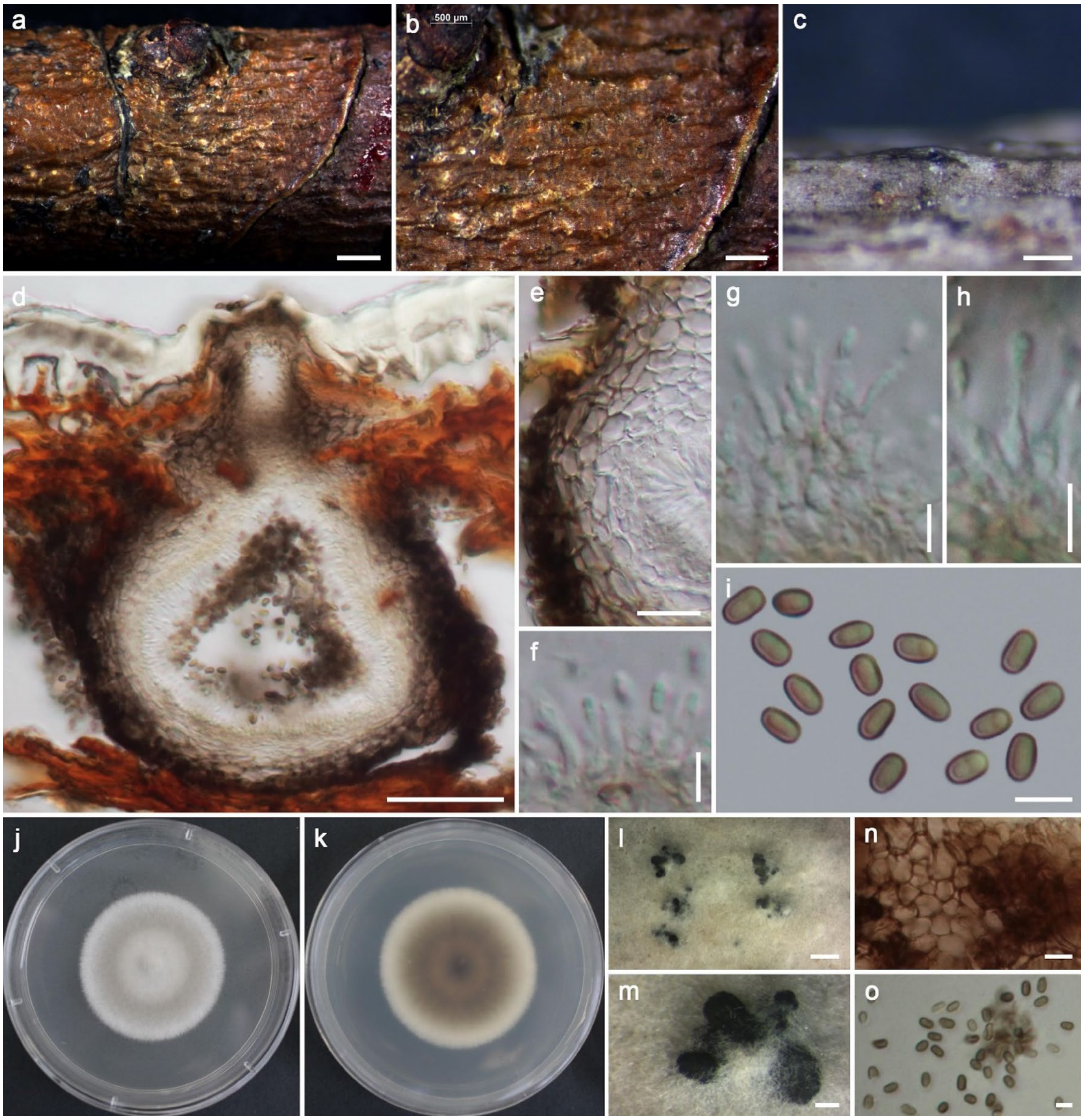


Fig. 15 ***Palmiascoma gregariascomum*** (MFLU 18–0845, new host record) **a-c** Conidiomata on the substrate. **d** Vertical section of conidioma. **e** Peridium. **f–h** Conidiogenous cells and conidiogenesis. **i,o** Conidia (o in culture), **j** Top view of culture in PDA. **k** Reverse view of culture. **l,m** Conidiomata on PDA. **n** Peridium. Scale bars: **a,l** = 1000 µm, **b** = 500 µm, **c,m** = 200 µm, **d** = 50 µm, **e** = 20 µm, **n** = 10 µm, **f-i,o** = 5 µm

vs 5–12 × 2–4 µm) and conidia (3.2–4.5 × 1.7–2.4 µm, 3.4–4.7 × 1.6–2.5 µm *vs* 4–6 × 2–3 µm) in morphologies compared to the type species (MFLU 11-0211). In multi-gene phylogeny, our strain clusters with MFLU 11–0211 with high statistical (81/ML, 1.00 BYPP) support. Based on similar morphology and phylogenetic analyses, here we provide a new host record of *Palmiascoma gregariascomum* on *Rosa* sp. from Thailand (Fig. 16).

Coniothyriaceae W.B. Cooke, Revta Biol., Lisb. 12: 289 (1983) [1980–1983]

Notes: Coniothyriaceae was introduced by Cooke (1983) to accommodate species of *Coniothyrium*. Kirk et al. (2008) synonymized Coniothyriaceae with Leptosphaeriaceae. De Gruyter et al. (2013) based on morphology and phylogenetic analyses showed that the type species *C. palmarum* is distinct from Leptosphaeriaceae and reinstated Coniothyriaceae in Pleosporales. Wijayawardene

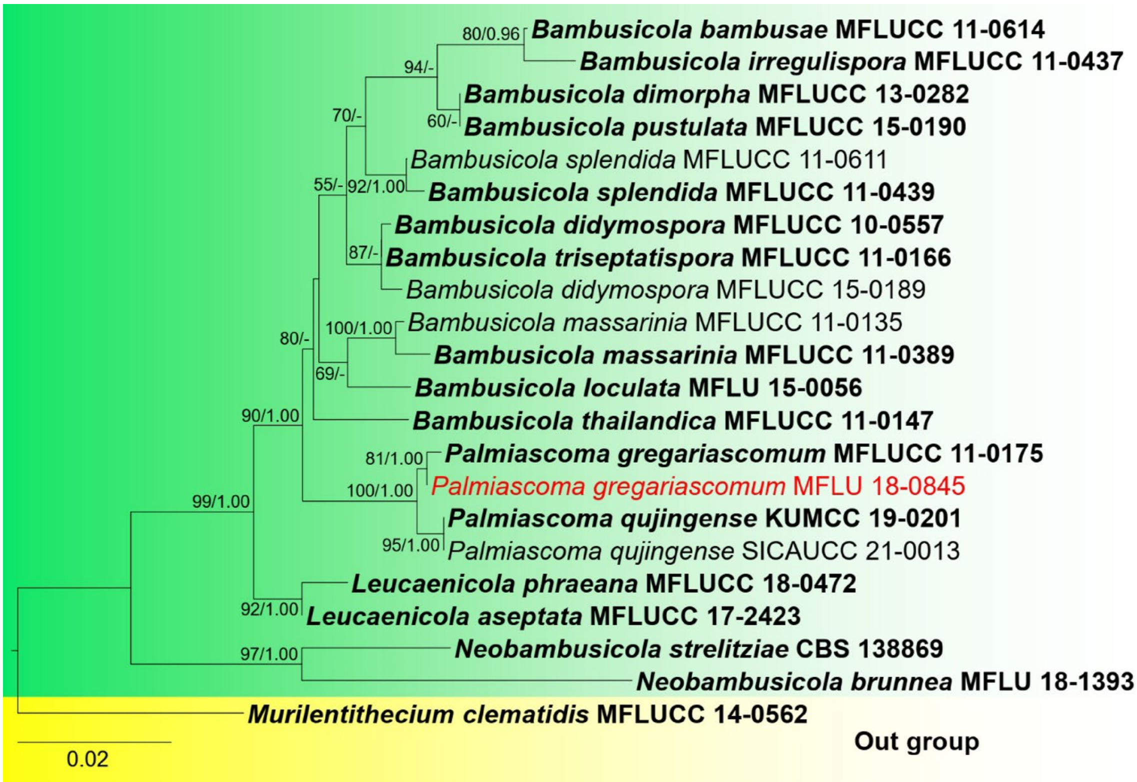


Fig. 16 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and *tef1* sequenced data for *Bambusicola* and allied genera Twenty-two strains are included in the combined sequence analyses, which comprise 2761 characters with gaps. *Murilentithecium clematidis* (MFLUCC 14–0562) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML ≥ 50% and BYPP ≥ 0.95 are given above the nodes. New strain is in red. Ex-type and representative strains are in **bold**

et al. (2022) accepted *Coniothyrium*, *Foliophoma*, *Neoconiothyrium*, *Ochrocladosporium* and *Staurosphaeria* in this family.

Coniothyrium Corda, Icon. fung. (Prague) 4: 38 (1840)

The genus is typified with *C. palmarum* Corda. In earlier studies *Contiothyrium* was considered as the asexual morph of *Leptosphaeria, Mycosphaerella* and *Massarina* (Sivanesan 1984). However, later studies based on molecular data transferred many species from *Contiothyrium* (Verkley et al. 2014; Hongsanan et al. 2020b). De Gruyter et al. (2013) reinstated Coniothyriaceae and included *Coniothyrium* as the family type.

Coniothyrium yuccicola Chaiwan, Jayaward., & K.D. Hyde, ***sp. nov.***

Index Fungorum number: *IF559467; Facesoffungi number: FoF08170; Fig. 17*

Etymology: Referring to the host *Yucca*

Holotype: MFLU 17–2529

Pathogenic on living leaves and peduncle stems of *Yucca filamentosa*. **Asexual morph**: *Conidiomata* 250–450 µm ($\bar{x}$ = 329 µm, n = 10) diam., superficial on or immersed in the host. *Conidiophores* not present. *Conidiogenous cells* lining entire cavity, hyaline, cylindrical, 8 ± 15 ($\bar{x}$ = 11.9 µm) 3 ± 8 µm ($\bar{x}$ = 5.1 µm), longer in culture than on host plants. *Conidiogenesis* holoblastic, proliferating percurrently. *Conidia* cylindrical, broadly rounded at apex, initially somewhat truncate at base, produced deep within the conidiogenous cells, secession rhexolytic, outer wall of conidiogenous cell often remaining on conidium, except at base, eventually disintegrating, olivaceous brown, 3-septate, lightly punctate, (2–)6.6–10.5(–14) × (1–)2–5(–6) µm ($\bar{x}$ = 7.3 × 3.6 µm, n = 40) brown, smooth-walled or verruculose, aseptate, curved, both sides gradually tapering towards the round to slightly acute apex and truncate base, guttulate. **Sexual morph**: Not observed.

Material examined: Russia, Donetsk People's Republic, Donetsk City, Donetsk Botanical Garden, flowerbed, on dying peduncle stem and live leaves of *Yucca filamentosa* L. (Asparagaceae), 20 May 2017, Timur S. Bulgakov, DNK-108 (MFLU 17–2529, **holotype**); ex-type living culture MFLUCC 18–0456.

GenBank numbers: OM235094 (SSU); OM235097(LSU)

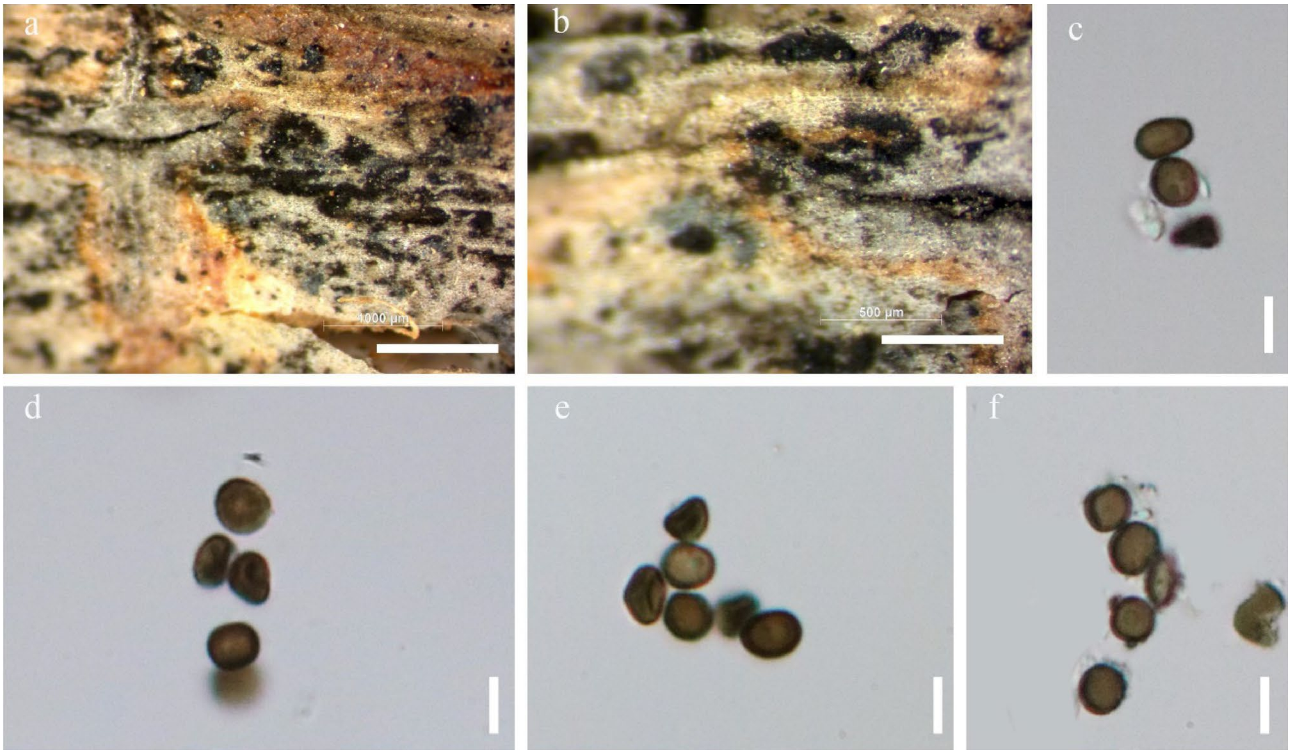


Fig. 17 ***Coniothyrium yuccicola*** (MFLU 17–2529, **holotype**) **a** Specimen with conidiomata. **b** Black acervuli. **c** Brown setae. **d** Conidiophores with basal parts of setae. **e** Hyaline conidiogenous cells. **f** Conidiomata on PDA. **g** Hyaline conidia. **h** Germinating conidium. **i** Appressoria. **j** Reverse view of the colony. **k** Upper view of the colony. Scale bars: **a** = 1000 μm, **b** = 500 μm, **c** = 20 μm, **d** = 15 μm, **e, f** = 10 μm

Notes: *Coniothyrium yuccicola* is an asexual morph. Based on our phylogenetic tree this species is closely related to *C. concentricum* (Fig. 18). Conidia of this species are brown aseptate, bacilliform, ellipsoid and often thick-walled (Fig. 17). Three *Coniothyrium* species are recorded on *Yucca* species (Farr and Rossman 2022): *Coniothryrium bartholomaei* from the USA (Oregon), *C. herbarum* from the USA (California), and *C. yuccae* from Argentina. *Coniothyrium bartholomaei* was reported as a plant pathogen that caused leaf spots of *Yucca* in Oregon (USA) (Pscheidt and Ocamb 2018; Barr 1992). *Coniothyrium herbarum* is known from USA (California) on the leaves of several closely related plants: *Dracaena indivisa*, *Sansevieria* sp. and *Yucca angustifolia* (Cash 1952), however, this species is invalid. *Coniothyrium yuccae* was found on dead leaves of *Yucca gloriosa* in Argentina (Buenos-Aires) (Farr 1973). *Phaeosphaeriopsis yuccae* is another morphologically similar taxon described from living leaves of *Yucca filamentosa* from Russia, Rostov region, Botanical Garden of Southern Federal University (Tibpromma 2017).

Didymellaceae Gruyter, Aveskamp & Verkley, Mycol. Res. 113(4): 516 (2009)

Members of this family have a wide host range and have different life modes: endophytic, pathogenic and saprobic (Hongsanan et al. 2020b). Forty-four genera are accepted in this family (Wijayawardene et al. 2022)

Ascochyta Lib., Pl. crypt. Arduenna, fasc. (Liège) 1(Praef.): 8 (1830)

Notes: *Ascochyta* was introduced by Libert (1830) with *A. pisi* as the type species. Species of *Ascochyta* are characterized by the globose locules with perithecial protuberances immersed in the stroma (Chen et al. 2015). Species are mostly endophytes, pathogens and saprobes with a wide host range and a geographical distribution (Hongsanan et al. 2020b; Farr and Rossman 2022). We provide a new host record of *Ascochyta medicaginicola* from *Prunus cerasifera* in Russia.

Ascochyta medicaginicola Q. Chen & L. Cai, in Chen et al., Stud. Mycol. 82: 187 (2015)

Index Fungorum number: *IF814129; Facesoffungi number: FoF08216; Fig. 19*

Pathogenic on living twigs of *Prunus cerasifera*, noticeable as black, circular dots on the host surface. **Asexual morph**: *Conidiomata* 165–190 µm high, 170–210 µm wide, black, scattered or gregarious, superficial to immersed, black, subglobose to globose, uniloculate. *Ostiolar neck*

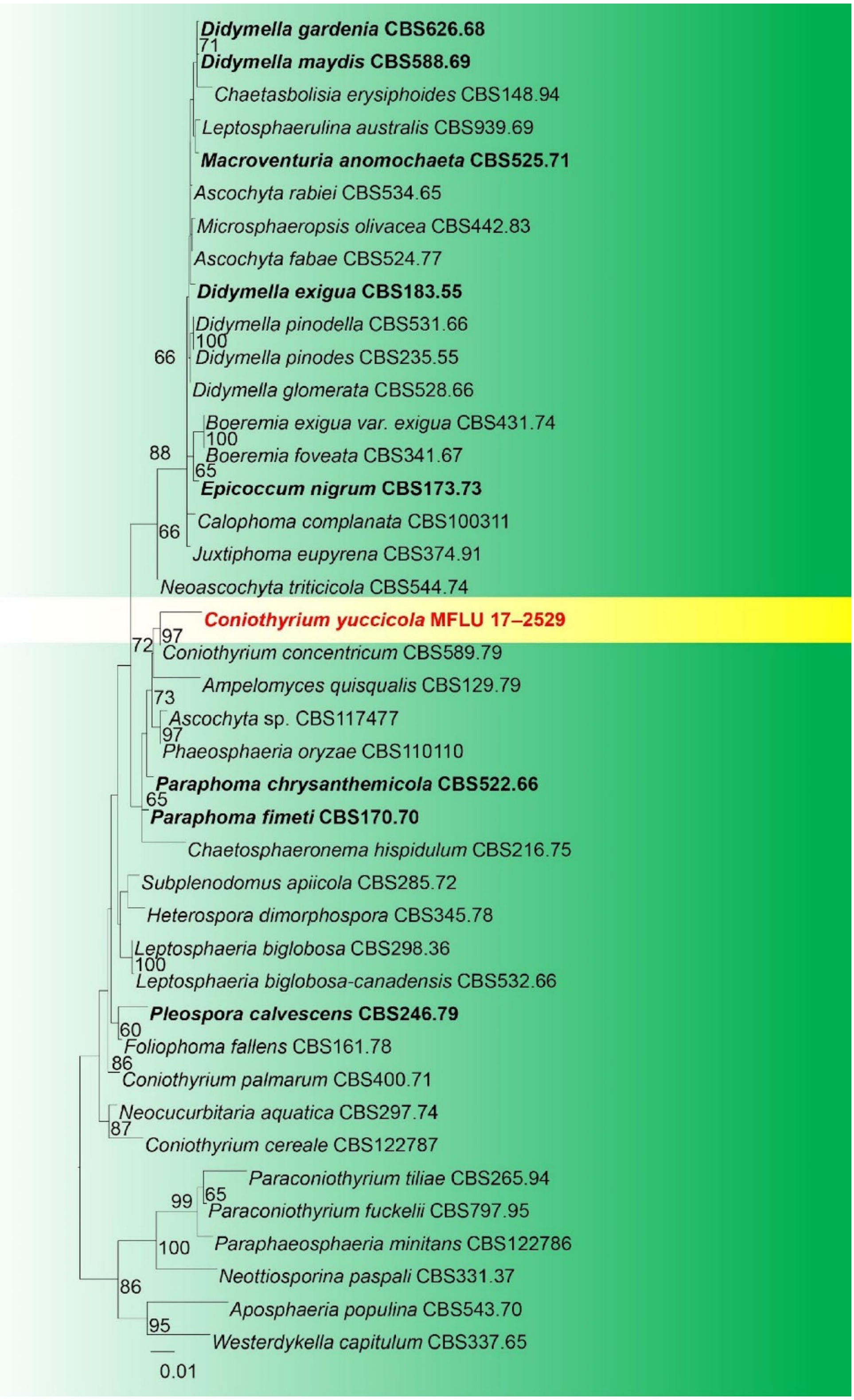


Fig. 18 Phylogram generated from ML analysis based on combined LSU and SSU sequence data of selected taxa. The combined dataset comprises 41 strains with 1834 characters including gaps. The tree is rooted to *Aposphaeria populina* (CBS543.70) and *Westerdykella capitulum* (CBS 337.65). Maximum Likelihood bootstrap values ≥ 65% and BYPP ≥ 0.90 are displayed on the nodes, respectively. Newly introduced taxa are indicated in red. Ex-type and representative strains are in **bold**

25–50 µm long, 3–5 µm wide, covered with 1-celled, thick-walled, dark brown to almost black. *Peridium* 15–25 µm wide at the base, 30–80 µm wide at the sides, thick, comprising 3–4 layers, outer most layer heavily pigmented, thick-walled, comprising blackish to dark brown loosely packed cells of *textura angularis*, inner layer composed 3–5 layers, pale brown to hyaline, cells towards the inside lighter,

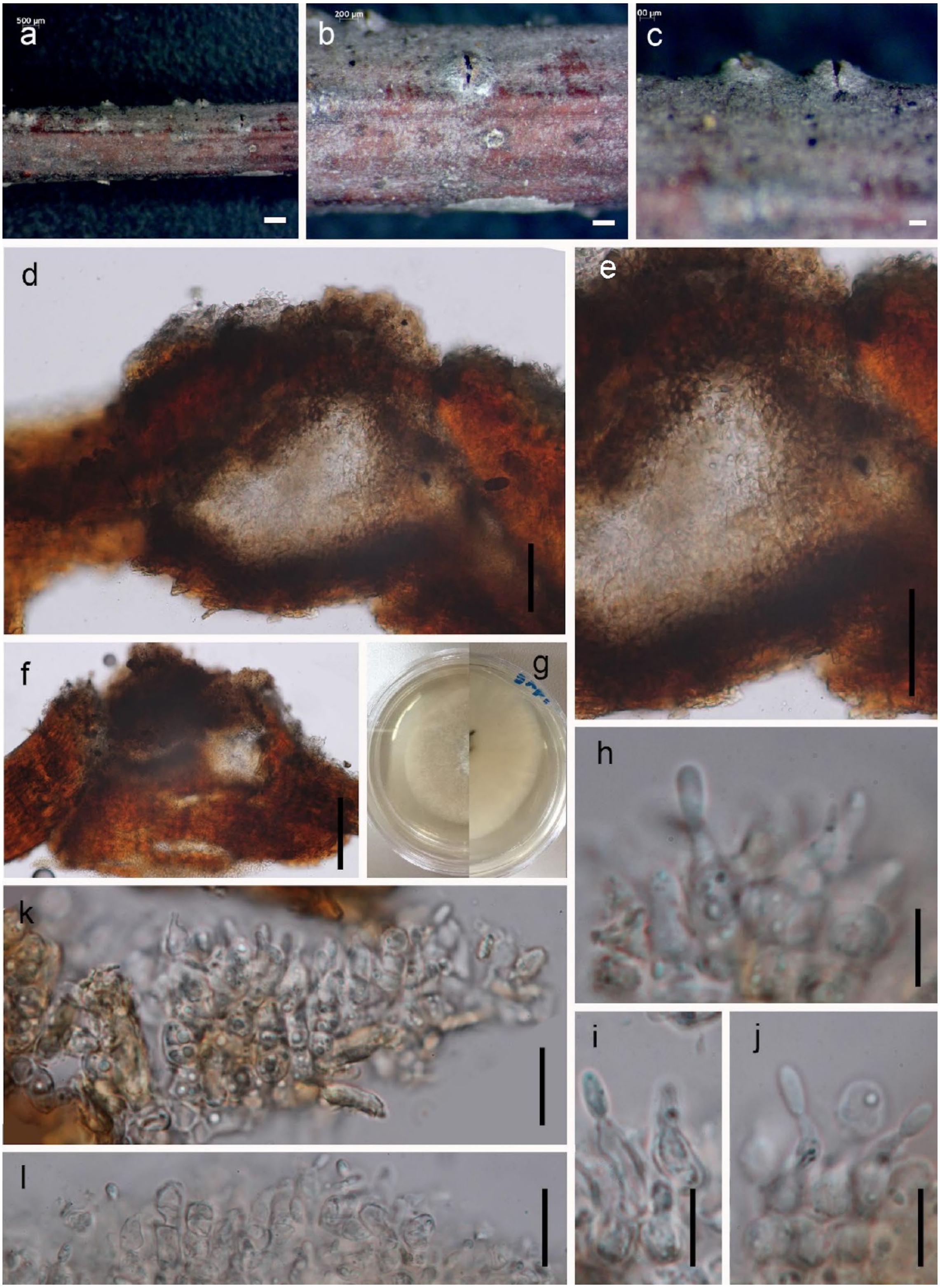


Fig. 19 ***Ascochyta medicaginicola*** (MFLU 17–2138, **new host record**) **a-c** Conidia observed on host substrate. **d-e** Conidiomata. **f–h** Conidia **i, k-l** Conidia **j** Conidiodenous cell. Scale bars: a = 500 µm, b-e, g = 100 µm, f, h = 50 µm, i-l = 10 µm

flattened, thick-walled cells of *textura angularis*. **Sexual morph**: Not observed.

Material examined: Russia, Rostov region, Shakhty, near a railroad, on dead twigs of *Prunus cerasifera* Ehrh.

(Rosaceae), 11 May 2017, Timur S. Bulgakov, T-1832 (MFLU 17–2138); living culture MFLUCC 18–0453.

Hosts: *Medicago albus*, *Medicago sativa*, *Medicago* sp. (Fabaceae, Hyde et al. 2020), *Prunus cerasifera* (Rosaceae, this study), *Scabiosa* sp. (Caprifoliaceae, Tibpromma et al. 2017) and *Trichosanthes dioica* (Cucurbitaceae, Sarkar et al. 2018-pathogenicity data are available).

Distribution: Canada, Czech Republic, France, Italy, USA (Hyde et al. 2020a, b, c), India (Sarkar et al. 2018), Thailand (this study)

GenBank number: OM235096 (ITS)

Notes: Our collection shares similar morphological characteristics with the ex-type strain of *A. medicaginicola* (Boerema et al. 2004; Chen et al. 2013). The multigene

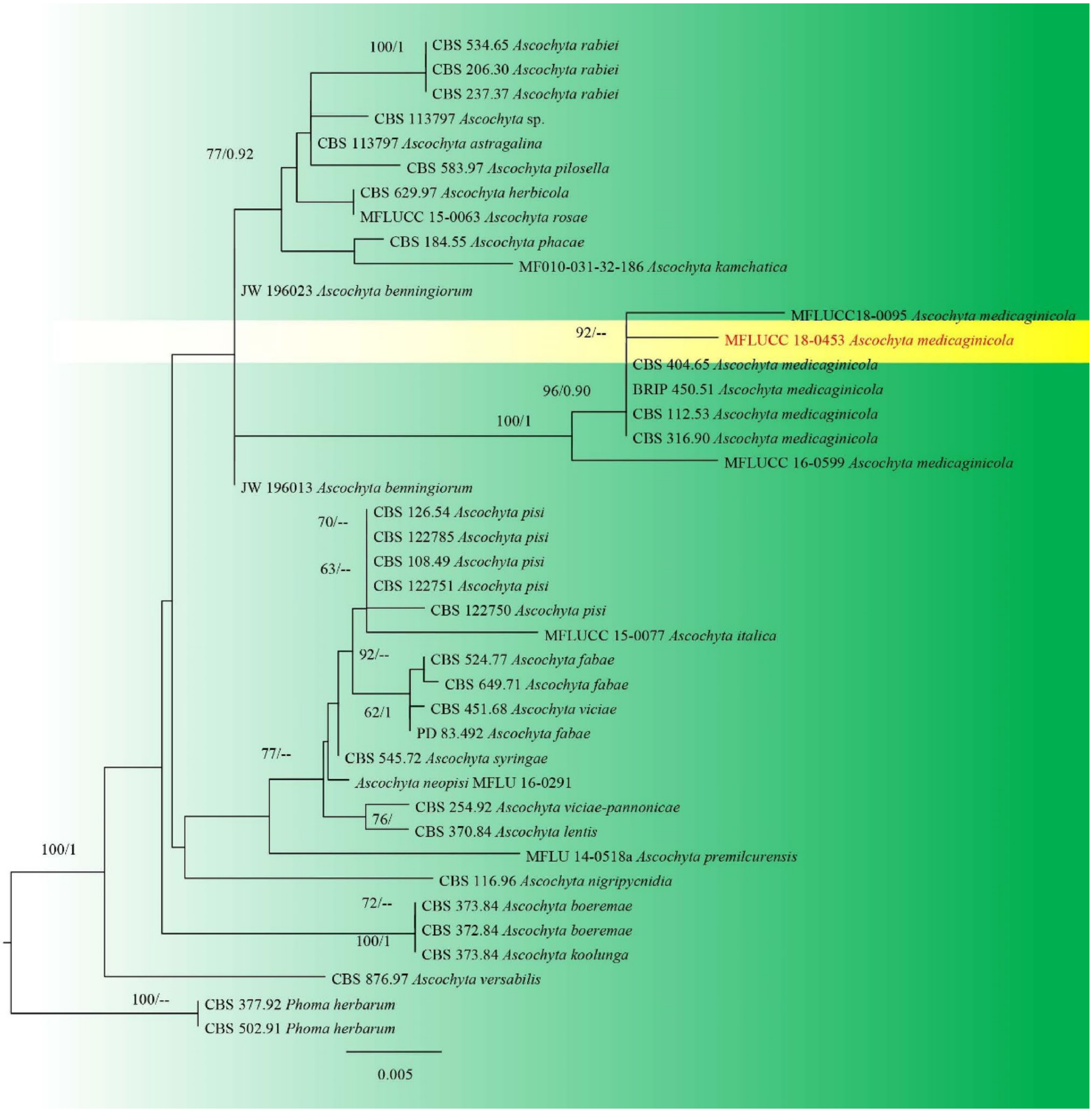


Fig. 20 Phylogram generated from maximum likelihood analysis based on combined, ITS, LSU and *tub2* sequence data of selected taxa. Related sequences were obtained from GenBank. Forty-one strains are included in the analyses, which comprise 633 characters including gaps. The tree was rooted with *Phoma herbarum* (CBS 377.92 and CBS 502.91). The maximum likelihood bootstrap (ML) values > 65%) are given above the nodes. The new isolate in red **bold**

phylogenetic analysis shows that our specimen groups in the *Ascochyta medicaginicola* clade with 96/0.90 ML/BYPP support (Fig. 20). Four *Ascochyta* species have been recorded based on the morphological description from Rosaceae plants in Russia (Melnik 2000; Farr and Rossman 2022): *Ascochyta idaei* on *Rubus idaeus* in the Leningrad region, Kursk region, and Stavropol region; *A. potentillarum* on *Potentilla reptans* in Arkhangelsk region (Melnik 2000), Lipetsk region (Sarycheva et al. 2009), Republic of Crimea (Ovcharenko 2011) and Voronezh region (Melkumov 2015); *A. pruni* on *Prunus padus* in Leningrad region; *Ascochyta sorbina* on *Sorbus torminalis* in Stavropol region. As these species were identified based on morphology alone, correct species identification is yet to be done. Our collection provides the first host record of *Ascochyta medicaginicola* on Rosaceae based on both morphological and phylogenetic data.

Didymosphaeriaceae Munk, Dansk bot. Ark. 15(no. 2): 128 (1953).

Didymosphaeriaceae represents an important family in Dothideomycetes. The family is typified by *Didymosphaeria*, with *D. epidermidis* as the type species (Hongsanan et al. 2020b). While taxa of Didymosphaeriaceae are often endophytic, pathogenic or saprobic on various plant hosts (Gonçalves et al. 2019; Hongsanan et al. 2020b), they can sometimes also be pathogenic to human beings (Hongsanan et al. 2020b). Species of Didymosphaeriaceae are mainly characterised by brown, 1–3-septate or muriform ascospores and cellular or trabeculate pseudoparaphyses in their sexual morphs while their asexual morphs are fusicladium-like or phoma-like (Hyde et al. 2013; Hongsanan et al. 2020b). After several taxonomic revisions, 32 genera have been accepted in the family (Hongsanan et al. 2020b).

Spegazzinia Sacc., Spegazzinia: [1] (1879)

Spegazzinia was introduced by Saccardo (1880), with *S. ornata* as the type species and it currently comprises hyphomycetous taxa. The genus was initially accommodated in Apiosporaceae (Sordariomycetes) based on morphology (Hyde et al. 1998). It was then transferred to Didymosphaeriaceae (Dothideomycetes) based on molecular evidence (Tanaka et al. 2015). Taxa in this genus are mainly characterised by a distinctive conidiophore ontogeny as well as two types of conidia (Samarakoon et al. 2020; Hongsanan et al. 2020b). The latest two taxa added to *Spegazzinia* are *S. musae*, reported as a saprobe on *Musa* sp., and *S. camelliae*, isolated as an endophyte from *Camellia sinensis* var. *assamica* (Samarakoon et al. 2020; Suwannarach et al. 2021).

Spegazzinia deightonii (S. Hughes) Subram., J. Indian bot. Soc. 35: 78 (1956).

Index Fungorum Number: IF306062; Facesoffungi number: FoF07238; Fig. 21

Saprobic on palm stem. **Asexual morph**: Hyphomycetous. *Sporodochia* powder-like, dark, dense, dry, 1–3.5 mm in diameter. *Conidiophores* 65–120 × 1–3 µm ($\overline{x}$ = 93.5 × 2.4 µm, n = 15), macronematous, micronematous, narrow, subspherical to doliiform, flexuous or erect, unbranched, hyaline to pale brown, verruculose. *Conidiogenous cells* 10–20 × 2–4 µm ($\overline{x}$ = 15.8 × 3 µm, n = 15), basauxic, terminal, erect, unbranched, hyaline to pale brown, verruculose, each producing a single, holoblastic conidium at the conidiophore apex. *Conidia* two types, disc-like and stellate; disc-like conidia 20–28 × 17–19 µm ($\overline{x}$ = 25.2 × 18.1 µm, n = 20), usually 8-celled, solitary, hyaline when immature, pale to dark brown on maturity, cross-septate, slightly constricted at the septa, with short and blunt spines at the periphery, frequently accompanied by attached conidiogenous cells post splitting from the conidiophores; stellate conidia 18–27 × 16–29 µm ($\overline{x}$ = 22.6 × 24.3 µm, n = 20), globose or variously shaped, frequently 4- to 6-celled, solitary, septate, deeply constricted at the septa, pale to dark brown, comprising spines 4–5 µm long. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 16–18 h. Colonies growing on PDA, reaching a diameter of 55 mm after 14 days at 25 °C, aerial, moderately dense, undulate margine, middle grey, periphery olive green at immature stage and brownish gray at maturity; reverse greyish white to white.

Material examined: Thailand, Chiang Rai, on dead stem of palm (Arecaceae), 20 December 2019, Binu C. Samarakoon, E003 MFLU 22-0277), living culture MFLUCC 22-0180.

Hosts: *Spegazzinia deightonii* has been reported from several hosts, including, *Andropogon glomeratus* (Arnold 1986), *Areca catechu* (Tianyu 2009; Matsushima 1980), *Arundo donax* (Tanaka et al. 2011), *Bambusa vulgaris* (Camino-Vilaro et al. 2019), *Calathea makoyana* (Tianyu 2009), *Cocos nucifera* (Tianyu 2009), *Imperata cylindrical* (Thaung 2008), *Musa* sp. (Samarakoon et al. 2018), *Panicum maximum* (Lu et al. 2000; Wong and Hyde 2003), *Phoenix hanceana* (Tianyu 2009), *Quercus xalapensis* (Heredia et al. 1995), *Saccharum spontaneum* (Mel'nik et al. 2000), *Thysanolaena latifolia* (Mel'nik et al. 2000) and *Tillandsia* sp. (Delgado-Rodriguez et al. 2002).

Distribution: China (Tianyu 2009), Cuba (Arnold 1986; Delgado-Rodriguez et al. 2002; Camino-Vilaro et al. 2019), Hong Kong (Lu et al. 2000; Wong and Hyde 2003), Japan (Tanaka et al. 2011), Mexico (Heredia et al. 1995), Myanmar (Thaung 2008), Philippines (Whitton et al. 2012), Taiwan (Matsushima 1980), Thailand (Samarakoon et al. 2020), United States (Delgado 2008), Vietnam (Mel'nik et al. 2000).

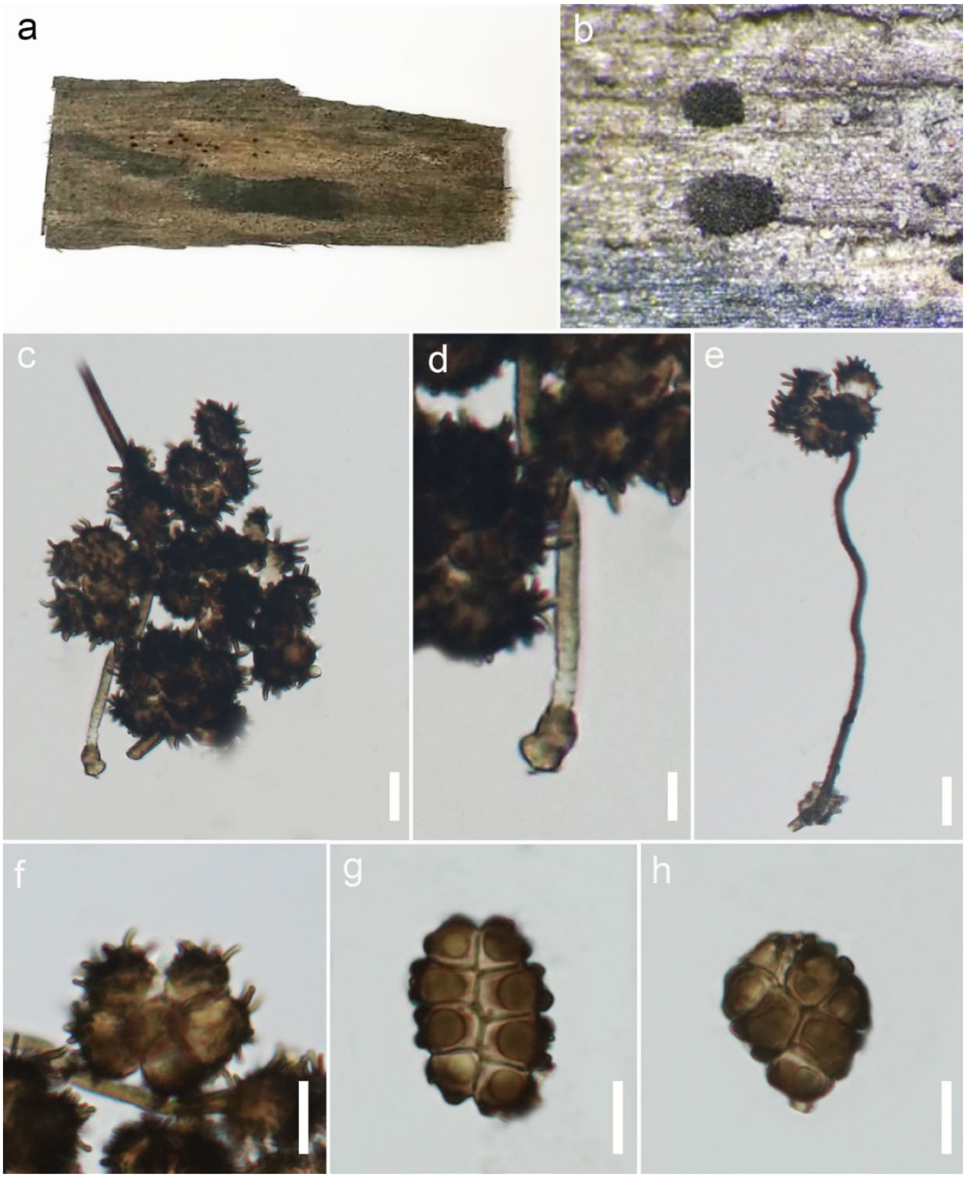


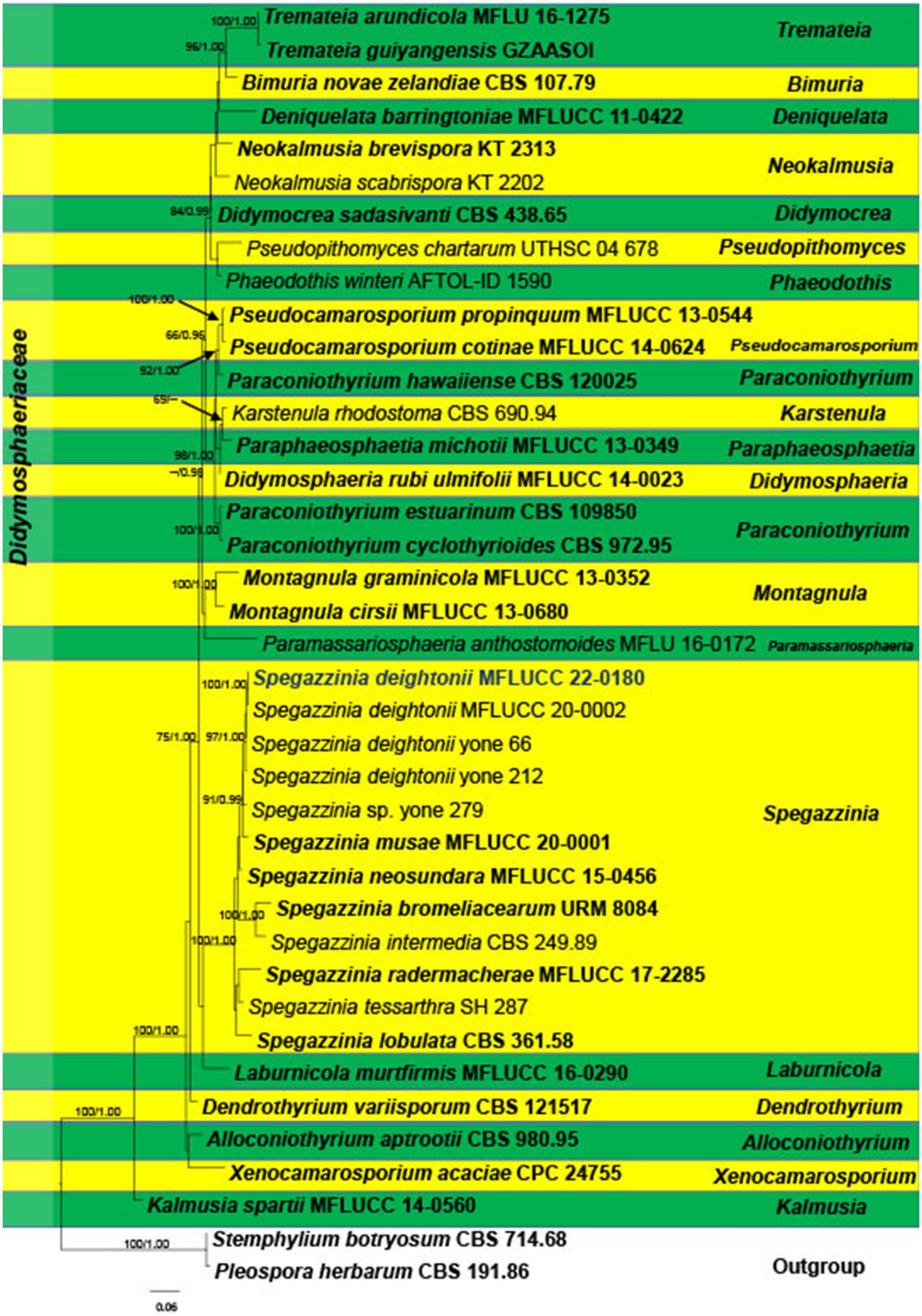
Fig. 21 *Spegazzinia deightonii* (MFLU 22-0277, **new host record**) **a** Host. **b** Close-up of conidia on host. **c** Mass of conidia. **d** Conidiogenous cell of stellate conidia. **e** Stellate conidium on a conidiophore. **f** Stellated conidium. **g** Disk-liked conidium. **h** Disk-like conidium with attached conidiogenous cell. Scale bars: **c–h** = 10 µm

GenBank numbers: ON885254 (SSU); ON873996(LSU); ON873998(ITS); ON885741 (*tef1*)

Notes: Our isolate (MFLUCC 22-0180) clusters with other strains of *Spegazzinia deightonii* with 95% ML, statistical support in the multi-loci phylogenetic tree (Fig. 22). Pairwise comparison of DNA sequence data shows insignificant differences among our strain (MFLUCC 22-0180) and the other strains of *S. deightonii*, following which our isolate is considered as *S. deightonii.* Furthermore, the isolate in the present study shares similar features with other strains of *S. deightonii,* including two types of pale to dark brown conidia which are multi-cellular, constricted at the septa and comprise either long (stellate conidia) or short (disc-like conidia) spines (Ellis 1961; Tanaka et al. 2011; Samarakoon et al. 2018). Small differences in sizes may be accounted for by host variations. *Spegazzinia deightonii* has been reported on a palm substrate in China, Taiwan and the United States (Matsushima 1980; Delgado 2008; Tianyu 2009). We recovered the species from Thailand and thus report it as a new record on Palm from Thailand. Recently this species was also reported to occur in Thailand, in the same Province and area, on *Musa* sp. (Samarakoon et al. 2020).

Lindgomycetaceae K. Hiray., Kaz. Tanaka & Shearer, in Hirayama et al., Mycologia 102(3): 733 (2010)

Notes: Lindgomycetaceae was introduced by Hirayama et al. (2010) with *Lindgomyces* (*L. ingoldianus*) as the generic type. Most Lindgomycetaceae members have been recorded from freshwater habitats and the freshwater isolates form a distinct lineage from other Dothideomycetes taxa based on ribosomal sequence data (Zhang et al. 2013; Hyde et al. 2013; Dong et al. 2021). There are seven


Didymosphaeriaceae
100/1.00 Tremateia arundicola MFLU 16-1275
96/1.00 Tremateia guiyangensis GZAASOI
Tremateia
Bimuria novae zelandiae CBS 107.79
Bimuria
Deniquelata barringtoniae MFLUCC 11-0422
Deniquelata
Neokalmusia brevispora KT 2313
Neokalmusia scabrispora KT 2202
Neokalmusia
84/0.99 Didymocrea sadasivanti CBS 438.65
Didymocrea
Pseudopithomyces chartarum UTHSC 04 678
Pseudopithomyces
Phaeodothis winteri AFTOL-ID 1590
Phaeodothis
100/1.00
Pseudocamarosporium propinquum MFLUCC 13-0544
66/0.96
Pseudocamarosporium cotinae MFLUCC 14-0624
Pseudocamarosporium
92/1.00
Paraconiothyrium hawaiiense CBS 120025
Paraconiothyrium
69/–
Karstenula rhodostoma CBS 690.94
Karstenula
98/1.00
Paraphaeosphaetia michotii MFLUCC 13-0349
Paraphaeosphaetia
–/0.98
Didymosphaeria rubi ulmifolii MFLUCC 14-0023
Didymosphaeria
Paraconiothyrium estuarinum CBS 109850
100/1.00
Paraconiothyrium cyclothyrioides CBS 972.95
Paraconiothyrium
100/1.00
Montagnula graminicola MFLUCC 13-0352
Montagnula cirsii MFLUCC 13-0680
Montagnula
Paramassariosphaeria anthostomoides MFLU 16-0172
Paramassariosphaeria
100/1.00 Spegazzinia deightonii MFLUCC 22-0180
Spegazzinia deightonii MFLUCC 20-0002
75/1.00 97/1.00 Spegazzinia deightonii yone 66
Spegazzinia deightonii yone 212
91/0.99 Spegazzinia sp. yone 279
Spegazzinia musae MFLUCC 20-0001
Spegazzinia neosundara MFLUCC 15-0456
100/1.00 Spegazzinia bromeliacearum URM 8084
100/1.00 Spegazzinia intermedia CBS 249.89
Spegazzinia radermacherae MFLUCC 17-2285
Spegazzinia tessarthra SH 287
100/1.00 Spegazzinia lobulata CBS 361.58
Spegazzinia
Laburnicola murtfirmis MFLUCC 16-0290
Laburnicola
100/1.00 Dendrothyrium variisporum CBS 121517
Dendrothyrium
Alloconiothyrium aptrootii CBS 980.95
Alloconiothyrium
Xenocamarosporium acaciae CPC 24755
Xenocamarosporium
Kalmusia spartii MFLUCC 14-0560
Kalmusia
100/1.00 Stemphylium botryosum CBS 714.68
Pleospora herbarum CBS 191.86
Outgroup
0.06

◂ **Fig. 22** Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *tef* sequence data of selected taxa in Didymosphaeriaceae. Bootstrap support values for ML ≥ 65% and BYPP ≥ 0.95 are indicated above or below the branches. Ex-type strains are in **bold**. The new isolate is in blue. The tree is rooted with *Laburnicola zaaminensis* (TASM 6152) and *L. murtfirmis* (MFLUCC 16-0290).

genera in the family, including *Hongkongmyces* which is also associated with human diseases (Tsang et al. 2014; Linqiang et al. 2020). The genus forms a close relationship to *Aquimassariosphaeria, Clohesyomyces, Lolia,* and *Trematosphaeria* in the phylogenetic analyses of the ribosomal DNA and protein-coding genes such as *tef* (Abdel-Aziz and Abdel-Wahab 2010; Hyde et al. 2016). We, therefore, encourage further taxonomic studies to include protein-coding regions for a better resolution of taxa in Lindgomycetaceae (Fig. 24).

Hongkongmyces Tsang et al., Medical Mycol. 52(7): 740 (2014)

Hongkongmyces was introduced as a monotypic genus associated with human infections, and typified by *H. pedis* (Tsang et al. 2014). Six species *H. aquaticus*, *H. brunneosporus*, *H. kokensis*, *H. pedis*, *H. snookiorum*, and *H. thailandicus* are listed in Species Fungorum (2022a, b). The species are commonly associated with freshwater habitats as saprobes. Hyde et al. (2016) introduced the second species of *Hongkongmyces* based on sexual morph characters, which was collected on submerged wood in a stream in Thailand. Later, an asexual morph of *H. snookiorum* was isolated from submerged wood (Crous et al. 2018). *Hongkongmyces snookiorum* was reported as an opportunistic fungal infection in a transplant patient (Deng et al. 2020). Schoch et al. (2012) and Aime et al. (2021) recommend using the fungal barcode locus such as the ITS region as well as any additional secondary barcode locus such as protein-coding region for the introduction of new species. Most *Hongkongmyces* species lack barcodes in public databases, and therefore, delineating species in the genus is a challenging task. In this paper, we introduce a new species of *Hongkongmyces* which was collected in a freshwater pond in Jilin Province of China based on comprehensive morphology and phylogeny analyses (Figs. 23 and 24).

Hongkongmyces changchunensis Phukhams., W.X. Su, & Y. Li, ***sp. nov.***

Index Fungorum number: *IF559493; Facesoffungi number: FoF10725; Fig.* 23

Etymology: The epithet reflects the locality, Changchun.

Holotype: HMJAU 60185.

Saprobic on decaying *Betula* twigs submerged in a freshwater stream. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* 77–188 × 85–174 µm diam, pycnidia scattered, semi-immersed, globose or ellipsoidal, black, coriaceous, ostiolate. *Peridium* 10–28 µm thick, composed of large, irregular, and dark brown cells arranged in a *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.6–23.5 × 1.6–4.9 µm ($\bar{x}$ = 10 × 3 µm, n = 20), enteroblastic, phialidic, determinate, cylindrical to subcylindrical, hyaline, thin-walled. Conidia 10–18 × 7–13 µm ($\bar{x}$ = 13 × 10 µm, n = 43), ellipsoidal, obovoid or irregular, aseptate, guttulate, hyaline, thin-walled, lacking mucilaginous sheath, turning brown at senescence stage.

Culture Characteristics: Colonies on PDA reaching 20 mm in 7 days at 20 °C, flat with entire margin, circular, grey to black, aerial mycelium becoming grey towards the edge; reverse grey-olivaceous to black, smooth.

Material examined: China, Jilin Province, Changchun District, Jingyuetan National Scenic Areas, on the submerged twigs in a stream of *Betula* sp. (Betulaceae), 12 May 2021, Chayanard Phukhamsakda (SWX32), (HMJAU 60185, **holotype**); ex-type living culture, CCMJ5008.

GenBank numbers: OL897173 (LSU), OL891809(SSU), OL996122 (ITS), OL944603 (*tef1*), OL944507(*rpb*2).

Notes: Phylogenetic analyses of LSU, SSU, ITS and *tef* sequence data show that *Hongkongmyces changchunensis* (CCMJ5008) is related to the type species *Hongkongmyces thailandicus* (MFLUCC 16–0406), with good support (92% ML/0.93 BYPP; Fig. 23). *Hongkongmyces changchunensis* was collected from submerged substrates in a freshwater habitat in Jilin Province of China. Both species were collected from fresh water habitats, but from different country (Hyde et al. 2016). *Hongkongmyces changchunensis* is similar to *Hongkongmyces aquaticus* in having phialidic conidiogenous cells and hyaline, variable shaped conidia, but it lacks sympodial proliferations (Dong et al. 2020). *Hongkongmyces changchunensis* is characterized by wet, globular, mass of conidia on natural substrates after drying and smooth surfaced conidia containing multiple small bubbles. Herein, we propose a new species based on both morphology and phylogenetic analyses.

Lindgomyces K. Hiray., Kaz. Tanaka & Shearer, in Hirayama et al., Mycologia 102(3): 733 (2010)

Notes: *Lindgomyces* was introduced in Lindgomycetaceae by Hirayama et al. (2010) based on the type species *L. ingoldianus* (Shearer & K.D. Hyde) K. Hiray., Kaz. Tanaka & Shearer. The morphology of the species of Lindgomyces is similar to *Massarina eburnea* and *Lophiostoma macrostomum*, but they differ from ascomata and ascospores (Raja et al. 2013; Hirayama et al. 2010). There are 14 epithets listed in *Lindgomyces* in Index Fungorum (2022a, b). Keys to the species of *Lindgomyces* were provided by Dong et al. (2020). In this study, we describe a novel species, *Lindgomyces guizhouensis* based on the unique morphological features

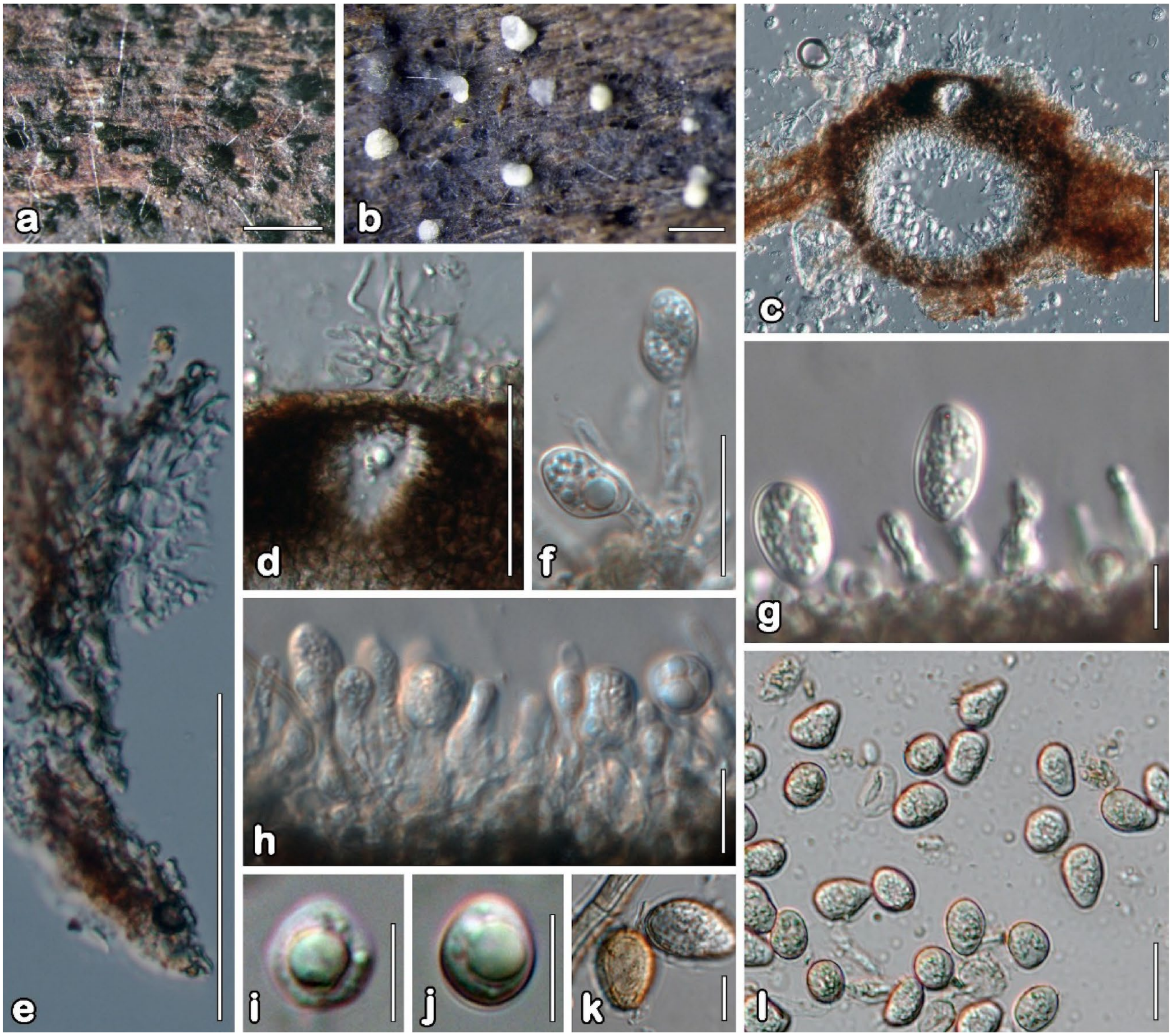


Fig. 23 ***Hongkongmyces changchunensis*** (HMJAU 60185, **holotype**) **a, b** Appearance of conidiomata on host surface. **c** Vertical section through conidioma. **d** Ostiole canal. **e** Section of partial conidioma peridium. **f–h** Conidiogenous cells and developing conidia. **i–l** Developmental state of conidia. Scale bars: **a** = 500, **b** = 200 μm, **c** = 100 μm, **d, e** = 50, **f, l** = 20 μm, **g–k** = 10 μm

and multi–gene phylogenetic analysis of a combined LSU and ITS sequence data (Fig. 26).

Lindgomyces guizhouensis J. Mai, Y.Z. Lu & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF559506; Facesoffungi number: FoF 10676; Fig. 25

Etymology: Referring to collecting site in Guizhou Province, China.

Holotypus: GZAAS 21–0383

Saprobic on decaying wood in terrestrial habitats. **Asexual morph**: *Ascomata* 396–548 μm high × 466–514 μm diam., superficial, black, smooth, scattered, solitary, erumpent, subglobose to broadly conical, with a centrally located ostiole. *Peridium* 44–79 μm thick, thick–walled, composed of pale brown cells of *textura angularis*. *Hamathecium* 1–2 μm wide, septate, branched, pseudoparaphyses above the asci. *Asci* 110–154 × 15–28 μm, bitunicate, fissitunicate, apically rounded with an indistinct ocular chamber, subsessile, broadly cylindrical to clavate. *Ascospores* 30–51 × 8–12 μm, ($\bar{x}$ = 44.7 × 10.5 μm, *n* = 25), obliquely uniseriate to 2–3–seriate, fusiform, slightly curved with narrowly rounded ends, 1–septate, 2–4 guttules in each cell, wall gray while in the ascus, smooth or slightly verruculose. **Sexual morph**: Not observed.

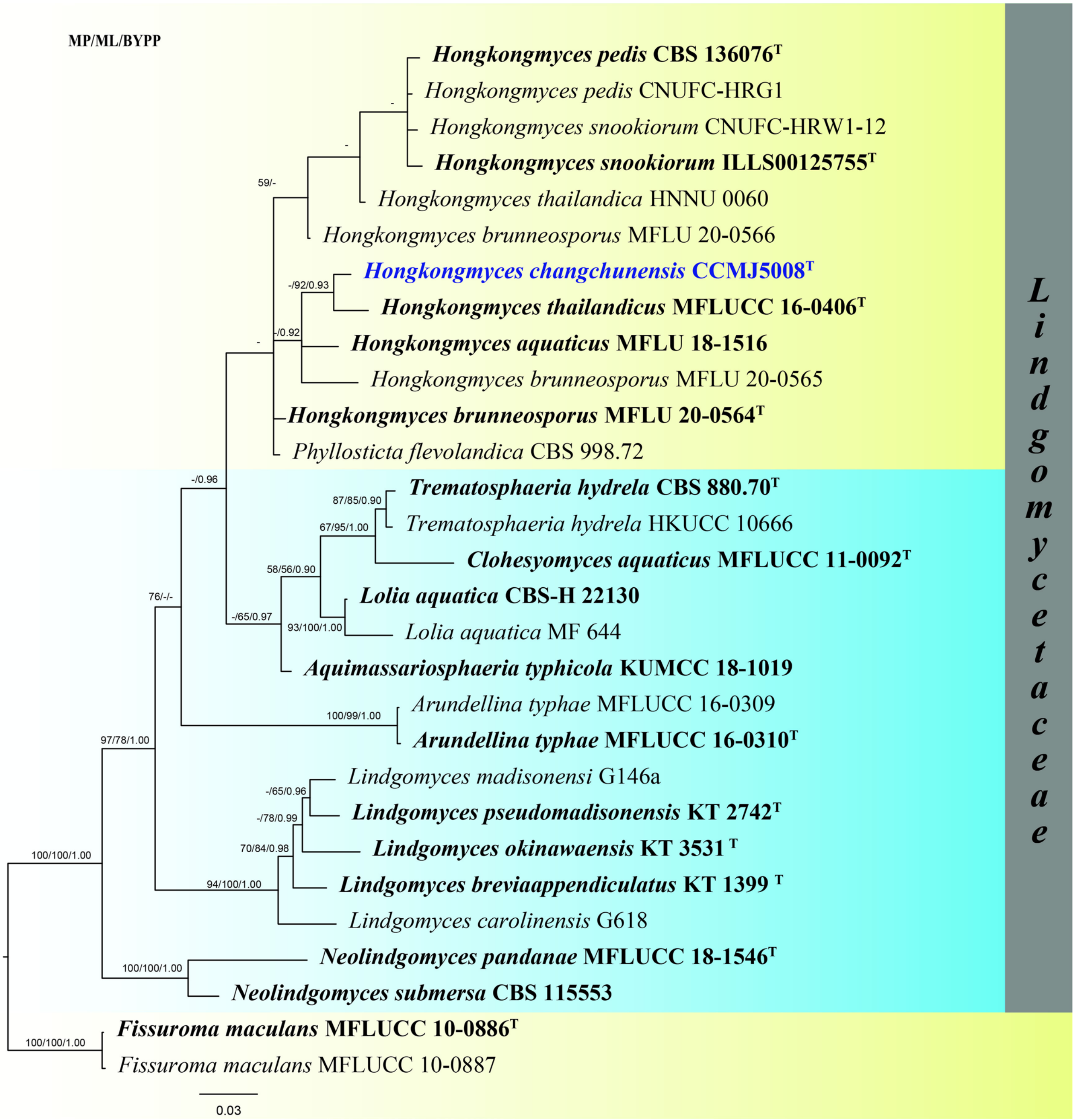


Fig. 24 Phylogram generated from Bayesian 50% majority-rule consensus phylogram based on combined LSU, SSU, ITS and *tef* sequence data of Lindgomycetaceae. The topology and clade stability of the combined gene analyses was compared to the single gene analyses. The tree is rooted with members of the Aigialaceae. Bootstrap values ≥ 50% (MP and ML) and BYPP ≥ 0.90 are given at the nodes. The type-delivered strains are in **bold**; the new isolates are in blue

Culture characteristics: Colonies on PDA reaching 43 mm in 20 days at 25 °C, flat, filiform, gray to near–black from center to edge, with moderate aerial mycelium, smooth, irregular; In reverse, gray to pale brown.

Material examined: China, Guizhou Province, Longli, on decaying wood submerged in a freshwater stream, 2 September 2020, Jian Ma, LLSB06 (GZAAS 21–0383, **holotype**); ex–type living culture, GZCC 21–0669.

GenBank numbers: OM339435 (ITS), OM339432 (LSU).

Notes: In a BLASTn search of NCBI GenBank, the closest match of LSU and ITS sequence data for *Lindgomyces guizhouensis* is 99.54% and 96.96% similar to *L. pseudomadisonensis* (KT 2742). The multi–loci phylogenetic

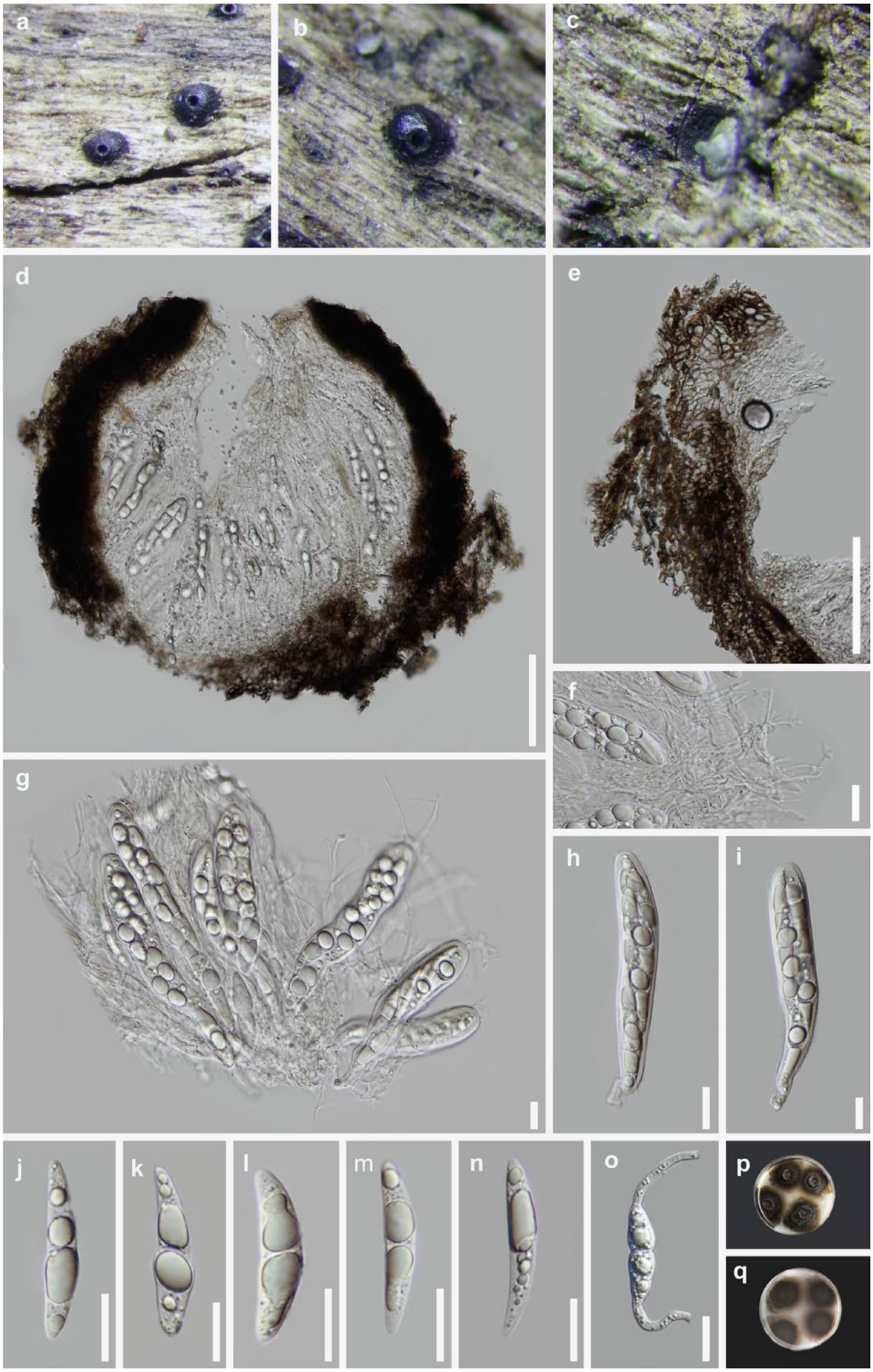


Fig. 25 ***Lindgomyces guizhouensis*** (GZAAS 21–0383, **holotype**). **a–c** Superficial ascomata on unidentified plant substrate. **d** Vertical section of an ascoma. **e** Peridium. **f** Hamathecium **g** Asci with hamathecium **h–i** Asci **j–n** Ascospores **o** Germinating ascospore **p–q** Colony on PDA from above and below. Scale bars: **d**, **e** = 100 µm, **f–o** = 20 µm

analyses of the combined LSU and ITS sequence dataset confirmed the new strain obtained belonging to *Lindgomyces*, where it is sister to *L. griseosporus* with 99% ML and 1.00 BYPP support (Fig. 25). Morphologically, *L. guizhouensis* is also most similar to *L. griseosporus* in having superficial, black with roughened surface ascomata; a thick peridium; bitunicate, clavate, subsessile asci and fusiform, 1-septate, guttules ascospores. However, our new collection differs from *L. griseosporus* in having larger ascomata (396–548 × 466–514 µm *vs* 240–290 × 320–350 µm), fragile peridium and smaller asci (110–154 × 15–28 µm *vs*

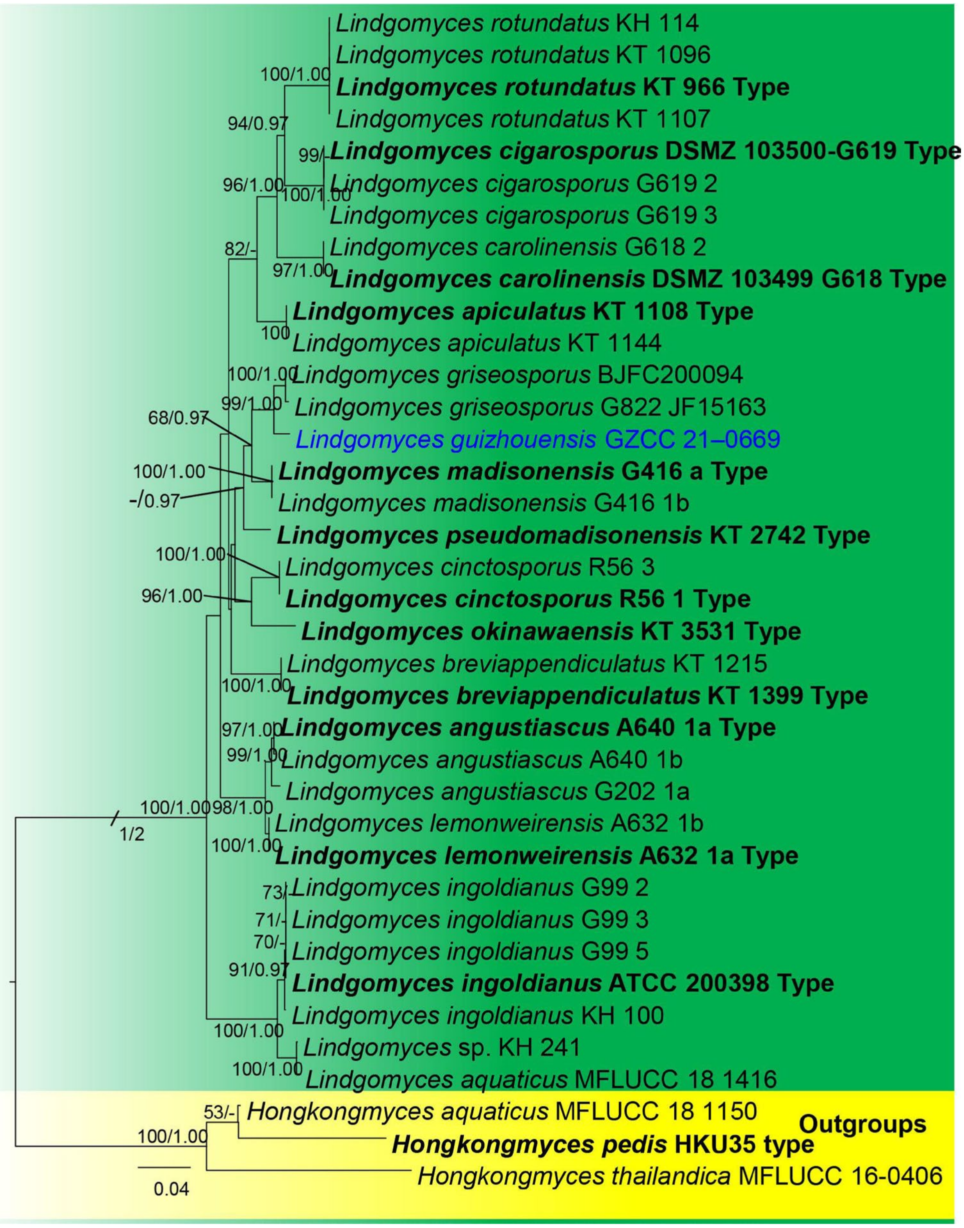


Fig. 26 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Twenty–two taxa were included in the combined analyses, which comprised 2096 characters (LSU: 841, ITS: 1255) after alignment. Bootstrap support values for ML ≥ 50% and BYPP ≥ 0.95 are given above the nodes. *Hongkongmyces aquaticus* (MFLUCC 18–1150), *H. pedis* (HKU35) and *H. thailandica* (MFLUCC 16–0406) were used as the outgroup taxa. The newly generated sequence is indicated in blue. The ex–type strains are indicated in **bold**

140–180 × 24–30). Therefore, we introduce *Lindgomyces guizhouensis* as a new species.

Lophiostomataceae Sacc.

Lophiostomataceae, typified by *Lophiostoma*, was first erected by Nitschke (1869) as ″Lophiostomeae″, but it was established by Saccardo (1883) as ″Lophiostomaceae″ and placed in Pleosporales. Lophiostomataceae species are mostly characterized by slot-like ostiole on apex of a flattened neck that are usually saprobes that grow on herbaceous and woody plants from terrestrial and aquatic environments (Holm and Holm 1988; Mugambi and Huhndorf 2009; Thambugala et al. 2015; Hashimoto et al. 2018). The historical account of Lophiostomataceae and recent generic notes of Lophiostomataceae were provided by Hyde et al. (2013) and Hongsanan et al. (2020a, b), respectively. Wijayawardene et al. (2022) outlined and accepted 30 genera of Lophiostomataceae with *Lophiostoma* as speciose genera (ca. 100). Calabon et al. (2022) listed 20 species under 10 genera of Lophiostomataceae from freshwater environments. In this series, we introduced two new species of Lophiostomataceae from terrestrial and freshwater habitats.

Neovaginatispora A. Hashim., K. Hiray. & Kaz. Tanaka.

Notes: *Neovaginatispora*, typified by *N. fuckelii*, was introduced by Hashimoto et al. (2018) based on their phylogenetic analysis and morphological differences of peridium (i.e., thinner peridium that is uniformly thick and composed of two cell layers) compared to *Vaginatispora*

(Thambugala et al. 2015). Recent phylogenetic analysis shows that *Neovaginatispora* strains form a separate subclade with *Lentistoma* and *Vaginatispora* (Bao et al. 2019; Phukhamsakda et al. 2020; Hyde et al. 2020a, b, c). Two *Neovaginatispora* species are accepted, *N. fuckelii* and *N. clematidis*. *Neovaginatispora fuckelii* has a cosmopolitan distribution that thrives on various hosts in terrestrial habitats (Wang and Lin 2004; Thambugala et al. 2015; Hyde et al. 2016; Hyde et al. 2020a, b, c) while Bao et al. (2019) reported this on freshwater habitats. The second species, *N. clematidis*, was introduced by Phukhamsakda et al. (2020) from the dead stems of *Clematis viticella* in Belgium. *Neovaginatispora clematidis* differs from *N. fuckelii* on their ascospore morphology (broad fusiform with a single eusepta). In this study, the third *Neovaginatispora* species is introduced based on the collection from dead stems of *Mangifera indica* in Taiwan.

Neovaginatispora mangiferae Tennakoon, M.S. Calabon, E.B.G. Jones & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF559843; Facesoffungi number: FoF12720; Fig. 27

Etymology: Name reflects the host *Mangifera indica*, from which the holotype was collected.

Holotype: MFLU 18–0069

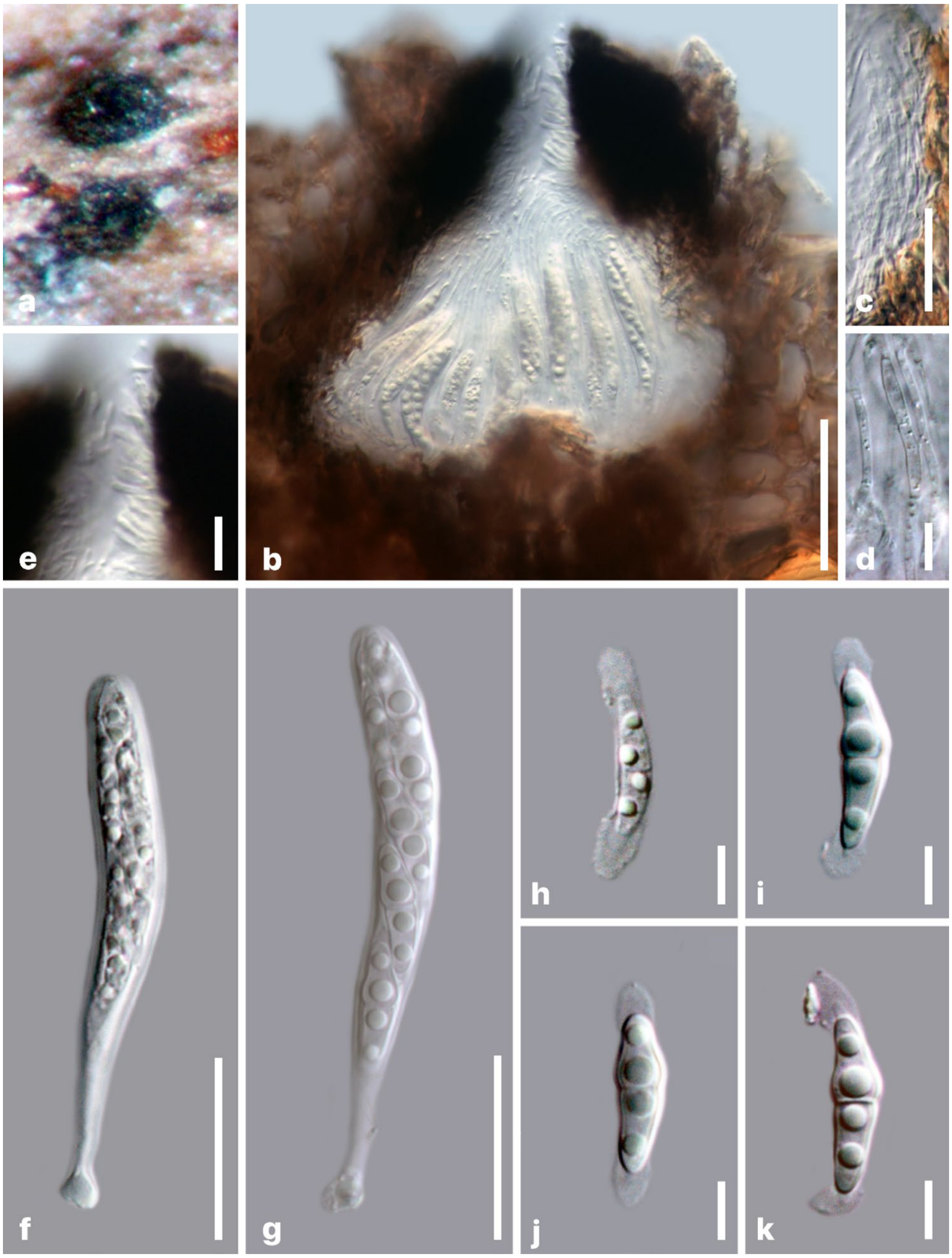


Fig. 27 ***Neovaginatispora mangiferae*** (MFLU 18–0069, **holotype**). **a** Appearance of ascomata in host substrate. **b** Vertical section of ascoma. **c** Peridium. **d** Pseudoparaphyses. **e** Ostiole with numerous periphysis. **f**, **g** Bitunicate asci. **h–k** Ascospores in different stages of maturity. Scale bars: **b** = 100 µm, **c**, **d**, **h–k** = 5 µm, **e**, **f**, **g** = 20 µm

Saprobic on decaying stem of *Mangifera indica*. **Sexual morph**: *Ascomata* 430–500 µm high, 320–350 µm diam., scattered, semi-immersed to immersed, papilla erumpent through host surface, coriaceous to carbonaceous, dark brown to black, globose to subglobose, ostiolate. *Ostiole* crest-like, variable in shape, central, periphysate, broadly papillate, with an irregular pore-like opening. *Peridium* 25–40 µm wide, thick, composing two layers of irregular cells arranged in a *textura angularis*, outer layer with darker, light brown to brown flattened cells, inner layer comprising several layers of hyaline cells. *Hamathecium* 1.5–3 µm wide, massive, long cylindrical cellular, anastomosed, cellular pseudoparaphyses, hyaline, septate with small guttules. *Asci* 60–80 × 7–9 µm ($\overline{x}$ = 60.9 × 7.2 µm, $n = 20$), 8-spored, bitunicate, cylindrical to cylindric-clavate, short pedicellate with furcate to obtuse ends, apically rounded with an indistinct ocular chamber. *Ascospores* 13–17 × 3.0–5.5 µm ($\overline{x}$ = 15.1 × 3.7 µm, $n = 25$), biseriate, overlapping, fusiform to sunbfusoid, strongly constricted at the median septum, straight or slightly curved, 1-septate at the center, enlarged near the septum at the upper cell, hyaline, guttulate, smooth-walled, mostly with 4 guttules, with a helmet-shaped to subcylindrical mucilaginous sheath at each end when immature, invisible at maturity, 2.1–5.6 µm long, 2.2–4.4 µm wide. **Asexual morph**: Not observed.

Culture characteristics: Conidia germinating on potato dextrose agar (PDA) within 24 h. Germ tubes produced from the apical cell of conidia. Colonies growing on PDA, reaching 25–30 mm in 2 weeks at 25 °C. Mycelia superficial, medium dense, irregular, flat, slightly raised, surface smooth with crenate edge, fluffy to velvety with smooth aspects, zonate with different sector yellowish-brown to moss brown at the margin brownish-grey at the center; from below**,** light moss brown at margin, dark gray at the middle, brown at the center, no pigmentation and sporulation.

Material examined: Taiwan, Chiayi, Fanlu Township area, Dahu village, dead stems of *Mangifera indica* (Anacardiaceae), 5 August 2017, D.S. Tennakoon, DTW 018C (18–0069, holotype), ex-type living culture, MFLUCC 17–2652.

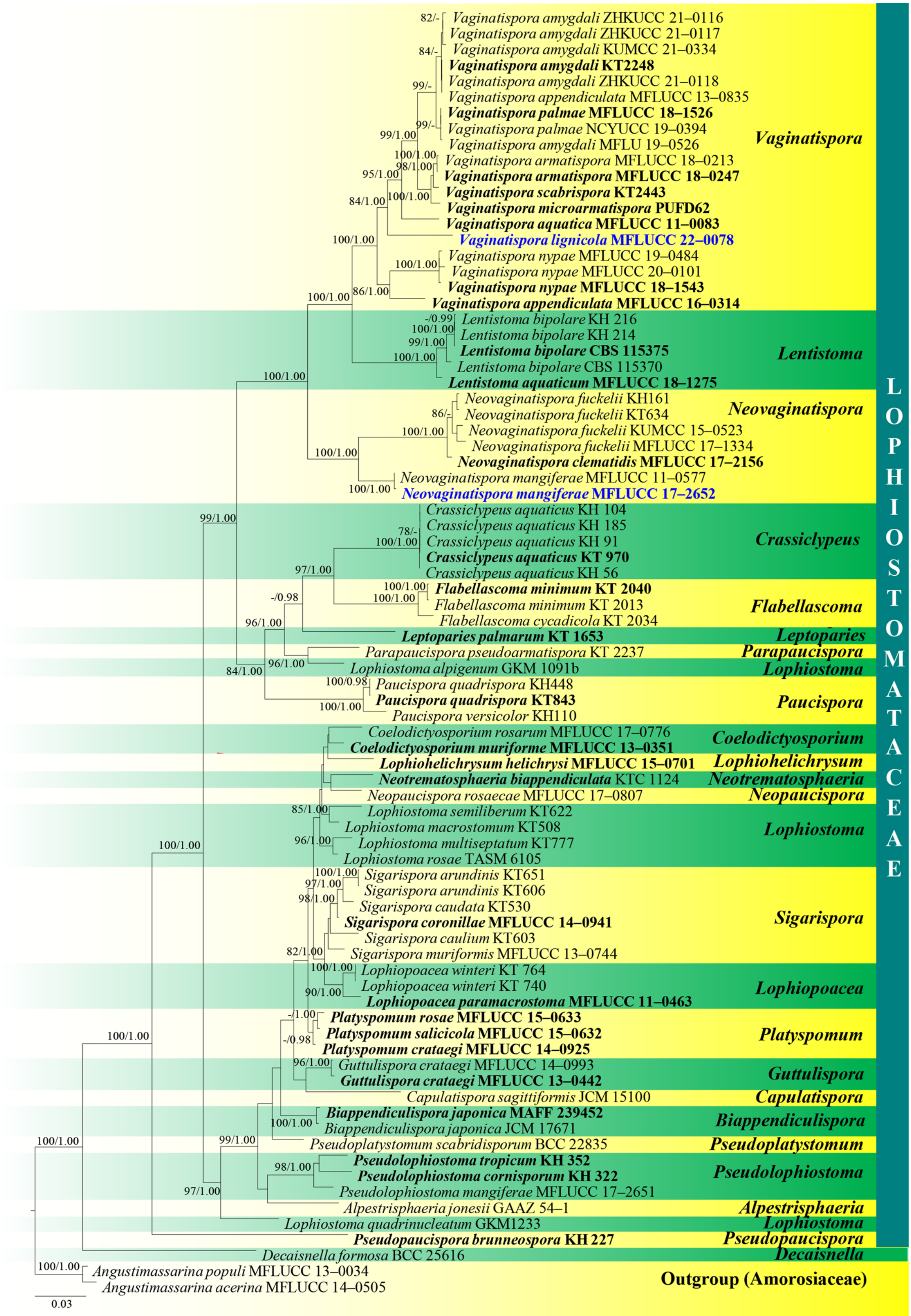
GenBank numbers: MG931027(LSU), MG931030 (SSU), MG931033 (ITS).

Notes: The isolate MFLUCC 17–2652 has formerly identified as *Neovaginatispora fuckelii* by Tennakoon et al. (2018) but in our phylogenetic analysis, it clustered with *Neovaginatispora* sp. MFLUCC 11–0577, and forms a separate subclade with *N. fuckelii* and *N. clematidis* with 100% MP, 1.00 BYPP support (Fig. 28). The pairwise nucleotide comparison of LSU and ITS of *N. mangiferae* MFLUCC 17–2652 show 2 bp (0/24%, 838 bp) and 1 bp (0.23%, 442 bp) differences with *Neovaginatispora* sp. MFLUCC 11–0577, respectively, with no differences on SSU sequence data. For this reason, we named the unidentified *Neovaginatispora* species (strain MFLUCC 11–0577) as another strain of *N. mangiferae*. In pairwise nucleotide comparisons of *Neovaginatispora mangiferae* MFLUCC 17–2652 with *N. fuckelii* MFLUCC 17**–**1334, there is a nucleotide difference of 6.94% (30/432 bp) in ITS, and 2.71% (22/813 bp) in LSU genes. A pairwise nucleotide comparisons of LSU, SSU, and ITS sequence data of *N. mangiferae* MFLUCC 17–2652 and *N. clematidis* reveals 22 bp (2.72%, 810 bp), 6 bp (0.64%, 938 bp), and 27 bp (7.03%, 384 bp) differences, respectively. *Neovaginatispora mangiferae* differs from *N. fuckelii* KT 634 by having larger ascomata (430–500 × 320–350 µm *vs* 150–180 × 200–250 µm) and thicker peridium (25–40 µm *vs* 15–25 µm), and periphyses in ostiole. The asci and ascospores are similar in size but ascospores of *N. mangiferae* is fusiform with acute ends but *N. fuckelii* has a fusiform ascospores with obtuse ends (Thambugala et al. 2015; Tennakoon et al. 2018; Bao et al. 2019). *Neovaginatispora mangiferae* has larger ascomata (430–500 × 320–350 µm *vs* 145–250 × 108–160 µm), shorter asci (60–80 × 7–9 µm *vs*. 53–105 × 9–12 µm), and smaller ascospores (13–17 × 3.0–5.5 µm *vs*. 16–19 × 5–7 µm) compared to *N. clematidis* (Phukhamsakda et al. 2020).

Vaginatispora K.D. Hyde, ***amended***

Saprobic on submerged wood, intertidal wood, dead twigs, endocarp or fallen fruit pericarp. **Sexual morph:** *Ascomata* solitary or scattered, immersed to erumpent, uniloculate, subglobose, glabrous, dark brown to black. *Ostiolar neck* slit-like, elongate, laterally compressed, composed of globose to elongate, brown to black cells, with a pore-like opening and hyaline periphyses. *Peridium* unequal in thickness, two-layered, outer layer comprising somewhat flattened cells, fusing and indistinguishable from the host tissues, inner layer comprising lightly pigmented to hyaline cells. *Pseudoparaphyses* numerous, cellular, hypha-like, hyaline, septate, anastomosing above the asci. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical to clavate, with a short or long pedicel, apically round with an ocular chamber. *Ascospores* uni- to bi-seriate, narrowly ellipsoidal or fusiform, straight to slightly curved, hyaline when immature, becoming yellow when mature, 1-septate, occasionally producing pseudosepta, septum mostly median, upper cell slightly broader than lower cell, smooth, thin-walled, with or without bipolar appendages or entire sheath. **Asexual morph**: Hyphomycetous. *Hyphae* septate, hyaline to lightly pigmented, mostly smooth, thick-walled, moniliform. *Chlamydospores* numerous, mostly in chains, globose to subglobose, smooth, initially hyaline then lightly pigmented at maturity, arising from the mycelium, formed intercalarily or terminally.

Type species: ***Vaginatispora aquatica*** K.D. Hyde


82/- Vaginatispora amygdali ZHKUCC 21–0116
Vaginatispora amygdali ZHKUCC 21–0117
84/- Vaginatispora amygdali KUMCC 21–0334
Vaginatispora amygdali KT2248
99/- Vaginatispora amygdali ZHKUCC 21–0118
Vaginatispora appendiculata MFLUCC 13–0835
Vaginatispora palmae MFLUCC 18–1526
99/1.00 99/- Vaginatispora palmae NCYUCC 19–0394
Vaginatispora amygdali MFLU 19–0526
100/1.00 Vaginatispora armatispora MFLUCC 18–0213
95/1.00 98/1.00 Vaginatispora armatispora MFLUCC 18–0247
100/1.00 Vaginatispora scabrispora KT2443
84/1.00 Vaginatispora microarmatispora PUFD62
Vaginatispora aquatica MFLUCC 11–0083
100/1.00 Vaginatispora lignicola MFLUCC 22–0078
100/1.00 Vaginatispora nypae MFLUCC 19–0484
Vaginatispora nypae MFLUCC 20–0101
86/1.00 Vaginatispora nypae MFLUCC 18–1543
100/1.00 Vaginatispora appendiculata MFLUCC 16–0314
Vaginatispora
-/0.99 Lentistoma bipolare KH 216
100/1.00 Lentistoma bipolare KH 214
99/1.00 Lentistoma bipolare CBS 115375
100/1.00 Lentistoma bipolare CBS 115370
100/1.00 Lentistoma aquaticum MFLUCC 18–1275
Lentistoma
Neovaginatispora fuckelii KH161
86/- Neovaginatispora fuckelii KT634
100/1.00 Neovaginatispora fuckelii KUMCC 15–0523
Neovaginatispora fuckelii MFLUCC 17–1334
100/1.00 Neovaginatispora clematidis MFLUCC 17–2156
Neovaginatispora mangiferae MFLUCC 11–0577
100/1.00 Neovaginatispora mangiferae MFLUCC 17–2652
Neovaginatispora
99/1.00 Crassiclypeus aquaticus KH 104
Crassiclypeus aquaticus KH 185
78/- 100/1.00 Crassiclypeus aquaticus KH 91
Crassiclypeus aquaticus KT 970
97/1.00 Crassiclypeus aquaticus KH 56
Crassiclypeus
100/1.00 Flabellascoma minimum KT 2040
-/0.98 100/1.00 Flabellascoma minimum KT 2013
Flabellascoma cycadicola KT 2034
Flabellascoma
96/1.00 Leptoparies palmarum KT 1653
Leptoparies
Parapaucispora pseudoarmatispora KT 2237
Parapaucispora
84/1.00 96/1.00 Lophiostoma alpigenum GKM 1091b
Lophiostoma
100/0.98 Paucispora quadrispora KH448
Paucispora quadrispora KT843
100/1.00 Paucispora versicolor KH110
Paucispora
Coelodictyosporium rosarum MFLUCC 17–0776
Coelodictyosporium muriforme MFLUCC 13–0351
Coelodictyosporium
Lophiohelichrysum helichrysi MFLUCC 15–0701
Lophiohelichrysum
Neotrematosphaeria biappendiculata KTC 1124
Neotrematosphaeria
Neopaucispora rosaecae MFLUCC 17–0807
Neopaucispora
85/1.00 Lophiostoma semiliberum KT622
Lophiostoma macrostomum KT508
100/1.00 96/1.00 Lophiostoma multiseptatum KT777
Lophiostoma rosae TASM 6105
Lophiostoma
100/1.00 Sigarispora arundinis KT651
97/1.00 Sigarispora arundinis KT606
98/1.00 Sigarispora caudata KT530
Sigarispora coronillae MFLUCC 14–0941
Sigarispora caulium KT603
82/1.00 Sigarispora muriformis MFLUCC 13–0744
Sigarispora
100/1.00 Lophiopoacea winteri KT 764
Lophiopoacea winteri KT 740
90/1.00 Lophiopoacea paramacrostoma MFLUCC 11–0463
Lophiopoacea
-/1.00 Platyspomum rosae MFLUCC 15–0633
100/1.00 -/0.98 Platyspomum salicicola MFLUCC 15–0632
Platyspomum crataegi MFLUCC 14–0925
Platyspomum
96/1.00 Guttulispora crataegi MFLUCC 14–0993
Guttulispora crataegi MFLUCC 13–0442
Guttulispora
Capulatispora sagittiformis JCM 15100
Capulatispora
Biappendiculispora japonica MAFF 239452
100/1.00 Biappendiculispora japonica JCM 17671
Biappendiculispora
100/1.00 99/1.00 Pseudoplatystomum scabridisporum BCC 22835
Pseudoplatystomum
Pseudolophiostoma tropicum KH 352
98/1.00 Pseudolophiostoma cornisporum KH 322
97/1.00 Pseudolophiostoma mangiferae MFLUCC 17–2651
Pseudolophiostoma
Alpestrisphaeria jonesii GAAZ 54–1
Alpestrisphaeria
Lophiostoma quadrinucleatum GKM1233
Lophiostoma
Pseudopaucispora brunneospora KH 227
Pseudopaucispora
Decaisnella formosa BCC 25616
Decaisnella
100/1.00 Angustimassarina populi MFLUCC 13–0034
Angustimassarina acerina MFLUCC 14–0505
Outgroup (Amorosiaceae)
0.03
LOPHIOSTOMATACEAE

◂ **Fig. 28** Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS, *tef1*, and *rpb2* sequence data representing Lophiostomataceae (Pleosporales). Eighty-one strains are included in the combined analyses which comprised 3726 characters (741 characters for LSU, 973 characters for SSU, 526 characters for ITS, 1001 characters for *tef1*, and 1011 characters for *rpb2*) after alignment. *Angustimassarina acerina* (MFLUCC 14–0505) and *Angustimassarina populi* (MFLUCC 13–0034) in Amorosiaceae (Pleosporales) were used as the outgroup taxa. Bootstrap support values for ML ≥ 75% are given above the nodes (left side) and BYPP ≥ 0.95 are given above the nodes (right side). Ex-type strains are in **bold** and newly generated sequences are in blue

Notes: Hyde (1995) introduced *Vaginatispora* to accommodate *Vaginatispora aquatica* K.D. Hyde (= *Lophiostoma vaginatispora* Huang Zhang & K.D. Hyde), which was previously placed in Massarinaceae. Eight species are included in this genus and members are characterized by depressed globose ascomata, immersed beneath a blackened neck, with a slot-like ostiole, numerous filamentous pseudoparaphyses, cylindrical to clavate asci and narrowly ellipsoidal, hyaline, 1-septate ascospores with a mucilaginous collar around its equator, having large guttules in each cell, and a spreading papilionaceous sheath (Thambugala et al. 2015; Hashimoto et al. 2018). We followed the treatment of Dong et al. (2020) and Hongsanan et al. (2020a, b) in this genus.

Vaginatispora lignicola M.S. Calabon, E.B.G. Jones & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF559844; Facesoffungi number: FoF12721; Fig. 29

Etymology: Referring to this taxon dwelling on wood

Holotype: MFLU 22**–**0116

Saprobic on decaying wood submerged in freshwater habitats. **Sexual morph**: *Ascomata* 200–360 × 220–415 µm diam. ($\overline{x}$ = 269 × 294 µm; *n* = 10), scattered to gregarious, immersed to semi-immersed, erumpent at maturity, coriaceous, black, subglobose, ostiolate. *Ostiole* slot-like, central, elongated, pore-like opening, plugged by hyaline, filamentous hyphae, periphysate. *Peridium* 40–65 µm wide, circular, symmetric, outermost layer heavily pigmented, comprising a blackish to dark brown amorphous layer, flattened and loosely packed cells of *textura angularis*, inner layer composed of hyaline cell layers, flattened, thick-walled cells of *textura angularis*. *Hamathecium* 1.3–2.5 µm wide ($\overline{x}$ = 1.9 µm, *n* = 30) comprising numerous, filamentous, branched, septate, pseudoparaphyses. *Asci* 125–145 × 15–30 µm ($\overline{x}$ = 137 × 23 µm, *n* = 20), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, short-pedicellate, apex rounded with a minute ocular chamber. *Ascospores* 50–72 × 14–17 µm ($\overline{x}$ = 62 × 16 µm, *n* = 30), uniseriate to bi-seriate, overlapping, straight or slightly-curved, initially hyaline, becoming yellowish at maturity, fusiform, mostly with narrow acute ends, 1–3-septate, strongly constricted at the septa, smooth-walled, with numerous small guttules and 2 distinct large guttules. **Asexual morph**: *Hyphae* 2–5 µm wide, septate, hyaline to lightly pigmented, mostly smooth, thick-walled, moniliform. *Chlamydospores* 6–19 × 4.5–16 ($\overline{x}$ = 10.9 × 8.4, *n* = 50), numerous, mostly in short chains, globose to subglobose, smooth, initially hyaline then becoming light brown at maturity, arising from the mycelium, formed intercalarily or terminally.

Culture characteristics: Conidia germinating on malt extract agar (MEA) within 24 h. Germ tubes produced from the basal and apical cell of conidia. Colonies growing on MEA, reaching 20–25 mm in 2 weeks at 25 °C. Mycelia superficial, circular, with entire margin, flat, smooth, from above greyish brown to grey, from below dark grey to black.

Material examined: Thailand, Tak Province, Tha Sing Yang, Ban Mae Ja Wang on decaying wood submerged in a freshwater river, 17 October 2019, N. Padaruth, CC43 (MFLU 22–0116, **holotype**), ex-type living culture, MFLUCC 22–0078.

GenBank numbers: MW287233 (LSU), MW287229(SSU), MW260329(ITS), MW512605(*tef1*), OP251197(*rpb2*)

Notes: Three species of *Vaginatispora* are recorded in freshwater habitats: *V. aquatica* (Hyde 1995; Tsui et al. 2000; Zhang et al. 2014a, b), *V. armatispora* (Hu et al. 2010; Bao et al. 2019; Hyde et al. 2019), and *V. nypae* (Hyde et al. 2020a, b, c; Boonmee et al. 2021). In this series, we introduce another novel species of *Vaginatispora*, *V. lignicola*, from a freshwater habitat in Thailand. *Vaginatispora lignicola* (MFLUCC 22–0078) confirms with the generic ascomatal morphology (erumpent, uniloculate, glabrous, slot-like ostiole, with numerous hyaline periphyses) but differs from the known members of the genus in having ascospores without a wide papilionaceous sheath or distinct hyaline appendages at both ends. Based on the phylogenetic analysis of combined LSU, SSU, ITS, *tef1*, and *rpb2* sequence data, *V. lignicola* is basal to *V. aquatica* with high bootstrap support (97 ML and 1.00 BYPP) (Fig. 28). The former differs from *V. aquatica* in the measurement (50–72 × 14–17 µm *vs* 36–48 × 11–16) and color of the ascospores (initially hyaline then becoming yellowish at maturity *vs* hyaline), and the absence of a sheath when stained in Indian ink wherein the latter have wide papilionaceous sheaths (Hyde 1995). The novel taxon differs from the freshwater strains of *V. armatispora* and *V. nypae* by having larger ascospores (50–72 × 14–17 µm *vs* 22–30 × 5.5–8 µm *vs* 26–29 × 6–7 µm) without a mucilaginous sheath and hyaline appendages at both ends (Bao et al. 2019; Hyde et al. 2019; Boonmee et al. 2021). Multi-locus phylogenetic analyses showed that *V. lignicola* is a distinct taxon in *Vaginatispora* with 49 bp (9.32%, 526 bp) and 14 bp (1.74%, 804) nucleotide differences in the ITS and LSU sequence data of the type

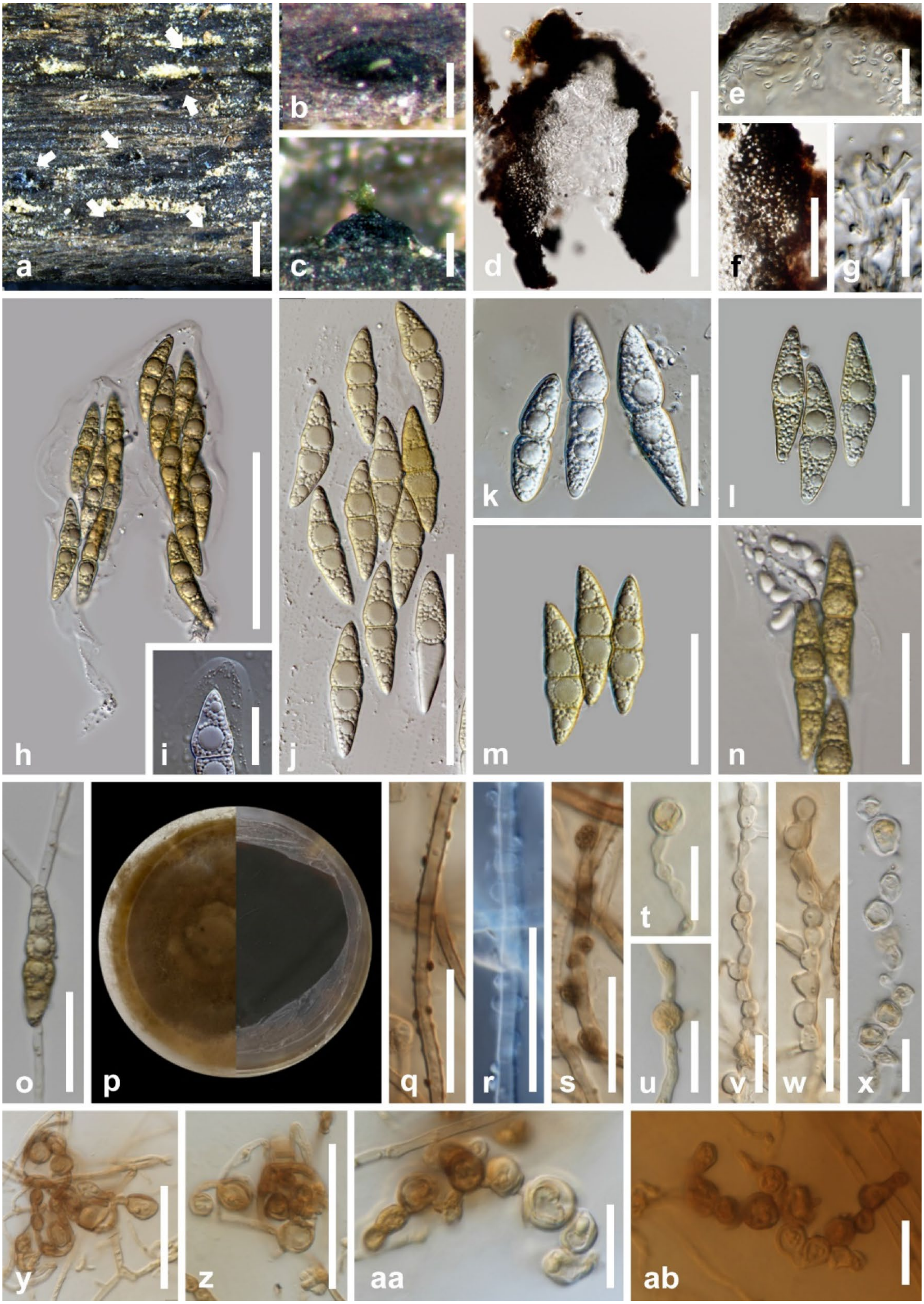


Fig. 29 ***Vaginatispora lignicola*** (MFLU 22–0116, holotype). **a** Host twig. **b**, **c** Appearance of erumpent ascomata in host substrate. **d** Vertical section of ascoma. **e** Slot-like ostiole with numerous periphysis. **f** Peridium. **g** Pseudoparaphyses. **h** Bitunicate asci. **i** Ocular chamber. **j–n** Ascospores in different stages of maturity. **o** Germinated ascospore. **p** Culture on MEA. **q–s** Hyphae. (**t**) Terminally and (**u**) intercalary swollen cells. **v–x** Moniliform hyphae with constricted septa. **y–ab** Multicellular bodies. Scale bars: **a** = 2 mm, **b–d** = 200 µm, **e, g** = 20 µm, **f** = 50 µm, **h, j** = 100 µm, **k–o**, **y**, **z** = 50 µm, **q–x**, **aa** = 20 µm

species, *V. aquatica*, respectively. The present work is the first report also of the morphological characteristics of the asexual morph of *Vaginatispora*. A simplified key to species of *Vaginatispora* is provided herein.

Key to species of *Vaginatispora*

1 Ascospores yellow at maturity, without sheath or appendages..*V. lignicola*

1 Ascospores hyaline, with either sheath or appendages... 2

2 Ascospores with wide papilionaceous sheath, lacking appendages..*V. aquatica*

2 Ascospores with or without a mucilaginous sheath, with distinct hyaline appendages..................................3

3 Ascospores < 25 µm long.................*V. scabrispora*

3 Ascospores > 25 µm long................................4

4 Ascomata lack slit-like ostiole.................*V. nypae*

4 Ascomata with slit-like opening.......................5

5 Appendages 2–8 µm long...........*V. microarmatispora*

5 Appendages 6–8 µm long................................6

6 Ascomata > 450 µm wide, peridium up to > 40 µm thick...*V. amygdali*

6 Ascomata < 450 µm wide, peridium up to < 40 µm thick..7

7 Ascospores up to < 40 µm long...........*V. armatispora*

7 Ascospores up to > 40 µm long..........................8

8 Ascospores 40–45 × 10–15 µm.......................... ....*V. appendiculata*

8 Ascospores 23–45 × 6–9 µm....................*V. palmae*

Phaeoseptaceae S. Boonmee, Thambugala & K.D. Hyde, Mycosphere 9(2): 323 (2018).

Notes: Phaeoseptaceae was introduced by Hyde et al. (2018) to accommodate *Phaeoseptum*, *Lignosphaeria* and *Neolophiostoma*. The LSU-SSU-*rpb2*-*tef1* multigene phylogeny in Hyde et al. (2018) showed a well-supported Phaeoseptaceae clade sister to Halotthiaceae. The species in Phaeoseptaceae share immersed or erumpent ascomata, dark brown to black outer peridium, cylindrical, branched, septate pseudoparaphyses, 8-spored, bitunicate, cylindrical-clavate, long pedicellate asci, and brown, muriform ascospores. Based on morphology and phylogeny, Thambugala et al. (2015) treated *Lignosphaeria* in Dothideomycetes, genera incertae sedis, and Liu et al. (2019a, b, c, d) treated *Neolophiostoma* in Halotthiaceae. In a recent revision of Dothideomycetes, Hongsanan et al. (2020b) accepted only *Phaeoseptum* and *Pleopunctum* in Phaeoseptaceae which was followed by Wijayawardena et al. (2020, 2022).

Phaeoseptum Ying Zhang, J. Fourn. & K.D. Hyde, in Zhang, Fournier, Phookamsak, Bahkali & Hyde, Mycologia 105(3): 606 (2013)

Notes: Zhang et al. (2013) introduced *Phaeoseptum*, which differs from *Mauritiana* in having dictyosporous ascospores. There are six *Phaeoseptum* species: *P. aquaticum* (on driftwood of *Salix* sp., France), *P. carolshearerianum* (on decaying wood of *Avicennia marina*, India), *P. hydei* (on dead twigs of *Delonix regia*, Thailand), *P. mali* (on dead stems of *Malus halliana*, China), *P. manglicola* (on decaying wood of *Avicennia marina*, India) and *P. terricola* (on dead wood, Thailand).

Phaeoseptum thailandicum Samarak. & K.D. Hyde, ***sp. nov***

Index Fungorum number: IF559754; Facesoffungi number: FoF11798; Fig. 30

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

Holotype: MFLU 19–2136

Saprobic on dead branches in terrestrial habitats. **Sexual morph:** *Ascomata* 270–350 µm high, 160–305 µm diam. ($\bar{x} = 309 \times 230.3$ µm, $n = 10$), scattered to gregarious, fully immersed under a small blackened pseudoclypeus, if appearing as black, elongated regions on host surface 540–915 µm ($\bar{x} = 640$ µm, $n = 8$) length; ascomata depressed spherical, laterally flattened. *Pseudoclypeus* composed of host cells with black deposits. *Peridium* 6–22 µm ($\bar{x} = 640$ µm, $n = 8$) wide, pseudoparenchymatous, of thin-walled cells, at apex comprising isodiametric angular cells that are more pigmented outwardly, at sides with flattened hyaline cells, at base of angular pigmented cells. *Hamathecium* comprising 1.4–2.5 µm ($\bar{x} = 1.9$ µm, $n = 20$), wide septate, cellular pseudoparaphyses, situated between and above the asci, embedded in a gelatinous matrix. *Asci* 100–155 × 20–28.5 µm ($\bar{x} = 129 \times 23.9$ µm, $n = 25$), 8-spored, rarely 32-spored, bitunicate, fissitunicate, cylindrical-clavate, with a distinct pedicel, apically rounded with a minute ocular chamber. Ascospores 25–35 × 8–11.8 µm ($\bar{x} = 30 \times 9.9$ µm, $n = 30$), uniseriate at base and overlapping 2–3-seriate at apex, pale to dark brown, broadly fusoid with broadly rounded ends, slightly curved, 11 (9–12-transversally septate, with a vertical septum in nearly all median cells, not constricted at the septa, the septa partly pale brown, having at maturity a thickened and heavily pigmented appearance, wall smooth, without sheath or appendages. **Asexual morph:** Not observed.

Material examined: Thailand, Nan, Pua District, on an unidentified dicotyledonous dead branch, 29 January 2019, MC Samarakoon (SAMC216), (MFLU 19-2136, **holotype**; HKAS 106993, **isotype**), Phrae, on an unidentified dicotyledonous dead branch, 24 January 2019, MC Samarakoon (SAMC203), (MFLU 19–2126; HKAS 106983, **paratypes**).

GenBank numbers: MFLU 19-2126—OM293748 (ITS), OM293743 (LSU), OM293754 (SSU), OM305061 (*tef1*), OM305067 (*tub2*)

MFLU 19-2136—OM293749 (ITS), OM293744 (LSU), OM305056 (*rpb2*), OM293755 (SSU), OM305062 (*tef1*), OM305068 (*tub2*)

Fig. 30 ***Phaeoseptum thailandicum*** (MFLU 19–2136, **holotype**) **a,b** Substarte, **c,d** Appearance of ascomata on the host, **e,f** Vertical section through ascoma, **g** Peridium, **h** Pseudoparaphyses, **i–l** Asci, **m–r** Ascospores. Scale bars: **a,b** = 1 cm, **c,d** = 1000 μm, **e,f** = 15 μm, **g-i** = 10 μm, **m-r** = 5 μm

HKAS 106993—OM293750 (ITS), OM293745 (LSU), OM305057 (*rpb2*), OM293756 (SSU), OM305063 (*tef1*), OM305069 (*tub2*)

Notes: Our two new collections of *Phaeoseptum thailandicum* share similar morphology of *Phaeoseptum* in having immersed ascomata under a small blackened pseudoclypeus, cylindrical-clavate asci with a distinct pedicel and broadly fusoid, brown ascospores with multi-transverse septa. Combined phylogeny shows that the novel taxon is sister to *P. mali* + *P. manglicola* clade with high statistical support (Fig. 31).

Pleopunctum N.G. Liu, K.D. Hyde & J.K. Liu, in Liu et al., Mycosphere 10(1): 767 (2019)

Notes: *Pleopunctum* was introduced to accommodate two hyphomycetous species based on phylogenetic analyses and divergence time which is the first asexual morph genus in Phaeoseptaceae (Liu et al. 2019a, b, c, d). There are five *Pleopunctum* species are accepted in Species Fungorum (2022a, b) with molecular data and all of them were found from China and Thailand in terrestrial habitate (Liu et al. 2019a, b, c, d; Phukhamsakda et al. 2020; Boonmee et al.2021).

Pleopunctum ellipsoideum N.G. Liu, K.D. Hyde & J.K. Liu, in Liu et al., Mycosphere 10(1): 767 (2019).

Index Fungorumnumber: IF556523; Facesoffungi number: FoF06114; Fig. 32

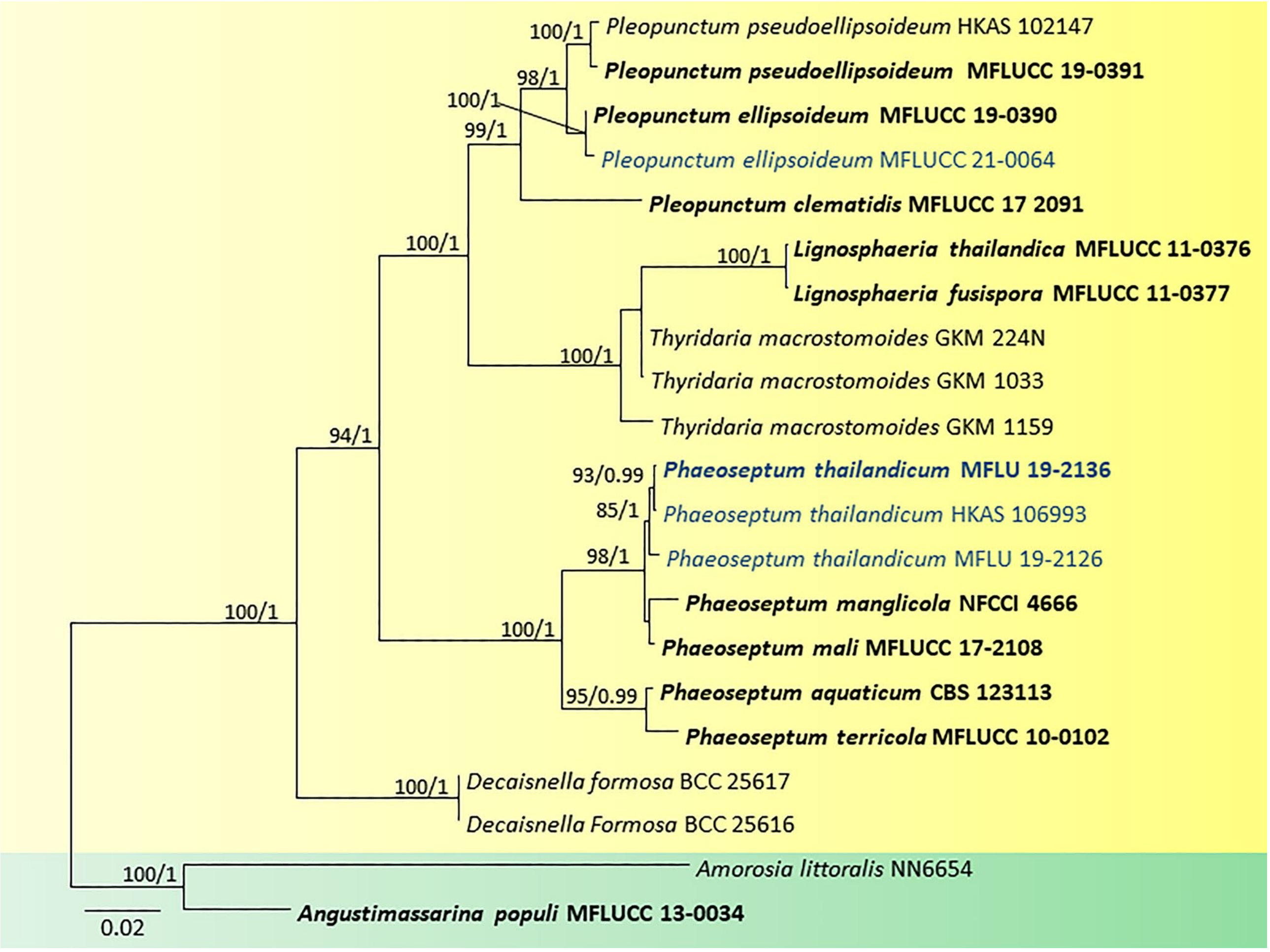


Fig. 31 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS and *tef1*sequence data of Phaeoseptaceae. Bootstrap support values for ML ≥ than 75% and BYPP ≥ 0.95 are given above the nodes. The ex-types are in **bold**; the new isolates are in blue. The tree is rooted with *Amorosia littoralis* (NN 6654) and *Angustimassarina populi* (MFLUCC 13–0034)

Saprobic on decaying wood. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate forming sporodochial conidiomata, superficial, black, scattered, velvety, glistening, orbicular. *Mycelium* immersed, composed of branched, septate, subhyaline to pale brown hyphae. *Conidiophores* and *conidiogenous cells* not observed. *Conidia* 33–45 × 16–20 µm ($\bar{x}$ = 38 × 18 µm, n = 35), acrogenous, solitary, oval to ellipsoidal, muriform, constricted at septa, yellowish brown to dark brown, broadly obtuse at apex, truncate at base. Basal cell 6.5–10.5 × 9.5–11.5 µm ($\bar{x}$ = 9–10.5 µm, n = 35), hyaline, elliptical to subglobose, smooth walled. **Sexual morph**: Not observed.

Culture characteristics: Conidium germinated on PDA within 12 h. Colonies on PDA reaching 20 mm in 4 weeks at 26 °C. Mycelia superficial, circular, entire, flat, rough, grey brown from above, dark brown from below.

Material examined: Thailand, Chiang Mai Province, Mae Taeng District, MRC, on bamboo culms, 15 July 2020, Y.R. Sun, M10 (MFLU 21–0091); living culture, MFLUCC 21–0064.

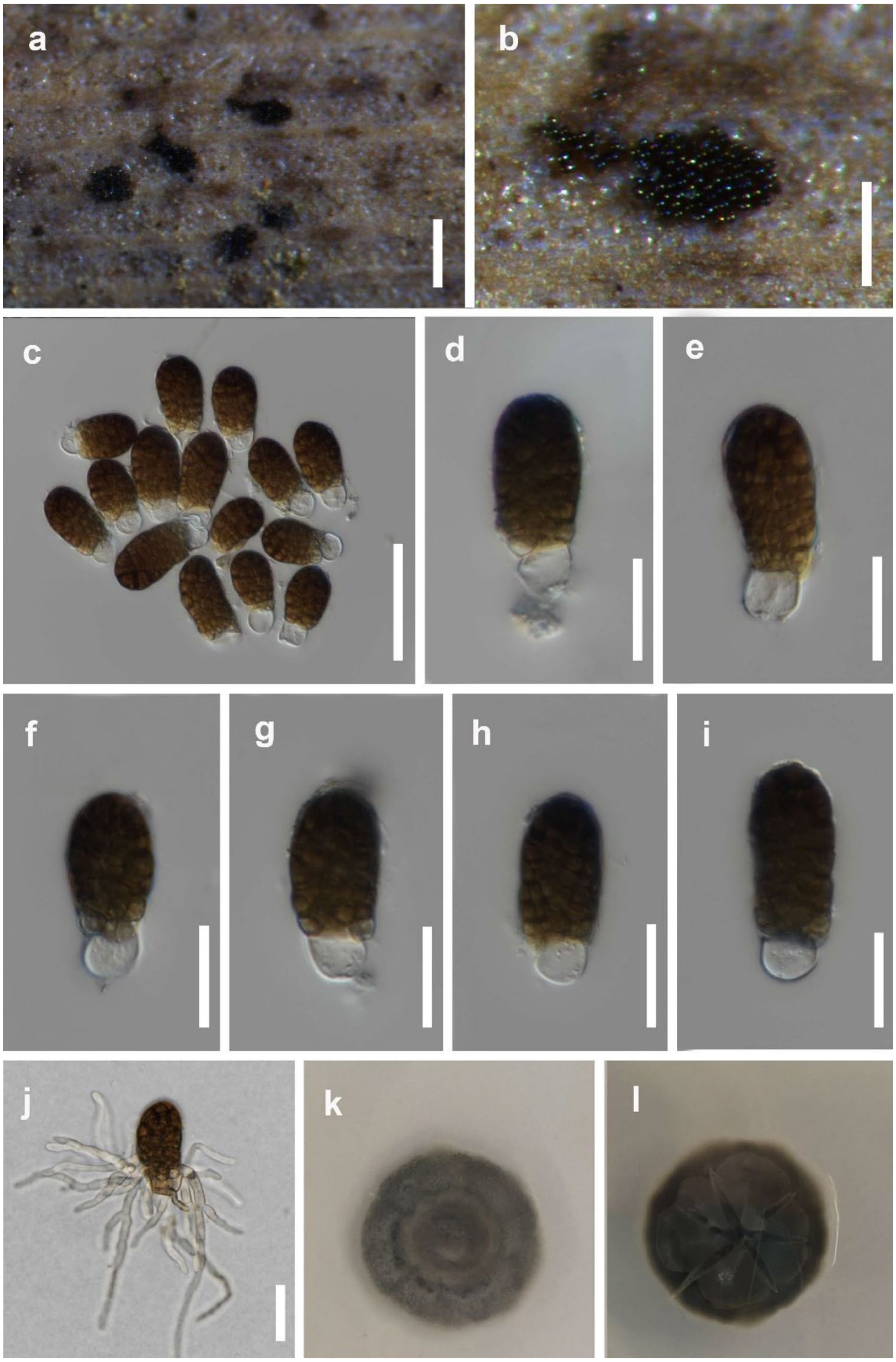
Hosts: decaying wood (Liu et al. 2019a, b, c, d) and bamboo (this study)

Distribution: China (Liu et al. 2019a, b, c, d) and Thailand (this study)

GenBank numbers: OM250079 (ITS), OM258687 (LSU)

Notes: *Pleopunctum ellipsoideum* was isolated from decaying wood in China by Liu et al. (2019a, b, c, d). The morphological characters of our collection are the same as in *P. ellipsoideum* (MFLUCC 19-0390). Phylogenetic analysis based on a combined LSU, ITS and *tef1* sequence data indicated that our isolate and *P. ellipsoideum* (MFLUCC 19–0390) clustered together with high support (ML 100% and 0.99 BYPP; Fig. 31). Based on both morphology and phylogeny, we identified our taxon as *P. ellipsoideum*. This is the first geographical and host report of *P. ellipsoideum* on bamboo in Thailand.

Fig. 32 ***Pleopunctum ellipsoideum*** (MFLU 21–0091, **new record**) **a**, **b** Colonies on natural substrates **c**–**i** Conidia with basal hyaline cells **j** Germinated conidium **k**, **l** Colonies on PDA media. Scale bars: a = 500 µm, b = 200 µm, c = 50 µm, d–j = 20 µm



Phaeosphaeriaceae M.E. Barr, Mycologia 71(5): 948 (1979)

Phaeosphaeriaceae has been subjected to various taxonomic changes since its establishment by Barr (1987). The inception of multi-gene phylogenetic analyses coupled with morphology has greatly resolved many taxonomic inconsistencies along with the introduction of several novel taxa (Phookamsak et al. 2014, 2017; Li et al. 2016; Crous et al. 2018; Hyde et al. 2020a, b, c). However, confusion in the placement of many taxa in the family still remains uncertain and problematic (Hongsanan et al. 2020b). Phaeosphaeriaceae at present accommodates more than 80 genera, with the taxa mainly exhibiting an endophytic, pathogenic and saprobic or hyperparasitic lifestyles (Hongsanan et al. 2020b).

Nodulosphaeria Rabenh., Klotzschii Herb. Viv. Mycol., Edn Nov, Ser. Sec., Cent. 8: no. 725 (in sched.) (1858)

Nodulosphaeria, was introduced by Rabenhorst (1858) and typified by *N. hirta* and was accommodated in *Phaeosphaeriaceae* by Barr (1987). The genus comprises endophytic, saprobic and pathogenic taxa which occur on a variety of hosts (Mapook et al. 2020; Chaiwan et al. 2019; Pasouvang et al. 2021). *Nodulosphaeria* taxa are principally characterised by ascomata with brown setae at the ostiole and three-to multi-septate ascospores with a swollen cell and often with terminal appendages (Shoemaker 1984; Mapook et al. 2016; Chaiwan et al. 2019). Molecular data for several *Nodulosphaeria* species listed in MycoBank (http://www.mycobank.org/, 07/2022) and Index Fungorum (http://www.indexfungorum.org/Names/Names.asp, 07/2022) are unavailable. A reference specimen for the type species *N. hirta* was recently designated by Mapook et al. (2016), who also provided molecular data for the same.

Nodulosphaeria digitalis W.J. Li, Camporesi, Bhat & K.D. Hyde, in Li et al., Mycosphere 6(6): 683 (2015)

Index Fungorum number: IF551664; Faces of fungi number: FoF 01302; Fig. 33

=*Nodulosphaeria thalictri* D. Pem, Camporesi & K.D. Hyde, in Hyde et al., Fungal Diversity: https://doi.org/10.1007/s13225-019-00429-2, [56] (2019)

Saprobic on stem of *Solidago virgaurea*. **Sexual morph**: *Ascomata* 185–200 µm high, 200–225 µm diam. ($\bar{x}$ = 192.3 × 213.1 µm, *n* = 5), appearing as black dots on host surface, immersed, unilocular, perithecial, solitary, usually scattered, globose to subglobose, dark brown, ostiolate. *Ostioles* 45–55 µm wide ($\bar{x}$ = 52.2 µm, *n* = 5), centric, comprising internal dark brown setae. *Ascomatal wall* 14–23 µm at the sides and base, 4–5-layered; 25–35 µm near the apex, 5–7-layered; outer layers made up of thick-walled, dark brown cells of *textura angularis*, innermost layer comprising thin-walled, pale brown to hyaline cells of *textura angularis* or flattened cells. *Pseudoparaphyses* 1–3 µm wide, numerous, filiform, hyaline, branched. *Asci* 55–90 × 8–12 µm ($\bar{x}$ = 74.1 × 9.2 µm, *n* = 40), 8-spored, bitunicate, cylindric-clavate, slightly curved, sessile to short-pedicellate, apically rounded with a minute ocular chamber. *Ascospores* (17–)20–27 × 3–4 µm ($\bar{x}$ = 22.6 × 3.7 µm, *n* = 45), overlapping 1–2-seriate, hyaline when immature, becoming yellowish-brown at maturity, long fusiform, ellipsoidal to subcylindrical, straight or slightly curved, with 4–5 transverse septa, second cell from the apex slightly swollen, constricted at second septum from the apex, thick- and smooth-walled, with rounded ends, with hyaline appendages (1–2.5 µm long, 2.5–4 µm wide) at both ends. **Asexual morph**: Illustrated in Li et al. (2015).

Material examined: Italy, Forlì Cesena, Valico del Tramazzo, on dead aerial stem of *Solidago virgaurea* L. (Asteraceae), 19 June 2021, Erio Camporesi, IT4714 (MFLU 22-0278)

Hosts: *Campanula trachelium* (Campanulaceae, Chaiwan et al. 2019), *Dactylis* sp. (Poaceae, Li et al. 2015), *Solidago virgaurea* (Asteraceae, this study), *Thalictrum* sp. (Ranunculaceae, Hyde et al. 2019)

Distribution: Italy (Li et al. 2015; Chaiwan et al. 2019; Hyde et al. 2019; this study)

GenBank numbers: ON873995 (LSU); ON873997(ITS); ON885742 (*tef1*)

Notes: The strain MFLU 22-0278 clustered with the strains *Nodulosphaeria digitalis* MFLUCC 15-2716 (type strain) and MFLUCC 17-2418, and *Nodulosphaeria thalictri* MFLUCC 18-1138 with a good statistical support (99% ML, 0.98 BYPP) in the SSU-LSU-ITS-*tef1* phylogenetic tree. Pairwise comparison among the two strains of *N. digitalis* MFLUCC 15-2716 and MFLUCC 17-2418, and *N. thalictri* MFLUCC 18-1138 is as follows: one base pair (bp) difference out of 1000 bp (0.1%) in SSU between *N. thalictri* MFLUCC 18-1138 and *N. digitalis* MFLUCC 17-2418; no bp difference among the three strains out of 844 bp in LSU and 504 bp in ITS respectively; two bp differences out of 891 bp (0.2%) in *tef1* between *N. thalictri* MFLUCC 18-1138 and *N. digitalis* MFLUCC 17-2418. The pairwise identity therefore reveals insignificant differences among the three strains (*N. digitalis* MFLUCC 15-2716 and MFLUCC 17-2418, and *N. thalictri* MFLUCC 18-1138) according to Jeewon and Hyde (2016). Therefore, *N. thalictri* MFLUCC 18-1138 is another strain of *N. digitalis*.

Morphologically, there are some differences between ‘*N. thalictri*’ and *N. digitalis* in terms of the position of ascomata (immersed or semi-immersed in ‘*N. thalictri*’ while superficial to semi-immersed in *N. digitalis*), ostiole (comprising internal brown to dark brown cells of *textura globulosa* in ‘*N. thalictri*’ while no such observation was made for *N. digitalis*) (Chaiwan et al. 2019, Hyde et al. 2019). Furthermore, there are some differences in size of the morphological structures between ‘*N. thalictri*’ and *N. digitalis* (Table 2) (Chaiwan et al. 2019; Hyde et al. 2019). However, all these differences may be the result of phenotypic plasticity which has arisen from the need to adapt to environmental variations and/or different hosts (Hyde et al. 2019). The differences in the morphological characters are not being reflected by any significant phylogenetic difference herein. Such occurrence has also been observed for other taxa (Mapook et al. 2016; Hyde et al. 2019; Pasouvang et al. 2021). Based on the above morpho-phylogenetic approach, ‘*N. thalictri*’ is considered as *N. digitalis*.

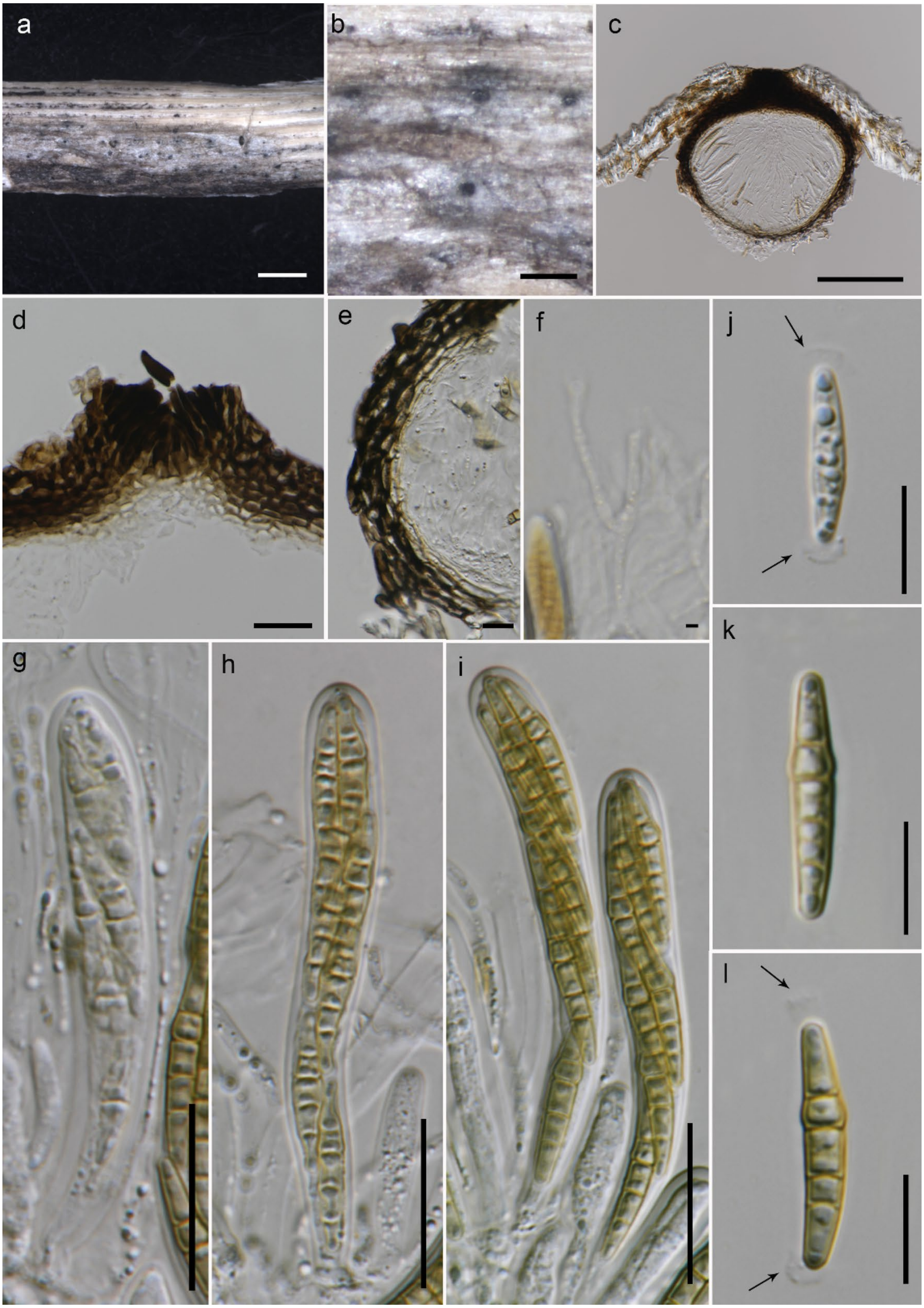


Fig. 33 ***Nodulosphaeria digitalis*** **(MFLU 22-0278)**. **a** Ascomata on dead aerial stem of *Solidago virgaurea*. **b** Close-up of ascomata on host. **c** Vertical section through an ascoma. **d** Close-up of an ostiole. **e** Vertical section of ascomatal wall. **f** Pseudoparaphyses. **g**–**i** Immature and mature asci. **j**–**l** Immature and mature ascospores (**j**, **l** arrows indicate appendages). Scale bars: **a–c** = 100 µm, **d, g–i** = 20 µm, **e, j–l** = 10 µm, **f** = 3 µm

Table 2 Morphological comparison among strains of *Nodulosphaeria digitalis* with sexual morph described

Strain	Host	Ascomata (µm)	Ostioles	Asci (µm)	Ascospores	Reference
N. digitalis MFLUCC 17–2418	*Campanula trachelium*	141.9 × 154	52.5 µm diam No setae	83 × 9	25 × 5 µm; 4-septate	Chaiwan et al. (2019)
N. digitalis MFLUCC 18–1138	*Thalictrum* sp.	263.7 × 217.9	71.2 µm diam No setae	84.1 × 10.1	32.3 × 4.5 µm; 7–8-septate	Hyde et al. (2019)
N. digitalis MFLU xx	*Solidago virgaurea*	192.3 × 213.1	52.2 µm diam Setae present	74.1 × 9.2	22.6 × 3.7 µm; 4–5-septate	This study

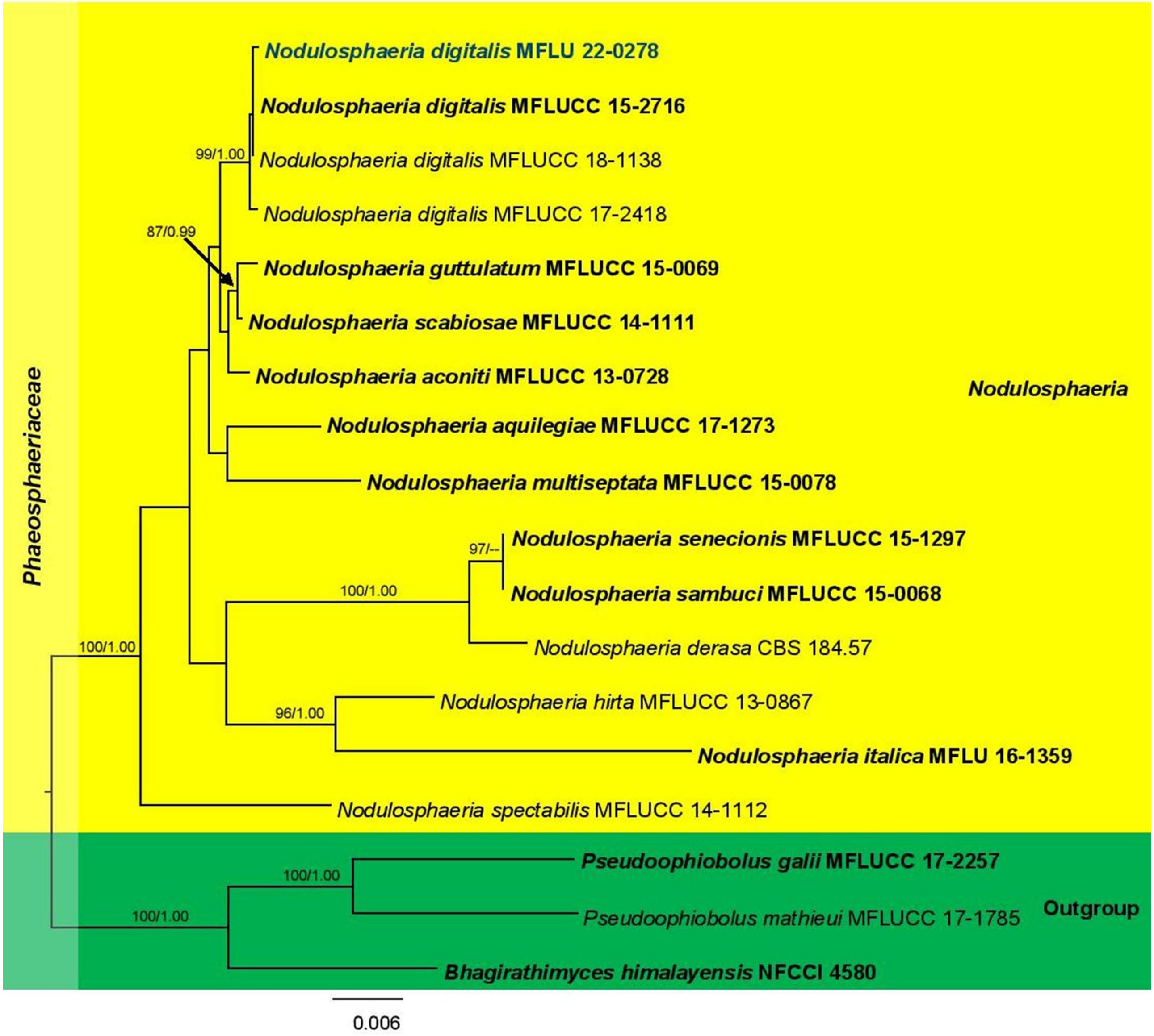


Fig. 34 Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, ITS and *tef* sequence data of selected taxa in Phaeosphaeriaceae. Bootstrap support values for maximum likelihood ≥ 65% and Bayesian posterior probabilities ≥ 0.95 are indicated above or below the branches. Type strains are in **bold**; the new isolate is in blue. The tree is rooted with *Bhagirathimyces himalayensis* NFCCI 4580, *Pseudoophiobolus galii* MFLUCC 17–2257 and *Pseudoophiobolus mathieui* MFLUCC 17–1785

The strain MFLU 22-0278 in this study clusters with the three strains of *N. digitalis* with 99% bootstrap support and 0.98 BYPP. There is no significant difference in the pairwise comparison among strains MFLU 22-0278 and MFLUCC 15-2716, MFLUCC 17-2418 as well as MFLUCC 18-1138 with regards to the LSU, ITS and *tef1* sequence data. Our strain MFLU 22-0278 resembles *N. digitalis* MFLUCC 17-2418 and MFLUCC 18-1138 (*N. digitalis* MFLUCC 15-2716 was described in its asexual morph) in having ascomatal wall made up of cells of *textura angularis*, sessile or short-pedicellate asci and septate ascospores with a swollen cell and terminal appendages (Chaiwan et al. 2019; Hyde et al. 2019). Our collection differs from *N. digitalis* MFLUCC 17-2418 and MFLUCC 18-1138 mainly in having ostioles with internal brown setae (Fig. 34). The morphological characters also vary in size (Table 2). This can be accounted for by environmental and host variations as stated above. These morpho-phylogenetic analyses therefore support MFLU 22-0278 as another strain of *N. digitalis*. The latter is herein reported as a new record from *Solidago virgaurea* in Italy.

Pleosporaceae Nitschke, Verh. naturh. Ver. preuss. Rheinl. 26: 74 (1869)

This family consists of endophytes, pathogens and saprobes and has a worldwide distribution (Hongsanan et al. 2020b). Twenty-three taxa are accepted in this family (Wijayawardene et al. 2022)

Bipolaris Shoemaker, Can. J. Bot. 33:882(1959)

Species of this genus are pathogens, saprobes and endophytes on a wide range of hosts with a worldwide distribution (Jayawardena et al. 2019a). Bhunjun et al. (2020), provided polyphasic approaches to delineate species in *Bipolaris*. There are 140 records in Index Fungorum (2022a, b) for this genus, however less than 50 species have molecular data.

Bipolaris luttrellii Alcorn, Mycotaxon 39: 378 (1990)

Index Fungorum number: *IF127658; Facesoffungi number: FoF01302; Fig. 35*

Saprobic on Poaceae sp. **Sexual morph**: Not observed. **Asexual morph**: *Conidiophores* up to 200 μm long and 7–10 μm thick, arising singly or in groups of a few conidia, simple, septate, straight or flexuous, sometimes geniculate at the upper part, smooth, pale to mid-brown. *Conidiogenous nodes* dark brown, distinct. *Conidia* (75–)90–125 × 17–26(–)28) μm ($\bar{x} = 107 \times 21$ μm, $n = 30$), straight or curved, broadly fusiform or obclavate fusiform, widest near centre, tapering towards rounded ends, pale to mid brown, 5–9-distoseptate, smooth-walled. *Hilum* slightly protuberant, single germ tubes arising from each end.

Material examined: China, Guizhou Province, Guizhou Academy of Agricultural Sciences, dead leaves of Poaceae sp., 20 July 2015, Kasun M. Thambugala CN020 (MFLU 16-2836), living culture MFLUCC 16–0281, GZCC 15–0045.

Host: *Dactyloctenium aegyptium*, on dead leaves of unidentified Poaceae host (Alcorn 1990; This study)

Distribution: Australia, China (Alcorn 1990; This study)

GenBank numbers: OQ154965 (ITS)

Notes: *Bipolaris luttrelli* is only known from the type specimen before this record. This species is morphologically similar to *B. setarieae* (Manamgoda et al. 2014). *Bipolaris luttrelli* can be distinguished from its sister taxa by having fewer conidiogenous loci on the conidiophores and its darker conidia with pale end cells (Manamgoda et al. 2014). In our phylogenetic analyses (Fig. 36), our strain clustered with the ex-type strain of *B. luttrelli* with a higher bootsrap support. There are 10 base pair differences between our strain and the ex-type strain in ITS. Both of these strains lack *tef1* gene region. Therefore, we identified our strain as *B. luttrelli* and provides the first report from China.

Curvularia Boedijn, Bull. Jard. bot. Buitenz, 3 Sér. 13(1): 123 (1933)

This is a species-rich genus which comprised of numerous pathogenic, saprobic and epiphytic fungi (Manamgoda et al. 2012a, b, 2015; Jayawardena et al. 2019a). Phytopathogenic species have been recorded mostly on poaceous hosts as well as non-poaceous hosts. Several *Curvularia* spp. have also been reported as opportunistic human pathogens on immunocompromised patients (Madrid et al. 2014; Manamgoda et al. 2011, 2015; Danish Khan et al. 2017; Tóth et al. 2020). There are more than 200 epithets recorded in Index Fungorum (2022a, b). To date, 130 species of *Curvularia* have been accepted within the genus (Ferdinandez et al. 2021).

Curvularia alcornii Manamgoda, L. Cai & K. D. Hyde, Sydowia 64(2): 259 (2012)

Index Fungorum number: *IF800665; Facesoffungi number: FOF10679; Fig. 37*

Saprobic on dried leaf of *Panicum virgatum*. *On CMA Hyphae* 4–5 μm, septate, branched. *Conidiophores* up to 241 μm long, micronematous to macronematous, pale brown to dark brown, simple or branched, septate, flexuous, highly geniculate. *Conidiogenous cells* (8–)9–17(–19) × (4–)5–6 μm ($\bar{x} = 13 \times 5$ μm, $n = 10$), hyaline to pale brown, smooth–walled, terminal or intercalary, monotretic to polytretic. *Conidia* (18–)20–26(–31) × (7–)8–10(–11) μm ($\bar{x} = 23 \times 9$ μm, $n = 30$) apical and basal cells hyaline or pale brown, matured conidia brown, straight, rarely curved, inequilateral ellipsoidal or clavate, dark brown septa, 3–4-distoseptate, enlarged middle cells; *hila* 1–2 μm distinctly protuberant, darkened. **Sexual morph:** Not observed.

Culture characteristics: Colonies on PDA reaching 57 mm in 7 days at 25 °C, slightly convex with entire margin, brown centre, sparse aerial mycelium becoming brown

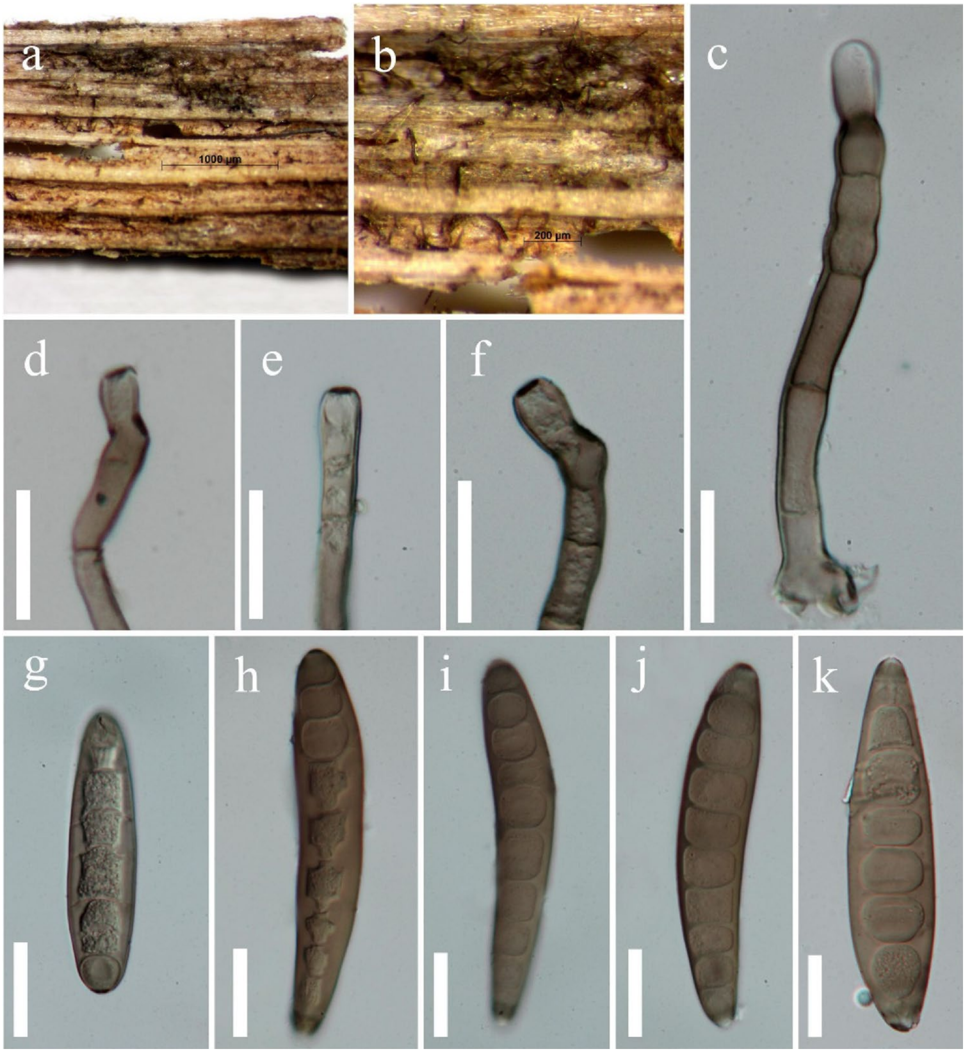


Fig. 35 **Bipolaris luttrelli** (MFLU 16–2836, **new host record**) **a**, **b**, Conidiophores and conidia on the host c-f. Conidiophores **g–k**, Conidia. Scale bars: **c–k** = 25 µm

to grey towards the edge, reverse black to dark brown, concentric. Colonies on CMA reaching 60 mm in 7 days at 25 °C, flat with entire margin, pale brown to dark brown, moderate aerial mycelium becoming dark brown to black towards the edge, reverse dark brown, concentric. Colonies on MEA reaching 67 mm in 7 days at 25 °C, flat with entire margin, dark green, sparse aerial mycelium becoming olivaceous green towards the edge, reverse black, concentric.

Material examined: Sri Lanka, Anuradhapura District, Thuruwila, N 8° 14′ 50.53859″, E 80° 25′ 9.24013″, on dried leaf of *Panicum virgatum* L. (Poaceae), 13 June 2019, D.S. Manamgoda, USJ-H-075, living culture USJCC-0088.

Hosts: Panicum spp.*, Pennisetum clandestinum, Oryza* spp. and *Zea mays* (Manamgoda et al. 2012a, b; Khemmuk et al. 2016)

Distribution: Australia and Thailand (Farr and Rossman 2022)

GenBank numbers: MZ948821 (ITS), MZ971267 (*gadph*), MZ971253 (*tef1*)

Notes: According to the phylogenetic result, isolate USJCC-0088 is identified as *Curvularia alcornii*. This taxon was originally described in Manamgoda et al. (2012a), as a saprobe on a leaf sample of *Zea mays* collected in Thailand (holotype MFLU 12-0397). In this study, the fresh isolate was identified as a saprobe on a dead leaf of *Panicum virgatum (*Fig. 38*)*. To our knowledge, this is a new record from Sri Lanka and a new fungus-host association.

Curvularia senegalensis (Speg.) Subram., Journal of the Indian Botanical Society. 35(4): 467 (1956)

≡ *Brachysporium senegalense* Speg., Anales del Museo Nacional de Historia Natural Buenos Aires 26: 133 (1914)

Index Fungorum number: *IF296254*; *Facesoffungi number: FoF13382; Fig. 39*

Saprobic on dead panicle of *Zea mays. On PDA Hyphae* 3–4 µm, septate, branched. *Conidiophores* up to 219 µm long, micronematous to macronematous, pale brown to dark brown, simple or branched, septate, straight to

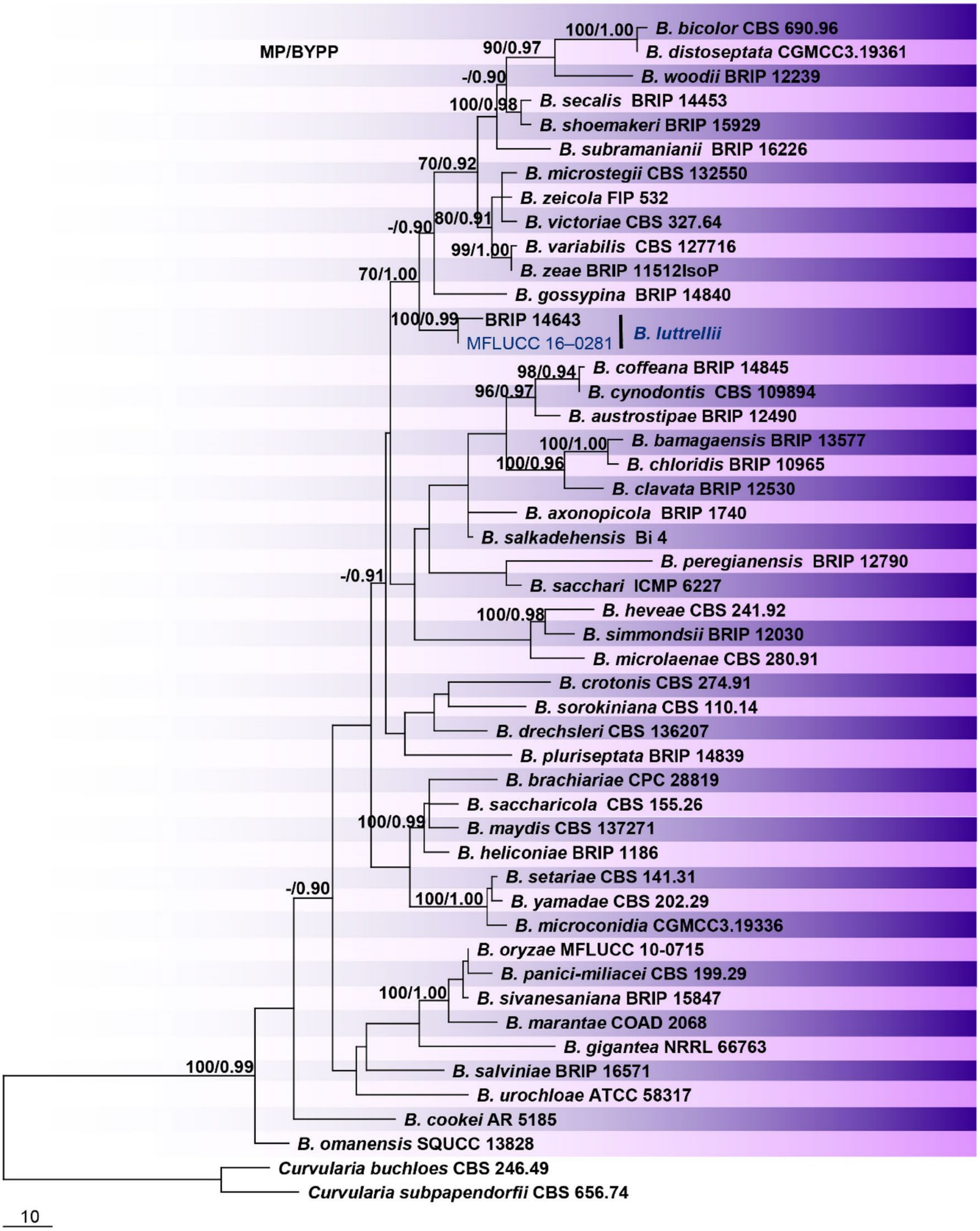


Fig. 36 One of the most parsimonious trees obtained in the combined analyses of ITS-*gapdh-tef1*. Maximum Parsimony values ≥ 70% and BYPP ≥ 0.90 are indicated above the nodes. The ex-types and reference strains are in **bold**; the new record is in blue**.** The tree is rooted with *Curvularia buchloes* (CBS 246.49) and *C. subpapendorfii* (CBS 656.74)

flexuous, geniculate at the apex. *Conidiogenous cells* (8–)9–15(–17) × 3–5 µm ($\bar{x}$ = 12 × 4 µm, *n* = 10), hyaline to pale brown, smooth–walled, terminal or intercalary, monotretic to polytretic. *Conidia* (17–)18–27(–34) × (7–)9–12(–13) µm ($\bar{x}$ = 22 × 11 µm, *n* = 30) apical and basal cells hyaline or pale brown, matured conidia brown, straight to curved, sometimes clavate, dark brown septa, 3–4-distoseptate, enlarged

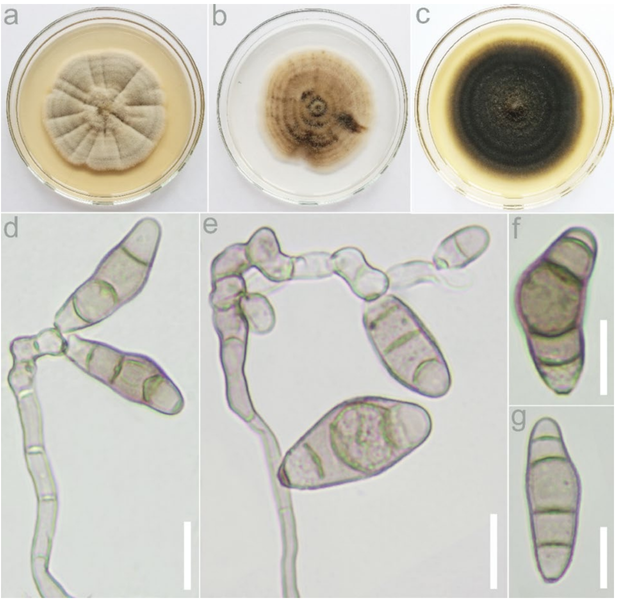


Fig. 37 ***Curvularia alcornii*** (USJCC–0088, **new host and geographical record**) **a** Seven-day old colony on PDA **b** Seven-day old colony on CMA **c** Seven-day old colony on MEA **d**, **e** Conidia attached to conidiophores **f, g** Conidia. Scale bars: **d–g** = 10 µm

middle cells; *hila* 1–2 µm flat, darkened. **Sexual morph:** Not observed.

Culture characteristics: Colonies on PDA reaching 73 mm in 7 days at 25 °C, flat with entire margin, grey to olivaceous black centre, abundant aerial mycelium becoming brown towards the edge, reverse black to dark brown, concentric. Colonies on CMA reaching 69 mm in 7 days at 25 °C, flat with entire margin, grey to pale brown, reverse white to pale brown, concentric. Colonies on MEA reaching 83 mm in 7 days at 25 °C, flat with entire margin, dark brown, abundant aerial mycelium becoming grey towards the edge, reverse dark brown to pale brown, concentric.

Material examined: Sri Lanka, Matale District, Palapathwela, N 7° 33′ 22.8″, E 80° 36′ 38.2″, on panicle of *Zea mays* L. (Poaceae), 08 November 2018, D.S. Manamgoda, USJ-H-031, living culture USJCC-0025.

Distribution: Australia, Brazil, China, Cuba, Hawaii, India, Malaysia, Mexico, Myanmar, Nigeria, Samoa, South Africa, Sri Lanka, Tanzania, Thailand, Texas, United States, Virginia and West Indies (Farr and Rossman 2022)

Hosts: Andropogon caricosus, Archontophoenix alexandrae, Bauhinia purpurea, Carya illinoensis, Citrullus vulgaris, Cymbopogon flexuosus, *Cynodon dactylon, Dichanthium caricosum, Gmelina arborea, Hevea brasiliensis, Hibiscus cannabinus, Jasminum sambac, Liquidambar macrophylla, Musa nana, Musa × paradisiaca, Oryza sativa, Ougeinia oojeinensis, Paspalum notatum, Paspalum paniculatum, Passiflora edulis, Persea Americana, Pinus caribaea, Pinus khasya*, *Quercus germana*, *Saccharum* sp., *Stigmaphyllon sagraeanum, Tamarindus indica*, *Thuja orientalis, Urena lobate, Vigna unguiculata, Zea mays* (Farr and Rossman 2022)

GenBank numbers: MT410577 (ITS), MZ971268 (GADPH), MZ971254 (*tef1*)

Notes: Isolate USJCC-0025 is identified as *Curvularia senegalensis* based on morphology and phylogeny (Fig. 38). The fresh isolate was collected from a dead panicle of *Zea mays*. *Curvularia senegalensis* has so far recorded in Sri Lanka only from *Hevea brasiliensis* (Adikaram and Yakandawala 2020). Moreover, it has only been reported on *Zea mays* from Brazil, Malaysia and Nigeria. To our knowledge, this is the first record of *Curvularia senegalensis* on *Zea mays* from Sri Lanka.

Pyrenophora Fr., Summa veg. Scand., Sectio Post. (Stockholm): 397 (1849)

Pyrenophora is a species-rich genus in Pleosporales which encompasses saprobic and phytopathogenic fungi associated mainly with poaceous hosts. The sexual morphs are characterized by black, thick-walled, subglobose to pyriform ascomata with an apical ostiole and conspicuous dark brown setae. Asci are bitunicate, show a large non-amyloid ring and usually contain eight pale yellowish brown or pale brown, muriform ascospores surrounded by a mucilaginous sheath. Asexual morphs show macronematous, brown, sympodial conidiophores with tretic conidiogenous cells and dematiaceous, rather straight, distoseptate conidia with a dark, non-protruding basal scar. Conidial germination occurs from polar or intermediate cells (Sivanesan 1987). This genus is monophyletic and genetically clearly distinct from other pleosporalean genera with a superficially similar conidial apparatus, such as *Bipolaris*, *Exserohilum* and *Porocercospora*. Multilocus DNA sequence data is currently available for at least 26 *Pyrenophora* species (Marin-Felix et al. 2019).

Pyrenophora verruculosa Madrid & Cantillo, ***sp. nov.***

Mycobank number: 844464; Facesoffungi number: FoF10420; Fig. 40

Etymology: The name refers to the verruculose conidia produced by this species

Holotype: SGO 168420

Probably saprobic or pathogenic to an unidentified member of *Poaceae.* **Sexual morph**: Not observed. **Asexual morph:** Hyphomycetous. Vegetative hyphae septate, branched, light olivaceous to mid olivaceous brown, thin to thick-walled, smooth, 2–6 µm wide, anastomosing, occasionally showing deposits of a mucilaginous dark brown material. *Conidiophores* macronematous, mononematous, solitary, septate, simple, slightly flexuous to strongly geniculate, light olivaceous brown to dark brown,

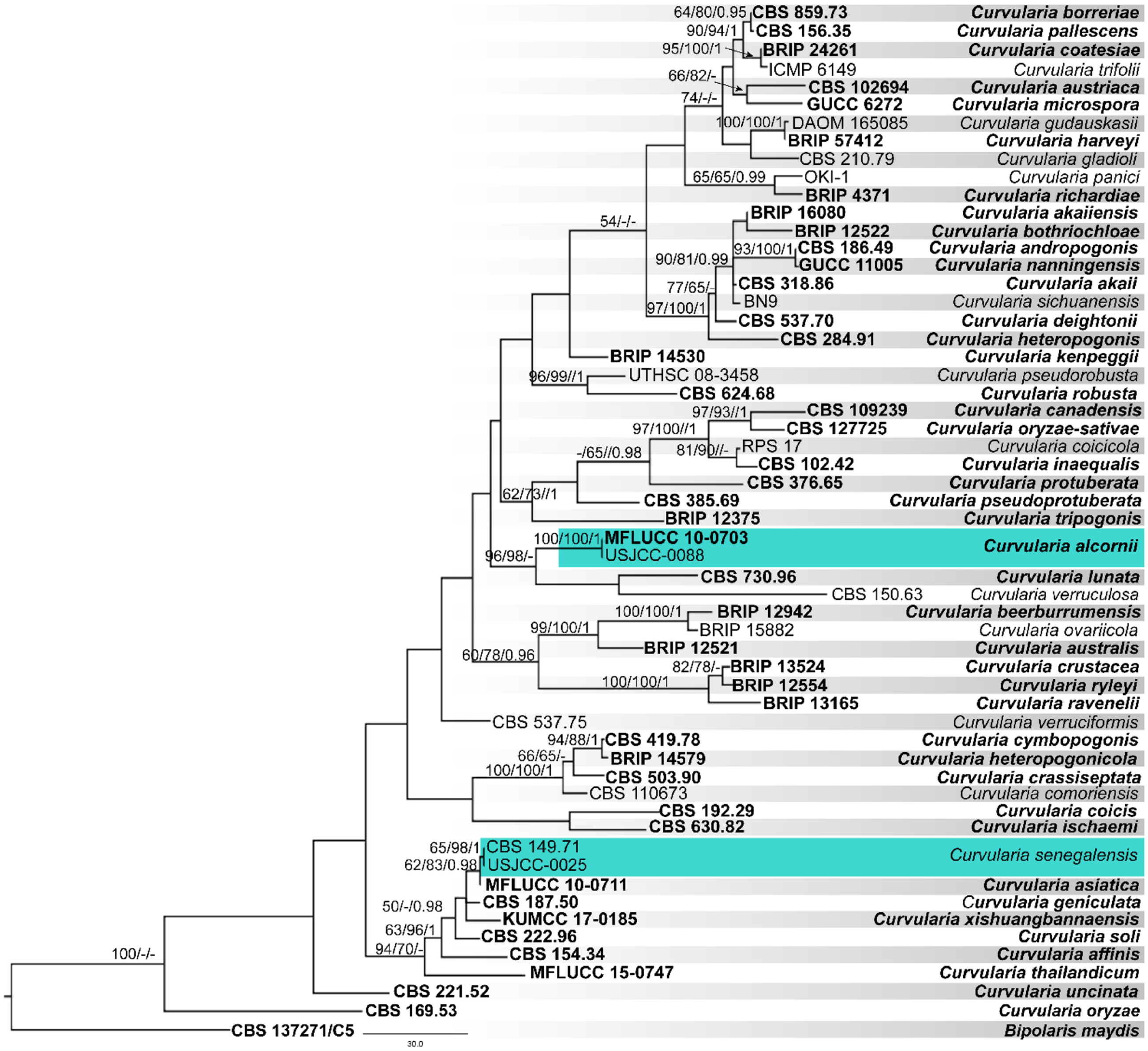


Fig. 38 Phylogram generated from parsimony analysis based on combined ITS, *gadph* and *tef1* sequence data of *Curvularia*. Bootstrap support values of MP and ML ≥ 50% and BYPP ≥ 0.95 are indicated above the nodes. The ex-types are in **bold**; the new records are highlighted in greenish-blue. The tree is rooted with *Bipolaris maydis* (CBS137271/C5)

often paler at the apex, smooth to verruculose, with cell walls often thicker than those of the supporting vegetative hyphae, 300–1270 × 5–9 µm with subnodulose to nodulose intercalary swellings up to 11 µm wide. *Conidiogenous cells* integrated, terminal and intercalary, mostly subcylindrical, mono- to polytretic, proliferating sympodially, 15–28 µm long. *Conidia* narrowly clavate, narrowly ellipsoidal to fusiform or subcylindrical, straight to slightly curved, light olivaceous brown to dark brown, verruculose, (26–)32–63(–74) × 12–21 µm, 3–5(mostly 4)-distoseptate, often constricted at the uppermost distoseptum, with a rounded apex and an obconically truncate or rounded base, basal cell sometimes delimited by a thick, dark septum. *Hilum* thick and dark. *Microsclerotia* abundant, mostly 45–240 µm wide.

Culture characteristics: Colonies on water agar with sterilized maize leaves dark brown, hairy, with abundant clumps of microsclerotia.

Material examined: Chile, El Loa Province, Atacama Desert, near Calama, isolated from unidentified dead *Poaceae*, 15 October 2015, H. Madrid & L. Linaje (SGO 168420, **holotype**).

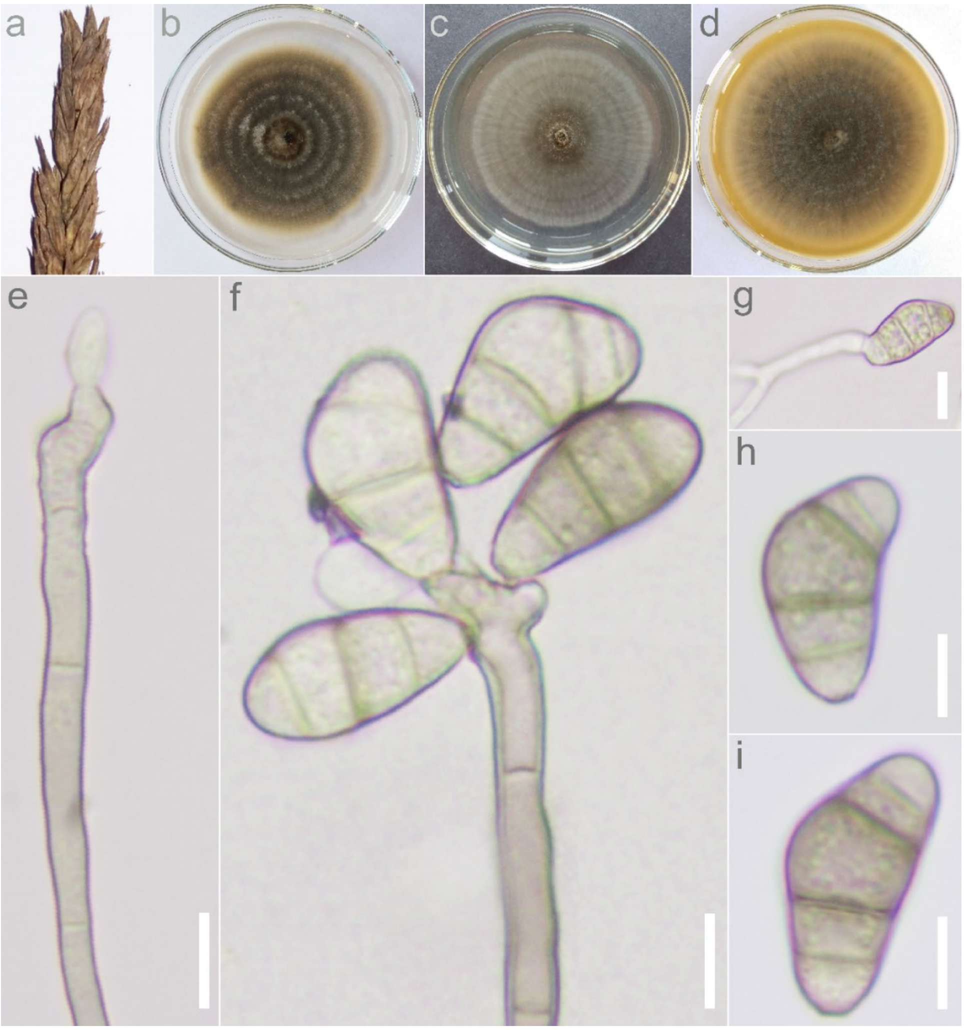


Fig. 39 ***Curvularia senegalensis*** (USJCC–0025, **new host record**) **a** Host: dead panicle of *Zea mays* **b** Seven day old colony on PDA **c** Seven day old colony on CMA **d** Seven day old colony on MEA **e** Conidiophore **f** Conidia attached to conidiophore **g** Germinating conidium **h, I** Conidia Scale bars: **e–i** = 10 µm

GenBank numbers: ON722346 (ITS), ON722346 (LSU), ON736764 (*gpdh*).

Notes: Due to mobility restrictions during the SARS-CoV-2 pandemic, the ex-type strain (HM 201), which had been preserved in sterile water, could not be properly maintained for several months. Recent attempts to reactivate the strain have been unsuccessful and the fungus probably died. However, the holotype was deposited at SGO and ex-type sequences of ITS, LSU and *gpdh* are available in GenBank. DNA sequence analyses revealed that *Pyrenophora verruculosa* is clearly distinct from all other members of *Pyrenophora* represented in GenBank. The closest hits in BLAST searches with the ITS sequence of strain HM 201 were *Pyrenophora novozelandica* (CBS 127934) (ex-type, GenBank MK539997, 96.55% similarity), *P. fugax* (CBS 509.77) (GenBank MK539985, 95.23% similarity), *P. nisikadoi* (CBS 190.29) (ex-type, as *Bipolaris brizae*, GenBank MH855213, 93.57% similarity), and *P. nobleae* (CBS 259.80) (GenBank MK539994, 91.33% similarity). BLAST searches with the *gpdh* sequence showed *P. fugax* (CBS 509.77) (GenBank AY004822, 95.70% similarity) and *P. nobleae* (CBS 966.87) (GenBank AY004824, 88.81% similarity) as the closest matches. With LSU, similar results were obtained, but with higher similarity percentages, as expected for this rather conserved locus. In the phylogenetic analysis, only ITS sequence data was used considering that LSU offers little resolution for closely related taxa in Pleosporales, and *gpdh* is available for a smaller number of species than ITS. In the ITS-based phylogenetic tree (Fig. 41), *P. verruculosa*, *P. novozelandica* and *P. fugax* formed a clade with 83% bootstrap support. These close relatives can easily be distinguished from *P. verruculosa* on the basis of conidial dimensions, i.e. smaller in *P. novozelandica*, 20.5–58 × 9.5–14 µm, and longer in *P. fugax*, 50–170 × 14–24 µm (Ellis 1961; Sivanesan 1987; Marin-Felix et al. 2019). Clumps of thick-walled, strongly pigmented cells superficially resembling the microsclerotia of *P. verruculosa*, have been reported in other *Pyrenophora* species, such as *P. nisikadoi* and *P.*

Fig. 40 ***Pyrenophora verruculosa*** (SGO 168420, **holotype**). **a, c, d** Conidia attached to conidiogenous cells. **b** Conidium passively released from a conidiogenous cell. **e–h** Conidia (verruculose ornamentation can be observed in e). **i** Hyphae with mucilaginous dark brown material. **j, k** Mycelia with microsclerotia. Scale bars*:* **a–d** = 40 µm, **e–i** = 20 µm, **j–k** = 45 µm

pseudoerythrospila (Marin-Felix et al. 2019). These species, however, are phylogenetically clearly distinct from *P. verruculosa* (Fig. 41).

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray., Stud. Mycol. 64: 177 (2009)

Tetraplosphaeriaceae was established to accommodate five genera, *viz Polyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Tetraplosphaeria* with *Tetraploa* sensu stricto asexual morphs (the type genus) and *Triplosphaeria* (Tanaka et al. 2011). Hyde et al. (2013) later treated *Tetraplosphaeria* as a synonym of *Tetraploa* which has been applied previously. Up to now, nine genera are accepted in

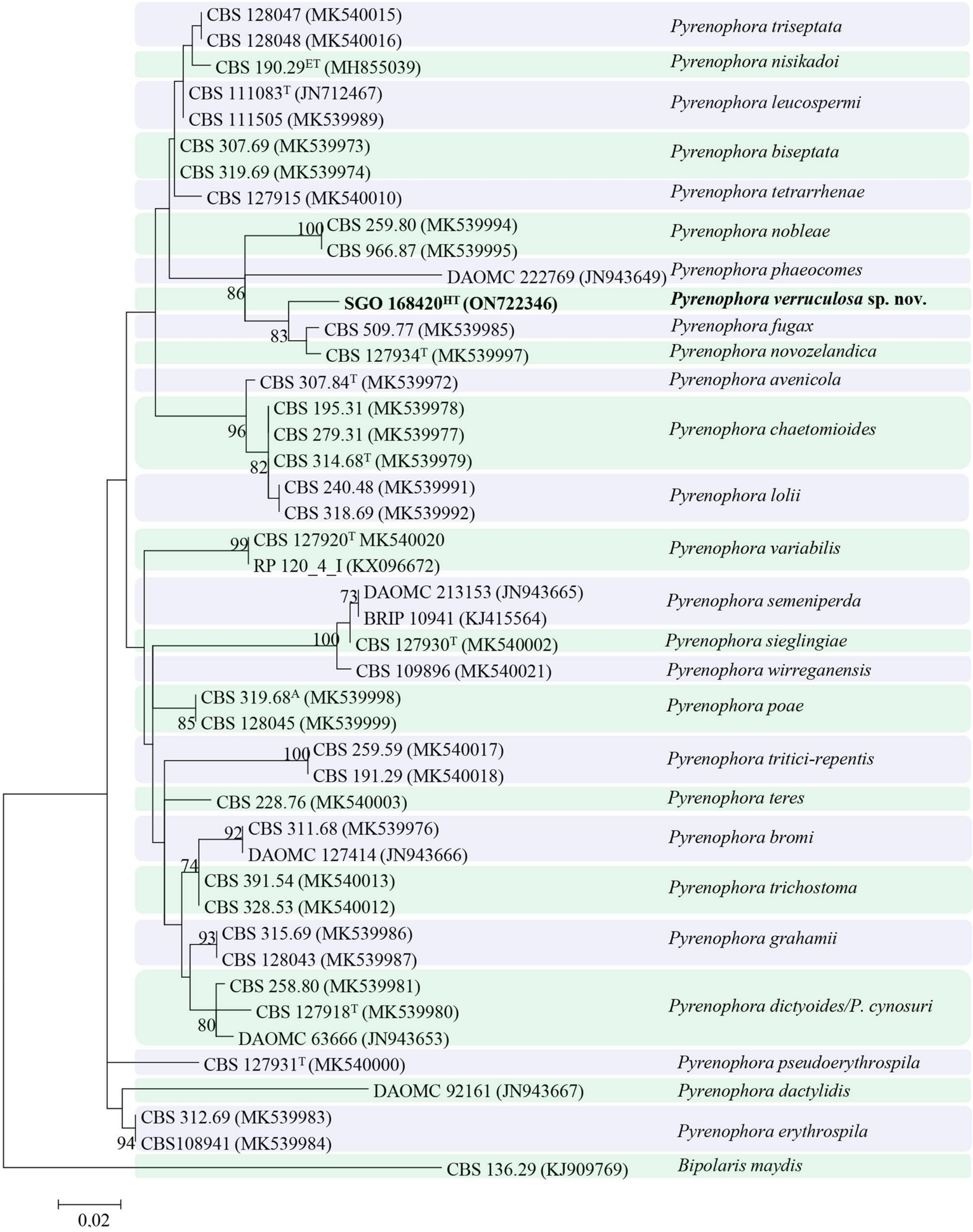


Fig. 41 Maximum likelihood tree based on ITS sequences, showing the phylogenetic relationships of *Pyrenophora* species. Bootstrap support values > 70% are shown near the internodes. The tree is rooted to *Bipolaris maydis*. GenBank accession numbers of ITS sequences are given, in parentheses, after each strain number. ^{A}authentic strain, ^{T}ex-type strain, ^{ET}ex-epitype strain, ^{HT}holotype material. New species is in **bold**

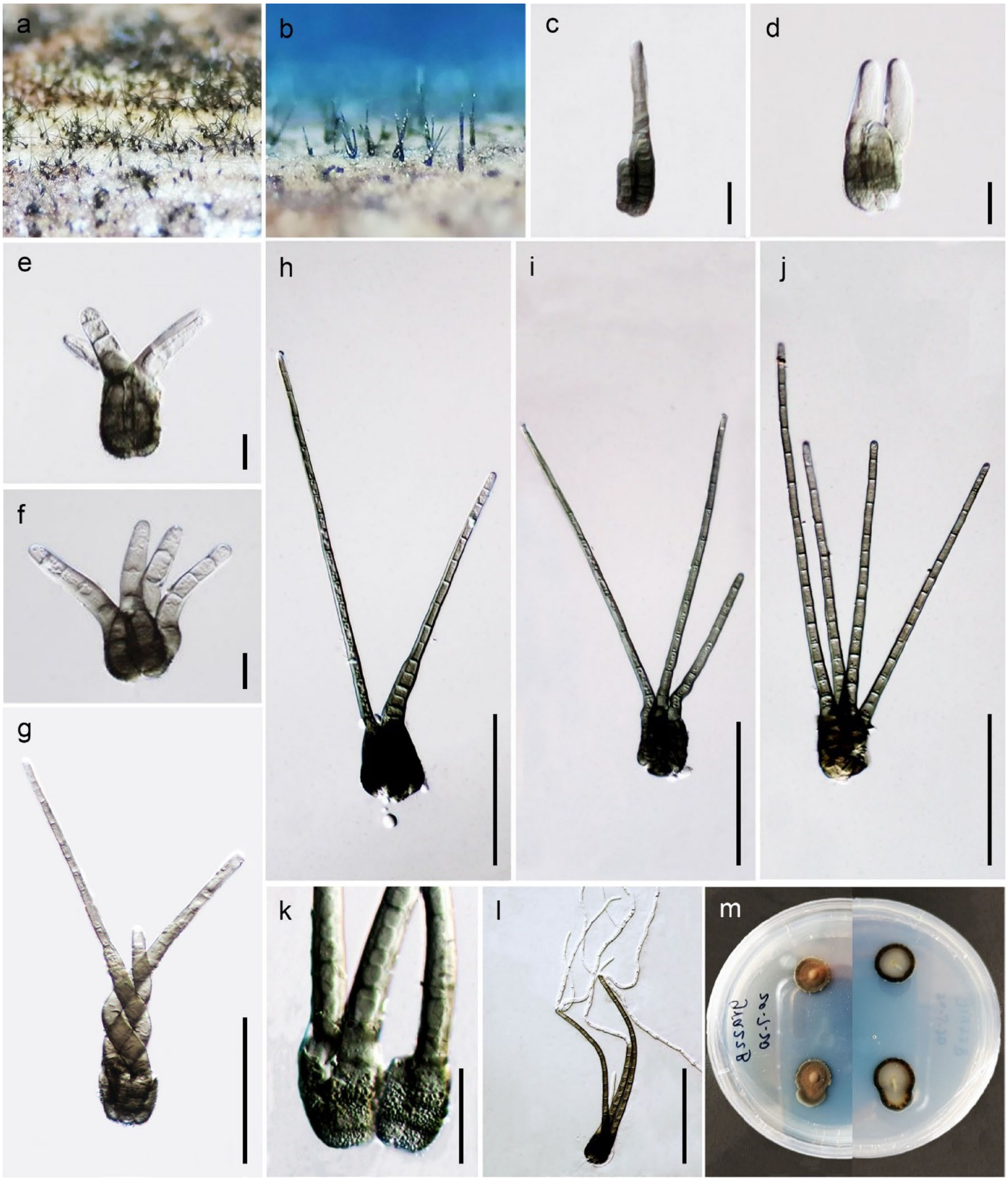


Fig. 42 ***Tetraploa dashaoensis*** (KUN–HKAS 107,636, **holotype**). **a–b**. Conidia on host substrate; **c–g**. Conidia; **k**. Verrucose conidia; **l**. Germinating conidium; **m**. Colony on PDA (left-front, right-reverse); Scale bars: **c–f, k** = 50 µm, **g–j,** l = 100 µm

Tetraplosphaeriaceae *viz Aquatisphaeria*, *Byssolophis*, *Ernakulamia*, *Polyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Shrungabeeja*, *Tetraploa* and *Triplosphaeria* (Wijayawardene et al. 2022). Members of this family are mostly reported as saprobe from aquatic and terrestrial habitats (Tibpromma et al. 2018; Hongsanan et al. 2020a, b; Hyde et al. 2020a, b, c; Li et al. 2021a, b).

Tetraploa Berk. & Broome, Ann. Mag. nat. Hist., Ser. 2 5: 459 (1850) MycoBank: MB10199

= *Tetraplosphaeria* Kaz. Tanaka & K. Hiray., in Tanaka et al., Stud. Mycol. 64: 177 (2009)

Notes: Tetraploa was introduced by Berkeley and Broome (1850) with *T. aristata* as the type species. The sexual morph is characterized by small globose ascomata, narrowly fusiform ascospores and appendage-like sheath. The asexual

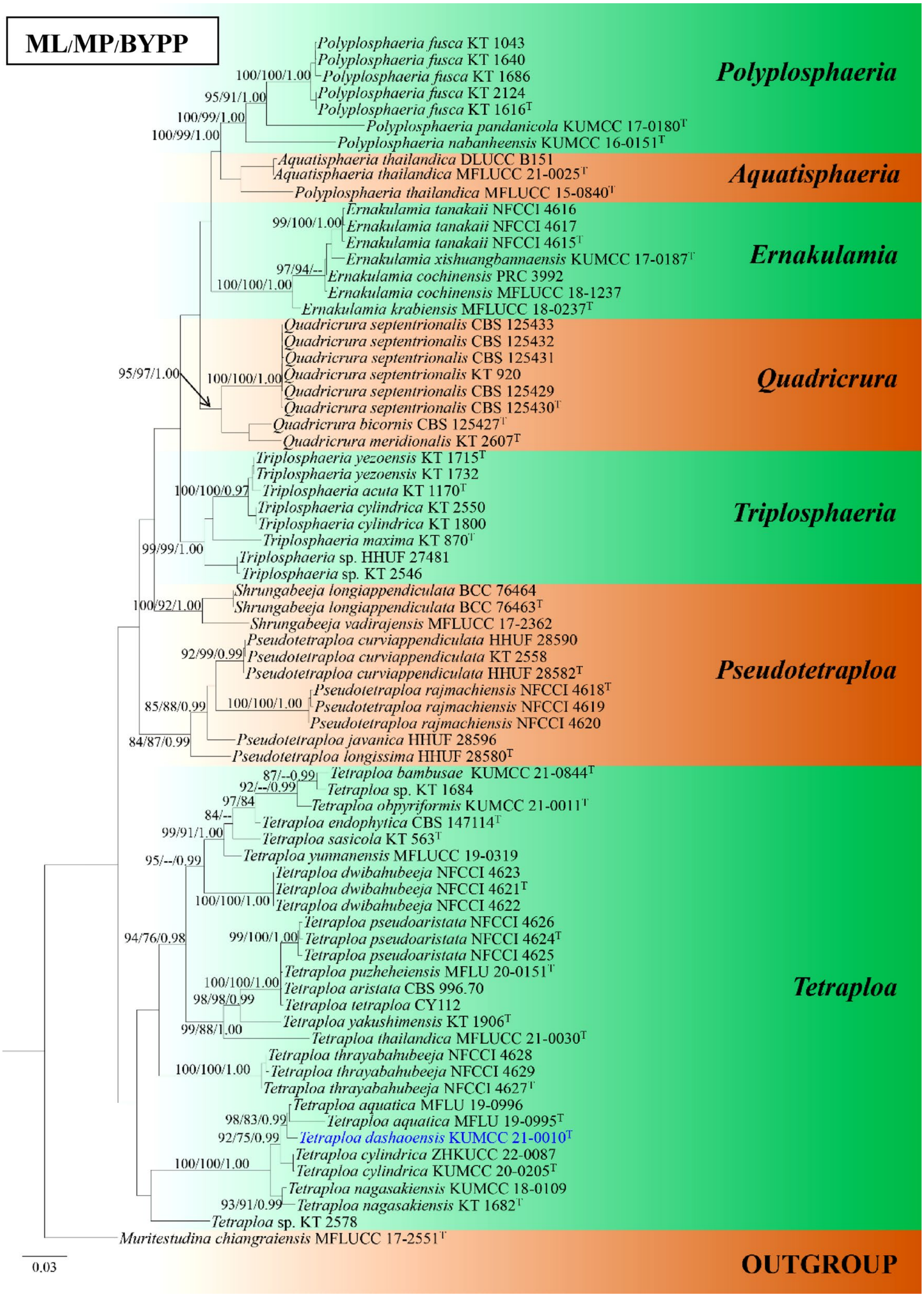


Fig. 43 Phylogram generated from maximum likelihood analysis of *Tetraploa* including related genera based on a combined LSU, ITS, SSU, *tub2* and *tef1* sequence data. Relevant sequences were referred from Dong et al. (2020), Hyde et al. (2020a), and Li et al. (2021a, b). The data set consisted of 3720 characters with gaps. Tree topology of the ML analysis was similar to the MP and BYPP tree topologies. Bootstrap support values of ML and MP ≥ 75% with BYPP ≥ 0.95 are given at the nodes. The ex-type cultures are indicated using "T"; the new isolate is in blue

morph belonging to *Tetraploa* sensu stricto has a columnar conidial body, with several prominent setose appendages at the apex (Hyde et al. 2013; Li et al. 2021a, b). Hyde et al. (2013) transferred species in *Tetraplosphaeria* to *Tetraploa*. In this study, we introduce one new species to *Tetraploa* based on morphology and molecular analysis with full description and illustration.

Tetraploa dashaoensis C.F. Liao & Doilom, ***sp. nov.***

Index Fungorum number: IF559273; Facesoffungi number: FoF10585; Fig. 42

Etymology: In reference to the location where the fungus was collected.

Holotype: KUN–HKAS 107636

Saprobic on dead stem of *Saccharum arundinaceum*. **Sexual morph**: Not observed. **Asexual morph**: hyphomycetous. *Colonies* superficial, effuse, gregarious, brown to dull green. *Mycelium* partly immersed in natural substratum, brunched, septate, hyaline. *Conidiophores* absent. *Conidiogenous cells* micronematous, integrated, monoblastic, intercalary, short cylindrical. *Conidia* 25–43 × 13–36 μm ($\bar{x} = 31 \times 23$ μm, $n = 30$), solitary, straight, septate, unbranched, mostly smooth-walled at the base of immature conidia, becoming verrucose at mature conidia, composed of 1–4 columns at the base, 1–3-septate in each column, with 1–4 apical appendages. *Appendage* 148–258 μm long ($\bar{x} = 186$ μm, $n = 30$), 6–15 μm wide at the base with dull green, 3–8 μm wide at the apex with hyaline, usually composed of three to four appendages, rarely one or two, euseptate, 6–23-septate, smooth, straight or divergent to intertwined; immature appendages 21–81 μm long ($\bar{x} = 43$ μm, $n = 30$), with 1–5-septate.

Culture characteristics: Conidia germinating on PDA, germination tube growing from both ends. Colonies on PDA reaching 10 to 14 mm diam. in 17 days at room temperature (25 ± 2 °C), mycelium dense, floccose, surface smooth, velutinous spot centre with flat substrate, circle or irregular margin, light brown to yellow–brown, dark brown towards to white margin in above; white at centre, dark brown towards margin in reverse. No pigment production.

Material examined: China, Yunnan Province, Kunming City, from dead stem of *Saccharum arundinaceum* (Retz.) (Poaceae), 4 July 2020, C.F. Liao, (KUN–HKAS 107636, **holotype**), ex-type living culture KUMCC 21-0010.

GenBank number: OL473549 (ITS), OL473555 (LSU), OL473556 (SSU), OL505601 (*tub2*), OL505599 (*tef1*).

Notes: Phylogenetic analyses of the combined LSU, ITS, SSU, *tub2* and *tef1* sequence data showed that our new collection *Tetraploa dashaoensis* KUMCC 21-0010 is related to *Tetraploa aquatica* (MFLU 19-0995, MFLU 19-0996), but forms a distinct linage with 98% ML, 83% MP and 0.99 BYPP values (Fig. 43). *Tetraploa dashaoensis* shares some morphological characteristics with the phylogenetically closest species *T. aquatica* in having cylindrical conidiogenous cells, a verrucose conidial base and 1–4 apical appendages with euseptate. However, *T. dashaoensis* differs from *T. aquatica* in having a different conidial colour (dull green *vs.* brown to pale brown), longer conidia (25–43 μm *vs.* 22.5–27 μm), longer appendages (148–258 μm *vs.* 98–134 μm), and more septate appendages (6–23-septate *vs.* 6–10-septate). In addition, *T. dashaoensis* has intertwined appendages, which were absent in *T. aquatic* (Li et al. 2021a, b). Phylogenetic analyses and morphological characters support our collection to be different species. Thus, we introduce *T. dashaoensis* as a new species based on morphology and phylogeny.

Torulaceae Corda, in Sturm, Deutschl. Fl., 3 Abt. (Pilze Deutschl.) 2: 71 (1829)

Notes: Sturm (1829) introduced Torulaceae with *Torula* as the type genus. There are six genera accepted in Torulaceae, namely *Dendryphion*, *Neotorula*, *Rostriconidium*, *Rutola*, *Sporidesmioides* and *Torula* (Hongsanan et al. 2020b). Torulaceae species are characterized by having erect, micro- or macronematous, straight or flexuous, subcylindrical conidiophores and doliiform to ellipsoid or clavate, brown, smooth to verruculose conidiogenous cells. Conidia are subcylindrical, phragmosporous, acrogenous, brown, dry, and smooth to verrucose, characteristically produced in branched chains (Hyde et al. 2016; Li et al. 2017a, b; Mapook et al. 2020). In this study, we follow Mapook et al. (2020) as the recent treatment for Torulaceae.

Torula Pers, Ann. Bot. (Usteri) 15: 25 (1795)

Notes: Persoon (1794) established *Torula* and was typified by *T. herbarum*. *Torula* species are characterized by having a terminal or lateral, monoblastic or polyblastic conidiogenous cells, which have a basally thickened and heavily melanized wall, with the apex thin-walled and frequently collapsing and becoming coronate (Crane and Miller 2016). There are 54 *Torula* species listed in Species Fungorum (2022a, b), however, only 18 taxa have molecular data.

Torula fici Crous, IMA Fungus 6: 192 (2015).

Index Fungorum number: *IF816154; Facesoffungi number: FoF02712, Fig. 44*

Saprobic on the dead pseudo stem parts of *Musa* sp. **Sexual morph**: Not observed. **Asexual morph**: *Colonies* effuse, black, powdery and thread-like. *Mycelium* slightly immersed, septate, branched, smooth, with pale brown hyphae. *Conidiophores* 2–3 μm long × 1–3 μm diameter ($\bar{x} = 2.77 \times 1.91$ μm, $n = 10$), macronematous, mononematous, solitary, erect, thick–walled, consisted of 2 distinct cells, first cell from the bottom is pale brown to sub hyaline, wide at the base and narrow at apex, the second

Fig. 44 ***Torula fici*** (MFLU 22-0251, **new collection**). Fungal colonies on host surface, **b, c, e–p** Budding, conidial formation and mature conidia, **d** Conidiogenous cell. Scale Bars: **a** = 500 µm, **b, i, k, m** = 20 µm, **e–h, j, l, n–p** = 15 µm, **c, d** = 5 µm

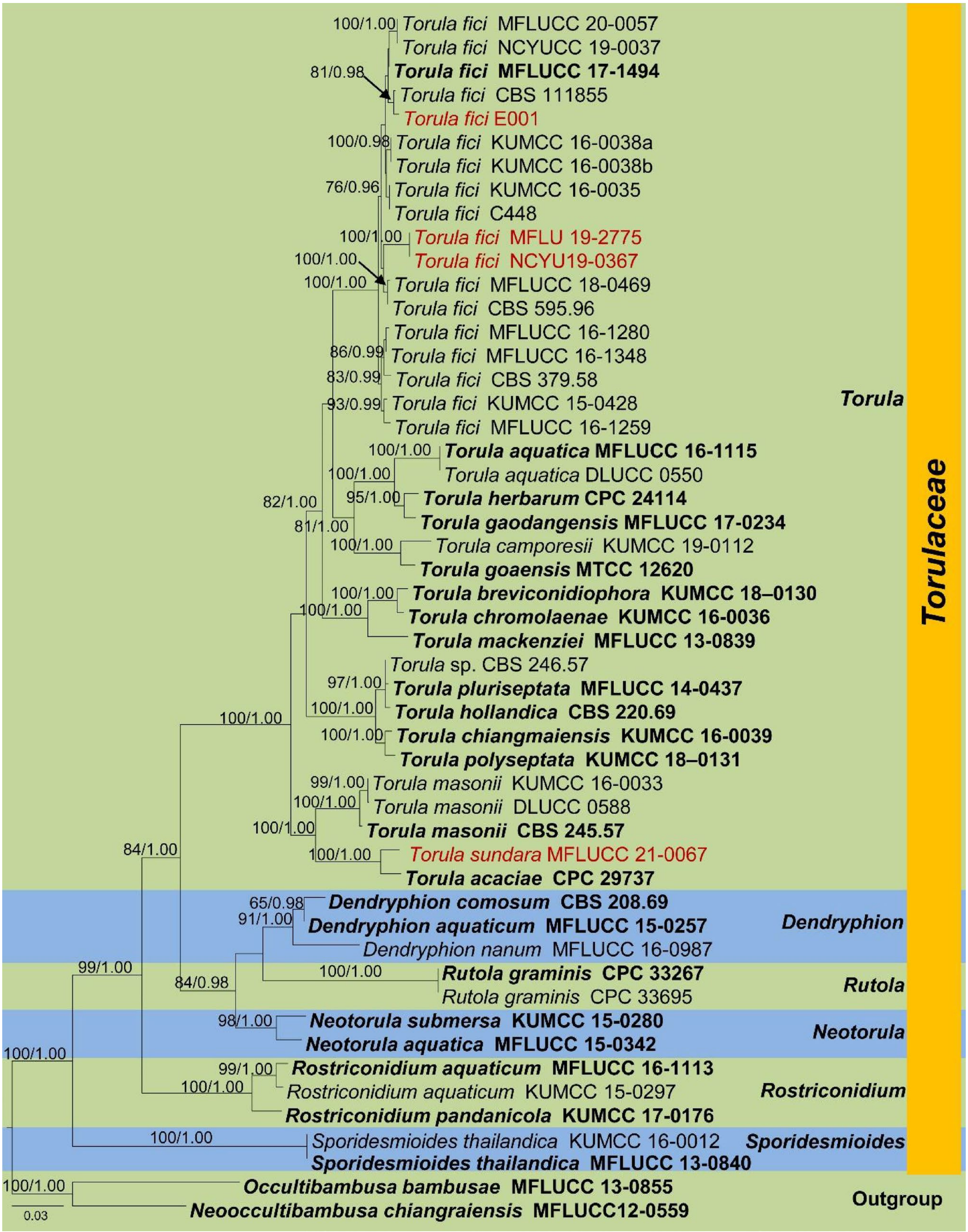
cell is pale brown to brown, different from the first cell by shape, cylindrical to subcylindrical at the base and globose to subglobose at apex, conidiophore arising from prostrate hypha. *Conidiogenous cells* 2–3 µm long × 1–2 µm diam, ($\bar{x} = 2.18 \times 1.33$ µm, $n = 10$) polyblastic, and terminal, dark brown to black, verruculose, thick-walled, ellipsoid, paler or sub hyaline at apex, dark and black at the bottom. *Conidia* 19– 25 µm long 2–3.5 µm wide ($\bar{x} = 18.56 \times 2.88$ µm, $n = 10$) solitary to catenate, acrogenous, simple, phragmosporous, dark brown, apical cell often pale brown, minutely verruculose, often 3–4 septate, rounded at both ends, composed of subglobose cells, slightly constricted at some septa. Immature conidia are sub hyaline to pale brown and arising to multi-angles from mature conidia. Conidial secession is rheixolytic.

Culture characteristics: Conidia germinating on PDA within 18 h and germ tubes produced from the tip cell. Colonies growing on PDA, reaching 5 cm in 5 days at 25 °C, mycelium partly immersed to superficial, slightly effuse, hairy, with regular edge, pink or pale brown.

Material examined: Thailand, Chiang Mai, Mushroom Research Center, on dead plant material of *Musa* sp. (Musaceae), 30 December 2018, Binu Samarakoon, E001 (MFLU 22-0251), living culture MFLUCC 22-0176.

Other material examined: Taiwan, Ali shan mountain, Fanlu Township area, Dahu forest, dead leaves of *Ficus septica* (Moraceae), 20 September 2018, D. S. Tennakoon, HAY029A (MFLU 19-2775); living culture, MFLUCC 20-0167, ibid., 10 July 2019, HAY029B (NCYU 19-0367); living culture, NCYUCC 19-0248.

Known hosts: *Chromolaena odorata* (Asteraceae), *Ficus septica* (Moraceae), *Ficus religiosa* (Moraceae), *Garcinia* sp. (Clusiaceae), *Magnolia grandiflora* (Magnoliaceae), *Olea europaea* (Oleaceae), *Pandanus sp.* (Pandanaceae),


100/1.00 Torula fici MFLUCC 20-0057
Torula fici NCYUCC 19-0037
81/0.98 Torula fici MFLUCC 17-1494
Torula fici CBS 111855
Torula fici E001
100/0.98 Torula fici KUMCC 16-0038a
Torula fici KUMCC 16-0038b
76/0.96 Torula fici KUMCC 16-0035
Torula fici C448
100/1.00 Torula fici MFLU 19-2775
100/1.00 Torula fici NCYU19-0367
100/1.00 Torula fici MFLUCC 18-0469
Torula fici CBS 595.96
Torula fici MFLUCC 16-1280
86/0.99 Torula fici MFLUCC 16-1348
83/0.99 Torula fici CBS 379.58
93/0.99 Torula fici KUMCC 15-0428
Torula fici MFLUCC 16-1259
100/1.00 Torula aquatica MFLUCC 16-1115
100/1.00 Torula aquatica DLUCC 0550
82/1.00
95/1.00 Torula herbarum CPC 24114
81/1.00 Torula gaodangensis MFLUCC 17-0234
100/1.00 Torula camporesii KUMCC 19-0112
Torula goaensis MTCC 12620
100/1.00 Torula breviconidiophora KUMCC 18–0130
100/1.00 Torula chromolaenae KUMCC 16-0036
Torula mackenziei MFLUCC 13-0839
Torula sp. CBS 246.57
97/1.00 Torula pluriseptata MFLUCC 14-0437
100/1.00 Torula hollandica CBS 220.69
100/1.00
100/1.00 Torula chiangmaiensis KUMCC 16-0039
Torula polyseptata KUMCC 18–0131
99/1.00 Torula masonii KUMCC 16-0033
100/1.00 Torula masonii DLUCC 0588
100/1.00 Torula masonii CBS 245.57
84/1.00
100/1.00 Torula sundara MFLUCC 21-0067
Torula acaciae CPC 29737
Torula
Torulaceae
65/0.98 Dendryphion comosum CBS 208.69
91/1.00 Dendryphion aquaticum MFLUCC 15-0257
Dendryphion nanum MFLUCC 16-0987
Dendryphion
99/1.00
100/1.00 Rutola graminis CPC 33267
84/0.98 Rutola graminis CPC 33695
Rutola
98/1.00 Neotorula submersa KUMCC 15-0280
Neotorula aquatica MFLUCC 15-0342
Neotorula
100/1.00
99/1.00 Rostriconidium aquaticum MFLUCC 16-1113
100/1.00 Rostriconidium aquaticum KUMCC 15-0297
Rostriconidium pandanicola KUMCC 17-0176
Rostriconidium
100/1.00 Sporidesmioides thailandica KUMCC 16-0012
Sporidesmioides thailandica MFLUCC 13-0840
Sporidesmioides
100/1.00 Occultibambusa bambusae MFLUCC 13-0855
Neooccultibambusa chiangraiensis MFLUCC12-0559
Outgroup
0.03

◀ **Fig. 45** The best scoring RAxML tree for combined dataset of LSU, SSU, ITS, *tef1* and *rpb2* sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses. The tree is rooted with *Neooccultibambusa chiangraiensis* (MFLUCC 12–0559) and *Occultibambusa bambusae* (MFLUCC 13–0855). Ex-type strains are in **bold** and newly generated sequences are in red. Bootstrap support values for ML ≥ 60% and BYPP ≥ 0.90 are given above the nodes

Musa sp. (Musaceae) (Crous et al. 2015a, b, c, Li et al. 2017a, b; Tibpromma et al. 2018; Jayasiri et al. 2019; Mapook et al. 2020; Samarakoon et al. 2021; Tennakoon et al. 2021; this study).

Known distribution: Taiwan (this study), Cuba, South Africa, Thailand (this study) (Crous et al. 2015a, b, c, Li et al. 2017a, b; Tibpromma et al. 2018; Jayasiri et al. 2019; Mapook et al. 2020; Samarakoon et al. 2021; this study).

GenBank numbers: MFLUCC 22-0176 – OP099550 (*LSU*), OP097673 (*SSU*), OP099562 (*ITS*), OP113821 (*tef1*) MFLUCC 20-0167 – MZ317501 (*LSU*); MZ317506 (*ITS*); MZ326657 (*tef1*); MZ326659 (*rpb2*) NCYUCC 19-0248 – MZ317502 (*LSU*); MZ317507 (*ITS*); MZ326658 (*tef1*); MZ326660 (*rpb2*)

Notes: In the multi-gene phylogeny, our strain (MFLUCC 22-0176) grouped with *T. fici* strains with moderate statistical support in ML analysis and a higher support in Baysian analysis (81% ML, 0.98 BYPP) (Fig. 45). Morphological comparisons revealed that our collection is similar to the holotype of *T. fici* (Crous et al. 2015a, b, c) by the distinct shape of the conidiophores and having 3–4 celled conidia. In addition, the conidiogenous cells of the type specimen are identical in shape with our collection. Therefore, based on both morphology and phylogeny evidence, we identify our specimen (MFLU 22-0251) as *T. fici* from Chiang Mai, Thailand. *Torula fici* was previously found from China on *Musa* sp. by Samarakoon et al. (2021). In this study, we report *T. fici* on *Musa* sp. for the first time from Thailand as a new collection. In addition, our strains (MFLU 19-2775 and NCYU 19-0367) share the size range of the conidial characters with *T. fici* (Crous et al. 2015a, b, c; Tibpromma et al. 2018; Mapook et al. 2020). The phylogeny also indicates that both strains were nested with other *Torula fici* strains in a 100% ML, 1.00 BYPP supported clade (Fig. 45). We conclude that our stains (MFLU 19-2775 and NCYU 19-0367) also belong to *T. fici* which was reported on *Ficus septica* from Taiwan as a new host record.

Torula sundara (*Subram.*) Y.R. Sun, Yong Wang bis & K.D. Hyde, ***comb.nov.***

≡ *Dwayabeeja sundara* Subram., J. Indian Bot. Soc.37: 56 (1958)

= *Pseudotorula sundara* (Subram.) J.L. Crane & A. Mill

Index Fungorum number: IF559464; Facesoffungi number: FoF09933; Fig. 46

Saprobic on decaying bamboo culms in terrestrial habitat. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate superficial, powdery, dark brown to black. *Mycelium* immersed, composed of branched, septate, pale brown to brown hyphae. *Conidiophores* 2.5–4 µm wide, micronematous to semi-macronematous, mononematous, solitary, erect, sample, straight or slightly flexuous, unbranched, paler brown to brown, thin-walled, septate, with ampulliform cells, arising from prostrate hypha. *Conidiogenous cells* polyblastic, terminal, with the apex thin-walled and freuently collapsing and becoming coronate, dark brown to black, ellipsoid to coronal. *Conidia* two types, short conidia and long conidia. Short conidia 41–60 × 9–15 µm ($\bar{x} = 53 \times 12$ µm, $n = 30$), acrogenous, phragmosporous, single or in chains, broadly fusiform, yellow brown to dark brown, 5–10-septate, slightly constricted at some septa, verruculose. Long conidia acrogenous, phragmosporous, single, straight or flexuous, cylindrical, up to 50-septate, constricted at the septa, brown to dark brown, up to 200 µm long. **Sexual morph**: Not observed.

Culture characteristics: Conidium germinated on PDA within 12 h. Colonies on PDA reaching 20 mm in two weeks at 26 °C. Mycelia superficial, circular, entire, flat, white from above, pale brown from below.

Material examined: Thailand, Chiang Mai Province, Mae Taeng District, MRC, on bamboo culms, 10 September 2020, H.W. Shen, M55 (MFLU 21-0089); living culture, MFLUCC 21-0067).

GenBank numbers: OM276824 (ITS), OM287866 (LSU)

Notes: *Dwayabeeja sundara* as the type species in *Dwayabeeja* was introduced by Subramanian (1958). It has dark blackish-brown colonies and two types of conidia. Crane and Miller (2016) transferred *D. sundara* to *Pseudotorula* based on catenate phragmoconidia. It was recollected and isolated from bamboo culms in Chiang Mai Province, Thailand. Here, we provided sequences for it. Phylogenetic analyses show it is a distinct clade in *Torula* and sister to *T. acaciae* with high support (ML 100% and 1.00 BYPP). According to the similarities in morphology along with phylogenetic analyses, we propose *Pseudotorula sundara* as a synonym of *Torula sundara*.

Periconiaceae (Sacc.) Nann., Repertorio sistematico dei miceti dell'uomo e degli animali 4: 482 (1934).

Periconiaceae was accommodated as a distinct lineage in Massarineae by Tanaka et al. (2011) based on morpho molecular data. Four genera (*viz. Bambusistroma*, *Flavomyces*, *Noosia* and *Periconia*) are accepted with endophytic, saprobic and pathogenic nutritional modes (Sarkar et al. 2019; Hongsanan et al. 2020b, Samarakoon et al. 2020; Wijayawardene et al. 2022).

Fig. 46 *Torula sundara* (MFLU 21–0089, **new combination**). **a, b** Colonies on the host **c–e** Conidiophores and conidia **f–l** Conidia **m** Germinated conidium. Scale bars: c = 10 µm, d–m = 20 µm

Periconia Tode, Fung. mecklenb. sel. (Lüneburg) 2: 2 (1791).

Periconia was introduced by Tode (1791) and typified by *P. lichenoides*. The asexual morph of the genus has pale to dark brown branched or unbranched conidiophores (also referred to as stipe). Conidiogenous cells of *Periconia* are monoblastic or polyblastic, and formed at the terminal ends or intercalary parts of the conidiophore. *Periconia* produces spherical, asepete, catenate or solitary conidia in pale to dark-brown. Both sexual and hypomycetous asexual morphs are recorded in this genus (Tanaka et al. 2015; Liu et al. 2017). There are 187 epithets listed in Index Fungorum (2022a, b). *Periconia* has been reported as a plant pathogen, endophyte and a common saprobe in terrestrial and aquatic habitats with a cosmopolitan distribution (Ellis 1961, 1976; Markovskaja and Kačergius 2014; Liu et al. 2017).

Periconia byssoides Pers., Syn. meth. fung. (Göttingen)1: 18 (1801)

*Index Fungorum number: 144538; Faceoffungi number: FOF*09319; *Figs. 47, 48*

Saprobic on leaves of *Vigna unguiculata.* **Sexual morph**: Not observed. **Asexual morph**: *Conidiophores* with conidial heads were observed on foliar lesions of cowpea. Conidiophores observed after 2–3 weeks, simple, micro- and semi-macronematous, unbranched and branched, initially

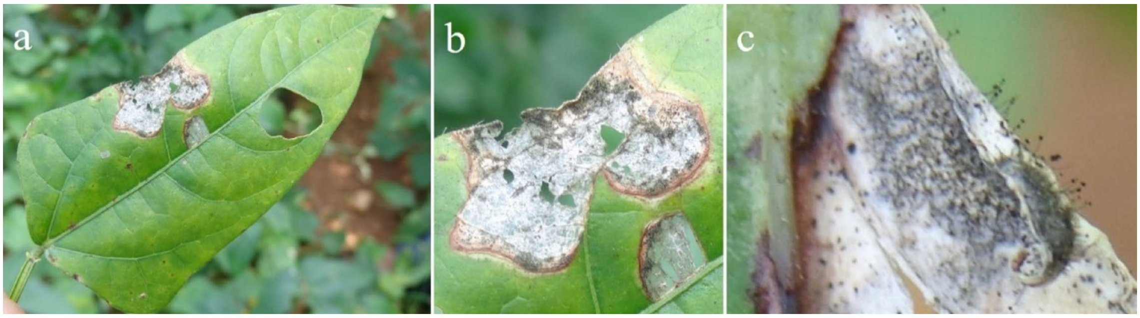


Fig. 47 Cowpea leaves showing the growth of *Periconia byssoides* on the necrotized lesions

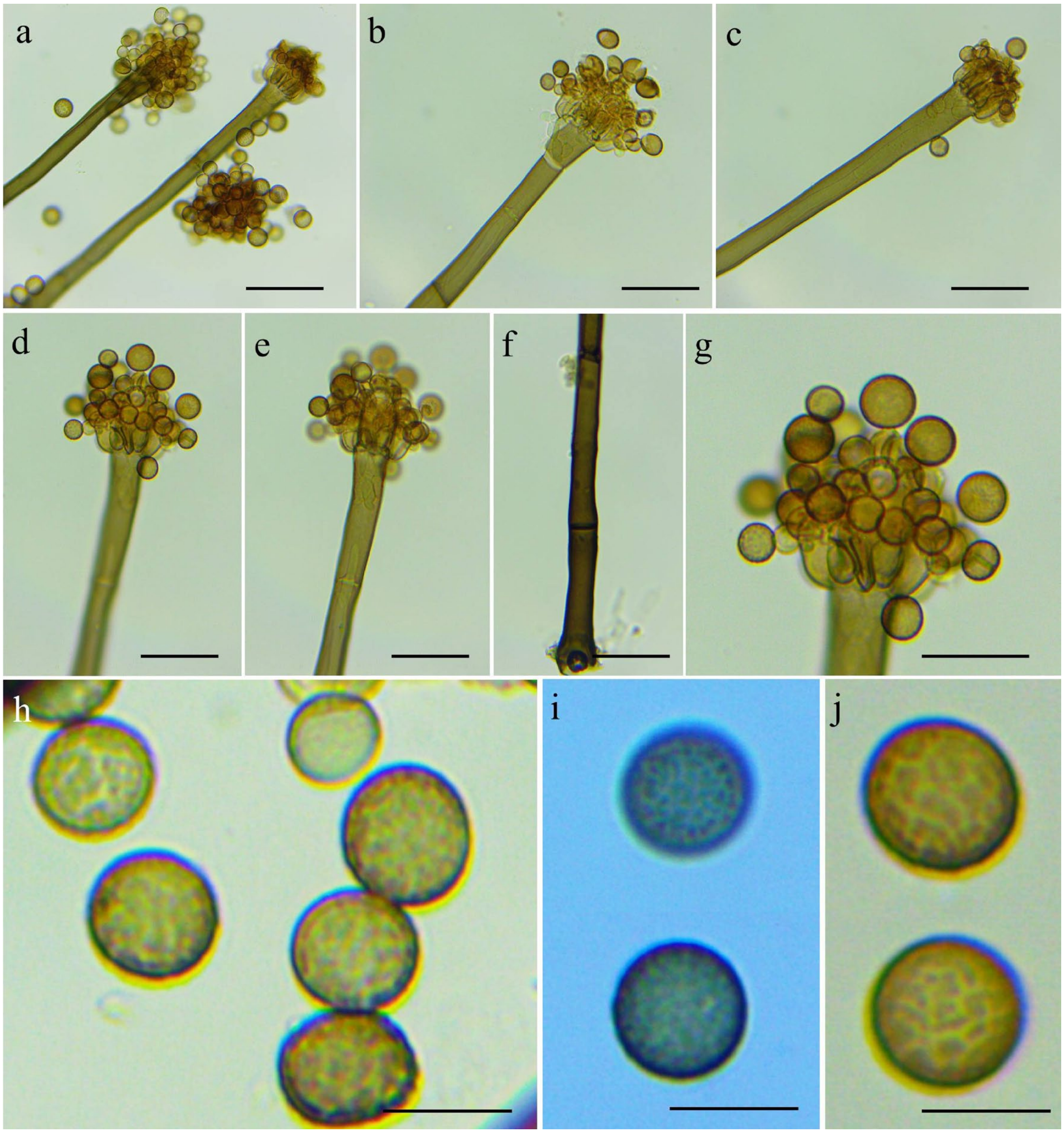


Fig. 48 ***Periconia byssoides*** (MD2, **new host and geographical record**): **a–c** Conidiophores terminating with heads of conidia **d–e** Heads of conidia showing phialides **f** – Basal part of conidiophores showing their distinct nature (color and septa) **g** Close view of the conidial head showing conidia and phialides **h–j** Conidia enlarged. Scale bars: **a – g** = 50 µm, **h – j** = 20 µm

Table 3 Comparative account of *Periconia* species with *P. byssoides* recorded on Cowpea from India

Species	Conidiophores	Conidia	Color	Habit	Reference
Periconia byssoides	Macronematous and proliferating with elongate apical cell and with branchlets	Spherical, verrucose; 8.5–14.4 (18.2) µm in diam	Pale brown to brown	On cowpea leaves	**Present study**
Periconia byssoides (Mason and Ellis 1953; Ellis 1971; Matsushima 1975)	Macronematous and proliferating with elongate apical cell and with branchlets	Spherical, verrucose; 10–12 (17) µm in diam	Pale brown to brown	Terrestrial saprobe	Markovskaja and Kačergius (2014)
Periconia pseudobyssoides (Markovskaja and Kačergius 2014)	Macronematous, with numerous proliferations and swollen apical cell without branchlets	Spherical to verrucose (12)15–17(20) µm in diam	Golden brown to reddish brown	Terrestrial saprobe	Markovskaja and Kačergius (2014)
Periconia cookei (Mason and Ellis 1953; Ellis 1971)	Macronematous and proliferations and swollen apex with without apical cell	Spherical, verrucose 13–16 µm in diam	Brown to dark brown	Terrestrial saprobe	Markovskaja and Kačergius (2014)
Periconia shyamala (Ellis 1971; Storey 2002)	Macronematous with elongate apical cell and branchlets	Spherical, verrucose 13–16(18)-22(25) µm in diam	Brown to dark brown	Terrestrial parasite or saprobe	Markovskaja and Kačergius (2014)
Periconia typhicola (Ellis 1976)	Macronematous branched inside the head	Spherical, verrucose; 11–17 µm in diam	Pale brown to brown	Terrestrial saprobe	Markovskaja and Kačergius (2014)
Periconia prolifica (Anastasiou 1963; Vrijmoed et al. 1982)	Micronematous, semimicronematous with proliferations	Subglobose, smooth, 7.5–15 µm in diam	Subhyaline to pale brown	Marine saprobe	Markovskaja and Kačergius (2014)

subhyaline to brownish, verruculose, and variable in length. *Conidiogenous cells* discrete, determinate, terminal or lateral, subglobose, mono- and polyblastic, smooth to verruculose, pale brown producing global verrucose conidia in acropetal chains (3–4 in number), 11.5–12.5 × 15 – 17 µm diam. ($\bar{x}$ = 11.9 × 15.2 µm, *n* = 20), conidia pale brown to brown verrucose. Conidiogenous cells were formed on an apical cell and in the collar region around the septa, sometimes on short hyaline or subhyaline branchlets. From primary, hyaline, globose conidiogenous cells numerous secondary conidiogenous cells arise, which produce short chains of spherical, commonly verruculose but sometimes verrucose, pale brown to brown conidia measured 8.5–11.4 µm diam.

Cultural characteristics: Culture on MEA reaching 35 mm after 20 days at 25 °C. Fungal colony appeared cottony with abundant white to orange-white aerial mycelium. In reverse colony dark olive to dark olivaceous-grey with concentric dark olivaceous-brown. Hyphae hyaline sometime greyish green, smooth and verruculose later becomes brown orange.

Material examined: India, Karnataka, Mysore, Doddamaragowdanahally, on foliar lesions of cowpea (*Vigna unguiculata* (*L.*) Walp.- Fabaceae) 18 May 2020, S. Mahadevakumar, Y.S. Deepika, N. Lakshmidevi (Specimen UOM-IOE 18/21), living culture (MD2).

GenBank numbers: OM811496 (ITS); OM811504 (LSU)

Notes: Detail descriptions and illustrations are presented in Mason and Ellis (1953) and Markovskaja and Kačergius (2014). Morphological inspection and measurements of conidiophores and conidia revealed that the fungal specimens described by Markovskaja and Kaergius (2014) for several Apiaceae hosts correspond well with the *P. byssoides*, which was based on lectotype material (Fries 1832). Phylogenetic analyses (Fig. 49) This is the first time that *P. byssoides* is reported from Fabaceae on *Vigna unguiculata* representing a new host record and geographical record (Table 3).

Periconia cortaderiae Thambugala & K.D. Hyde, in Thambugala et al., Mycosphere 8(4): 734 (2017)

Index Fungorum number: IF553165; Facesoffungi number: FoF03226; *Fig. 50*

Saprobic on decaying leaves of *Musa basjoo*. **Sexual morph:** Not obersved. **Asexual morph:** hyphomycetous. *Colonies* on host black, powdery, conidial masses are clearly visible on the host. *Mycelium* sub hyaline to pale brown or brown branched, having black conidial clusters *Conidiophores* 60–130 × 3 – 4 µm ($\bar{x}$ = 76.5 × 3.5 µm, *n* = 15), macronematous, mononematous, appear as single or a cluster, erect, rough-walled, sub hyaline, brown to dark brown, septate at some points, significantly branched and flexuous. Conidiogenesis can be observed at the apices of the branches or from the middle of the conidiophores. *Conidiogenous cells* 3.5–4.5 µm × 2.5–3.5 µm ($\bar{x}$ = 3.5 × 2.8 µm, *n* = 10), annellidic, monoblastic, discrete on the stipe, percurrent proliferations present as scars at the apex of the conidiophore. *Conidia* 4–8 × 4–7 µm ($\bar{x}$ = 6.8 × 6.2 µm, *n* = 40), appear as chains or single, globose, one-celled, immature conidia are hyaline to pale brown, mature conidia are brown to dark brown, smooth or minutely verruculose, thick- walled.

Culture characteristics: Conidia germinating on PDA within 36–48 h. Colonies on PDA, reach 15 mm after 18 days at 25 °C, at maturity, unevenly distributed radial furrows or linear marks were observed, surface notably rough at maturity with crenulate to crenate margin, the colony is completely black and powdery at maturity, moderately dense, reverse white to black.

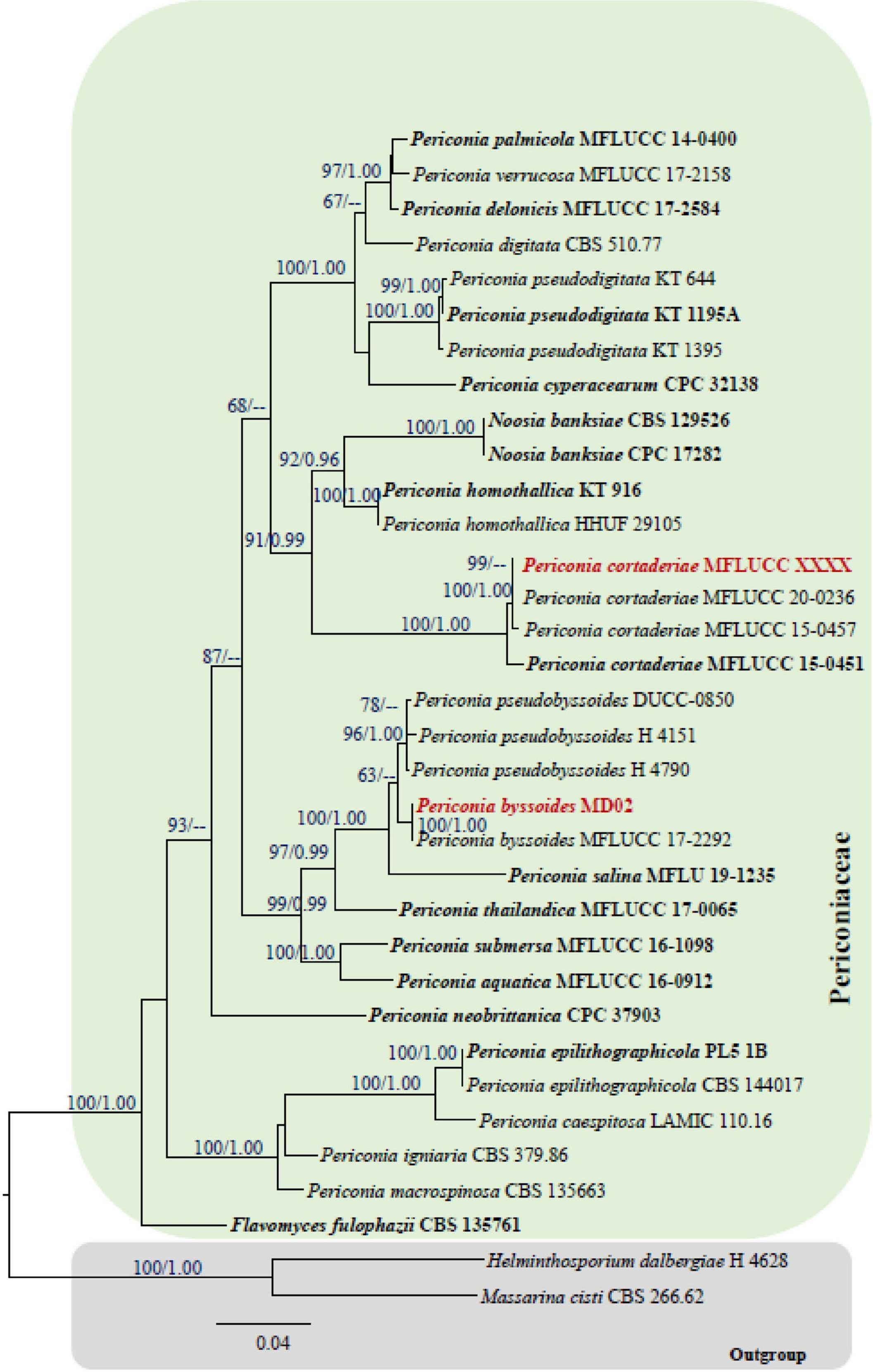
Material examined: Russia, Krasnodar region, Sochi, Khstinsky City District, M.V. Frunze Health Care Resort, park, on a dying leafstalk of *Musa basjoo* Siebold & Zucc. ex Iinuma (Musaceae), 15 October 2018, Timur S. Bulgakov, BNR-001 (MFLU 18–1896), living culture MFLUCC 22-0178.

Known hosts: *Cortaderia* sp. (Poaceae, Monocotyledon) (Thambugala et al. 2017); on *Caragana arborescens* (Fabaceae, Dicotyledon) (Phookamsak et al. 2019); on *Musa* sp. (Musaceae, Monocotyledon) (Samarakoon et al. 2021 and this study).

Distribution: From Russia (This study), from Thailand (Thambugala et al. 2017, Samarakoon et al. 2021; this study), from Yunnan, China (Phookamsak et al. 2019)

GenBank numbers: OP097674 (LSU), OP099358 (SSU), OP099551 (ITS), OP113822 (*tef1*)

Notes: Based on BLASTn search results of SSU, LSU, ITS sequence data, MFLUCC 22-0178, showed high similarity to *Periconia cortaderiae* (MFLUCC 18-0668) as follows; SSU = 99.76%, LSU = 99.88%, ITS = 99.80%. Our new collection is similar to the holotype of *P. cortaderiae* (Thambugala et al. 2017), except the length and the shape of the conidiophores. Our collection has short conidiophores with respect to the holotype (60–130 × 3–4 µm *vs*. 400–800 × 4–9.4 µm). The conidiophore of our strain is notably curved and branched compared to other collections. The conidiogenesis is also found as terminal and intercalary on the conidiophores in our strain. The other collections of *P. cortaderiae* only had terminal conidial formation with respect to our finding. There is no significant difference in the nucleotide base pair comparison of our strain with the ex-type strain. In our multigene phylogeny, MFLUCC 22-0178 grouped with *P. cortaderiae* (MFLUCC 15-0451, MFLUCC 18-0668, MFLUCC 20-0236) with strong statistical support (ML = 100%, BYPP = 1.00). In this study, we identify our new collection as *P. cortaderiae*, from *Musa* sp. (Monocotyledon), from Russia for the first time as a new geographical record.


Periconia palmicola MFLUCC 14-0400
97/1.00
Periconia verrucosa MFLUCC 17-2158
67/--
Periconia delonicis MFLUCC 17-2584
Periconia digitata CBS 510.77
100/1.00
99/1.00
Periconia pseudodigitata KT 644
100/1.00
Periconia pseudodigitata KT 1195A
Periconia pseudodigitata KT 1395
Periconia cyperacearum CPC 32138
68/--
100/1.00
Noosia banksiae CBS 129526
Noosia banksiae CPC 17282
92/0.96
100/1.00
Periconia homothallica KT 916
Periconia homothallica HHUF 29105
91/0.99
99/--
Periconia cortaderiae MFLUCC XXXX
100/1.00
Periconia cortaderiae MFLUCC 20-0236
100/1.00
Periconia cortaderiae MFLUCC 15-0457
87/--
Periconia cortaderiae MFLUCC 15-0451
78/--
Periconia pseudobyssoides DUCC-0850
96/1.00
Periconia pseudobyssoides H 4151
Periconia pseudobyssoides H 4790
63/--
Periconia byssoides MD02
100/1.00
100/1.00
Periconia byssoides MFLUCC 17-2292
93/--
97/0.99
Periconia salina MFLU 19-1235
99/0.99
Periconia thailandica MFLUCC 17-0065
100/1.00
Periconia submersa MFLUCC 16-1098
Periconia aquatica MFLUCC 16-0912
Periconiaceae
Periconia neobrittanica CPC 37903
100/1.00
Periconia epilithographicola PL5 1B
100/1.00
Periconia epilithographicola CBS 144017
100/1.00
Periconia caespitosa LAMIC 110.16
100/1.00
Periconia igniaria CBS 379.86
Periconia macrospinosa CBS 135663
Flavomyces fulophazii CBS 135761
100/1.00
Helminthosporium dalbergiae H 4628
Massarina cisti CBS 266.62
0.04
Outgroup

◂ **Fig. 49** Maximum likelihood tree revealed by RAxML from an analysis of a concatenated SSU, LSU, ITS and *tef*1 sequence dataset of the species in Periconiaceae, showing the phylogenetic position of *Periconia delonicis* (MFLUCC 20–0235). Bootstrap supports ≥ 60% and BYPP ≥ 0.95 are given above the branches as ML/BYPP. The tree is rooted with *Helminthosporium dalbergiae* (MAFF 243853) and *Massarina cisti* (CBS 266.62). Strains generated in this study are indicated in red bold. Ex–type strains are indicated in black **bold**. The scale bar 0.02 represents the expected number of nucleotide substitutions per site

Tubeufiales S. Boonmee & K.D. Hyde.

Notes: Tubeufiales includes three families *viz*. Bezerromycetaceae, Tubeufiaceae and Wiesneriomycetaeae with 56 genera (Wijayawardene et al. 2022).

Tubeufiaceae M.E. Barr, Mycologia 71(5): 948 (1979).

Notes: Barr (1979) defined Tubeufiaceae based exclusively on the generic type, *Tubeufia*, and treated it in Pleosporales. Based on unique morphology and multigene phylogenetic investigations, Boonmee et al. (2012) formed the order Tubeufiales and designated Tubeufiaceae as the typical family. Previously, 19 genera were compared in Tubeufiaceae (Boonmee et al. 2012). Following that, Lu et al. (2018) reappraised Tubeufiaceae and accepted 43 taxa to this family based on phylogenetic analyses and morphological evidence. With the expansion of fungal investigations, the family Tubeufiaceae presently contains 47 genera (Lu et al. 2018; Liu et al. 2019a, b, c, d; Wijayawardena et al. 2022).

Helicoma Corda, Icon. fung. (Prague) 1: 15 (1837)

Notes: *Helicoma* was introduced by Corda (1837) who treated *H. muelleri* as the type species. It is one of the earliest described helicosporous hyphomycete genera (Liu et al. 2019a, b, c, d). *Helicoma* species have been found in tropical and temperate locations (Boonmee et al. 2012, 2014; Lu et al. 2018; Brahmanage et al. 2017), and there are 59 records in the genus (Lu et al. 2018; Liu et al. 2019a, b, c, d; Barreto et al. 2021).

Helicoma aquaticum Y.Z. Lu, J.C. Kang & K.D. Hyde, in Lu et al. Fungal Diversity 92: 174 (2018).

Index Fungorum: 554836; Facesoffungi number: FoF04712; Fig. 51

Saprobic on decaying fruits of *Dipterocapus* sp. **Asexual morph**: Hyphomycetous, helicosporous. *Colonies* on the substratum superficial, gregarious, brown. *Mycelium* composed of partly immersed, partly superficial, hyaline to pale brown, septate, hyphae. *Conidiophores* macronematous, mononematous, cylindrical, erect, straight, unbranched, septate, 119–180 µm long, 6.5–7 µm wide, the lower part brown to dark brown, the upper part pale brown, smooth-walled. *Conidiogenous cells* holoblastic, mono- to polyblastic, integrated, intercalary, cylindrical, with denticles, arising laterally from the lower part of conidiophores, 10–15 × 5–9 µm ($\bar{x}$ = 12 × 7 µm, *n* = 20), brown, smooth-walled. *Conidia* solitary, pleurogenous, helicoid, tapering towards apex, rounded at tip, 33–37 µm diam. and conidial filament 3.5–6 µm wide ($\bar{x}$ = 5 µm, *n* = 20), 290–376 µm long ($\bar{x}$ = 321 µm, *n* = 20), 20–27-septate, constricted at septa, coiled $1^1/_2$–$4^1/_4$ times, becoming loosely coiled or uncoiled in water sometimes, hyaline to pale brown, smooth-walled. **Sexual morph**: Not observed.

Culture characteristics: Colonies growing on PDA at 25 °C, edge undulate, flat, circular, spreading, with fluffy pale brown air-mycelium, pale brown to brown mycelium. reverse dark brown, pale brown at the edge side, lobate at the center, without pigmented.

Material examined: Thailand, Chiang Mai Province, MRC, on dead fruits of *Dipterocarpus* sp. (Dipterocarpaceae), 15 August 2019, Xia Tang, Dip 18 (MFLU 21-0176), living culture MFLUCC 21-0141.

GenBank numbers: OM232106 (ITS), OM248446 (LSU), OM272846 (*tef1*)

Hosts: Unindentified submerged decaying wood (Lu et al. 2018), dead fruits of *Dipterocarpus* sp. (*Dipterocarpaceae*) (this study).

Distribution: Thailand (Lu et al. 2018, this study).

Notes: *Helicoma aquaticum* was described and illustrated by Lu et al. (2018) from an unidentified submerged decaying wood in Thailand. Based on the morphological characteristics, our collection shares similar morphology with the ex-type strain (Fig. 52). Comparisons of ITS, LSU and *tef1* sequence data between our collection and the holotype showed that they are 2/ 549 bp (0.3%) of ITS, 9/1201 (0.7%) of LSU and 9/879 bp (1%) of *tef1*. We consider that our collection is the same as *Helicoma aquaticum* following the guidelines for species delineation proposed by Jeewon and Hyde (2016). This is the first report of *Helicoma aquaticum* on a *Dipterocarpus* sp. in Thailand.

Wiesneriomycetaceae Suetrong, Rungjind., Somrith. & E.B.G. Jones

Based on morphology and molecular phylogeny, Suetrong et al. (2014) introduced Wiesneriomycetaceae as order incertae sedis. Pratibha et al. (2015) placed Wiesneriomycetaceae in Tubeufiales. Bezerra et al. (2017) introduced Wiesneriomycetales to accommodate Wiesneriomycetaceae based on morphological characteristics and phylogenetic analyses. Based on phylogenetic inference and divergence times estimates, Liu et al. (2017) considered Wiesneriomycetales as a synonym of Tubeufiales. Hongsanan et al. (2020b) and Wijayawardena et al. (2020, 2022) accepted this family in Tubeufiales.

Wiesneriomyces Koord., Verh. K. Akad. Wet., tweede section 13(4): 246 (1907).

Fig. 50 ***Periconia cortaderiae*** (MFLU 18–1896, **new host and geographical record**). **a – b** Colonies on host **c – f, i, j** Conidiophores bearing conidia **g, h, k** Conidiogenesis from terminal and intercalary parts of the conidiophore **l-p** Conidial chains and conidia. Scale bars: **a** = 3 mm, **b** = 3.5 mm, **c** = 50 µm, **e – j** = 15 µm, **d, k – p** = 5 µm

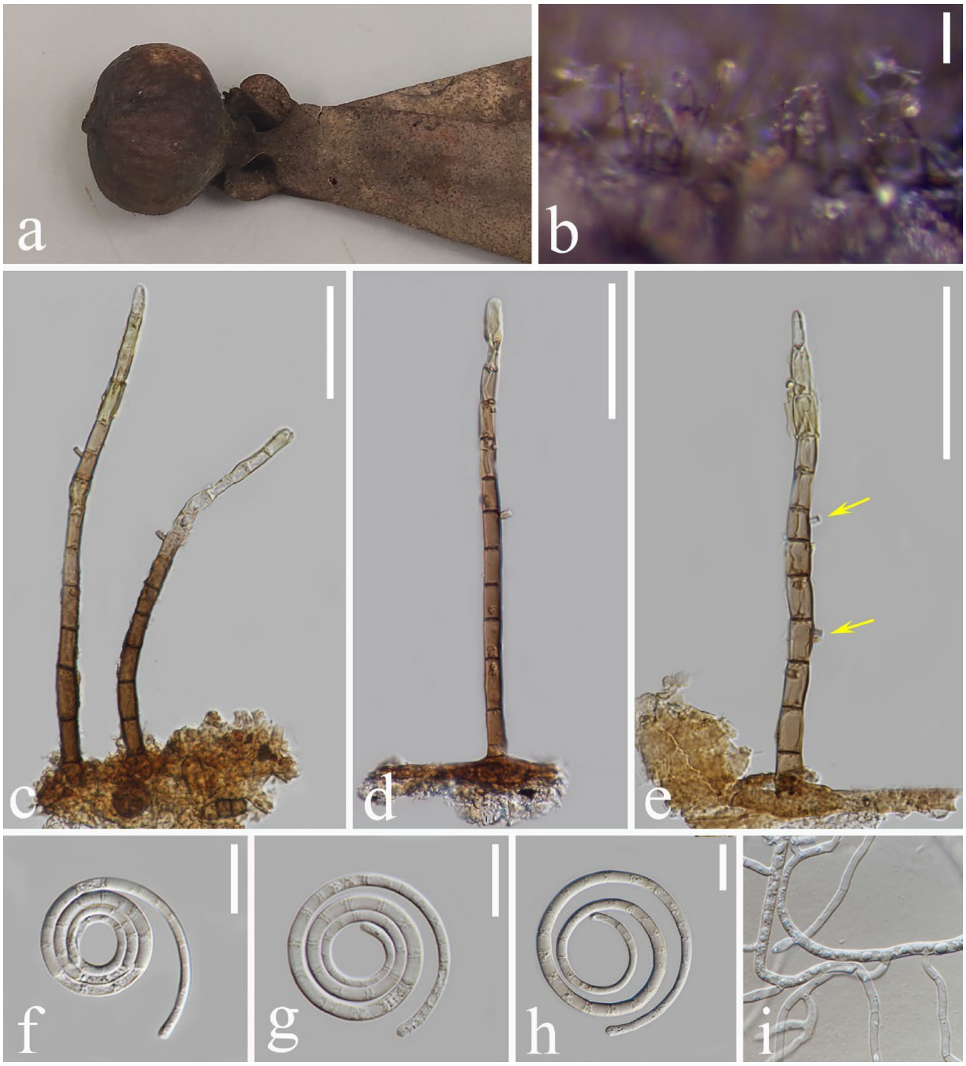


Fig. 51 ***Helicoma aquaticum*** (MFLU 21–0176, **new host record**) **a, b** Host. **c, d** Conidiophores. **e** Conidiophore with conidiogenous cells. **f–h** Conidia. **i** Germinated conidium. Scale bars: **b** = 100 µm, **c–e** = 50 µm, **f–h** = 10 µm

Notes: *Wiesneriomyces* species have setose, branched conidiophores, single-chain hyaline conidia, with a short isthmi separating the conidia (Suetrong et al. 2014; Hongsanan et al. 2020b). The sexual morph for this genus is not yet reported.

Wiesneriomyces laurinus (Tassi) P.M. Kirk, Trans Br Mycol Soc 82: 748 (1984)

Index Fungorum number: *IF107371; Facesoffungi number: FoF09126, Fig. 53*

Saprobic on dead leaves of *Dimocarpus longan*. **Sexual morph**: Not observed. **Asexual morph**: Colonies effuse, yellowish-brown. *Conidiomata* sporodochial, solitary, 3–10 setae arising from the margins of the sporodochial stalk. *Setae* 140–300 × 3–8 µm ($\bar{x}$ = 180 × 5 µm, *n* = 30), subulate, apex acute, septate, thick-walled, deep brown, arising on leaf surface. *Conidiophores* 30–50 × 2–4 µm ($\bar{x}$ = 40 × 3 µm, *n* = 21), emi-mucronematous, close to one another, brown to sub-hyaline at the base, hyaline towards the apex, septate, irregularly branched. *Conidiogenous cells* 6–9 × 2–4 µm ($\bar{x}$ = 7 × 3 µm, *n* = 26), located at the conidiophores terminal, cylindrical, hyaline, integrated. *Conidia* 50–70 × 2–4 µm ($\bar{x}$ = 60 × 3 µm, *n* = 30), solitary, clumped together into a semi-mucus, hyaline, smooth, sandy, cylindrical, taper towards both ends that are obtusely rounded, 5–6-septate, prominently constricted at septa, median cells 6–10 × 2–4 µm long, terminal cells 6–10 × 2–4 µm.

Culture characteristics: Colonies on PDA, 37–42 mm diam. after 3 weeks, colonies from above: medium dense, flat, slightly raised, rough surface with irregular edges, fluffy not smooth, leaden grey to light grey at the margin, black to ollvnceous black in the centre; reverse: grey to light grey at the margin, grey-brown to grey in the centre.

Material examined: China, Guangdong Province, Guangzhou City, Haizhu District, Zhongkai University of Agriculture Engineering, 23° 6′ 32″ N, 113° 16′ 37″ E, alt. 20 m, on the dead leaves of *Dimocarpus longan* Lour. (Sapindaceae),

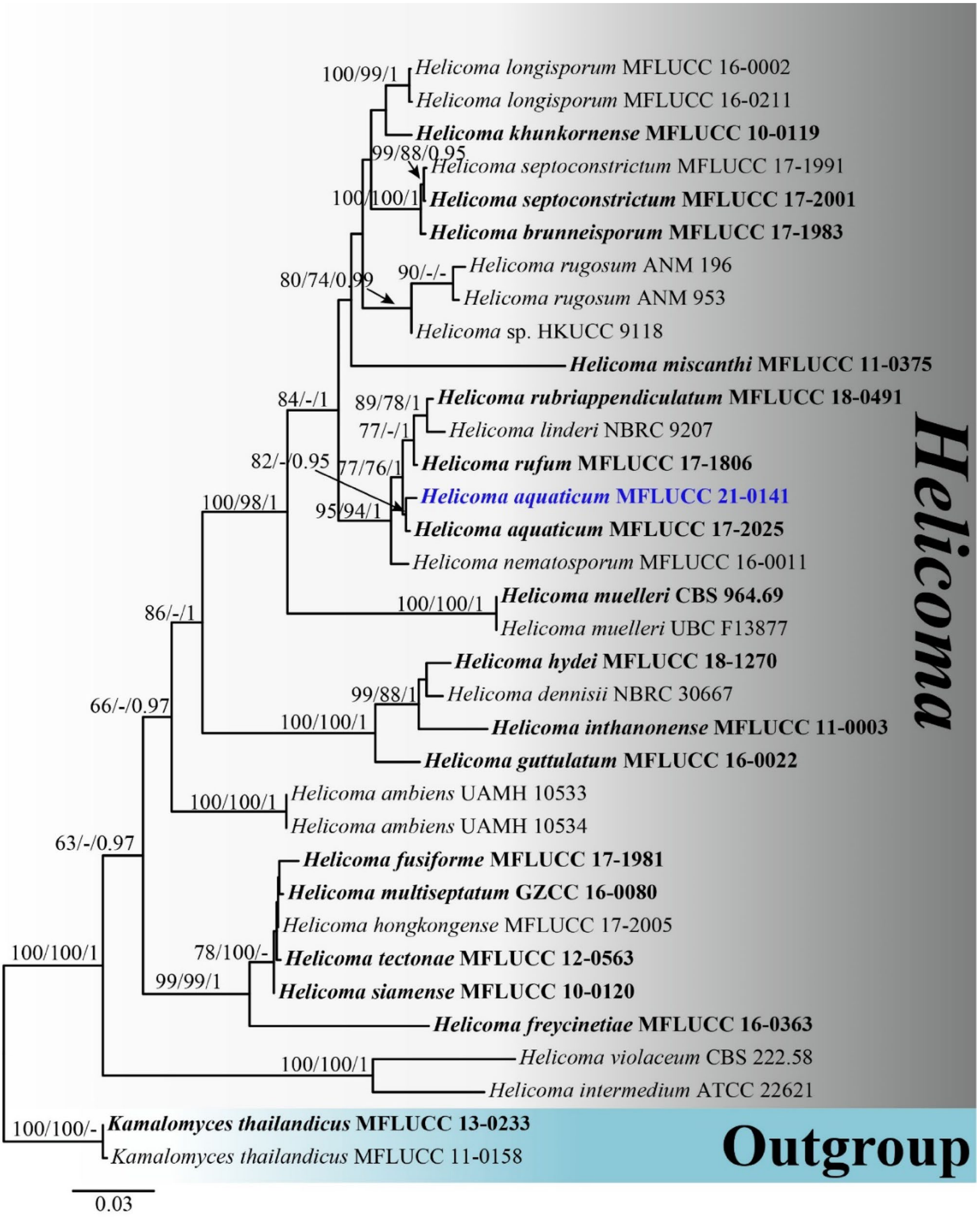


Fig. 52 Phylogram generated from parsimony analysis based on combined ITS, LSU and *tef1* sequence data of *Helicoma*. ML and MP bootstrap support values ≥ 70% are indicated above the nodes, and branches with Bayesian posterior probabilities ≥ 0.95 are given above the nodes. The ex-types (reference strains) are in **bold**; the new isolates are in blue bold. The tree is rooted with *Kamalomyces thailandicus* (MFLUCC 13–0233) and *Kamalomyces thailandicus* (MFLUCC 11–0158)

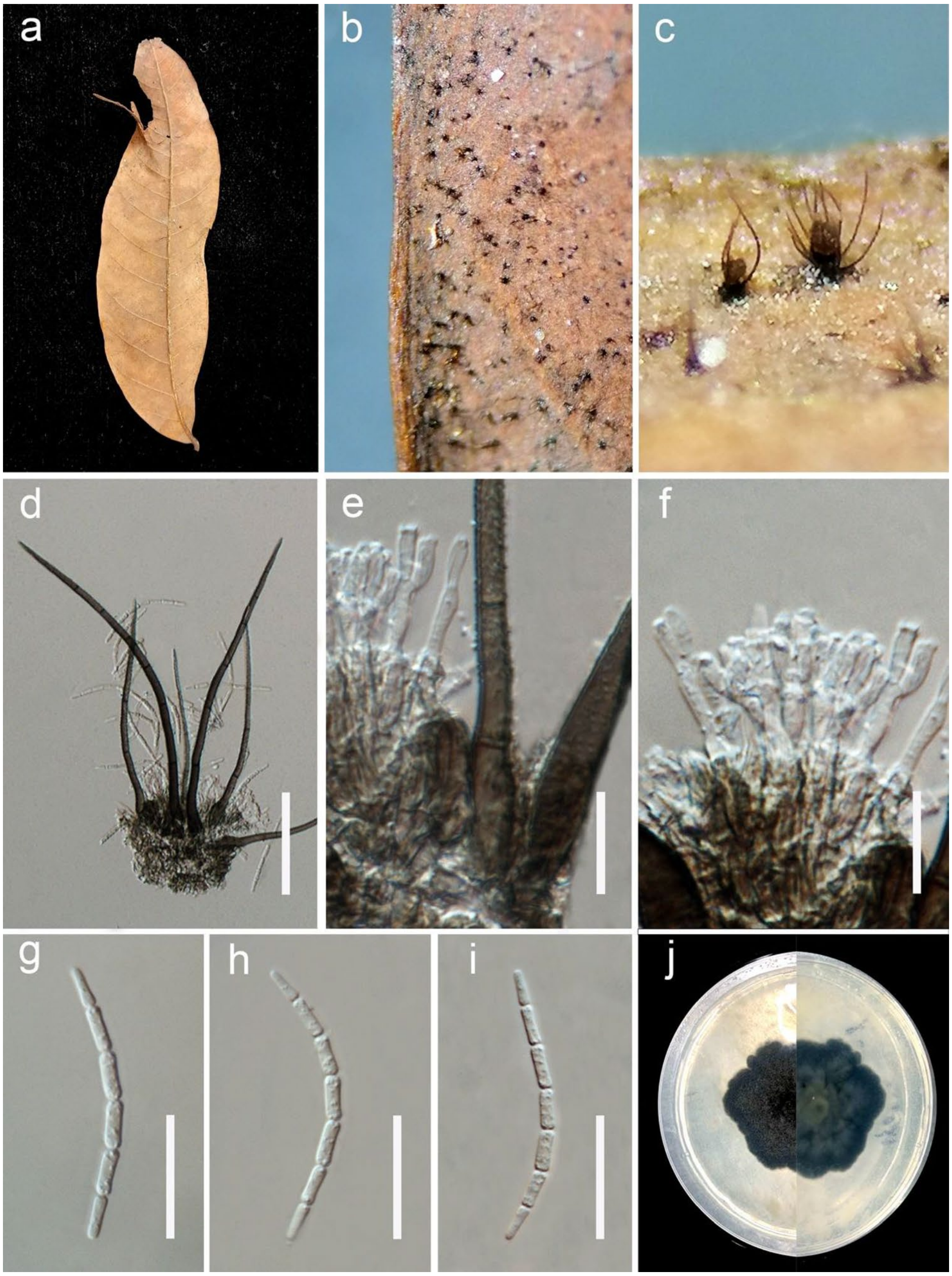


Fig. 53 ***Wiesneriomyces laurinus*** (ZHKU 22–0008, **new host record**) **a–c** Appearance of sporodochia on host. **d** Squash mount of sporodochium. **e, f** Conidiophores with setae. **g–i** Conidia. **j** Colonies on PDA. Scale bars: **d** = 100 μm, **e, f** = 20 μm, **g, i** = 25 μm

23 July 2021, YH. Yang & CF. Liao (ZHKU 22-0008); living cultures ZHKUCC 22-0008, ZHKUCC 22-0009.

Known hosts: *Carissa carandas* (Apocynaceae), *Clusia rosea* (Clusiaceae), *Hibiscus elatus* (Malvaceae), *Ficus ampelas* (Moraceae), *Gyranthera caribensis* (Malvaceae), leaf litter of *Caesalpinia echinata* (Fabaceae), *Laurus nobilis* (Lauraceae), *Ocotea leucoxylon* (Lauraceae), *Pandanus urophyllus* (Pandanaceae), *Psidium guajava* (Myrtaceae), *Roystonea regia* (Arecaceae), *Talipariti elatum*, *Theobroma cacao* (Malvaceae), *Thuja occidentalis* (Cupressaceae), *Dimocarpus longan* (Sapindaceae)

Distribution: Brazil (da Silva and Grandi 2008), China (this study), Cuba (Delgado-Rodriguez et al. 2002), Hong Kong (Lu et al. 2000; Zhuang 2001), Mexico (Begerow et al. 2018), Myanmar (Thaung 2008), Russia (Melnik and Popushoi 1992), United Kingdom (Dennis 1986), Venezuela (Castaneda-Ruiz et al. 2003).

GenBank numbers: ZHKUCC 22-0008—OM780294 (LSU), OM780298 (SSU), OM780284(ITS)

ZHKUCC 22-0009—OM780295 (LSU), OM780306 (SSU), OM780286 (ITS)

Notes: Our two strains (ZHKUCC 22-008 and ZHKUCC 22-009) share similar characters with *Wiesneriomyces*

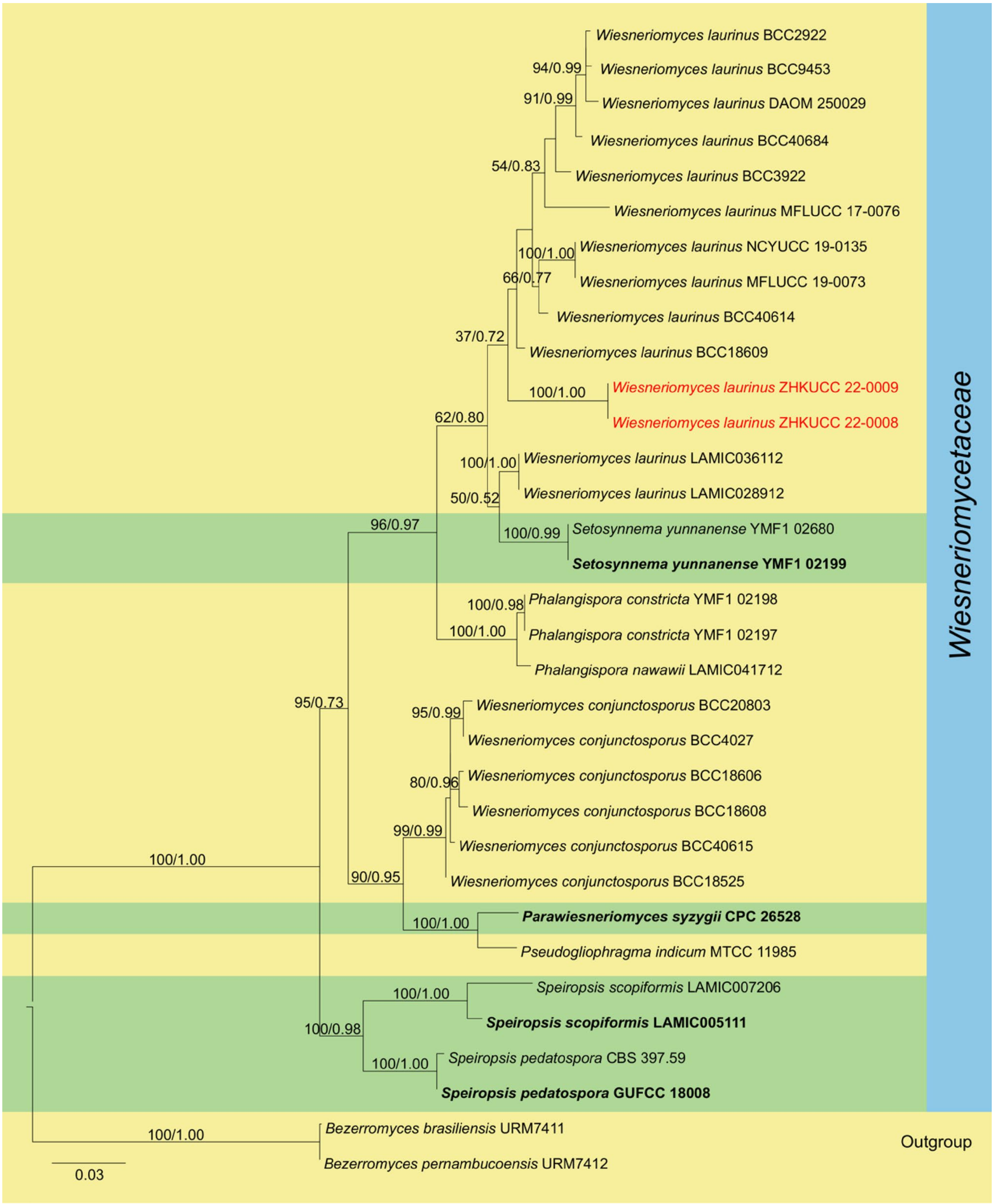


Fig. 54 The best scoring RAxML tree for *Wiesneriomycetaceae*, for combined dataset of LSU, SSU and ITS sequence data. The tree is rooted with *Bezerromyces brasiliensis* (URM7411) and *Bezerromyces pernambucoensis* (URM7412). Ex-type strains are in **bold** and newly generated sequences are in red. Bootstrap support values for ML ≥ 50% and BYPP ≥ 0.95 are given above the nodes

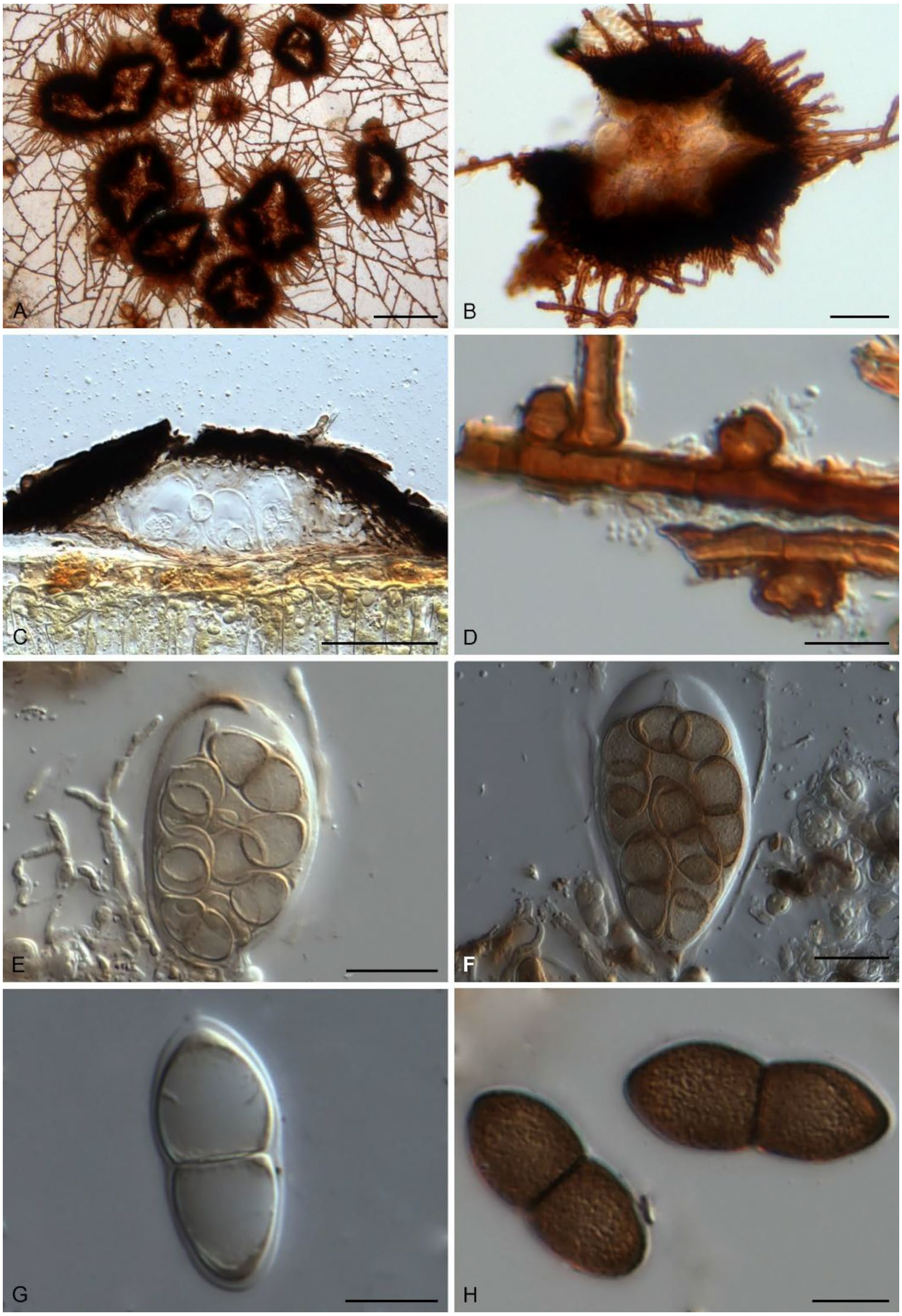


Fig. 55 ***Asterina brigadeirensis*** (VIC 44217, **holotype**) **a** Colony with open thyriothecia and surface mycelium. **b** Ascomata opened by a central star-shaped fissure. **c** Cross section of the ascomata. **d** Globose to pyriform unicelular appressoria. **e** Immature ascus with pseudoparaphyses. **f** Mature ascus. **g** Immature ascospores**. h** Brown and verruculose ascospore. Scale bars: **a** = 200 µm, **b–c** = 50 µm, **d–e–f** = 20 µm, **d** = 10 µm, **g–h** = 10 µm

laurinus (Heredia et al. 2000; Rajashekhar and Kaveriappa 2000; Suetrong et al. 2014; Pratibha et al. 2015; Tennakoon et al. 2021). The phylogeny also showed that our strains (ZHKUCC 22-008 and ZHKUCC 22-009) clustered with other *Wiesneriomyces laurinus* strains (closer to BCC18609), with moderate statistical support (Fig. 54). This is the first report of *Wiesneriomyces laurinus* on *Dimocarpus longan*.

Dothideomycetes orders incertae sedis

Asterinales M.E. Barr ex D. Hawksw. & O.E. Erikss.

Notes: The order was introduced by Hawksworth and Eriksson (1986), based on the type species of the order, *Asterina melastomatis* Léveillé, which had its DNA extracted, sequenced and studied phylogenetically for the first time by Guatimosim et al. (2015), demonstrating that the Asterinales is polyphyletic. Based on molecular data of the type species, Asterinales *stricto* sensu includes two families, namely: Asterinaceae and Parmulariaceae (Guatimosim et al. 2015; Giraldo et al. 2017; Phookamsak et al. 2019; Johnston and Park 2019; Hongsanan et al. 2020a; Le Renard et al. 2020; Firmino and Pereira 2021).

Asterinaceae Hansford, Mycol. Pap. 15: 188 (1946)

Notes: Asterinaceae was proposed by Hansford (1946), undergoing several modifications over time in relation to the genera belonging to the family. Asterinaceae is polyphyletic and the Asterinaceae *stricto* sensu comprises the species grouping with the type species, *Asterina melastomatis*.

Asterina Léveillé, Annls Sci. Nat., Bot., sér. 3 3: 59 (1845)

Notes: The genus was described by Léveillé (1845), having *Asterina melastomatis* as the type species. The genus is characterized by having circular shaped ascomata, opening by a star-shaped fissure, with absence of hypostroma, adhering to the host by superficial hyphae with lateral appressoria (hyphopodia), bitunicate asci disposed as an upright palisade layer, and 2–celled brownish ascospores.

Asterina brigadeirensis A.L. Firmino & O.L. Pereira, ***sp. nov.***

Index Fungorum number: *IF900066*; *Facesoffungi number*: *FoF13383; Fig. 55*

Etymology: Name refers to the mountain range, where the fungus was collected, Serra do Brigadeiro.

Holotype: VIC 44217

Sexual morph*:* *Colonies* amphigenous, circular to irregular, single to confluent, dark brown, black, 0.1–5 mm diam. *Hyphae* straight to slightly flexuous, branching irregularly, brown, septate, hyphal cells cylindrical, 4.5–7.5 µm diam., smooth. *Appressoria* numerous, entire to lobate, sessile, lateral, alternate to unilateral, never opposed, globose to pyriform, unicellular, straight to angular, 7.5–10 × 6–9.5 µm, brown, penetration peg central on the appressorial cell. *Ascomata* superficial, thyriothecia, scutiform, on top of mycelial mat, circular to ellipsoid, single to confluent, fringed at margins, randomly distributed in the colony, 135–262.5 µm diam., opening by a central star-shaped fissure to an irregular fissure, dark brown to black; wall of *textura radiata to irregulate* on cells isodiametric to cylindrical. *Pseudoparaphyses* cylindrical, filiform, septate, unbranched, hyaline, up to 2.5 µm wide. *Asci* bitunicate in structure, fissitunicate, disposed as an upright palisade layer, ovoid to cylindrical, 8-spored, hyaline, 65–95 × 35–45 µm. *Ascospores* cylindrical to oblong, ends rounded, straight or slightly arched, 1-septate, constricted at the median septum, hyaline, becoming brown at maturity, verruculose, 30–35 × 12.5–16 µm. **Asexual morph*:*** Not observed*.*

Material examined: Brazil, Minas Gerais, Araponga, on living leaves of *Miconia cinnamomifolia* Naudin (Melastomataceae), 10 September 2014, A.L. Firmino (VIC 44217, **holotype**).

GenBank numbers: MZ475298 (LSU)

Notes: *Asterina brigadeirensis* differs from the species previously reported on Melastomataceae (Léveillé 1845; Hennings 1904, 1909; Theissen 1912, 1913; Sydow and Sydow 1916; Yates 1917; Maublanc 1920; Ryan 1924, 1928; Sydow 1927, 1930; Sydow and Petrak 1929; Chardón and Toro 1930; Orejuela 1944; Petrak 1950; Hansford 1954; Yamamoto 1957; Hosagoudar and Abraham 2000). It is closest to *A. venezuelana*, which has smaller and ovoid to conoid appressoria, smaller and ovoid to clavate asci, and smaller and dark brown ascospores. *Asterina brigadeirensis* is easily separated from *A. amadelpha*, *A. belluciae*, *A. centroniae*, *A. chrysophylli*, *A. confertissima*, *A. hypophyla*, *A. maublancii*, *A. melanotes*, *A. melastomatis*, *A. melastomatis-candidi*, *A. memecylonicae*, *A. pulla*, *A. schlechteriana*, *A. sinsuieiensis*, *A. uribei* in having verruculose ascospores. *Asterina antioquensis* is distinct from the new species in having ovoid to ellipsoid appressoria, smaller asci, and smaller ascospores with an upper third septum. *Asterina astroniae* has narrow hyphae, smaller and ovoid appressoria, smaller and subglobose to ovoid asci, and finally smaller ascospores. *Asterina denigrata* differs from *Asterina brigadeirensis* in the hypophyllous colonies, smaller ascomata and asci with 2–6 spores, and smaller and dark brown ascospores. *Asterina hughesii* differs in the narrow appressoria, smaller and spatulate asci, lacking pseudoparaphyses, and smaller ascospores. *Asterina melastomatacearum* differs from *Asterina brigadeirensis* in the smaller asci, and smaller and ellipsoid-ovoidal ascospores. *Asterina madikeriensis* differs in the colonies epiphyllous, entire appressoria and smaller ascospores with tuberculate wall. *Asterina melastomaticola* differs in the narrow hyphae, lacking pseudoparaphyses, and much smaller ascospores with echinulate ornamentations. *Asterina miconiae* differs from *Asterina brigadeirensis* in the smaller and cylindrical to subglobose appressoria, smaller and elliptical-clavate asci, and smaller ascospores. *Asterina miconiicola* differs in the much smaller ascospores with an upper third septum. *Asterina theissenii* differs in having narrow and dark brown hyphae, cylindrical to hemispherical appressoria, lacking pseudoparaphyses, and much smaller asci and ascospores. *Asterina transiens* differs from new species in the cylindrical appressoria, smaller and elliptical asci, and much smaller ascospores. *Asterina venezuelana* differs in the narrow and dark brown hyphae, smaller and ovoid to clavate asci, and smaller and dark brown ascospores. Finally, *Asterina lopi*, described below differs from the new species in having smaller and cylindrical to globose appressoria, smaller and ovoid to subclavate asci, and much smaller ascospores. (Léveillé 1845; Hennings 1904, 1909a; Theissen 1912, 1913; Sydow and Sydow 1916; Yates 1917; Maublanc 1920; Ryan 1924, 1928; Sydow 1927, 1930; Sydow

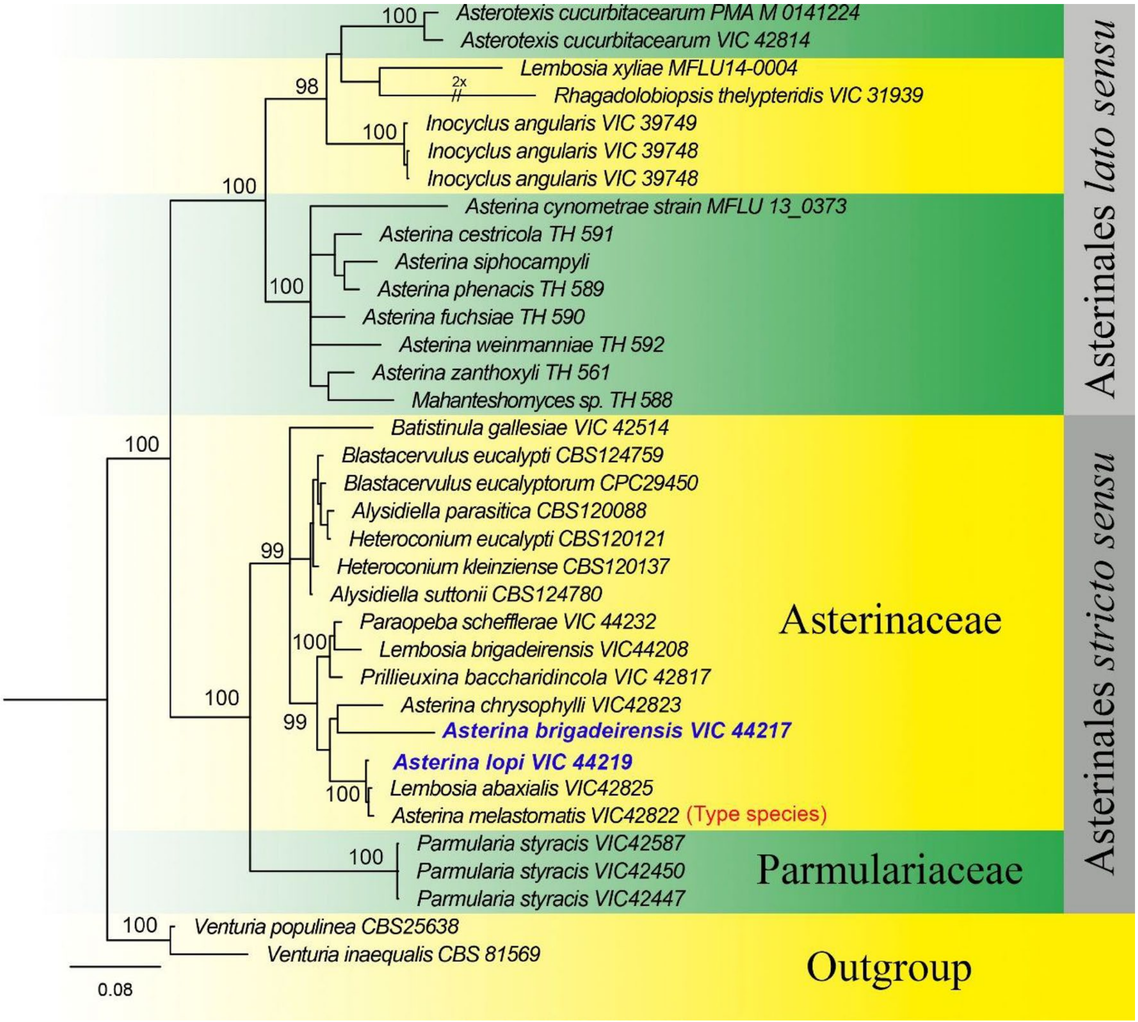


Fig. 56 The phylogenetic tree was obtained by Bayesian inference methods using the sequences of the LSU region. The posterior probability values are indicated at the nodes. Strain numbers are indicated after species names. New sequence data is in bold and blue. The analyses included 33 strains including representative genera of Asterinales *stricto* sensu and Asterinales *lato* sensu. The tree is rooted with *Venturia populina* (CBS 256.38) and *V. inaequalis* (CBS 815.69) (Pleosporales) as outgroup

and Petrak 1929; Chardón and Toro 1930; Orejuela 1944; Petrak 1950; Hansford 1954; Yamamoto 1957; Hosagoudar and Abraham 2000; Hosagoudar 2006). Based on our phylogenetic analyses (Fig. 56) and morphological analyses, herein we introduce a new species, *A. brigadeirensis*. *Asterina brigadeirensis* is the tenth species of *Asterina* reported on hosts belonging to Melastomataceae in Brazil, and the twelfth on *Miconia*.

Asterina lopi A.L. Firmino & O.L. Pereira, ***sp. nov.***

Index Fungorum number: IF900067; Facesoffungi number: FoF13384; Fig. 57

Etymology: The name refers to the mountain range, where the fungus was collected, Serra do Lopo.

Holotype: VIC 44219

Sexual morph*:* *Colonies* epiphyllous, circular to irregular, single to confluent, black, 1–6 mm diam. *Hyphae* straight to flexuous, branching unilaterally or irregularly, brown, septate, hyphal cells cylindrical, 4–4.5 µm diam., smooth. *Appressoria* numerous, entire to irregularly lobate, sessile, lateral, alternate to unilateral, never opposed, cylindrical to globose, unicellular, straight to angular, 5–7.5 × 5–6 µm, brown, penetration peg central on the appressorial cell. *Ascomata* superficial, thyriothecia, scutiform, on top of mycelial mat, circular to ellipsoid, single to confluent, fringed at margins, randomly distributed in the colony, 112–212.5 µm diam., opening by a central star-shaped fissure, dark brown; wall of *textura radiate* to *irregulata*, cells isodiametric to cylindrical to irregular. *Pseudoparaphyses* cylindrical, filiform, septate, unbranched, hyaline, up to 2.5 µm wide. *Asci* bitunicate

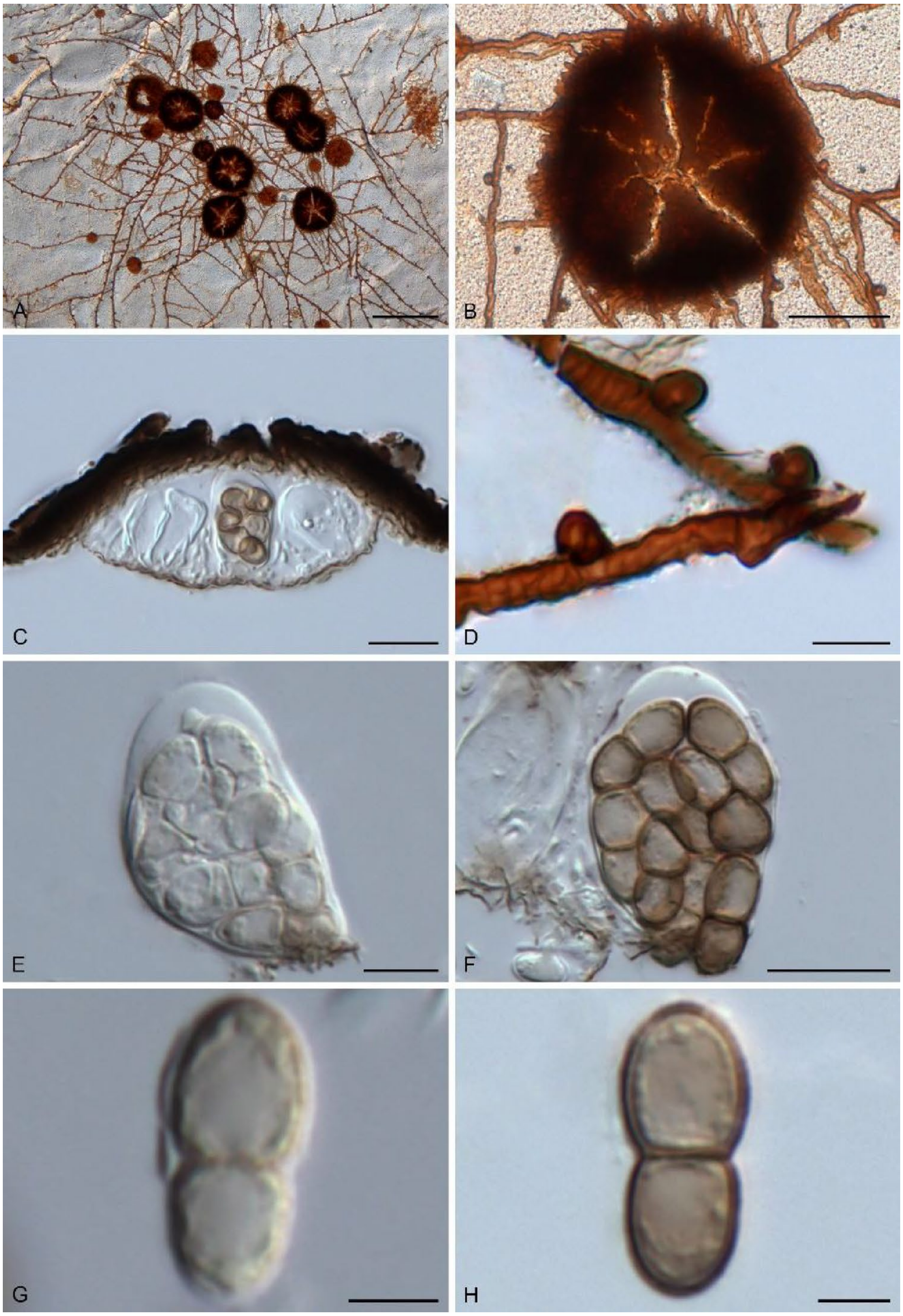


Fig. 57 ***Asterina lopi*** (VIC 44219, **holotype**) **a** Colony with open thyriothecia and surface mycelium. **b** Ascoma opened by a central star-shaped fissure. **c** Cross section of the ascoma. **d** Cylindrical to globose unicelular appressoria. **e** Immature ascus. **f** Mature ascus. **g** Immature ascospores. **h** Mature brown ascospores. Scale bars: **a** = 200 µm, **b** = 50 µm, **c–f** = 20 µm, **d–e** = 10 µm, **g–h** = 5 µm

in structure, fissitunicate, disposed as an upright palisade layer, ovoid to subclavate, 8-spored, and hyaline, 35–55 × 20–25 µm. *Ascospores* cylindrical to oblong, ends broadly rounded, straight, 1-septate, constricted at the median septum, hyaline, becoming pale brown to brown at maturity, verruculose, 12.5–15 × 6–7 µm. **Asexual morph***:* Not observed.

Material examined: Brazil, Minas Gerais, Extrema, on living leaves of *Miconia* sp. (Melastomataceae), 24 December 2014, A.L. Firmino & S.R. Pacheco (VIC 44219, **holotype**).

GenBank numbers: MZ475299 (LSU)

Notes: Twenty-seven species of *Asterina* have been reported previously in association with living leaves of melastomataceous hosts. *Asterina guianensis* on *Miconia guianensis* from Costa Rica and *Miconia mirabilis* from Puerto Rico and Virgin Islands, *A. racemosae* on *Miconia racemose* from Puerto Rico, and *A. tetrazygiae* on *Tetrazygia*

Table 4 Host, country and source details of *Asterina* species in Melastomataceae

Species on	Host	Source and country
A. amadelpha Syd	*Conostegia oerstediana*	Sydow & Petrak (1929), Costa Rica
A. antioquensis (Toro) Garcés	*Miconia ciliate*. *M. milleflora* and *M. dodonaea*	Chardón & Toro (1930), Colombia, Venezuela
A. astroniae H.S. Yates	*Astronia* sp.	H.S. Yates (1917), Philippines
A. belluciae Henn	*Bellucia* sp.	Hennings (1904), Brazil
***A. brigadeirensis* A.L. Firmino & O.L. Pereira**	***Miconia cinnamomifolia***	**This study, Brazil**
A. centroniae Petr	*Centronia excelsa*	Petrak (1950), Ecuador
A. confertissima Speg	*Arthrostemma campanulare*	Syd. & P. Syd. (1916), Brazil
A. chrysophylli Henn	*Miconia acinodendron*, *M. laevigata*, *M. prasina* and *Henriettea succosa*	Guatimosim et al. (2015), Brazil, Trinidad and Tobago. Puerto Rico and the Virgin Islands
A. denigrata Petr	*Blakea* sp.	Sydow & Petrak (1929), Costa Rica
A. hughesii Hosag. & T.K. Abraham	*Miconia racemosa*	Hosagoudar & Abraham (2000), Puerto Rico
A. hypophyla Berk. ex Theiss	Melastomataceae member	Berkeley ex Theissen (1912), Guatemala
***A. lopi* A.L. Firmino & O.L. Pereira**	***Miconia* sp.**	**This study, Brazil**
A. madikeriensis Hosag	*Memecylon* sp.	Hosagoudar (2006), India
A. maublancii (G. Arnaud) Maubl	Melastomataceae member	Maublanc (1920), Brazil
A. melanotes Syd	*Blakea* sp. and *Miconia granulosa*	Sydow & Petrak (1929), Costa Rica, Colombia
A. melastomatacearum (Henn.) Theiss	*Melastoma* sp.	Theissen (1913), Brazil
A. melastomaticola Hansf	*Melastoma malabathricum*	Hansford (1954), Indonesia
A. melastomatis Lév	*Miconia* sp.	Léveillé (1845), Brazil
A. melastomatis-candidi W. Yamam	*Melastoma candidum*	Yamamoto (1957), China
A. memecylonicae R.W. Ryan	*Memecylon edule*	Ryan (1928), India
A. miconiae Theiss	*Miconia* sp. and *M. rubiginosa*	Theissen (1913), Brazil
A. miconiicola R.W. Ryan	*Miconia racemosa*	Ryan (1924), Puerto Rico, Dominican Republic
A. pulla Lév	Melastomataceae member	Léveillé (1845), Bolivia
A. schlechteriana Syd	*Clidemia dentata*	Sydow (1927), Costa Rica
A. sinsuieiensis W. Yamam	*Barthea formosana*	Yamamoto (1957), China
A. theissenii R.W. Ryan	*Miconia* sp.	Ryan (1924), Puerto Rico
A. transiens Theiss	*Miconia candolleana*	Theissen (1913), Brazil
A. uribei Toro	*Miconia toroi* and *M. ciliate*	Chardón & Toro (1930), Colombia, Venezuela
A. venezuelana Syd	*Clidemia* sp., *C. bonplandii* and *C. hirta*	Sydow (1930), Venezuela

sp., and *Tetrazygia elaeagnoides* from Puerto Rico and Virgin Islands, were described by Ryan (1924) and not used in the comparisons for having an ostiolar opening, a characteristic that does not belong to *Asterina*.

Asterina lopi differs from the species previously reported on Melastomataceae (Léveillé 1845; Hennings 1904, 1909; Theissen 1912, 1913; Sydow and Sydow 1916; Yates 1917; Maublanc 1920; Ryan 1924, 1928; Sydow 1927, 1930; Sydow and Petrak 1929; Chardón and Toro 1930; Orejuela 1944; Petrak 1950; Hansford 1954; Yamamoto 1957; Hosagoudar and Abraham 2000; Hosagoudar 2006) in morphology and on host association (Table 4). It is morphologically closer to *A. melastomatacearum*, which has larger and ellipsoid-ovoidal ascospores. *Asterina lopi* is easily separated from *A. amadelpha*, *A. belluciae*, *A. centroniae*, *A. chrysophylli*, *A. confertissima*, *A. hypophyla*, *A. maublancii*, *A. melanotes*, *A. melastomatis*, *A. melastomatis-candidi*, *A. memecylonicae*, *A. pulla*, *A. schlechteriana*, *A. sinsuieiensis*, and *A. uribei* in having verruculose ascospores; *A. antioquensis*, *A. madikeriensis, A. miconiae*, *A. transiens* and *A. venezuelana* in having lobate appressoria. *Asterina astroniae* is distinct from the new species in having ovoid appressoria, ascomata with irregular fissure, wider asci, and larger ascospores. *Asterina denigrata* has hypophyllous colonies, wider and dark brown hyphae, dark brown and subglobose to conoid appressoria, wider and ovoid to ellipsoid asci with 2–6 spores, and larger and dark brown ascospores. *Asterina hughesii* differs from *Asterina lopi* in the wider hyphae, larger appressoria, narrow and spatulate asci, lacking pseudoparaphyses, and larger ascospores. *Asterina melastomaticola* differs in the pulvinate to conoid appressoria, globose to ovoid asci, lacking pseudoparaphyses, and larger ascospores. *Asterina miconiicola* differs from *Asterina lopi* in the wider hyphae, larger appressoria, and narrow ascospores with an upper third septum. *Asterina theissenii* differs in having narrow and dark brown hyphae, globose to ovoid asci, lacking pseudoparaphyses, and larger ascospores (Léveillé 1845; Hennings 1904, 1909; Theissen 1912, 1913; Sydow and Sydow 1916; Yates 1917; Maublanc 1920; Ryan 1924, 1928; Sydow 1927, 1930; Sydow and Petrak 1929; Chardón and Toro 1930; Orejuela 1944; Petrak 1950; Hansford 1954; Yamamoto 1957; Hosagoudar and Abraham 2000). Based on our phylogenetic analyses (Fig. 56) and morphology, herein we introduce a new species, *A. lopi*. *Asterina lopi* is the ninth species of *Asterina* reported on hosts belonging to Melastomataceae in Brazil, and the eleventh on *Miconia*.

Botryosphaeriales C.L. Schoch, Crous & Shoemaker.

Notes: Botryosphaeriales was introduced to accommodate a single family Botryosphaeriaceae by Schoch et al. (2006). Schoch et al. (2009a) accepted its position in the Pleosporomycetidae. Later, Planistromellaceae was recognised as a distinct family within Botryosphaeriales (Minnis et al. 2012) Phyllostictaceae was reinstated for *Phyllosticta* (Wikee et al. 2013). Another three families were introduced by Slippers et al. (2013), namely Saccharataceae for *Saccharata*, Aplosporellaceae for *Aplosporella* and Melanopsaceae for *Melanops*. Wyka and Broders (2016) introduced Septorioideaceae for *Septorioides*. Yang et al. (2018) raised *Endomelanconiopsis* and *Pseudofusicoccum* to familial status as Endomelanconiopsidaceae and Pseudofusicoccaceae, respectively. Wijayawardene et al. (2018) accepted the above nine families in the order. However, Phillips et al. (2019) synonymised Endomelanconiopsidaceae with Botryosphaeriaceae, Pseudofusicoccaceae with Phyllostictaceae, and Septorioideaceae with Saccharataceae based on morphology, phylogeny and evolutionary divergence times. Therefore, six families, i.e. Aplosporellaceae, Botryosphaeriaceae, Melanopsaceae, Phyllostictaceae, Planistromellaceae, Saccharataceae, are phylogenetically proved in the order now (Hongsanan et al. 2020a, b; Wijayawardene et al. 2020).

Aplosporellaceae Slippers, Boissin & Crous, Stud. Mycol. 76(1): 41 (2013)

Aplosporellaceae was introduced in Botryosphaeriales with two genera *Aplosporella* and *Bagnisiella* (Slippers et al. 2013). Sharma et al. (2017) added *Alanomyces* as a new genus in this family based on four loci phylogeny. Two genera are accepted in Aplosporellaceae *viz. Alanomyces* and *Aplosporella* (Dissanayake et al. 2021a, b; Wijayawardene et al. 2022).

Aplosporella Speg. Anal. Soc. cient. argent 10(4): 157 (1880).

Aplosporella was treated as a type genus of Aplosporellaceae in Botryosphaeriaceae (Crous et al. 2006; Schoch et al. 2006; Damm et al. 2007; Liu et al. 2012). The genus was established by Spegazzini (1880) and typified by *Aplosporella chlorostroma*. Later, Aplosporellaceae was introduced as a new family by Slippers et al. (2013). Wijayawardene et al. (2014a, b, 2016, 2020, 2022) also confirmed the phylogenetic placement and accepted Aplosporellaceae in Botryosphaeriaceae. There are 342 epithets of *Aplosporella* listed in Index fungorum (2022a, b). *Aplosporella* is characterized by muti-locular conidiomata, with hyaline to brown, aseptate conidia and, filiform paraphyses (Damm et al. 2007; Ekanayaka et al. 2016; Dissanayake et al. 2021a, b; Hyde et al. 2021). *Aplosporella* species are not easy to identify based on only morphology because of their wide range of host and morphological similarities. Many species were introduced based on their host occurrence and suggested that species in *Aplosporella* are not host-specific (Damm et al. 2007; Fan et al. 2015; Ekanayaka et al. 2016; Dou et al. 2017).

Aplosporella artocarpi Trakun., L. Lombard & Crous, in Trakunyingcharoen et al., Persoonia 34: 91 (2014)

Index Fungorum number: IF810167; *Facesoffungi number: FoF10747, Fig. 58*

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* (280–) 300–350 × 370–450 (–500) µm ($\bar{x}$ = 300 × 415 µm, n = 5), solitary, immersed to semi-immersed with 2–3 locules, globose to subglobose, black. *Ostiole* absent. *Peridium* 45–50 (–60) µm wide, multi-layered, comprised of dark brown cells of *Textura angularis*. *Hamanthecium* 3–5 µm wide, numerous, hyaline, aseptate, paraphyses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 1–2 µm wide, holoblastic, cylindrical, hyaline. *Conidia* 15–20 × 5–10 µm ($\bar{x}$ = 17 × 7 µm, n = 15), aseptate, rough-walled, granular appearance, hyaline to dark brown, ellipsoidal, without appendages.

Culture characteristics: Conidia germinating on PDA within 24 h, reaching 85 mm after 7 days at room temperature, concentric, flat, irregular, rough surface, greenish-grey.

Material examined: Thailand, Chiang Rai Province, Doi Pui, on the dead stems of *Chromolaena odorata* (L.) (Asteraceae), 10 July 2020, Zin Hnin Htet, SW23 (MFLU 22–0108), living culture MFLUCC 22-0010.

Known hosts and distribution: On asymptomatic twig of *Artocarpus heterophyllus* (Moraceae) in Chiang Mai Province, Thailand (Trakunyingcharoen et al. 2015); on asymptomatic leaves of *Stoechospermum marginatum* (Dictyotaceae) and *Caulerpa taxifolia* (Caulerpaceae) in India (Sahoo et al. 2021); on dead branches of *Mangifera indica* (Anacardiaceae) in China (Yang et al. 2022); on dead stems of *Chromolaena odorata* (Asteraceae) in Chiang Rai Province, Thailand (this study)

GenBank numbers: ON834371(LSU), ON823183(ITS)

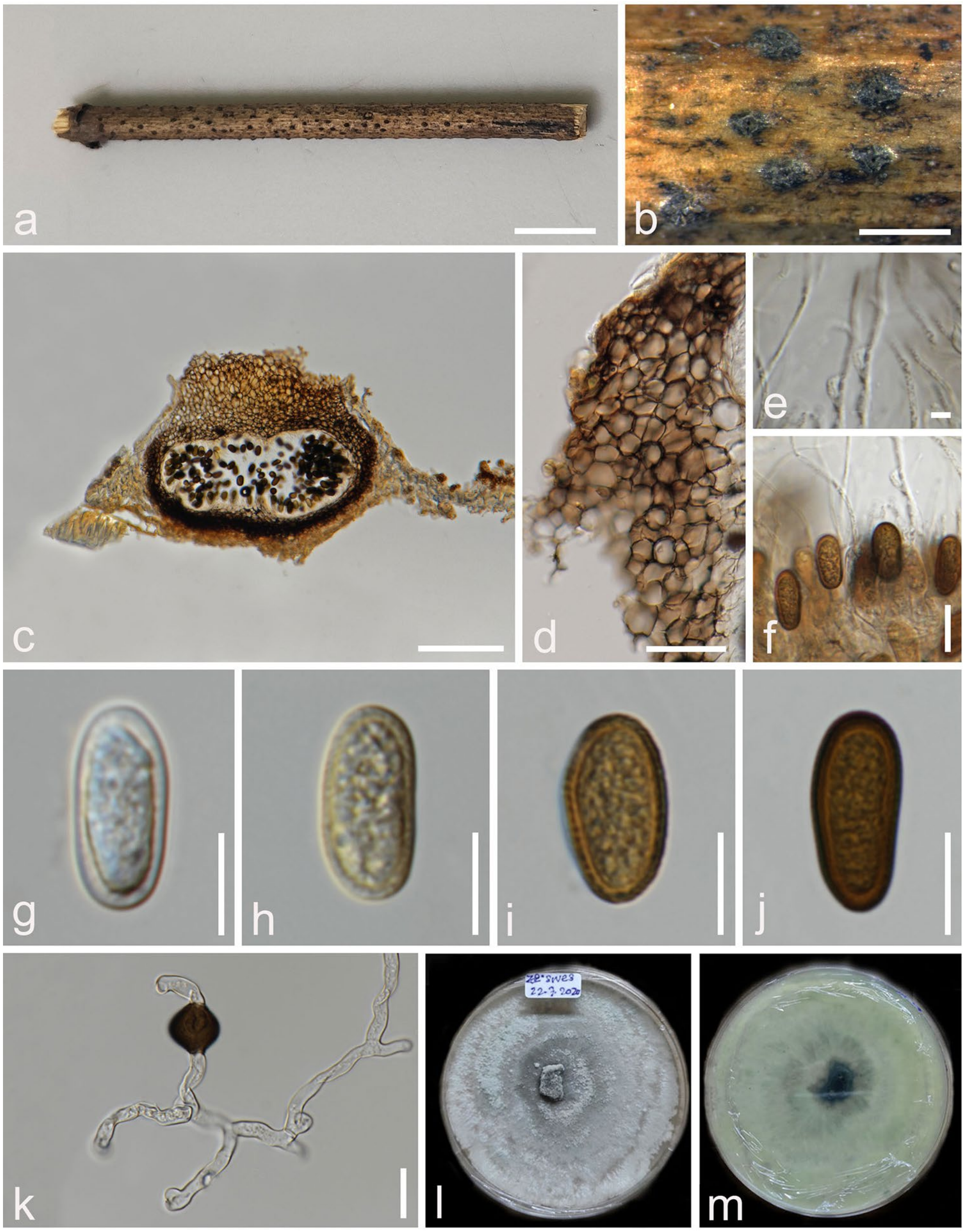


Fig. 58 ***Aplosporella artocarpi*** (MFLU 22–0108, **new host record**). **a, b** Appearance of conidiomata on host substrate. **c** Section through conidoma. **d** Peridium. **e** Pseudoparaphyses. **f** Conidia on the conidiogenous cells. **g-j** Conidia. **k** Sporulation **l–m** Culture on PDA from surface and reverse. Scale bars. **a** = 1000 µm, **b** = 500 µm, **c** = 100 µm, **d** = 30 µm, **e** = 5 µm, **f, l, m** = 20 µm, **g,h,I,j,k** = 10 µm

Notes: *Aplosporella artocarpi* was introduced by Trakunyingcharoen et al. (2015). The species has morphologically similar to other *Aplosporella* species such as *A. hesperidica*, *A. prunicola*, and *A. thailandica* in having dark-brown, multilocular conidiomata with aseptate, hyaline to dark-brown conidia (Damm et al. 2007; Ekanayaka et al. 2016; Dissanayake et al. 2021a, b). In our phylogenetic analysis, *Aplosporella artocarpi* (MFLUCC 22-0010) is closely related to *Aplosporella artocarpi* (CPC 22,791) with ML = 70%, BYPP = 0.54. (Fig. 59). According to BLASTn result, the closest match for the LSU sequence was *Aplosporella artocarpi* (CPC 22791) with 99.83% similarity. The closest match for the ITS sequence was *Aplosporella prunicola* (CBS 121167) with 97.81% similarity. Furthermore, comparisons of ITS region between our taxon, *Aplosporella artocarpi* (MFLUCC 22-0010) and ex-type strain of *A. artocarpi* (CPC 22791) show one base pair difference (0.18%) across 531 nucleotides. *Aplosporella* species can be found on a wide range of hosts such as Anacardiaceae, Asteraceae, Caulerpaceae, Cupressaceae, Dictyotaceae, Fabaceae, Gingkoaceae, Moraceae, Myrtaceae, Proteaceae, and Rosaceae (Du et al. 2017; Mapook et al. 2020; Sahoo et al. 2021; Yang et al. 2021). We collected *Aplosporella artocarpi* (MFLU 22-0108) from Thailand and reported here as a new host record associated with *Chromolaena odorata*.

Botryosphaeriaceae Theiss. & Syd. [as 'Botryosphaeriacae'], Annls mycol. 16(1/2): 16 (1918)

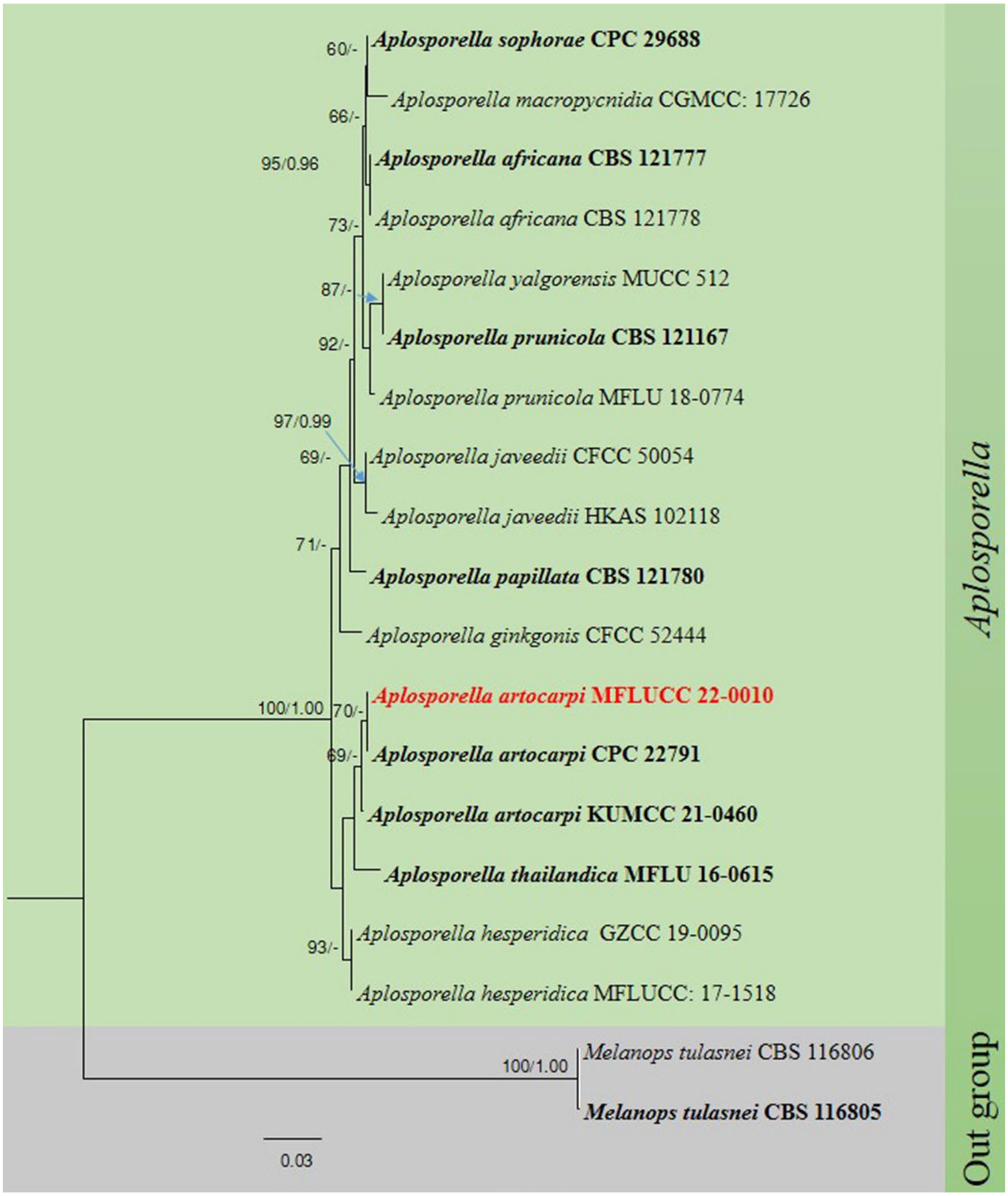


Fig. 59 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, and *tef1* sequence data for the *Aplosporella*. The combined dataset consists of 19 taxa from *Aplosporella* and our taxon, *Aplosporella artocarpi* (MFLUCC 22–0010). *Melanops tulasnei* (CBS 116805 and CBS 116806) are used as outgroup. The topology of the maximum likelihood analysis is similar to Bayesian analysis. Bootstrap support value for ML ≥ 60% and BYPP ≥ 0.95 are given above the branches. The ex-type strains are **bold**. The newly generated sequence is indicated in bold and red

Notes: Botryosphaeriaceae was introduced by Theissen and Sydow (1918) for three genera, *Botryosphaeria*, *Phaeobotryon* and *Dibotryon*. Initially, the family had been successively put into the orders Dothideales (Müller and von Arx 1950) and Pleosporales (Luttrell 1955), until Schoch et al. (2006) raised Botryosphaeriaceae to orderal status as Botryosphaeriales. Over decades of taxonomic revisions and updates based on morphology, the family has become increasingly complex. Kirk et al. (2008) estimated that there are 26 genera and 1517 species in the family, while Liu et al.

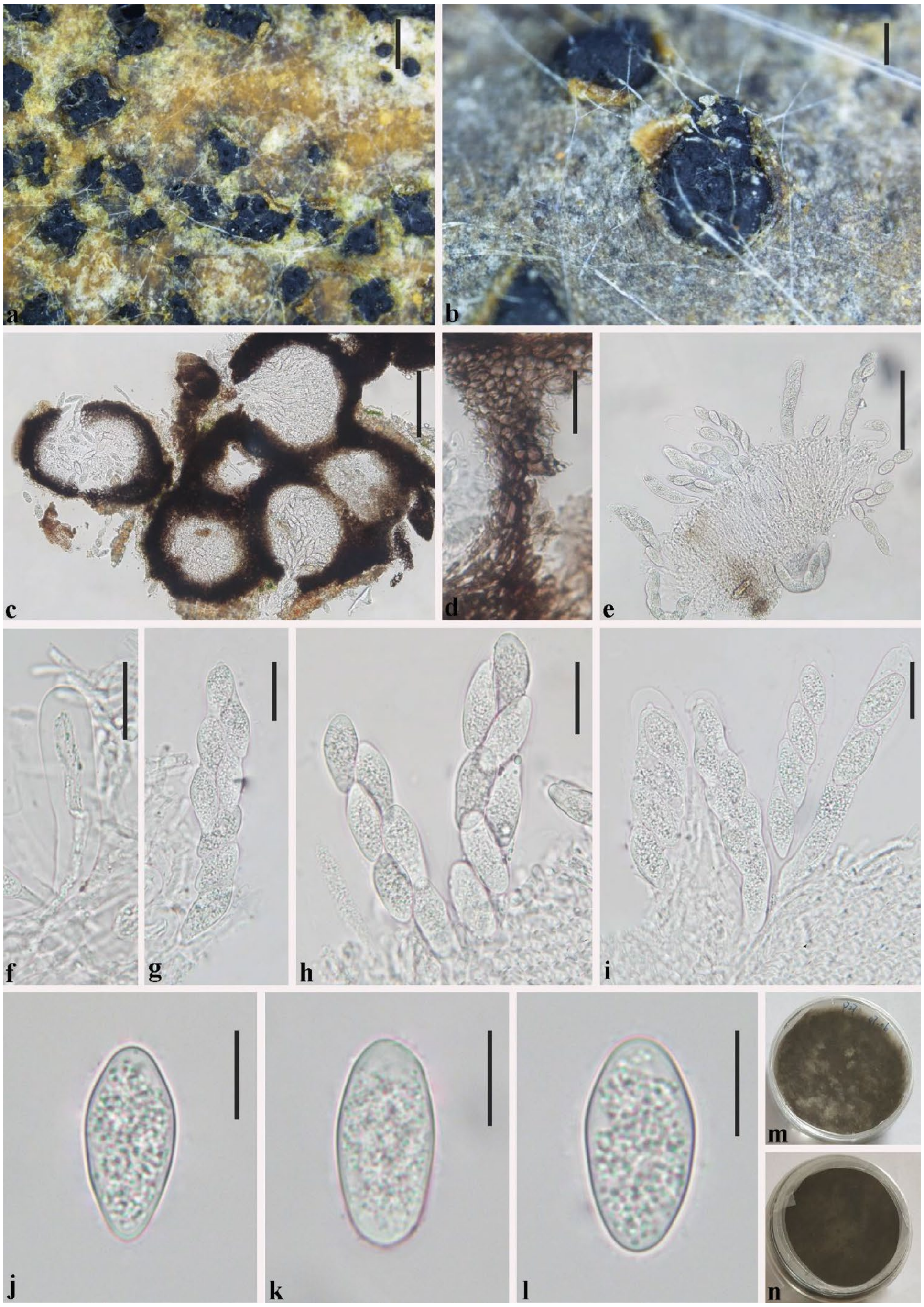


Fig. 60 ***Botryosphaeria dothidea*** (IFRD500–008, **new geographic and habitat record**) **a, b** Appearance of ascomata on host substrate. **c** Section of ascomata. **d** Peridium. **e** Pseudoparaphyses and asci. **f–i** Asci. **j–l** Ascospores. **m–n** Colony on PDA (**m** from front, **n** from reverse). Scale bars: **a** = 500 µm, **b** = 200 µm, **c, e** = 100 µm, **d** = 30 µm, **f–i** = 20 µm, **j–l** = 10 µm

(2012) accepted 29 genera and approximately 1485 species. Phillips et al. (2013) consider morphological characters alone as inadequate to define genera or identify species, and they detailed described 17 genera and 110 species which has molecular data. Thereafter, Dissanayake et al. (2017) introduced six new genera and 85 new species/species combinations. So far, 22 genera are accepted in Botryosphaeriaceae (Phillips et al. 2019; Hongsanan et al. 2020a).

Botryosphaeria Ces. & De Not., Comm. Soc. crittog. Ital. 1(fasc. 4): 211 (1863)

Notes: *Botryosphaeria* was introduced by Cesati and De Notaris (1863) based on the type species *B. dothidea*. However, as the type material was immature, *B. dothidea* was epitypified by Slippers et al. (2004) based on morphology and phylogenetic data which combined ITS, *tef1* and *tub2* genes. The sexual morphs are characterized by brown to black, globose ascostromata, comprising a botryose aggregate, or sometimes solitary, with a central ostiole, papillate or not, bitunicate, clavate asci, with a short pedicellate and a small ocular chamber, intermixed with hyphae-like, wide, septate pseudoparaphyses, and hyaline, aseptate, fusoid to ovoid ascospores, with or without a mucilaginous sheath (Liu et al. 2012). The asexual morphs of *Botryosphaeria* were reported as *Dichomera*, *Diplodia*, and *Fusicoccum* (Crous and Palm 1999; Slippers et al. 2004; Crous et al. 2006). They are characterized by uni- to multilocular pycnidial, frequently embedded in stromatic tissue, holoblastic, hyaline, subcylindrical conidiogenous cells, with 1–2 percurrent proliferation, and hyaline, aseptate, narrowly fusiform, or irregularly fusiform conidia, rarely forming a septum before germination, smooth with granular contents (Slippers et al. 2004). So far, 286 species names are recorded in Index Fungorum (2022a, b), in which 30 species known from culture are accepted in the genus.

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

See Species fungorum for synonyms.

Index Fungorum number: IF183247; Faces of fungi number:FoF03512; Fig. 60

Saprobic on submerged wood of freshwater. **Sexual morph:** *Ascomata* 300–500 µm diam., black, circular or subglobose to globose, scattered, gregarious, uni- to multiloculate, immersed to erumpent on host tissue, with visible black dots or papilla. *Ostiole* circular, central, papillate. *Peridium* composed of two-layered locules, outer layer composed of dark brown or brown thick-walled cells of *textura angularis*, inner layer composed of hyaline thin-walled cells of *textura angularis* lining the locule. *Pseudoparaphyses* 2–4 µm wide, hyphae-like, septate. *Asci* 96–144 × 18–25 µm ($\bar{x} = 116 \times 23$ µm, $n = 10$), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellatea, pically rounded with an ocular chamber. *Ascospores* 21–32 × 10–14 µm ($\bar{x} = 26.3 \times 11.7$ µm, $n = 40$), biseriate, hyaline, aseptate, fusoid to ovoid, sometimes with tapered ends, spindle-shaped, thin-walled, smooth with granular contents. **Asexual morph:** Not observed.

Cultural characteristics: Ascospore germinating on PDA within 24 h. Colonies on PDA fast-growing, reaching 7–8 cm diameter in 50 days at 20–25 °C, with dense, hairy, black mycelium on the surface, reverse black.

Material examined: China, Yunnan Province, a small river of Puzhehei wetland, on dead submerged decaying wood of unidentified plants, 23 June 2019, Hao Yang, p27 (IFRD500–008), living culture KUMCC 20–0186.

Known hosts and distribution: broad range of hosts and wide geohraphical distribution (Farr and Rossman 2022)

GenBank numbers: MT559116 (LSU), MT559099 (ITS)

Notes: *Botryosphaeria dothidea* is the type species of the genus, and was reported extensively from all around the world (Fries 1823; Arx and Müller 1954). It was epitypified by Slippers et al. (2004) based on morphology and phylogeny. This taxon was collected from southwest China and its ITS sequence data of our isolate are 100% identical to the verified sequences of *B. dothidea* (MH992666 and MH973592). Based on morphology and phylogenetic analyses (Fig. 61), we identify the strain as *B. dothidea*. It is a new geographic record from China and a new habitat record from freshwater.

Class Laboulbeniomycetes Engler

Laboulbeniales Lindau

Notes: This order includes more than 2000 species described as obligate ectosymbionts on Arthropods. Wijayawardena et al. (2022) accepted three families *viz*. Ceratomycetaceae, Euceratomycetaceae and Laboulbeniaceae in this order.

Laboulbeniaceae G. Winter [as 'Laboulbenieae'], Rabenh. Krypt.-Fl., Edn 2 (Leipzig) 1.2: 918 (1886)

Notes: Goldman and Weir (2018) based on SSU rDNA sequence data identified this family to be consist of essentially terrestrial and sexually reproducing taxa with simple or compound endogenous antheridia. Santamaria and Pedersen (2021) accepted 147 genera in this family.

Rhachomyces Thaxt., Proc. Amer. Acad. Arts & Sci. 30: 468 (1895) [1894]

Notes: *Rhachomyces* is quite numerous: with six species described very recently, the number of accepted species in the genus is now 91 (Rossi and Christian 2020; Rossi and Leonardi 2020; Santamaria et al. 2020; Buyck et al. 2021). This genus is characterized by a series of superposed, usually short cells forming an axis that remembers a spinal column (hence the name, from Greek *rachis* = spine); these cells produce laterally both sterile appendages of various lengths and antheridial appendages, the latter ending with a single antheridium consisting of a simple phialide. In mature thalli the perithecia are usually found in an apical position and more frequently are single, but can be two or even more in a few species. The cells forming the outer wall of perithecia are arranged in four rows, each consisting of four unequal cells. Most of the species of *Rhachomyces* occur on ground beetles (Carabidae), but a few are associated with rove beetles (Staphylinidae) and two were found on small carrion beetles (Leiodidae Cholevinae). A single sequence is available for species in this genus (Goldmann and Weir 2018).

Rhachomyces cruralis W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: IF559505; Facesoffungi number: FoF13385; Fig. 62

Etymology: From Latin *crus* = leg, because the thalli of the new species are found only on the legs of the host insect.

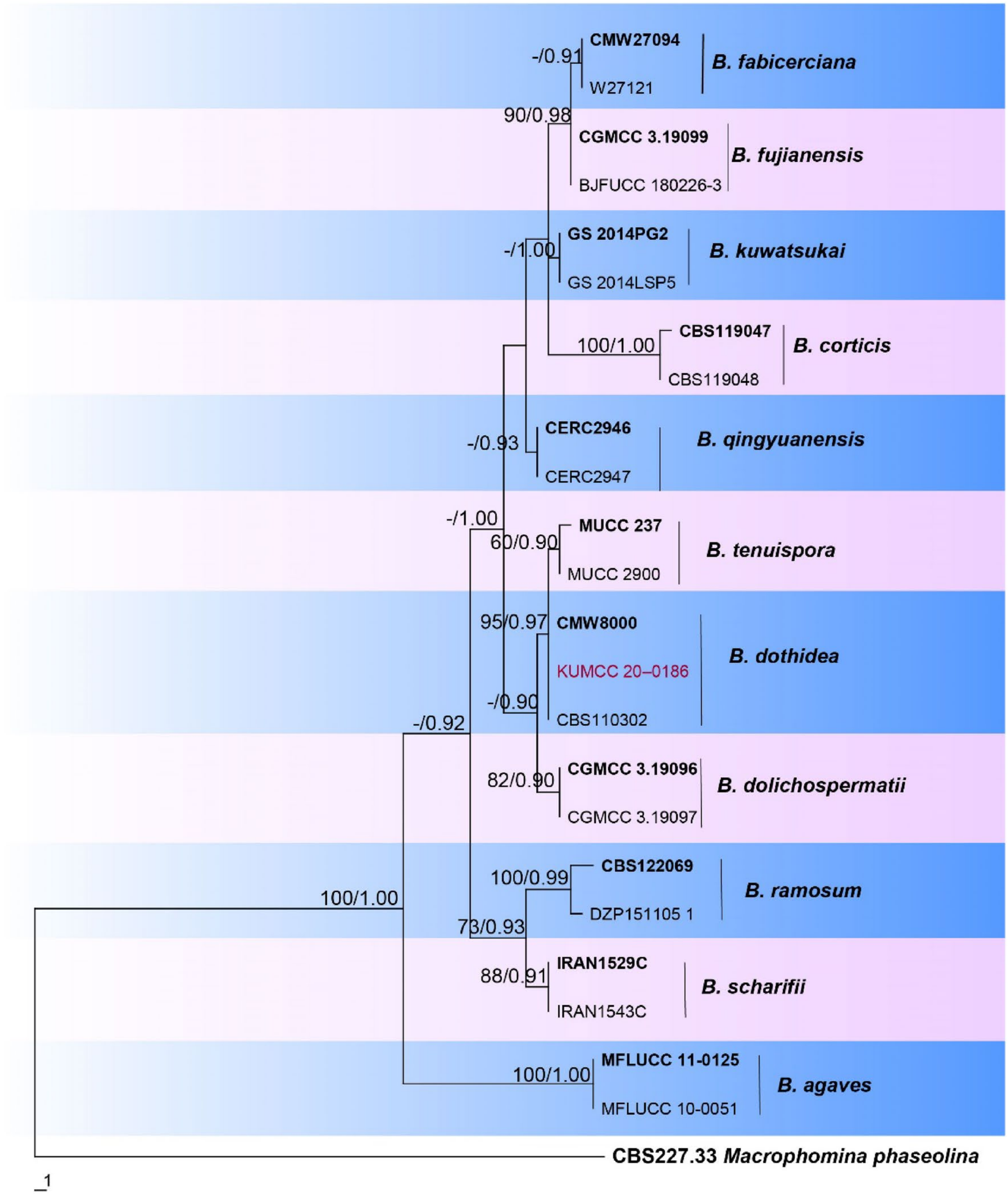


Fig. 61 Phylogram generated from maximum likelihood analysis based on combined ITS, and *tef1* sequence data for the *Botryosphaeria*. The combined dataset consists of 23 taxa from *Botryosphaeria* with our strain. The tree is rooted with *Macrophomina phaseolina* (CBS 227.33). The topology of the maximum likelihood analysis is similar to Bayesian analysis. Bootstrap support value for ML ≥ 60% and BYPP ≥ 0.90 are given above the branches. The ex-type strains are in **bold**. The newly generated sequence is in red

Holotype: FI WR1997

Axis of the receptacle is straight or slightly curved, consisting of 10–15 brownish cells gradually increasing in size and bearing a dark brown band in the lower portion. *Appendages* almost straight, more numerous in the upper portion of the thallus, usually consisting of 5–6 dark brown cells separated by back septa and slight constriction, the distal one being distinctly longer and gradually paler, with the lower portion slightly inflated and the tip hyaline or almost so. *Antheridial appendages* very few, consisting of a short and brownish lower cell followed by a straight hyaline antheridium. *Perithecium* reddish-brown, subsessile, symmetrically

Fig. 62 ***Rhachomyces cruralis*** (FI WR1997, **holotype**). Scale bar = 50 µm

Fig. 63 ***Rhachomyces hyperommae*** (FI WR2331, **holotype**). Scale bar = 50 µm

elliptical, about twice as long as it is broad, regularly tapering to the darker, subconical tip and almost hyaline, rounded apex. Length from foot to perithecial apex 270–350 µm. Perithecium, including basal cells 125–175 × 60–80 µm. Longest appendages 100 µm.

Material examined: South Africa, E Transvaal, Mt. Sheba Nat. Res., 14–15.II.1995, S. Zoia, on posterior legs of *Pachydesus rufipes* (Boheman) (Carabidae, Trechini) (FI WR1997, **holotype**). Same data as the type, M. Zapparoli legit (FI WR1987 and WR 2000, **paratypes**); same data as the type, A. Vigna Taglianti legit, FI WR1998 and WR1999, **paratypes**).

Fig. 64 ***Rhachomyces magrinii*** (FI WR4049, **holotype**). Scale bar = 100 µm

Notes: The species is more similar to *Rhachomyces cruralis* and *R. moreti* W. Rossi et Proaño, parasitic on *Trechisibus calathiformis* Deuve from Ecuador. The latter fungus, however, has an oblong perithecium, the axis of the receptacle consists of 16–18 cells, and the appendages are paler and slenderer (Rossi and Proaño Castro 2009).

Rhachomyces hyperommae W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: *IF559509; Facesoffungi number: FoF13386; Fig. 63*

Etymology: Named after the host insect genus.

Holotype: CAMB WR2331a

Axis of the receptacle composed of 12–17 cells very different in size, shape, and color: the basal and the suprabasal are blackened, narrow, and elongate; the following 2 or 3 are relatively small, dark and isodiametric; the others gradually broader and paler from below upwards. *Appendages* short, stiff, one-sided, projected obliquely upwards, consisting of 4 cells, of which the lower 3 are dark brown while the upper has a paler and curved tip. *Antheridial appendages* similar to the sterile ones but shorter and paler, each bearing distally a brown, elongate antheridium tapering in a curved and truncate paler tip. *Perithecium* broadly fusiform, with the posterior side more convex, nearly hyaline or tinged with pale yellow, brownish yellow near the base in older specimens, the hyaline and conical tip ending in a blunt apex. Length from foot to perithecial apex 280–380 µm. Perithecium, including basal cells 110–145 × 35–42 µm. *Antheridia* 20–25 µm. Longest appendage 90 µm.

Material examined: Autralia, NSW Border Ranges N. P., Tweed Range Rd., 4.6 km SW of Bridle Ck. Rd., alt. 580 m, 4.II–9.IV.1993, M. Gray & G. Cassis, on a femur and the abdomen of *Hyperomma* sp. (Staphylinidae, Paederinae, Paederini, Cryptobiina), CAMB WR2331a, **holotype**; FI WR2331b **isotype**).

Notes: The new species seems to be allied to *Rhachomyces arbusculus* Thaxt., described on an unidentified rove-beetle from Liberia, West Africa (Thaxter 1896). The two parasites have similar appendages and are also somewhat similar in the general habitat. However, *R. abusculus* is distinctly more slender and more elongate, with the cells forming the receptacle more numerous (20–25) and not strongly different from each other, and with a much narrower perithecium suffused with brown at the apex.

Rhachomyces magrinii W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: IF559510; Facesoffungi number: FoF13387; Fig. 64

Etymology: Named after the entomologist Paolo Magrini, who supplied us with the material utilized for the description of the new species.

Holotype: FI WR4048

Axis of the receptacle from almost straight to distinctly curved or slightly sigmoid, consisting of (14)18–29 cells; basal and suprabasal cells slender, elongate and dark brown colored, the others gradually larger and paler. *Appendages* occurring in the lower part of the thallus are slender, consisting of 5–6 brownish, elongate cells; these appendages are visible only on young thalli, but are broken off in very early stages of development. The upper and more lasting appendages are thicker, generally consisting of 5 relatively short, subequal cells, the series ending with a 6th cell distinctly longer and much paler, with an almost hyaline tip. *Antheridial appendages* consist of a single, pale brown cell bearing apically a hyaline antheridium with a tapering and distinctly curved efferent neck. *Perithecium* subsessile, pale grayish brown, more or less bent as to the axis of the receptacle, symmetrical or slightly asymmetrical, about three times longer than broad, slightly more inflated below, the truncate-conical and paler tip ending in a broad and blunt apex. Length from foot to perithecial apex 525–950 µm. Perithecium 135–180(200) × 45–60(70) µm. *Antheridial* appendages 40–45 µm. Longest sterile appendages 150 µm.

Material examined: Mexico, Querétaro, Pinal de Amoles, Ojo de Agua, 9.III.2011, G. Trezzi, on *Mexaphaenops elegans* Barr (Carabidae, Trechini) (FI WR4048, **holotype**; FI WR4049, WR4488, **paratype**).

Fig. 65 ***Rhachomyces platyprosophi*** (FI WR3973a, **holotype**). Scale bar = 100 µm

Notes: The only previously described species in *Rhachomyces* on a cave-dwelling Trechini from Central America is *R. quetzalcoatl* Balazuc, occurring on *Paratrechus* spp. from Mexico and Guatemala. The two species of fungi share the absence of dark pigmentation on the perithecial tip and the structure of the upper appendages, but differ greatly in other characteristics, as the much shorter receptacle of *R. quetzalcoatl*, consisting of dozens of cells, and its more inflated perithecium (Rossi and Cesari-Rossi 1977, Fig. 63).

Rhachomyces platyprosophi W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: *IF559511; Facesoffungi number: FoF13388; Fig. 65*

Etymology: Named after the host insect genus.

Holotype: FI WR3973.

Axis of the receptacle from almost straight to variably curved or sigmoid, consisting of 15–22 brownish cells gradually enlarging upwards and separated by oblique septa. *Appendages* spreading, nearly opaque except for the gradually paler and curved tip, longer and more numerous in the upper portion of the receptacle, reaching and sometimes exceeding the perithecial apex. *Antheridial appendages* relatively numerous, chestnut brown colored, consisting of a slender and elongate cell followed by a very slender antheridium with a paler and sigmoid tip. *Perithecium* long and slender, subsessile, oblong, light brown colored, the tip gradually tapering, hardly distinguished except for the darker color, the apex hyaline and subtruncate. Length from foot to perithecial apex 500–830 µm. Perithecium 190–290 × 50 µm. *Antheridial* appendages 50–65 µm. Longest sterile appendage 520 µm.

Material examined: Indonesia, Sumatra, Palembang, s. d., s. c. (from the collection of A. Fauvel in the Institut Royal des Sciences Naturelles, Bruxelles), on abdomen and legs of *Platyprosopus indicus* Motschulski (Staphylinidae, Staphylininae, Platyprosopini) (FI WR3973a, **holotype**; FI WR3973b and WR3973c **isotypes**).

Notes: Due to the large dimensions and the oblong perithecium, the new species can be compared with *Rhachomyces carbonii* W. Rossi & M. Leonardi, recently described on a rove beetle from Sierra Leone, which however bears a slender and much darker receptacle, shorter and slender appendages and has perithecium with spirally twisted wall cells with an abruptly distinguished tip (Rossi and Leonardi 2018).

Class Lecanoromycetes O.E. Erikss. & Winka

Subclass Lecanoromycetidae P.M. Kirk et al.

Caliciales Bessey.

Notes: Caliciales is an order of lichenized fungi, including mostly crustose, but also foliose forms (Lücking et al. 2016)

Caliciaceae Chevall. [as 'Calicineae'], Fl. gén. env. Paris (Paris) 1: 314 (1826)

Notes: Caliciaceae is a family of lichenized fungi, including mostly crustose, but also foliose forms (Lücking et al. 2016)

Buellia De Not., G. bot. ital. 2(1.1): 195 (1846)

Notes: *Buellia* is a large, heterogeneous and probably a polyphyletic genus. Some species groups are relatively well-defined and may warrant formal recognition. This includes the *Buellia subalbula* (Nyl.) Müll. Arg. aggregate (Bungartz et al. 2011). Below we describe a new species that belongs to this group.

Buellia pruinocalcarea Aptroot, M.F. Souza & Spielmann, *sp. nov*.

Index Fungorum number: *IF900068; Facesoffungi number*: *FOF13389; Fig. 66*

Saxicolous *Buellia* on limestone with thallus thick, white, apothecia flush with the thallus, densely white pruinose, and ascospores 12–14 × 6–7 µm.

Holotype: Aptroot 77815.

Etymology: Named after the white pruina and the calcareous habitat.

Sexual morph: *Thallus* crustose, covering areas up to 20 cm diam., marginal 3 mm continuous, remaining parts rather regularly cracked with areoles flat, c. 0.5 mm diam., not corticate, dull, almost pure white, very regularly c. 0.3 mm thick, not surrounded by a prothallus, but margin thinner though at least 0.1 mm thick. Isidia and soredia absent. *Ascomata* numerous, singly or aggregated, partly in concentrical zones (especially the outer rim of apothecia at 3 mm from the margin), immersed, flush with the thallus, rather uniformly 0.3–0.5 mm diam., sparse, solitary, disc flat, grey, margin barely raised, c. 0.05 mm thick, white, both disc and margin densely white pruinose. *Excipulum* uniformly dark brown in section. *Epihymenium* a layer of c. 15 µm high of brown paraphysal tips overlain with an c. 25 µm high epipsamma composed of many grey crystals that do not dissolve in K (calcium oxalate). *Hymenium* 70–90 µm high, hyaline, not inspersed, amyloid, paraphyses 1–1.5 µm wide, with dark brown upper. *Hypothecium* dark brown, in the central part up to 75 µm high, towards the margin tapering to c. 25 µm high. *Ascospores* 8/ascus, brown, 1-septate, ellipsoid, 12–14 × 6–7 µm. **Asexual morph**: not observed.

Chemistry: Thallus and apothecia UV + patchily salmon-orange, especially in the submarginal zone, C–, P–, K–. TLC: nil.

Ecology and distribution: On exposed limestone in Atlantic rain forest biome; only known from Brazil.

Material examined: Brazil, Mato Grosso do Sul: Serra da Bodoquena, Bodoquena, Dente de Cão, summit, alt. 450 m, 20° 47′ 05″ S, 56° 45′ 03″ W, on exposed limestone in Atlantic rain forest biome, 7 November 2018, Aptroot 77815 (**holotype**, CGMC).

GenBank number: MW322683 (ITS).

Notes: This species is not keyed out in Malme (1912). It shows similarities with species of the *Buellia subalbula* (Nyl.) Müll. Arg. aggregate (Bungartz et al. 2011) and seems most similar to *Buellia amabilis* de Lesd. (see Bungartz and Nash 2004), which differs by the ornamented ascospores and the apothecia that become more convex, and the absence of UV luminescence. Phylogenetically, it clusters deep inside *Buellia* De Not. in the current sense (Fig. 66). Sequences of other species of the *B. subalbula* aggregate are not available.

As part of a continuous effort to explore lichenologically relatively unidentified regions in Brazil, we investigated the microlichens on an isolated limestone outcrop in a tropical south-western inland region, *viz.* the Dente de Cão in the Parque Nacional da Serra da Bodoquena in the state of Mato Grosso do Sul, close to the borders with Paraguay and Bolivia. This range of hills is the only larger forested area still in existence in this state. Many microlichens were recently reported from the area (Aptroot and Spielmann 2020). This area is close to the venue of IAL9, the nearby town of Bonito.

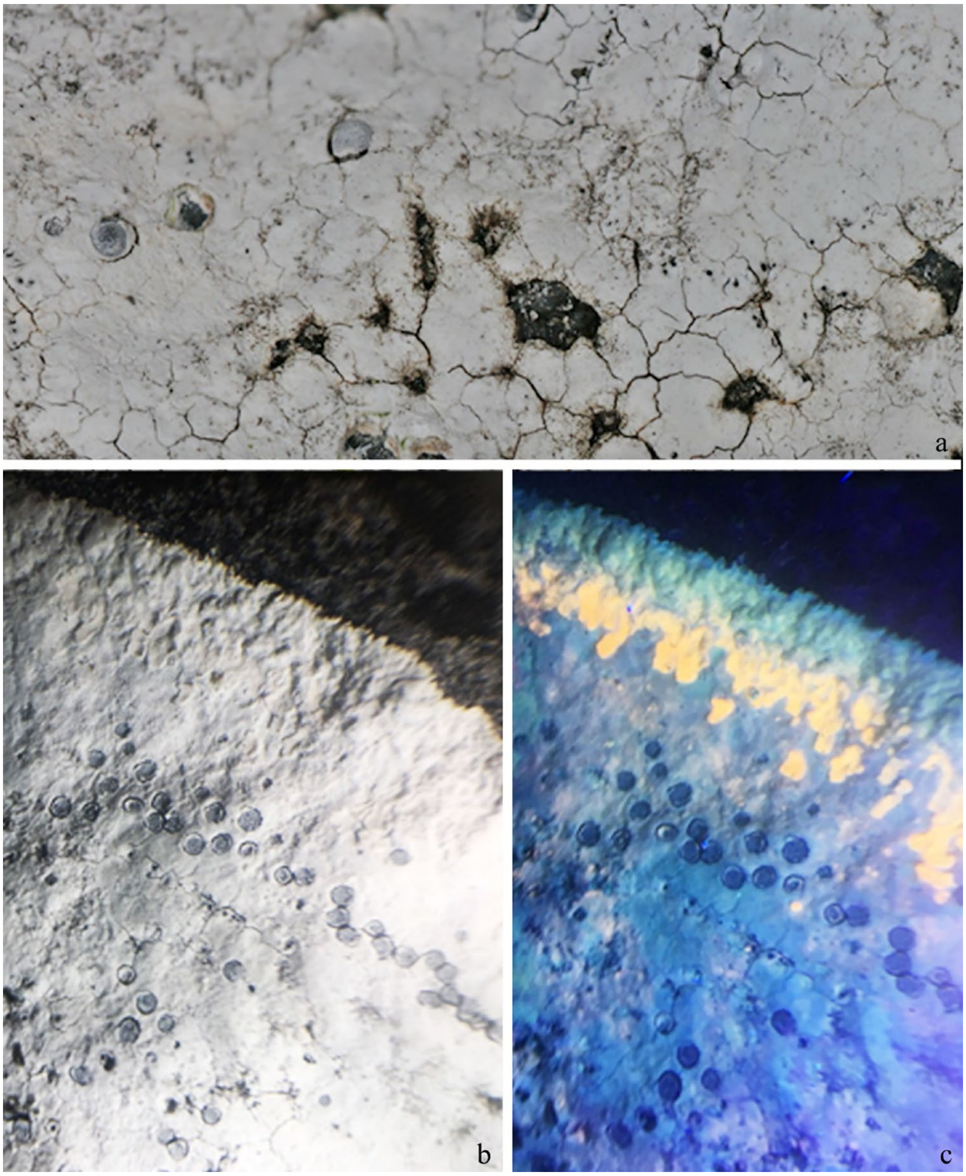


Fig. 66 ***Buellia pruinocalcarea*** (Aptroot 77815 **holotype**) **a.** habitat. **b.** Upper and lower left in daylight. **c.** lower right in 365 nm UV light. Scale bars: **a-c** = 20 mm

The natural vegetation of the Serra da Bodoquena is the Atlantic rain forest, a biome that stretches all along the coast from north-eastern to south-eastern Brazil. In fact, it is the most western patch of Atlantic rainforest in existence, and as such unique. Exposed limestone outcrops occur in various places in the tropics, but their extent is often limited and they tend to be soon grown over by vegetation. The Dente de Cão is formed of white Precambrian (neoproterozoic, see Boggiani 1997) limestone known as the Bocaiana formation, and reaches 450 m alt. It weathers into karst and the name of the rock outcrop is after the sharp tooth-like rock points. Somewhat to our surprise, the exposed limestone outcrop, although only scarcely colonized by fanerogams, was not completely covered by lichens. Cyanobacteria were more abundant. The most common lichens were the species of Collemataceae and Lichinaceae (Fig. 67).

Lecanorales Nannf.

Notes: Lecanorales is the largest order of lichenized fungi, one of the largest containing crustose lichens and the largest containing foliose lichens (Lücking et al. 2016).

Lecanoraceae Körb. [as 'Lecanoreae'], Syst. lich. germ. (Breslau): 104 (1855).

Notes: Lecanoraceae is a family of lichenized fungi, one of the largest containing crustose lichens (Lücking et al. 2016).

Lecanora Ach., in Luyken, Tent. Hist. Lich.: 90 (1809).

Fig. 67 Phylogram generated from maximum likelihood analysis based on ITS. Bootstrap support values for ML ≥ 80% and Bayesian posterior probabilities ≥ 0.95 are given near nodes respectively. The tree is rooted in *Diplotomma rivas-martinezii* (13365 BA). Ex-type strains are in bold. The newly generated sequences are indicated in bold blue

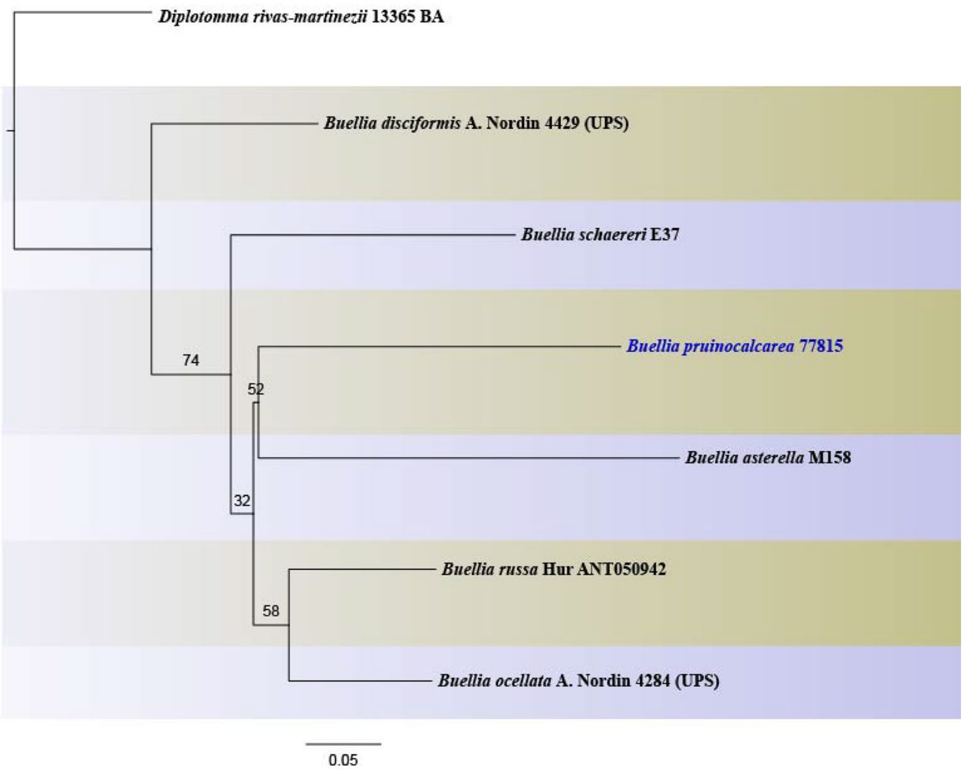


Fig. 68 ***Lecanora immersocalcarea*** (Aptroot 77822, **holotype**). Habitat. Scale bar = 23 mm

Notes: *Lecanora* is a large, heterogeneous and possibly paraphyletic genus. Some species of this group are well-defined. Below we describe a new species in the somewhat aberrant *Lecanora marginata* (Schaer.) Hertel & Rambold group (Rambold 1989).

Lecanora immersocalcarea Aptroot, M.F. Souza & Spielmann, ***sp. nov***.

Index Fungorum number: IF900069; Facesoffungi:FOF13390; Fig. 68

Saxicolous Lecanora on limestone with thallus 0.5–0.8(-2.0) mm thick, very pale ochraceous white, apothecia immersed in the thallus, black, immature.

Etymology: Named for the immersed apothecia and the calcareous habitat.

Holotype: Aptroot 77822.

Thallus crustose, superficial, covering areas up to 10 cm diam., dull, cretaceous, very pale ochraceous white, regularly cracked with the areoles angular, slightly convex and c. 0.5–0.9 mm diam., c. 0.5–0.8 mm thick but in some places with lobate superficial outgrowths of up to 2 mm thick, not surrounded by a prothallus, but margin thick and raised, sharply delimited, not lobed or fissured. Isidia and soredia absent. *Ascomata* immature apothecia, several per areole, flush with the thallus, rounded, 0.2–0.4 mm diam.; disc black, margin thin, black. *Epihymenium* grey, without crystals. *Excipulum* without crystals. *Hypothecium* hyaline. *Mature ascospores* not observed. *Pycnidia* not observed.

Chemistry: Thallus UV–, C–, P + yellow, K + yellow. TLC: atranorin.

Distribution: On exposed limestone outcrop in Atlantic rain forest biome; only known from Brazil.

Material examined: Brazil. Mato Grosso do Sul: Serra da Bodoquena, Bodoquena, Dente de Cão, summit, alt. 450 m, 20° 47′ 05″ S, 56° 45′ 03″ W, on exposed limestone in an

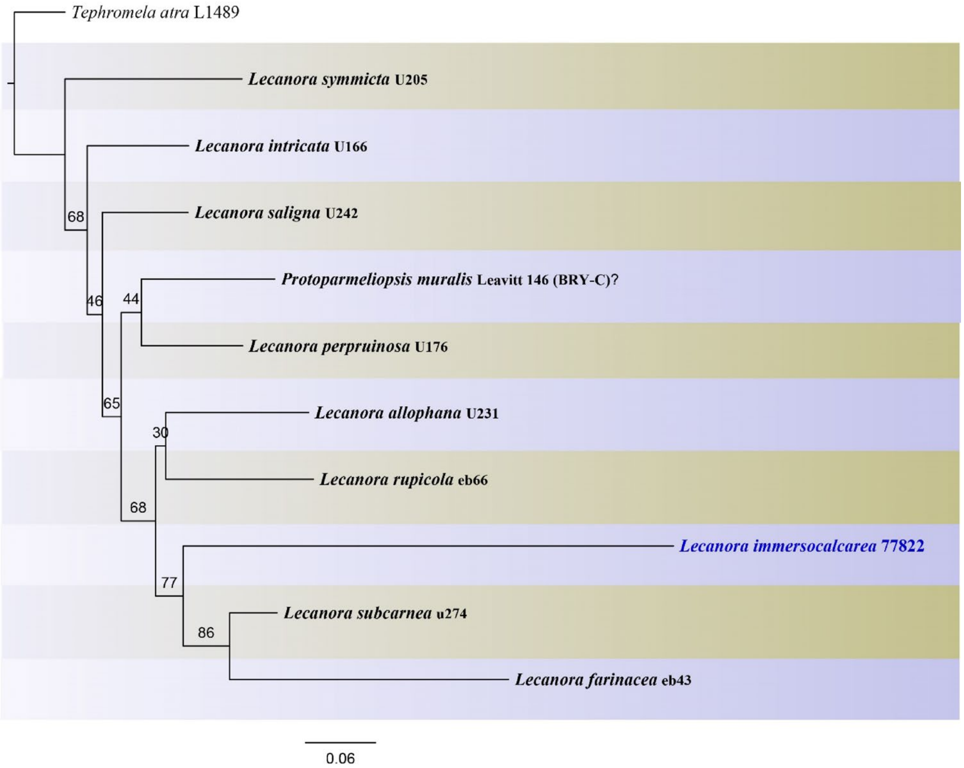


Fig. 69 Phylogram generated from maximum likelihood analysis based on ITS. Bootstrap support values for ML ≥ 80% and Bayesian posterior probabilities ≥ 0.95 are given near nodes respectively. The tree is rooted in *Tephromela atra* (L1489). Ex-type strains are in bold. The newly generated sequences are indicated in **bold** blue

Atlantic rain forest biome, 7 November 2018, Aptroot 77822 (**holotype, CGMC**).

GenBank number: MW322682 (ITS)

Notes: This species is locally abundant. Fully fertile material was not found, but the type specimen was sequenced and clustered inside *Lecanora* Ach. in the current sense. Morphologically it would belong to the *Lecanora marginata* (Schaer.) Hertel & Rambold group, in which indeed calciferous species or at least specimens are known. Only one described species seems close, however, *viz*. *Lecanora oreinodes* (Körb.) Hertel & Rambold (Rambold 1989), which differs by the flatter, flush areoles and the somewhat fractured/lobate thallus margin, and which is not known to occur on pure limestone. Phylogenetically, it clusters deep inside *Lecanora*, where it clusters with several species with usnic acid instead of atranorin, but with low support (Fig. 69). Sequences of other species of the *L. marginata* group are not available. This species is described from the same locality as *Buellia pruinocalcarea* (for details see under *Buellia pruinocalcarea*).

Teloschistales D. Hawksw. & O.E. Erikss.

Notes: Teloschistales is a large order of lichenized fungi, one of the largest containing crustose lichens (Arup et al. 2013).

Teloschistaceae Zahlbr. [as 'Theloschistaceae'], in Engler, Syllabus, Edn 2 (Berlin): 45 (1898).

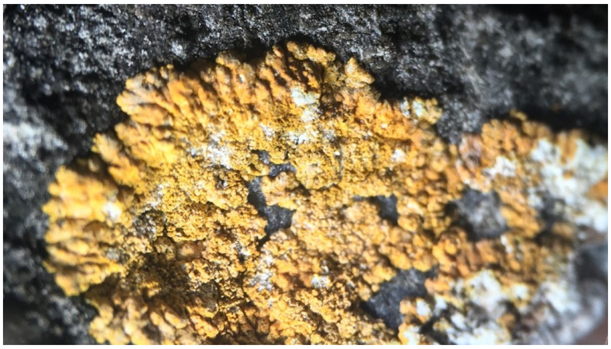


Fig. 70 ***Wetmoreana blastidiocalcarea*** (*Aptroot* 77,806, **holotype**). Habitat. Scale bar = 17 mm

Notes: Teloschistaceae is a family of lichenized fungi, one of the largest containing crustose lichens. Most species are generally still treated under the genus *Caloplaca* Th. Fr. (Schumm and Aptroot 2019).

Wetmoreana Arup, Søchting & Frödén, in Arup, Søchting & Frödén, Nordic Jl Bot. 31(1): 66 (2013)

Notes: *Wetmoreana* is a recently split genus in Teloschistaceae (Arup et al. 2013). At the moment, three to five species are recognized in this genus, depending on whether or not *Fulgogassparrea* S.Y. Kondr., N.-H. Jeong, Kärnefelt, Elix, A. Thell & Hur (Kondratyuk et al. 2013) is recognized as a separate genus.

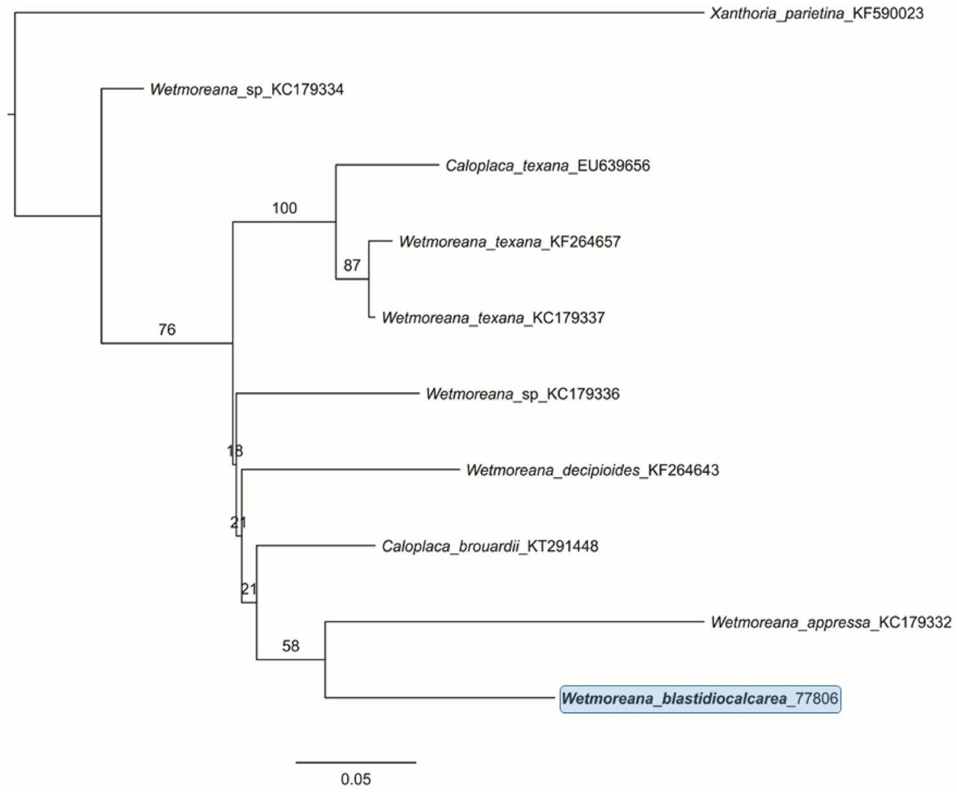


Fig. 71 Phylogram generated from maximum likelihood analysis based on ITS. Bootstrap support values for ML ≥ 80% and Bayesian posterior probabilities ≥ 0.95 are given near nodes respectively. The tree is rooted in *Xanthoria parietina* (pop4_26). Ex-type strains are in bold. The newly generated sequences are indicated in **bold** blue

Wetmoreana blastidiocalcarea Aptroot, M.F. Souza & Spielmann *sp. nov.*

Index Fungorum number: *IF900070; Facesoffungi number*: *FOF13391; Fig. 70*

Saxicolous Wetmoreana on limestone with thallus thick, yellow-orange, radially lobate, central part of the thallus areolate, covered by c. 0.05 mm diam, semiglobose corticate bulbs of thallus color that might serve as blastidia.

Etymology: Named after the calcareous and the blastidious habitat.

Holotype: Aptroot 77806.

Thallus placodioid, up to 2 cm diam., corticate, dull, yellow-orange, white pruinose on the marginal lobes, up to 0.3 mm thick. The central part of the thallus areolate, covered by c. 0.05 mm diam, semiglobose corticate bulbs of thallus colour that might serve as (and would in former species of *Fulgensia* usually being called) blastidia, sometimes partly dissected into secondary lobes resembling the marginal lobes. Marginal lobes much radially divided into less than 0.1 mm wide lobuli, gradually thinning towards the margin. Isidia and soredia absent. *Ascomata* and pycnidia not observed.

Chemistry: Thallus and apothecia UV + red, C−, P−, K+ crimson. TLC: anthraquinones.

Distribution: On exposed limestone in Atlantic rain forest biome; only known from Brazil.

Material examined: Brazil. Mato Grosso do Sul: Serra da Bodoquena, Bodoquena, Dente de Cão, summit, alt. 450 m, 20° 47′ 05″ S, 56° 45′ 03″ W, on exposed limestone in Atlantic rain forest biome, 7 November 2018, Aptroot 77806 (**holotype; CGMC**).

GenBank number: MW322681 (ITS).

Notes: Morphologically, this species shows similarities with several genera in the Teloschistaceae. The corticated granules in the central part of the thallus resemble the blastidia known from several species of *Fulgensia* A. Massal. & De Not. In this sense, it was used for most of the past century. Sequencing of the type showed that this species belongs to *Wetmoreana*. None of the species in this genus are blastidiate. Phylogenetically, it clusters deep inside *Wetmoreana* (Fig. 71). Note that *Caloplaca brouardii* de Lesd. is phylogenetically also a *Wetmoreana* (Wilk et al. in prep). This species is described from the same locality as *Buellia pruinocalcarea* (for details see under that species).

Class Leotiomycetes O.E. Erikss. & Winka

Phacidiales C.E. Bessey

Phacidiales was placed in Leotiomycetes by Bessey (1907). Quijada et al. (2018) included three families in Phacidiale (*viz*. Helicogoniaceae, Phacidiaceae, Tympanidaceae) and one informal taxonomic lineage with 29 genera. Wijayawardene et al. (2022) accepted two families *viz*.

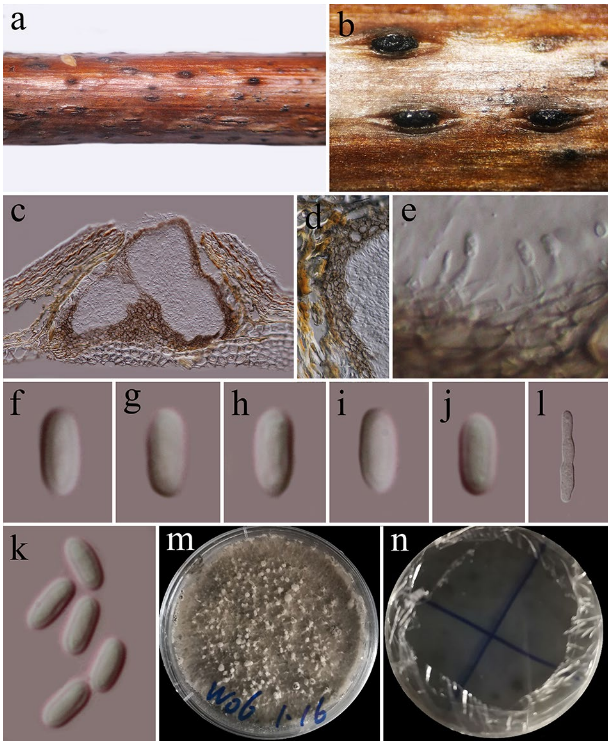


Fig. 72 ***Phacidium chinense*** (KUN-HKAS 112899, **holotype**). **a** Herbarium. **b** Conidiomata on the host. **c** Vertical sections of conidioma. **d** Sections of peridium. **e** Conidiogenous cells and developing conidia. **f–k** Conidia. **l** Germinating conidium. **m, n** Culture on PDA. Scale bars: **c** = 100 µm, **d** = 50 µm, **e, k** = 10 µm, **f–j** = 5 µm, **l** = 20 µm

Helicogoniaceae and Phacidiaceae in this order and accepted Tympanidaceae in Leotiales.

Phacidiaceae Fr. [as 'Phacidiacei'], Summa veg. Scand., Sectio Post. (Stockholm): 367 (1849).

Phacidiaceae was introduced by Fries (1849) and typified by *Phacidium* (Crous et al. 2014). Six genera (*Allantophomopsiella*, *Allantophomopsis*, *Bulgaria*, *Darkera*, *Phacidium* and *Potebniamyces*) were included in Phacidiaceae based on DNA sequence data (Crous et al. 2014; Li et al. 2020). Wijayawardene et al. (2022) accepted nine genera in this family.

Phacidium Fr., Observ. mycol. (Havniae) 1: 167 (1815).

The generic name *Phacidium* was introduced by Fries (1815) with *Phacidium lacerum* as the type species. *Phacidium* species are widely distributed throughout the globe and has been reported as pathogens on dead leaf tips and as saprobic on dead leaves of several host families (Crous et al. 2014; Li et al. 2020). Both asexual morph and sexual morph of this genus are known (Li et al. 2020). There are 43 taxa are listed in Species Fungorum (2022a, b) (http://www.speciesfungorum.org/Names/Names.asp). However, it is a poorly studied genus due to the lack of molecular data. Here we introduce a new species of *Phacidium* from decaying wood in terrestrial habitats in China.

Phacidium chinense G.C. Ren & K.D. Hyde ***sp. nov.***

Index Fungorum number: IF559693; Facesoffungi number: FoF10836, Fig. 72

Etymology: The species epithet reflects the country where the species was collected.

Holotype: KUN-HKAS 112899

Saprobic on dead wood of *Rosa* sp. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 170–200 µm high, 150–240 µm diam. ($\bar{x} = 180 \times 200$ µm, n = 5), black, pseudostromatic, solitary or gregarious, semi-immersed to superficial, multi-locular, with 3–10 locules embedded in the pseudostroma. *Ostioles* $60–85 \times 45–70$ ($\bar{x} = 73.5 \times 58.5$, $n = 5$) µm, centrally located, circular. *Conidiomata wall* 15–35 µm thick, 3–5 layered, comprising brown cells of *textura angularis*, thick-walled at basal, thin-walled at side. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* $3.5–5.5 \times 1.2–2.0$ µm ($\bar{x} = 4.8 \times 1.5$, $n = 10$), hyaline, enteroblastic, phialidic, discrete, cylindrical, smooth-walled, arising from stratum. *Conidia* $4.5–6 \times 2.0–2.4$ µm ($\bar{x} = 5.2 \times 2.1$ µm, $n = 30$), hyaline, oblong, unicellular, thick- and smooth-walled.

Culture Characters: Colonies on PDA, reaching 80–90 mm diam., after four weeks at 20–25 °C, medium dense, circular, rough, fluffy, cotton, gray, with white papillate on the surface, reverse dark-gray.

Material examined: China, Yunnan Province, Diqing Autonomous Prefecture, Xianggelila (27.28′ 8° N, 99.50′ 45° E), 2958 m, on dead wood of *Rosa* sp. (Rosaceae), 30 August 2020, Guang-Cong Ren, W06 (KUN-HKAS 112899, **holotype**), ex-type living culture KUMCC 20-0168.

GenBank numbers: ON490924 (LSU), ON490925(ITS), ON506923(*tef1*), ON506922 (*rpb2*)

Notes: Phacidium chinense is introduced as a new species based on its distinct morphology, which is supported by phylogenetic analyses. In the phylogenetic analyses, *P. chinense* is distinct from extant species in *Phacidium* and formed a sister clade to *Phacidium calderae*, however, there is no bootstrap support (Fig. 73). *Phacidium chinense* is different to *P. calderae* in having oblong conidia and phialidic, cylindrical conidiogenous cells, while *P. calderae* in having subcylindrical conidia with apical mucoid appendage and proliferating with periclinal thickening conidiogenous cells (Crous et al. 2014).

Class Sordariomycetes O.E. Erikss. & Winka

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

Diaporthales Nannf

Diaporthales containing numerous important endophytic, saprobic and phytopathogenic ascomycetous families. Even

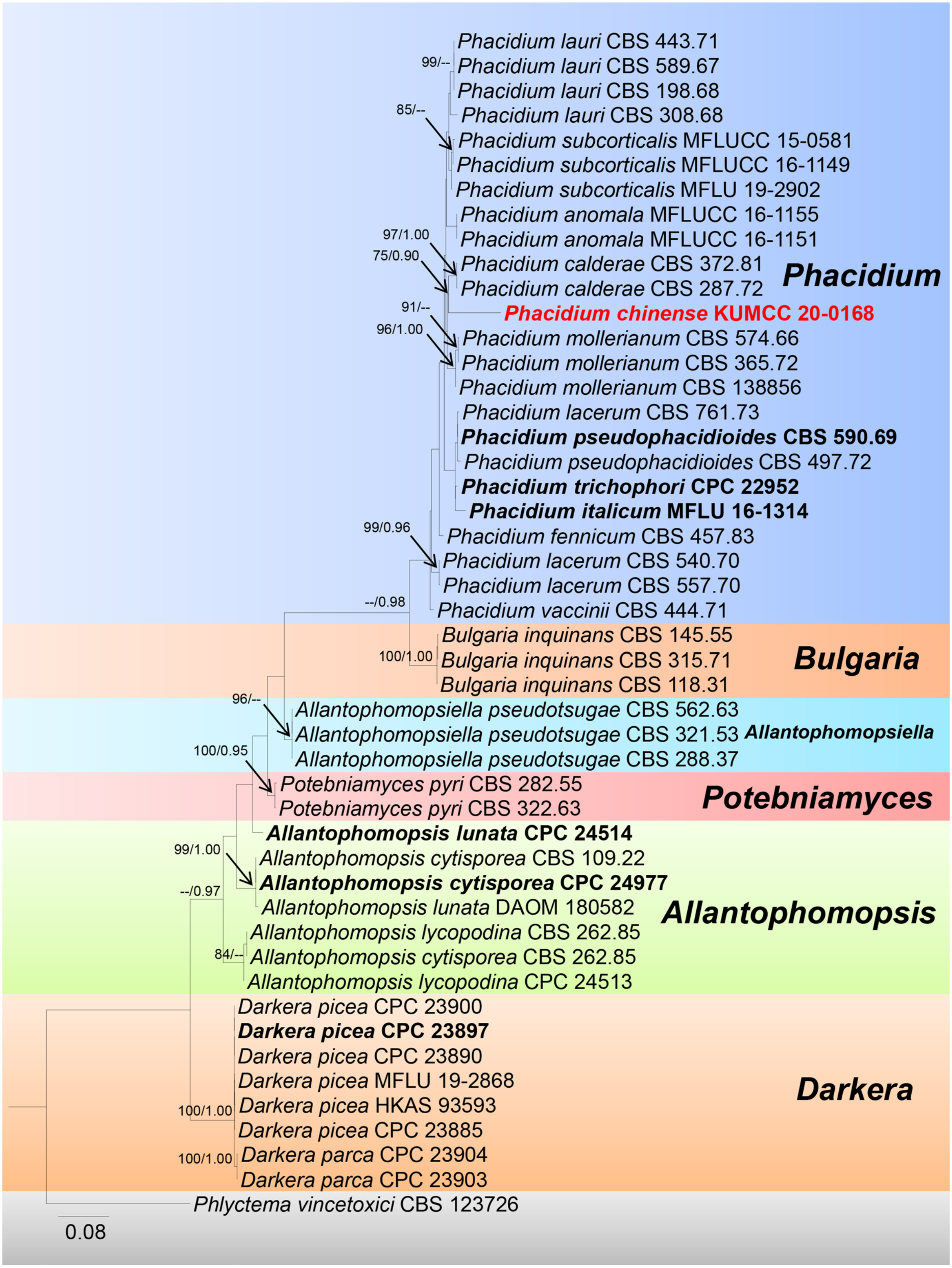


Fig. 73 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *tef1*, and *rpb2* sequence data. Forty-eight strains are included in the combined analyses which comprised 3378 characters (8200 characters for LSU, 546 characters for ITS, 879 characters for *tef1*, 1133 characters for *rpb2*) after alignment. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The evolutionary model SYM + G applied to ITS sequence data, while SYM + I + G applied to LSU, GTR + G *tef1* and *rpb2* gene regions. Bootstrap support values for ML ≥ 80% and BYPP ≥ 0.95 are given near nodes respectively. The tree is rooted in *Phlyctema vincetoxici* (CBS 123,726). Ex-type strains are in **bold**. The newly generated sequences are indicated in **bold** red

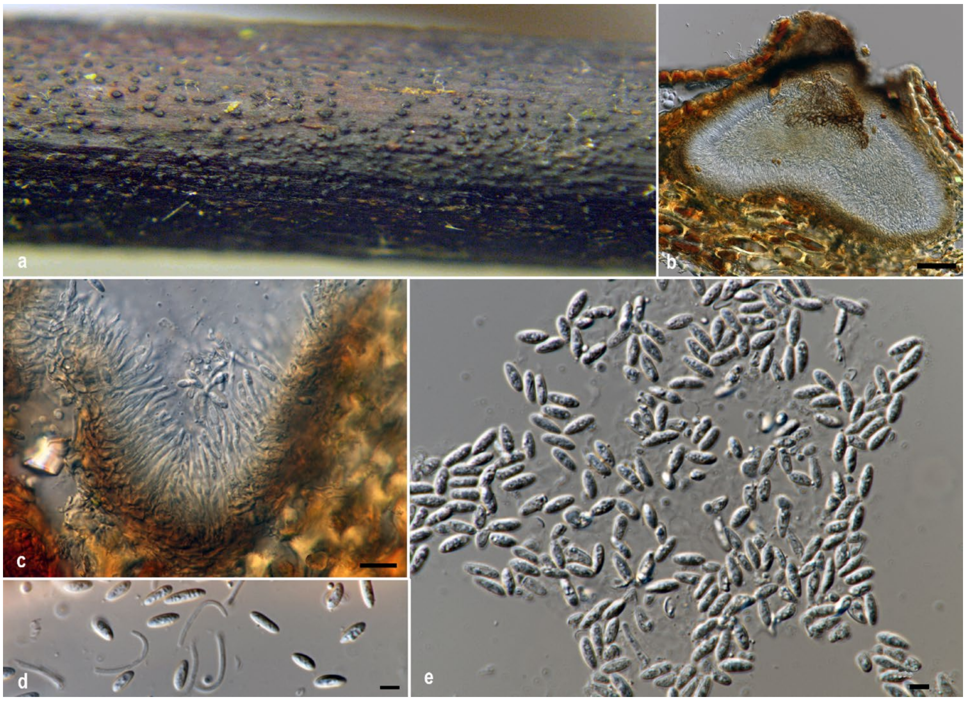


Fig. 74 ***Diaporthe foeniculina*** (**JZB320201, new host record**) **a**. Appearance of conidiomata on the host. **b**. Section through the conidiomata. **c**. Mature conidia attached to the conidiophore and the conidioma cell wall. **d**. Alpha and beta conidia. **e**. Mature conidia. Scale bars: **b, c** = 20 µm, **d, e** = 5 µm

though, families, and genera in this order showed high distinct morphological diversity, taxonomic placements are still problematic (Senanayake et al. 2017).

Diaporthales introduced by Nannfeldt (1932), to accommodate Höhnel's Eu-Diaportheen and Valseen taxa (Senanayake et al. 2018) and currently 30 families are in this order named: Apiosporopsidaceae, Apoharknessiaceae, Asterosporiaceae, Auratiopycnidiellaceae, Coryneaceae, Cryphonectriaceae, Cytosporaceae, Diaporthaceae, Diaporthosporellaceae, Diaporthostomataceae, Dwiroopaceae, Erythrogloeaceae, Gnomoniaceae, Harknessiaceae, Juglanconidaceae, Lamproconiaceae, Macrohilaceae, Melanconidaceae, Melanconiellaceae, Neomelanconiellaceae, Phaeoappendicosporaceae, Phaeochorellaceae, Prosopidicolaceae, Pseudomelanconidaceae, Pseudoplagiostomataceae, Schizoparmaceae, Stilbosporaceae, Sydowiellaceae, Synnemasporellaceae and Tubakiaceae (Hyde et al. 2020a, b, c; Wijayawardena et al. 2022).

Diaporthaceae Höhn. ex Wehm., Am. J. Bot. 13: 638 (1926)

Diaporthaceae was introduced and placed in Diaporthales by von Höhnel (1917). The members of Diaporthaceae are known to be endophytic, pathogenic and saprobic. Species in Diaporthaceae mostly inhabit in terrestrial hosts and rarely on aquatic hosts (Udayanga et al. 2011; Dissanayake et al. 2017; Senanayake et al. 2017). There are 15 genera accepted in Diaporthaceae, *viz. Apioporthella, Apiosphaeria, Chaetoconis, Chiangraiomyces, Diaporthe, Hyaliappendispora, Leucodiaporthe, Massariothea, Mazzantia, Ophiodiaporthe, Paradiaporthe, Phaeocytostroma, Phaeodiaporthe, Pustulomyces,* and *Stenocarpella* (Hyde et al. 2020a, b, c).

Diaporthe Nitschke, Fungi rhenani exsic., suppl., fasc. 5: no. 1988 (1867)

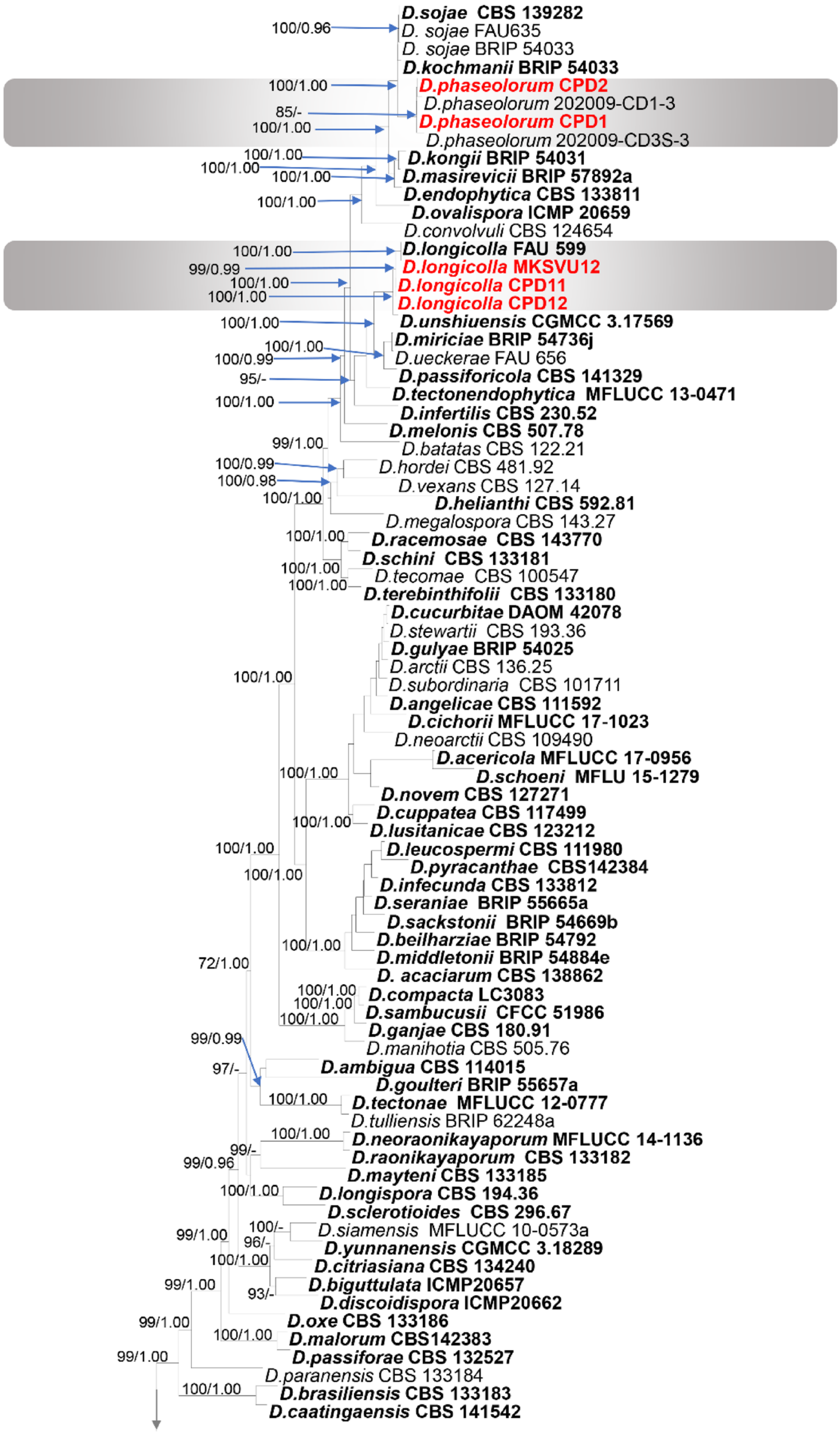
Diaporthe is the type genus of Diaporthaceae, and it was established by Nitschke (1867). *Diaporthe* species have been recorded as endophytes or saprobes on a wide range of host plants in different geographical areas (Udayanga et al. 2011; Dissanayake et al. 2017; Abeywickrama et al. 2020). Many economically significant crops are infected by pathogenic *Diaporthe* species leading to severe crop losses (Manawasinghe et al. 2019; Abeywickrama et al. 2020), with blights, fruit and root rots, cankers, diebacks, wilts and leaf spots (Manawasinghe et al. 2019; Abeywickrama et al. 2020). The genus contains 1152 epithets in Index Fungorum (assessed in 29.08.2022; Index Fungorum 2022a, b).

Diaporthe foeniculina (Sacc.) Udayanga & Castl., in Udayanga et al., Persoonia 32: 95 (2014).

Index Fungorum number: IF803929; Facesoffungi number: FoF02183; Fig. 74

Saprobic on dead aerial branch of *Ficus carica*. **Sexual morph:** See Udayanga et al. (2014). **Asexual morph:** coelomycetous. *Conidiomata* observed as small black dots on the host, semi-immersed to immersed, pycnidial, pyriform, scattered, ostiolate, 150–300 µm diam. *Conidiomata wall* consisting of 3–4 layers of pale brown, thick-walled cells of *textura angularis*. *Conidiophores* hyaline, smooth, unbranched. *Alpha conidia* hyaline, smooth-walled,

Fig. 75 Phylogram generated from maximum likelihood analysis based on ITS, *cal*, *his*, *tef1* and *tub2* sequenced data of given *Diaporthe* species. Related sequences were obtained from GenBank, and 223 strains are included in the sequence analyses, with 2674 columns, 1972 distinct patterns 1439 parsimony-informative, 340 singleton sites, 894 constant sites. *Diaporthella corylina* (CBS121124) is used as the outgroup taxon. Bootstrap support values for ML ≥ 65%, BYPP ≥ 0.90 are given near the nodes. Type strains are in **bold**. Newly generated strains are in red **bold**



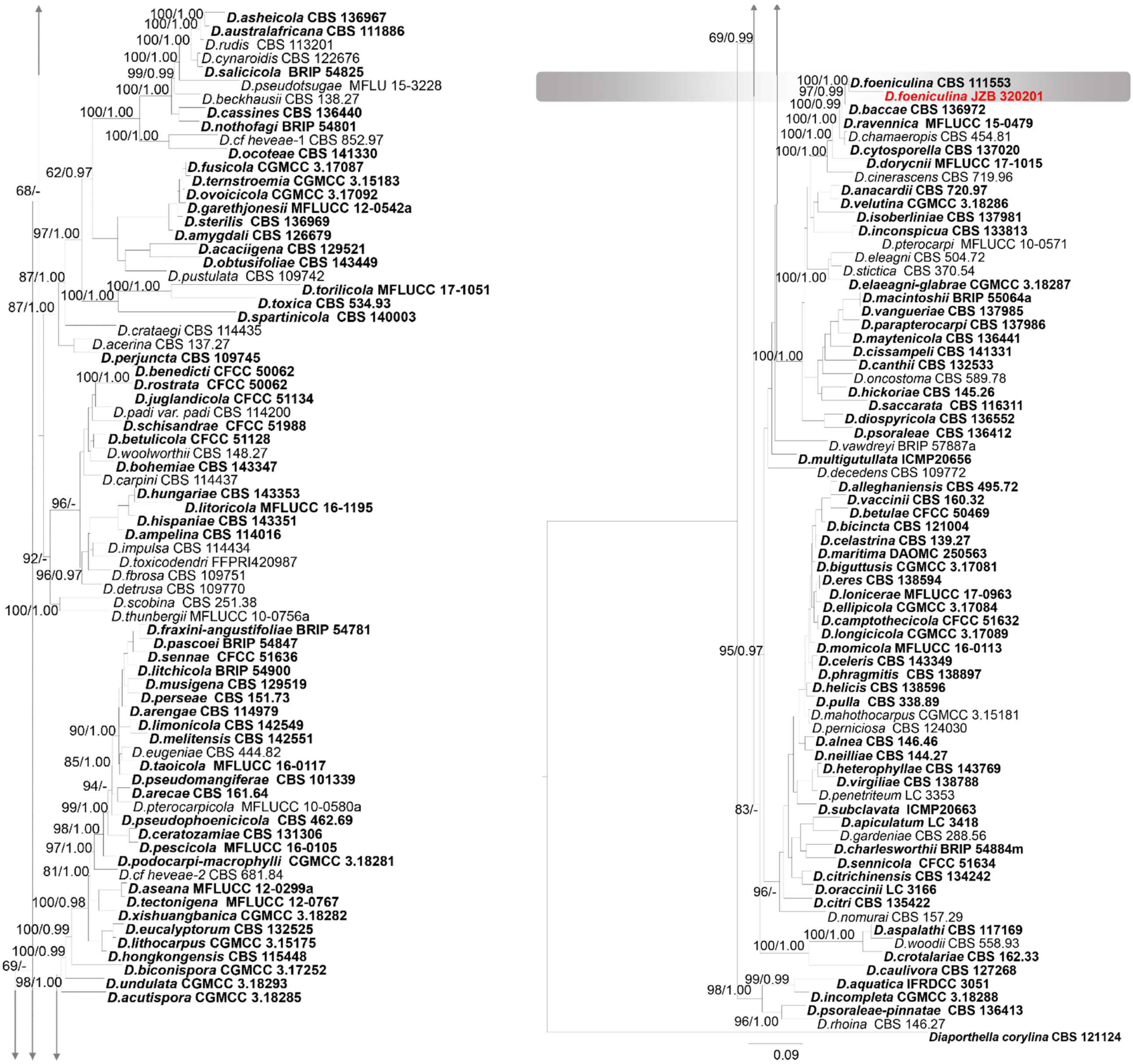


Fig. 75 (continued)

bi- to multi-guttulate, ovate to ellipsoidal, base sub-truncate, 5–7.5 × 1.5–3 µm ($n = 20$). *Beta conidia* aseptate, hyaline, smooth, apex and base bluntly rounded, slightly curved, 15–25 × 0.5–2 µm ($n = 10$).

Culture characteristics: Colonies on PDA entirely white both on surface and reverse. Aerial mycelium cottony, colonies reaching 60 mm diam. after 7 days in room temperature.

Material examined: Italy, Province of Forlì-Cesena [FC], near Pianetto—Galeata, on dead and aerial branch of *Ficus carica* L. (Moraceae), 21 December 2018, E. Camporesi, IT 4192 (JZBH 320201), living culture JZB 320201.

Hosts: Wide host range, including *Achillea*, *Ailanthus*, *Amorpha*, *Angelica*, *Arctium*, *Asparagus*, *Camellia*, *Castanea*, *Chenopodium*, *Citrus*, *Cupressus*, *Diospyros*, *Eucalyptus*, *Ficus carica Hemerocallis*, *Lunaria*, *Melilotus*, *Microcitrus*, *Persea*, *Platanus*, *Prunus*, *Rosa*, *Rubus*, *Vicia* and *Wisteria* (Farr and Rossman 2022; this study).

Distribution: Wide geographical range, including in Chile, Greece, Iran, Italy, Malta, New Zealand, Portugal, Serbia, South Africa, Spain, Thailand, Turkey, Uruguay, US (Farr and Rossman 2022; this study).

GenBank numbers: OP002068 (ITS), OP837431(*his*), OP837429 (*tub2*)

Notes: Diaporthe foeniculina (JZB 320201) was recovered from a dead aerial branch of *Ficus carica* in Italy. Our strain shared similar morphology with the type strain of *D.*

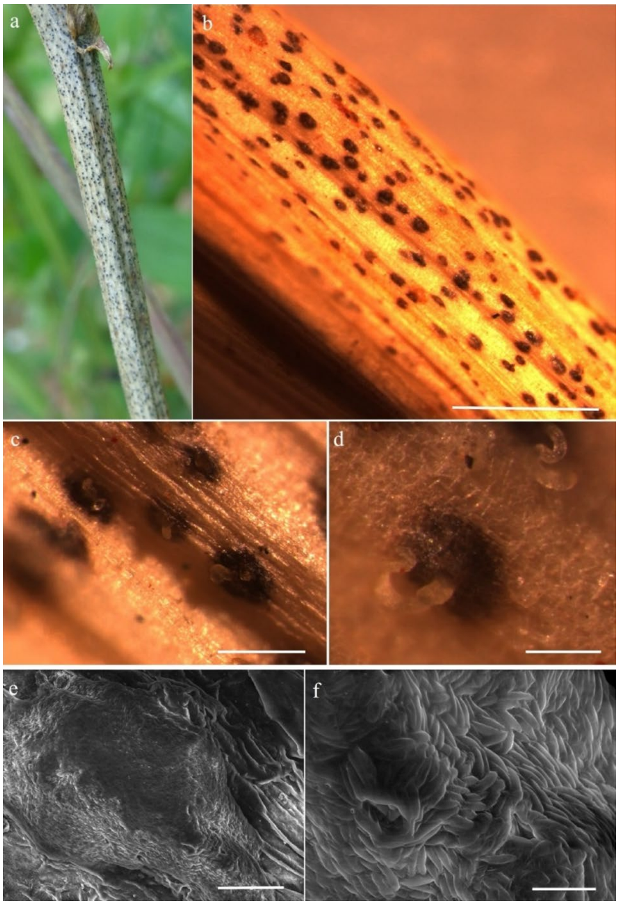


Fig. 76 Micromorphological features of *D. longicolla* (CPDI21, **new host record**) **a.** Cowpea stem affected by *Diaporthe longicolla.* **b.** Stereo view of infected region showing pycnidial structures. **c–d.** Stereo view showing cirri of spores erupted from pycnidia. **e.** SEM image of pycnidium. **f.** Conidia of *D. longicolla* observed in SEM. Scale bars: **b** = 10 mm; **c– d** = 2 mm; **e – f** = 10 µm

foeniculina (CBS 111553) which was introduced by Udayanga et al. (2014), with minor dimensional differences. Conidiomata of our strain (JZB 320201) are comparatively smaller than those of *D. foeniculina* (CBS 111553) (150–300 µm diam. *vs* 400– 700 µm diam.). Further we have observed smaller alpha conidia in our strain than CBS 111553 (5–7.5 × 1.5–3 µm *vs* 8.8 ± 0.3 × 2.4 ± 0.1 µm) (Udayanga et al. 2014). These morphological differences probably due to environmental factors and host variations. Phylogenetic analyses using combined ITS, *cal*, *his*, *tef1*, *tub2* sequence data confirmed that our strain is *D. foeniculina* and it is clade with the strain MFLUCC 20-0151 with high statistical support (92/1.00) (Fig. 75). Comparisons of base pair differences for ITS, *tub2* and *his* genes between our strain (JZB 320201) and the ex-epitype strain of *D. foeniculina* (CBS 111553) reveal less than 1% base pair differences in ITS and *tub2* gene regions (ITS = 0.57%, *tub2* = 0.97%). However, we observe 5.77% base pair difference in HIS gene (94.23% similarity). We were unable to obtain *cal* and *tef1* sequence data for our strain, and we could not compare the base pair difference for them. Thus, based on the multi-gene phylogeny and morphology; this study presents the first report of *D. foeniculina* from a *Ficus carica* from Italy.

Diaporthe longicolla (Hobbs) J.M. Santos, Vrandečić & A.J.L. Phillips, in Santos, Vrandečić, Čosić, Duvnjak & Phillips, *Persoonia* 27: 13 (2011)

Index Fungorum number: *IF164797*; *Faceoffungi number: FOF11682; Figs.* 76, 77

Pathogenic and associated with stem of *Vigna unguiculata*. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* 80–130 µm high, 230–320 µm diam. $\bar{x}$ = 118 × 290 µm, n = 20, pycnidial, pyriform, initially immersed, erumpent at maturity, globose to pyriform, black, elongated neck, often with light yellowish white conidial cirrus extruding from ostiole. *Pycnidial wall* parenchymatous consisting of 4–7 layers of pale brown, thick-walled cells of *textura angularis*, *Pycnidia* globose locules and prominent beaks, which immersed in medium, black, solitary, discoid or irregular. *Conidiophores* 4–7 × 4.1–7.3 µm ($\bar{x}$ = 4.4 × 6.3 µm, *n* = 30), ampulliform, straight to sinuous, unbranched, hyaline, smooth. *Conidiogenous cells* 7.8–13.8 × 1.4–2.7 µm ($\bar{x}$ = 10.9 × 2.1 µm, n = 30), phialidic, terminal, cylindrical, slightly tapering towards the apex. *Alpha-conidia* 5.1–7.5 × 1.2–3.4 µm ($\bar{x}$ = 6.1 × 2.6 µm, n = 20), aseptate, hyaline, smooth, ovate to ellipsoidal, guttulate. *Beta-conidia* 5.8–7.5 × 2.5–3.5 µm ($\bar{x}$ = 6.4 × 2.8 µm, n = 10), hyaline, filiform, hamate.

Cultural characteristics: On potato dextrose agar, the fungus initially produced white fluffy aerial hyphae, forming relatively dense concentric pattern colony, which subsequently exhibited light yellow pigmentation.

Material examined: India, Karnataka, Mysuru Doddamaragowdanahally, on infected stem of cowpea plants as pathogen. July, 2020, S. Mahadevakumar, Y.S. Deepika (UOM-IOE 20/25), living cultures CPDI21, CPDI22, MKSVu012.

Hosts: Wide host range, including *Abutilon*, *Acer*, *Actinidia*, *Ambrosia*, *Arachis*, *Chamaesyce*, *Cucumis*, *Euphorbia*, *Glycine*, *Helianthus*, *Ipomoea*, *Kalanchoe*, *Phaseolus*, *Pisum*, *Pyrus*, *Rumex*, *Solanum*, *Trichilia*, *Vigna* and *Xanthium* (Farr and Rossman 2022; this study).

Distribution: Wide geographical range, including in Argentina, Australia, Brazil, China, Croatia, Greece, India, Italy, Malaysia, Missouri, South Korea, US (Farr and Rossman 2022; this study).

GenBank Numbers: CPDI21—MW737797 (ITS), OM934823 (*tub2*), OM934820 (*tef1*)

CPDI22–MW737798 (ITS), OM934824 (*tub2*), OM934821(*tef1*)

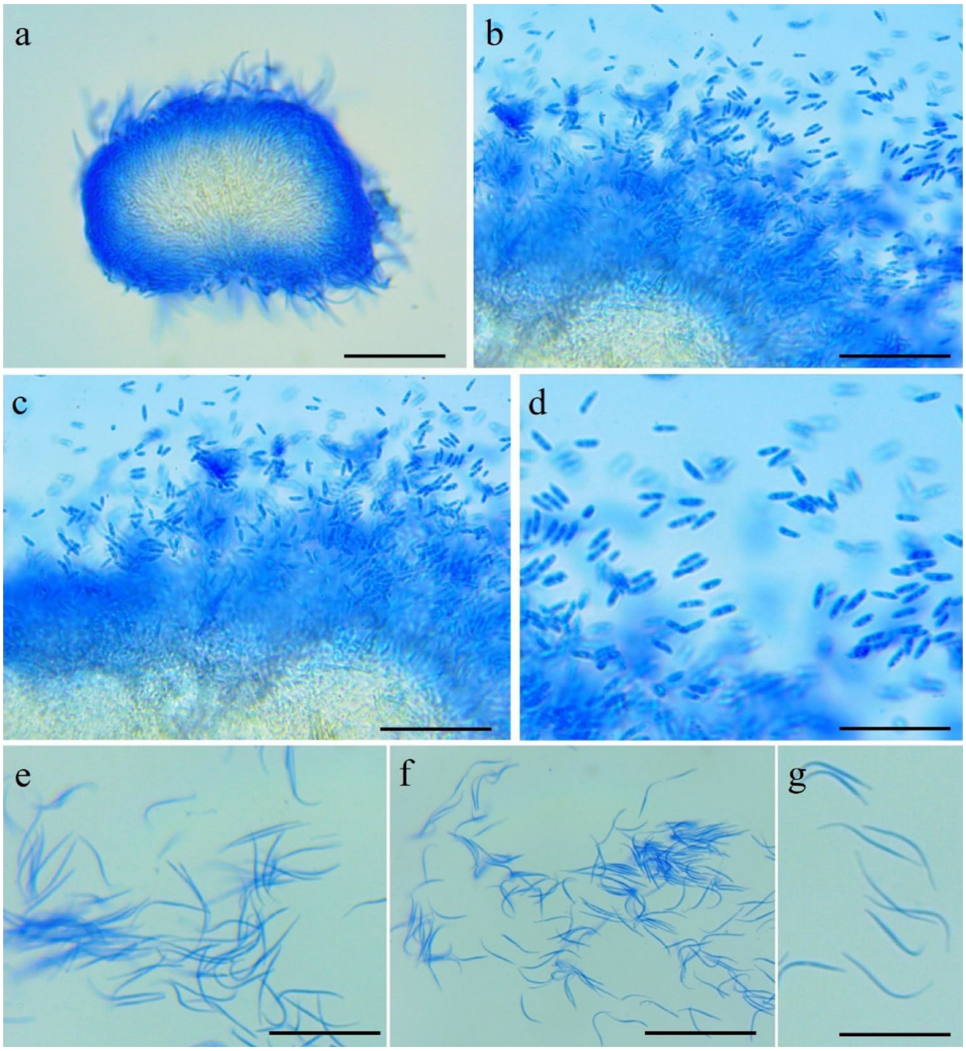


Fig. 77 Micromorphological features of *D. longicolla*: **a–d.** Conidial mass with spores observed under compound microscope. **e–g** Beta conidia of *Diaporthe longicolla* recorded on cowpea plants. Scale bar: **a–g** = 20 µm

MKSVu012– KT819767 (ITS), OM934825(*tub2*), OM934822 (*tef1*)

Notes: The symptoms were observed on stems of cowpea. Initial symptoms appeared as small lesions, more or less circular, later elongated, blackish-brown lesions, eventually pycnidia developed (Fig. 76). Stem girdling occurs and the shoot above the infected area wilts and dries up. Pathogenicity tests were conducted and proved to be pathogenic on healthy cowpea plants. Morphologically our strain shares similar morphology with the ex-type strain of *D. longicolla* (Fig. 77). In the multigene phylogenetic analyses, our strain clusters with *D. longicolla* with a high bootstrap support (Fig. 75). Previously, *Phomopsis longicolla* is known to be associated with cowpea seeds. However, no reports are available on the association of *D. longicolla* of cowpea in India. This is the first report of *D. longicolla* associated with cowpea from India.

Diaporthe phaseolorum (Cooke & Ellis) Sacc., Syll. Fung. (Abellini) 1: 692 (1882).

Index Fungorum number: IF164797; *Faceoffungi number: FoF10638; Figs: 78, 79.*

Pathogenic and associated with stem of *Vigna unguiculata*. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* 105–192 µm high, 165–285 µm diam. $\bar{x} = 122 \times 255$ µm, $n = 30$, pycnidial, pyriform, initially immersed, erumpent at maturity, globose to pyriform, black, elongated neck, often with light yellowish white conidial cirrus extruding from ostiole. *Pycnidial wall* parenchymatous consisting of 3–6 layers of pale brown, thick-walled cells of *textura angularis*. *Pycnidia* globose locules and prominent beaks, which immersed in medium, black, solitary, discoid or irregular. *Conidiophores* 3.8–7.5 × 3.8–7.5 µm ($\bar{x} = 4.2 \times 5.8$ µm, $n = 30$), ampulliform, straight to sinuous, unbranched, hyaline, smooth. *Conidiogenous cells* 8.2–12.8 × 1.6–2.5 µm ($\bar{x} = 9.8 \times 2.2$ µm, $n = 30$), phialidic, terminal, cylindrical, slightly tapering towards the apex. *Alpha-conidia* 5.3–7.7 × 1.5–4.6 µm ($\bar{x} = 6.5 \times 2.8$ µm, $n = 30$), aseptate, hyaline, smooth, ovate to ellipsoidal, guttulate. *Beta-conidia*

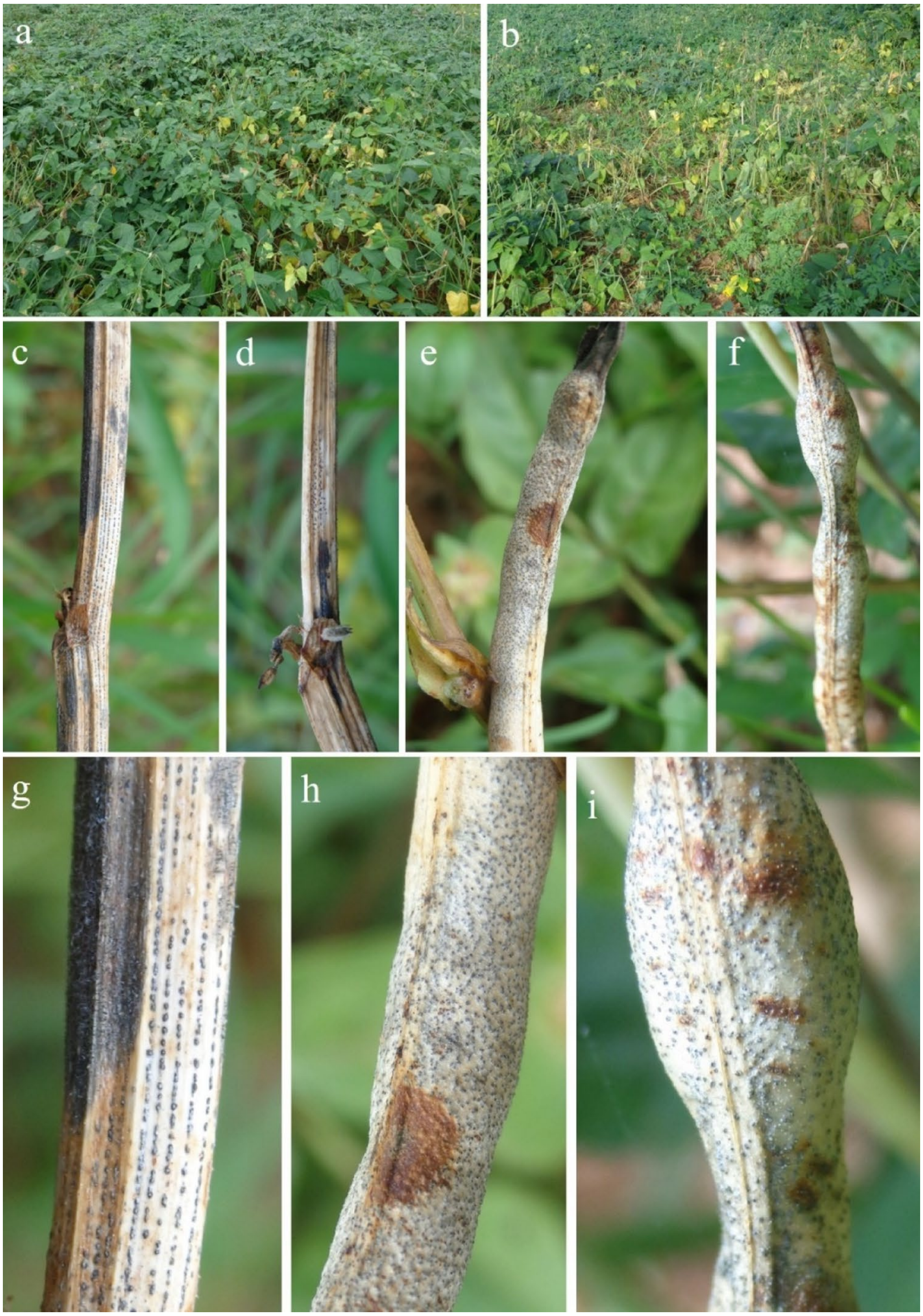


Fig. 78 Diagnostic features of cowpea stem blight and pod blight disease caused by *Diaporthe phaseolorum* and *D. longicolla*: **a–b.** field view of cowpea plants affected with Diaporthe stem blight and pod blight disease. **c, d, g.** Stem blight disease caused by *D. longicolla*. **e,f,h,i.** pod blight disease symptoms caused by *D. phaseolorum*

10.2–17.5 × 1.2–2.3 µm ($\bar{x}$ = 12.6 × 1.2 µm, n = 30), hyaline, filiform, hamate.

Culture characteristics: On PDA, colonies with white, floccose, aerial mycelium were recorded after 7 days of incubation. Pure cultures obtained from the colonies expressed from infected pod and stem samples.

Material examined: India, Karnataka, Mysuru Doddamaragowdanahally, on infected stem of cowpea plants as pathogen, July, 2020, S. Mahadevakumar, Y.S. Deepika, N. Lakshmidevi (UOM-IOE 20/26), living cultures CPDp1, CPDp2.

Hosts: Wide host range, including *Acer*, *Actinidia*, *Aeschynomene*, *Arctium*, *Aspalathus*, *Aster*, *Calopogonium*, *Cannabis*, *Caperonia*, *Capsicum*, *Centrosema*, *Clitoria*, *Cyphomandra*, *Desmanthus*, *Desmodium*, *Eriobotrya*, *Euphorbia*, *Glycine*, *Helianthus*, *Hylocereus*, *Ipomoea*, *Jatropha*, *Lablab*, *Lupinus*, *Lycopersicon*, *Macroptilium*, *Macrotyloma*, *Maytenus*, *Ocimum*, *Olearia*, *Panicum*, *Phalaris*,

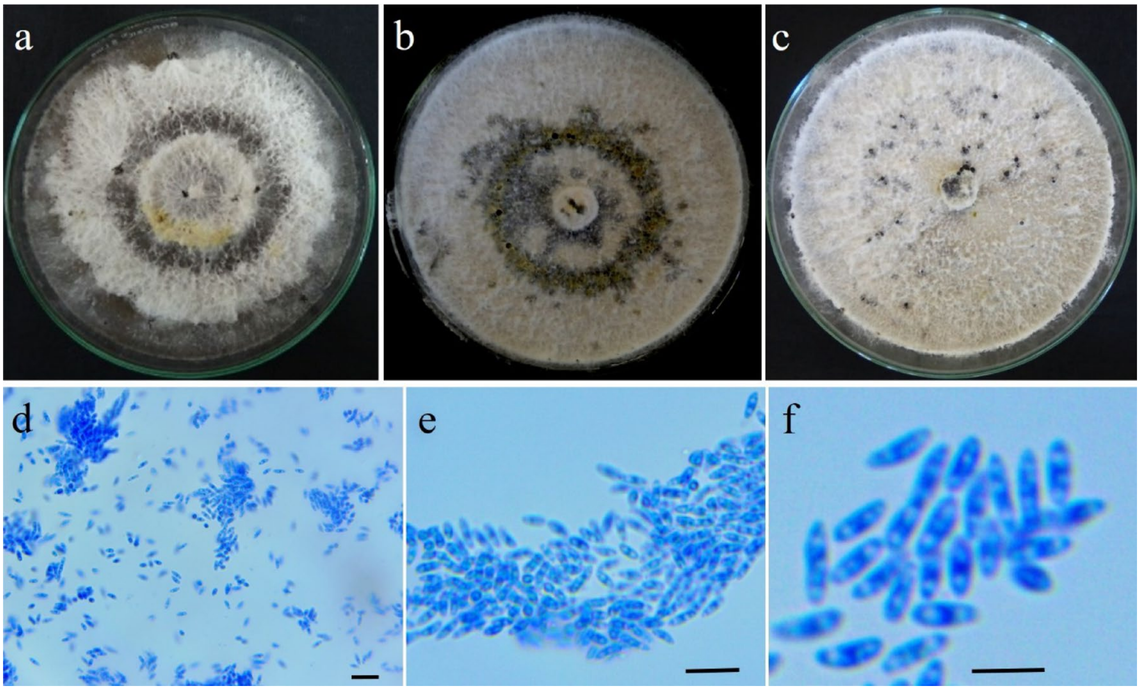


Fig. 79 Cultural and micromorphological characteristics of *Diaporthe phaseolorum* isolated from Cowpea: **a–c.** Pure cultures of *D. phaseolorum* on PDA (15 days old). **d–f.** Alpha conidia of *D. phaseolorum*. Scale bar: **d–f** = 10 µm

Phaseolus, *Pyrus*, *Stokesia*, *Vigna*, *Vitis* and *Zea* (Farr and Rossman 2022; this study).

Distribution: Wide geographical range, including in Australia, Barbados, Brazil, Brunei Darussalam, Cameroon, Canada, China, Colombia, Cook Islands, Croatia, Cuba, Dominican Republic, Fiji, India, Italy, Jamaica, Korea, Maryland, Mauritius, Missouri, New Zealand, Papua New Guinea, Spain, South Africa, Switzerland, Thailand, Tonga, Trinidad and Tobago, United Kingdom, United States, Uruguay, Venezuela and West Indies (Farr and Rossman 2022; this study).

GenBank Numbers: CPDp1– MW737799 (ITS), OM934818 (*tub2*), OM934816 (*tef1*)

CPDp2– MW737800 (ITS), OM934819 (*tub2*), OM934817 (*tef1*)

Notes: Morphologically our strain is similar to the ex-type strain of *D. phaseolorum* (Fig. 78). In the multigene phylogenetic analyses, our strain clustered with the ex-type strain of *D. phaseolorum* (Fig. 75). Pathogenicity tests were conducted and proved to be pathogenic on healthy cowpea plants. *Diaporthe longicolla* causes stem blight of cowpea while *D. phaseolorum* causes pod blight of the same host (Fig. 79). This is the first report of *D. phaseolorum* associated with cowpea from India and worldwide.

Melanconiellaceae Senan., Maharachch. & K.D. Hyde, in Senanayake et al., Stud. Mycol. 86: 275 (2017).

Melanconiellaceae was invalidly introduced (Locquin 1984) for *Melanconiella* and it was validated by Senanayake et al. (2017). The type species of *Melanconiella* is *M. spodiaea* (Tul. & C. Tul.) Sacc. (Fan et al. 2018). Fan et al. (2018) accepted *Melanconiella*, *Microascospora* and *Sheathospora* and Senanayake et al. (2018) accepted *Greeneria*, *Melanconiella* and *Microascospora* in the family. Hyde et al (2020c) accepted five genera; *Greeneria*, *Melanconiella*, *Microascospora*, *Septomelanconiella* and *Sheathospora* in the family.

Melanconiella Sacc., Syll. fung. *(*Abellini*)* 1: 740 *(*1882*)*

Melanconiella was established by Saccardo (1882) for the type species *M. spodiaea* Tul. & C. Tul. and second species *M. chrysostroma* (Fr.) Tul. & C. Tul. *Melanconiella* species are found in overwintered plants as saprobes or as mild canker causing agents (Voglmayr et al. 2012; Senanayake et al. 2018). There are 40 species epithets recorded in Index Fungorum (January 2022).

Melanconiella meridionalis Voglmayr & Jaklitsch, in Voglmayr et al., Fungal Diversity 57(1):33 (2012).

Index Fungorum number: IF800123; Facesoffungi number: FoF10701, Fig. 80

Saprobic on dead twigs of *Fagus sylvatica*. **Sexual morph:** *Pseudostromata* indistinct, less commonly distinct and circularoutline, causing minute bumps in the bark. *Ectostromatic disc* flat, 2–2.3 mm long, well-defined,

Fig. 80 ***Melanconiella meridionalis*** (MFLU 15–2604, **new host and geographical record**) **a, b** Appearance of pseudostromata on dead branch of *Fagus sylvatica* **c** Pseudostroma in transverse section **d, e** Pseudostroma in vertical sections **f** Peridium. **g** Paraphyses.**h**–**j** Asci. **k**–**n** Ascospores. Scale bars: **d** = 50 µm, **e** = 80 µm, **f** = 10 µm, **h–j** = 25 µm, **k–n** = 10 µm

with circular or elliptic outline, cream, light or pale yellow. *Central column* dark brown. *Entostroma* yellowish hyphae. *Ostiole* central. *Perithecia* 200–600 µm, subglobose, immersed, coriaceous, brown to black, *Perithecia wall* 8–10 µm wide, comprising brown cells of *textura angularis* of inner layer and 15–18 µm wide, unequally thick, comprising irregular dark brown cells of *textura prismatica* of outer layer. *Hamathecium* comprising 1–1.5 µm septate, unbranched, cellular pseudoparaphyses. *Asci* (85–)95–100(–115) × (8–)10–12(–15) µm ($\bar{x}$ = 97 × 11 µm, *n* = 20), broadly cylindrical to fusoid, 8-spored, distinct apical ring with short pedicel or sessile. *Ascospores* uni- or irregularly biseriate, hyaline, fusoid, constricted at the septum, (20–)23–25(–28) × (4–) 5–6(–7) µm, ($\bar{x}$ = 24 × 5.2 µm, n = 30); ends rounded, upper cell mostly larger and some guttules. **Asexual morph:** Not observed.

Material examined: Italy, Province of Forlì-Cesena, Santa Sofia, on twigs of *Fagus sylvatica* L. (Fagaceae), 3 August 2015, E. Camporesi, IT2575 (MFLU 15-2604).

Host and distribution: *Ostrya carpinifolia* in China (Voglmayr et al. 2012; Fan et al. 2018), Europe and North

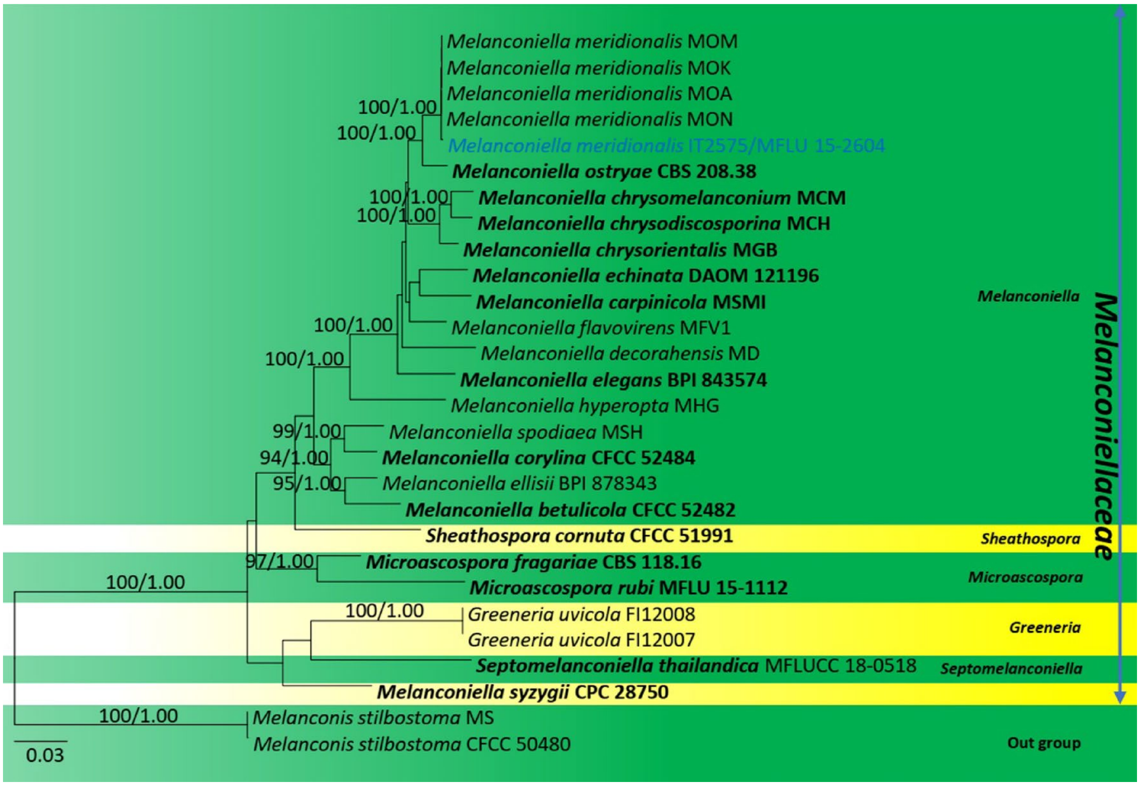


Fig. 81 Phylogram generated from the maximum likelihood analysis based on combined LSU, ITS, *rpb2* and *tef1* sequence data representing family Melanconiellaceae. Related sequences are taken from Fan et al. (2018) and Senanayake et al. (2018). *Melanconis stilbostoma* (CFCC 50,480) and *M. stilbostoma* (MS) are used as the outgroup taxa. Twenty-eight strains are included in the combined gene analyses comprising 3380 characters after alignment (880 characters for LSU, 500 characters for ML ≥ 75% and BYPP ≥ 0.95 are given above the nodes. Ex-type strains are in **bold** and new strain is indicated in blue

America (Voglmayr et al. 2012), *Fagus sylvatica* in Italy (this study).

GenBank numbers: OM403250 (ITS), OM403249 (LSU)

Notes: The new strain shares a close phylogenetic affinity to *Melanconiella meridionalis* in our combined LSU, ITS, *rpb2* and *tef1* sequence data analyses (Fig. 81). This species was previously recorded from dead corticated twigs and branches of *Ostrya carpinifolia* (Betulaceae) from different localities i.e. Australia, Croatia, Greece, Italy and Slovenia (Voglmayr et al. 2012). *Melanconiella meridionalis* has not been reported from Fagaceae and here we provide the first association of sexual morph of species with *Fagus sylvatica*.

Pararamichloridiales Crous

Notes: Pararamichloridiales was introduced by Crous et al. (2017) to accommodate a monotypic family including two genera, namely *Pararamichloridium* and *Woswasia*. However, *Woswasia* (Woswasiaceae) was treated in Diaporthomycetidae families incertae sedis by Zhang et al. (2017) based on morphological and phylogenetical analyses. This result was supported by Hyde et al. (2020a, b, c). Divergence time estimates for Pararamichloridiales are crown age of 50.08 Mya and stem age of 101.46 Mya (Hyde et al. 2020a, b, c). The data of divergence time estimates for Pararamichloridiales is line with recommendations for ranking families.

Pararamichloridiaceae Crous, in Crous et al., Persoonia 39*:* 357 (2017*)*

Notes: Pararamichloridiaceae was introduced as a monotypic family by Crous et al. (2017) for *Pararamichloridium* Crous. However, Zhang et al. (2017) established a new family Woswasiaceae to accommodate *Cyanoannulus* and *Xylomelasma* while *Woswasia* was placed in Diaporthomycetidae families incertae sedis based on its close phylogenetic affinity, and this was conferred in later studies (Hyde et al. 2020a, b, c; Wijayawardene et al. 2020). Members of Pararamichloridiaceae are pathogenic on plant leaves (Crous et al. 2017, 2018).

Pararamichloridium Crous, in Crous et al., Persoonia 39: 357 (2017)

Notes: *Pararamichloridium*, the type genus of Pararamichloridiaceae, was established by Crous et al. (2017) to

Fig. 82 ***Pararamichloridium aquisubtropicum*** (GZAAS 21–0382, **holotype**) **a–b** Colony on decaying wood **c–e** Conidiophores with attached conidia **d–g** Conidiogenous cells and conidia **h** Conidia **i** Germinating condium **j–k** Colony on PDA from above and below. Scale bars: **c–e** = 20 µm, **f–i** = 10 µm

accommodate two species, *P. livistonae* Crous (as the type species) and *P. verrucosum* (V. Rao & de Hoog) Crous. Crous et al. (2018) introduced the third species of *Pararamichloridium* based on blast search and phylogenetic analysis. In this study, morphological characteristics and multi-gene phylogenetic analysis of a combined LSU and ITS sequence data reveals the fourth new species of *Pararamichloridium* from dead wood collected in freshwater from China (Figs. 82, 83).

Pararamichloridium aquisubtropicum J.Y. Zhang, Y.Z. Lu & K.D. Hyde, ***sp. nov***.

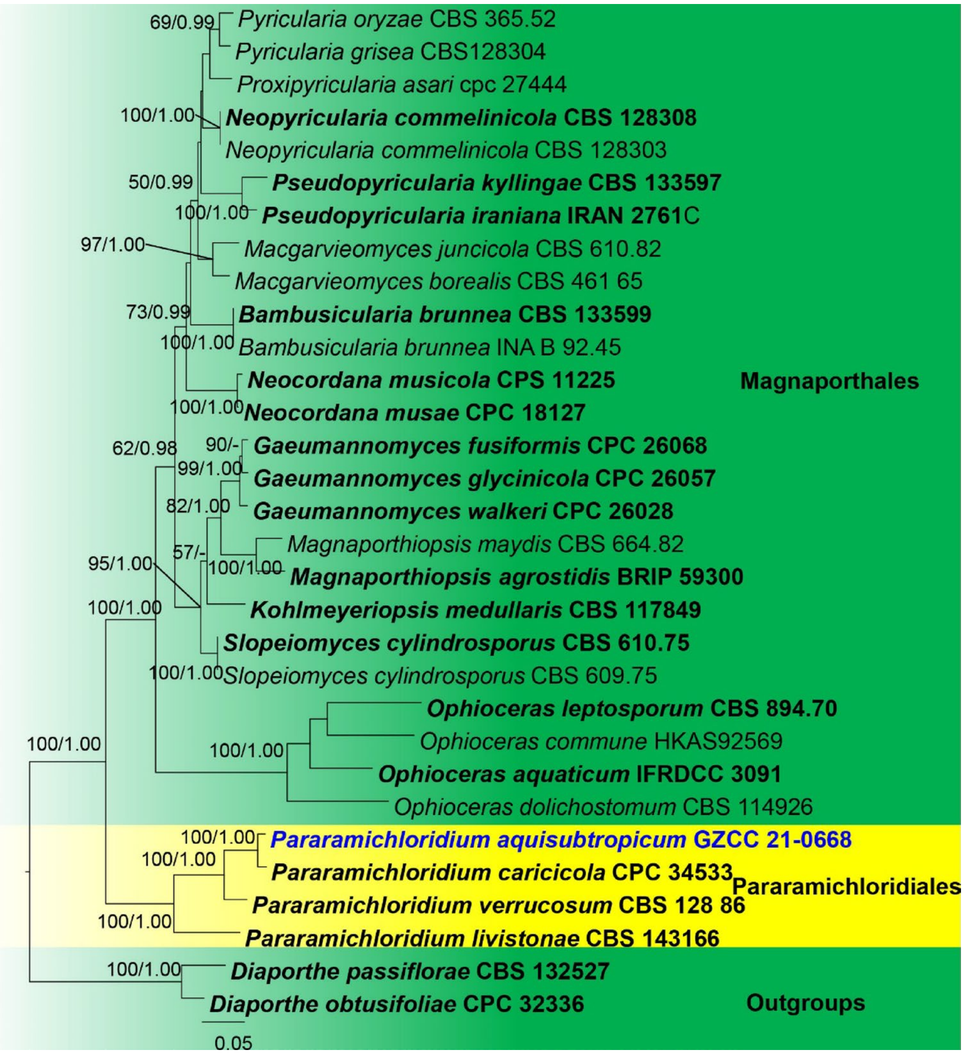


Fig. 83 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Twenty–two taxa were included in the combined analyses, which comprised 1524 characters (LSU: 885, ITS: 639) after alignment. Bootstrap support values for ML ≥ 50% and BYPP ≥ 0.95 are given above the nodes. The tree is rooted with *Diaporthe passiforae* (*CBS* 132,527) and *D. obtusifoliae* (CPC 32,226). The ex–type strains are indicated in **bold**. The newly generated sequence is indicated in blue

Index Fungorum number: *IF559507; Facesoffungi number: FoF10677*; Fig. 82

Etymology: Referring to the aquatic habitat and collecting site in subtropical country, China

Holotype: GZAAS 21–0382

Saprobic on submerged decaying wood. **Asexual morph:** Colonies on natural substrate superficial, brown, smooth, solitary. *Mycelium* partly immersed, consisting of branched, smooth, brown hyphae. *Conidiophores* 119–202 × 2.6–4.7 µm ($\bar{x}$ = 161.4 × 3.6 µm, *n* = 24), macronematous, mononematous, sucylindrical, straight, unbranched, brown, smooth, 6–9-septate. *Conidiogenous cells* 27.3–37 × 2.6–3.8 µm ($\bar{x}$ = 27.6 × 3.3 µm, *n* = 15), holoblastic, polyblastic, integrated, terminal, subhyaline to pale brown, subcylindrical. *Conidia* 4–8 × 3–4.7 µm ($\bar{x}$ = 5.2 × 3.7 µm, *n* = 25), acrogenous, solitary, aseptate, pale brown, globose to subglobose. **Sexual morph:** Not observed.

Culture Characters: Colonies on PDA reaching 33 mm in 44 days at 25 °C, flat, curler, near–round or round, gray, smooth, middle erumpent; In reverse, yellow at the center, lightly brown or gray at the margin.

Material examined: China, Guizhou Province, Xishui County, on decaying wood submerged in a freshwater stream, 16 September 2020, Jian Ma, XY2(GZAAS 21–0382, **holotype**); ex–type living culture, GZCC 21–0668.

GenBank numbers: OM339437 (ITS), OM339434 (LSU).

Notes: The phylogenetic analysis (Fig. 83) revealed that *Pararamichloridium aquisubtropicum* forms distinct lineage belonging to *Pararamichloridium,* where it is sister to *P. caricicola* with 100% BS, 1.00 BYPP, high support. *Pararamichloridium caricicola* is the closest species based on BLASTn result of LSU and ITS region with 99.55% and 96.11% similarity, respectively. *Pararamichloridium caricicola* is found in culture, while our new collection was saprobic on submerged decaying wood. *Pararamichloridium aquisubtropicum* shares the same morphology with *P. caricicola* in having brown, septate, smooth conidiophores integrated, terminal, subcylindrical conidiogenous cells and ellipsoid, pale brown aseptate, conidia. However, *P.*

aquisubtropicum differs from *P. caricicola* by it darker and longer (119–202 × 2.5–4.7 µm *vs* 35–100 × 2.5–3 µm) conidiophores. Thus, *P. aquisubtropicum* is introduced here as a distinct novel species based on its distinct morphological features and phylogenetic placement.

Distoseptisporales Z.L. Luo, K.D. Hyde & H.Y. Su Fungal Diversity 99: 482 (2019).

Distoseptisporaceae was established by Su et al. (2016) with a single genus, *Distoseptispora*. Based on morphology and phylogenetic analysis of combined LSU, SSU, *rpb2*, and *tef1* sequence data, Luo et al. (2019) established a new order, Distoseptisporales. Previously, the order Distoseptisporales was classified under the class Sordariomycetes, subclass Diaporthomycetidae. *Aquapteridospora* was described by Yang et al. (2015) and assigned to the Diaporthomycetidae genus *incertae sedis*. Later, Dong et al. (2021) performed a molecular phylogeny study using combined LSU, ITS, *tef1*, and *rpb2* sequence data and established a new family, Aquapteridosporaceae K.D. Hyde & Hongsanan, to accommodate a single genus, *Aquapteridospora*, and placed Aquapteridosporaceae in the order Distoseptisporales. Distoseptisporales currently consists of two families (Aquapteridosporaceae and Distoseptisporaceae), with Distoseptisporaceae serving as the type family.

Distoseptisporaceae K.D. Hyde & McKenzie, Fungal Diversity 80: 402 (2016)

Su et al. (2016) identified two Sporidesmium-like taxa with distinct morphology and phylogenetic relationships. They can be distinguished from Sporidesmiaceae based on strong molecular evidence and morphological investigation. As a result, the family Distoseptisporaceae was established to include Sporidesmium-like species under the type genus *Distoseptispora*. In the previous study, there was no sexual morph known for this family (Su et al. 2016; Yang et al. 2018; Hyde et al. 2019, 2020a, b, c, 2021; Luo et al. 2019; Sun et al. 2020a, b). Recently, Yang et al. (2021) proposed a sexual morph of *Distoseptispora* and this is the first time that the sexual morph of *Distoseptispora* has been found.

Distoseptispora K.D. Hyde, McKenzie, Maharachch. Fungal Diversity 80:375–409 (2016)

Su et al. (2016) defined *Distoseptispora* as a genus with *Distoseptispora fluminicola* as the type species. Yang et al. (2018) updated the *Distoseptispora* genus description. In addition, the sexual morph of this species is unidentified in the previous study (Su et al. 2016; Yang et al. 2018; Hyde et al. 2019, 2020a, b, c; Luo et al. 2019; Sun et al. 2020a, b). There is only one species of sexual morph described in *Distoseptispora* (Yang et al. 2021). The sexual morph is characterized by being solitary or gregarious, immersed to semi-immersed, perithecial, subglobose to ellipsoidal, ostiolate, dark brown ascomata with a short neck and hyaline, 0–3-septate, ascospores with a mucilaginous sheath (Yang et al. 2021). The asexual morph is distinguished by hyphomycetous, macronematous conidiophores, percurrent, elongate conidiogenous cells, olivaceous, brown, yellowish, or reddish brown, euseptate or distoseptate conidia, and rarely muriform conidia. (Su et al. 2016; Xia et al. 2017; Luo et al. 2018a, b; Tibpromma et al. 2018; Yang et al. 2018; Hyde et al. 2020a, b, c). The genus now has 46 recognized species, 14 of which are from terrestrial habitats and 32 from freshwater habitats (Su et al. 2016; Hyde et al. 2016, 2019, 2020, 2021; Xia et al. 2017; Yang et al. 2015, 2018; Luo et al. 2018a, b, 2019; Monkai et al. 2020; Song et al. 2020; Sun et al. 2020a, b; Li et al. 2021a, b; Yang et al. 2021, Hyde et al. 2021, Index Fungorum 2022a, b). *Distoseptispora hyalina* J. Yang and K.D. Hyde is the first sexual morph reported in the genus based on molecular DNA data (Yang et al. 2021).

Distoseptispora bambusicola X. Tang, Jayaward, J.C Kang & K.D. Hyde ***sp. nov.***

Index Fungorum number: IF558533; Facesoffungi number: FoF09940; Fig. 84

Etymology: Named after the host bamboo from which the holotype was found.

Holotypus: GZAAS21-0379.

Saprobic on decaying stems of bamboo submerged in a freshwater stream habitat. **Sexual morph:** Not observed. **Asexual morph:** Colonies effuse, scattered, hairy, brown to dark brown. Mycelium mostly immersed, composed of branched, septate, brown, smooth hyphae. *Conidiophores* macronematous, mononematous, pale brown to brown, solitary, 4–7-septate, erect, straight or flexuous, unbranched, slightly constricted at septa, smooth, cylindrical, 64–116 µm × 4–7 µm ($\bar{x} = 90.5 \times 5.5$ µm, $n = 30$), truncate at the apex. *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, determinate, brown, cylindrical. *Conidia* 72–193 µm × 7.5–14.5 µm ($\bar{x} = 126 \times 14$ µm, $n = 30$) acrogenous, solitary, obclavate or lanceolate, rostrate, straight or slightly curved, multi-distoseptate, up to 16-distoseptate, guttulate, pale brown, tapering towards the rounded apex, truncate at the base, slightly constricted at septa, smooth-walled, rounded at apex, with a truncate base and faintly to heavily pigmented scar.

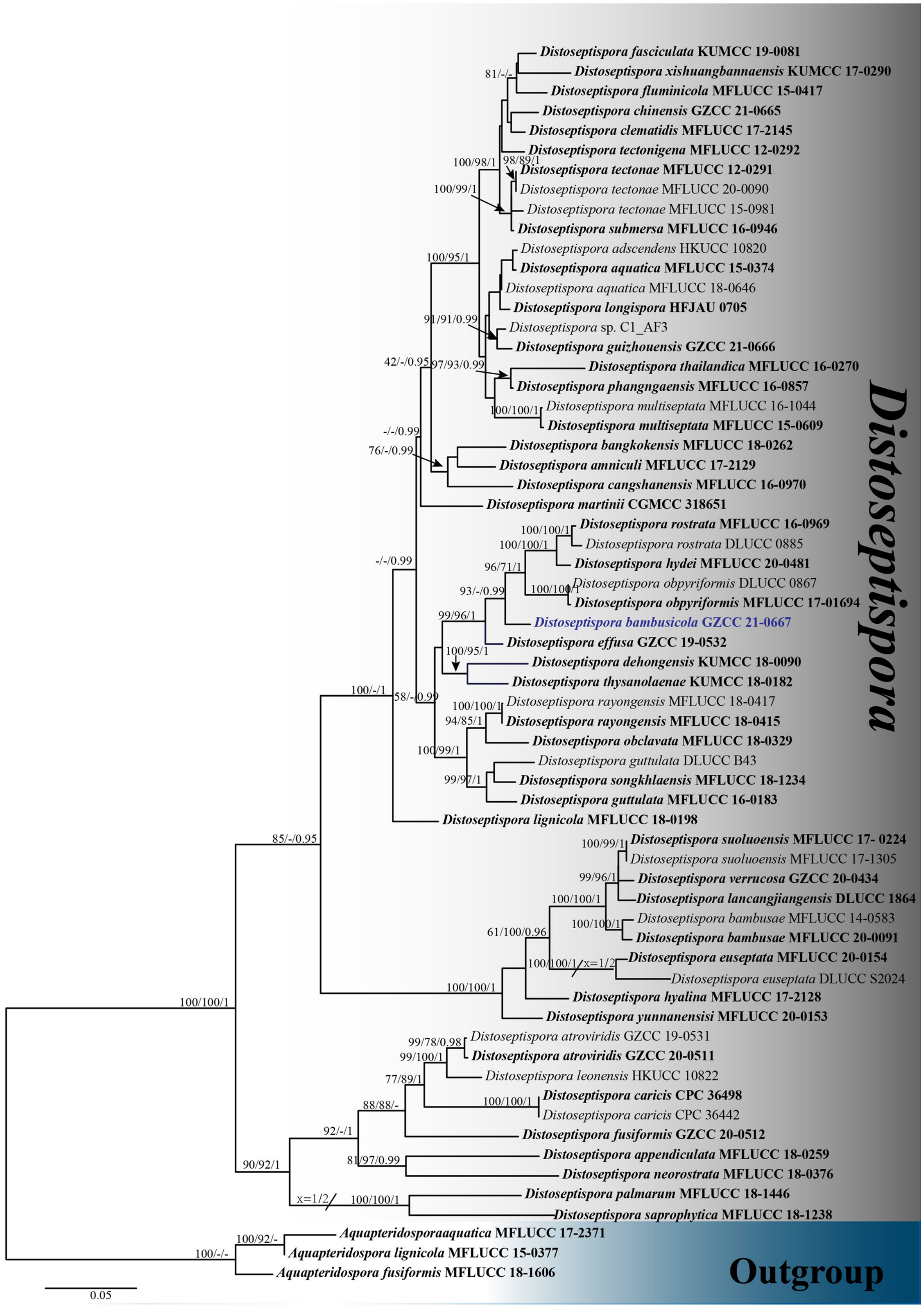
Culture characters: Colony grown on PDA in room temperature, circular, fluffy, white, dense in the center, but sparse, slightly olivaceous in the outside. In reverse, deeply olivaceous in the center, slightly yellow at the entire margin. Refer to the pigment produced on PDA and OA, purpure.

Material examined: China, Guizhou Province, Zunyi City, on decaying stems of bamboo submerged in a freshwater stream, 21 February 2021, Xia Tang, K1 (GZAAS21-0379, **holotype**), ex-type living culture, GZCC21-0667.

Fig. 84 ***Distoseptispora bambusicola*** (GZAAS21-0379, **holotype**). **a, b** Colonies on dead wood **c–e** Conidiophores **f** Cnidiogenous cell **g–n** Conidia **o** Germinated conidia **p, q** Colony on PDA (up-front, down-reverse). Scale bars: **c–j** = 20 μm, **k–o** = 50 μm

GenBank numbers: MZ474873 (ITS), MZ474872 (LSU), MZ474866 (SSU), OM272845 (*tef1*).

Notes: Distoseptispora bambusicola clustered with *D. hydei*, *D. obpyriformis,* and *D. rostrata* with a 100%ML, 99%MP and 1.00 BYPP support. According to the morphological comparisons (Fig. 85), our novel species can be distinguished from closely related species. *Distoseptispora bambusicola* differs from *D. rostrata* by its smaller conidiophores (64–116 μm × 4–7 μm *vs* 82–126 μm × 5–7 μm), larger conidia (72–193 μm × 7.5–14.5 μm *vs* 115–155 μm × 9–11 μm) and less distosepta (16-distosepta *vs* 23-distosepta). *Distoseptispora bambusicola*


Distoseptispora fasciculata KUMCC 19-0081
81/-/-
Distoseptispora xishuangbannaensis KUMCC 17-0290
Distoseptispora fluminicola MFLUCC 15-0417
Distoseptispora chinensis GZCC 21-0665
Distoseptispora clematidis MFLUCC 17-2145
Distoseptispora tectonigena MFLUCC 12-0292
100/98/1
98/89/1
Distoseptispora tectonae MFLUCC 12-0291
100/99/1
Distoseptispora tectonae MFLUCC 20-0090
Distoseptispora tectonae MFLUCC 15-0981
Distoseptispora submersa MFLUCC 16-0946
100/95/1
Distoseptispora adscendens HKUCC 10820
Distoseptispora aquatica MFLUCC 15-0374
Distoseptispora aquatica MFLUCC 18-0646
Distoseptispora longispora HFJAU 0705
91/91/0.99
Distoseptispora sp. C1_AF3
Distoseptispora guizhouensis GZCC 21-0666
42/-/0.95
97/93/0.99
Distoseptispora thailandica MFLUCC 16-0270
Distoseptispora phangngaensis MFLUCC 16-0857
100/100/1
Distoseptispora multiseptata MFLUCC 16-1044
Distoseptispora multiseptata MFLUCC 15-0609
-/-/0.99
76/-/0.99
Distoseptispora bangkokensis MFLUCC 18-0262
Distoseptispora amniculi MFLUCC 17-2129
Distoseptispora cangshanensis MFLUCC 16-0970
Distoseptispora martinii CGMCC 318651
100/100/1
Distoseptispora rostrata MFLUCC 16-0969
100/100/1
Distoseptispora rostrata DLUCC 0885
-/-/0.99
96/71/1
Distoseptispora hydei MFLUCC 20-0481
93/-/0.99
100/100/1
Distoseptispora obpyriformis DLUCC 0867
Distoseptispora obpyriformis MFLUCC 17-01694
99/96/1
Distoseptispora bambusicola GZCC 21-0667
Distoseptispora effusa GZCC 19-0532
100/95/1
Distoseptispora dehongensis KUMCC 18-0090
Distoseptispora thysanolaenae KUMCC 18-0182
100/-/1
58/-/0.99
100/100/1
Distoseptispora rayongensis MFLUCC 18-0417
94/85/1
Distoseptispora rayongensis MFLUCC 18-0415
Distoseptispora obclavata MFLUCC 18-0329
100/99/1
Distoseptispora guttulata DLUCC B43
99/97/1
Distoseptispora songkhlaensis MFLUCC 18-1234
Distoseptispora guttulata MFLUCC 16-0183
Distoseptispora lignicola MFLUCC 18-0198
85/-/0.95
100/99/1
Distoseptispora suoluoensis MFLUCC 17- 0224
Distoseptispora suoluoensis MFLUCC 17-1305
99/96/1
Distoseptispora verrucosa GZCC 20-0434
100/100/1
Distoseptispora lancangjiangensis DLUCC 1864
61/100/0.96
100/100/1
Distoseptispora bambusae MFLUCC 14-0583
Distoseptispora bambusae MFLUCC 20-0091
100/100/1
x=1/2
Distoseptispora euseptata MFLUCC 20-0154
Distoseptispora euseptata DLUCC S2024
100/100/1
Distoseptispora hyalina MFLUCC 17-2128
Distoseptispora yunnanensisi MFLUCC 20-0153
100/100/1
99/78/0.98
Distoseptispora atroviridis GZCC 19-0531
99/100/1
Distoseptispora atroviridis GZCC 20-0511
Distoseptispora leonensis HKUCC 10822
77/89/1
Distoseptispora caricis CPC 36498
100/100/1
Distoseptispora caricis CPC 36442
88/88/-
Distoseptispora fusiformis GZCC 20-0512
92/-/1
Distoseptispora appendiculata MFLUCC 18-0259
81/97/0.99
Distoseptispora neorostrata MFLUCC 18-0376
90/92/1
Distoseptispora palmarum MFLUCC 18-1446
x=1/2
100/100/1
Distoseptispora saprophytica MFLUCC 18-1238
Distoseptispora
100/92/-
Aquapteridosporaaquatica MFLUCC 17-2371
100/-/-
Aquapteridospora lignicola MFLUCC 15-0377
Aquapteridospora fusiformis MFLUCC 18-1606
Outgroup
0.05

◀ **Fig. 85** Phylogram generated from parsimony analysis based on combined ITS, LSU, SSU, *rpb2* and *tef1* sequence data of *Distoseptispora*. The ML and MP bootstrap support values ≥ 70% are and branches with BYPP ≥ 0.95 are given above the nodes. The ex-types (reference strains) are in bold; the new isolates are in blue **bold**. The tree is rooted with *Aquapteridospora fusiformis* (MFLU 18–1601), *Aquapteridospora lignicola* (MFLUCC 15–0377) and *Aquapteridospora aquatica* MFLUCC 17–2371)

shares similar morphological characteristics with *D. obpyriformis* in the size, shape, color of conidiophores, but differ in conidial size (72–193 µm × 7.5–14.5 µm *vs* 53–71 µm × 12–16 µm). *Distoseptispora bambusicola* differs from *D. obpyriformis* by having obclavate or lanceolate, longer conidia. *Distoseptispora bambusicola* can be distinct from *Distoseptispora hydei* by conidal shape and size (72–193 µm × 7.5–14.5 µm *vs* 32–58 µm × 10–15 µm; obclavate or lanceolate *vs* obpyriform to fusiform). *Distoseptispora hydei* is characterized with a gelatinous sheath around the tip of conidia, while *D. bambusicola* lacks this character. According to the comparisons of our novel species with other phylogenetically related taxa based on a pairwise nucleotide comparison of ITS (Jeewon and Hyde 2016), *D. bambusicola* differs from *D. rostrata* in 13/ 517 bp (2.5%), *D. hydei* in 8/ 395 bp (2.0%) and differs from *D. obpyriformis* in 25/571 bp (4.0%). Pairwise nucleotide comparison of LSU and *tef1* also showed that *D. bambusicola*

Fig. 86 ***Colletotrichum aeschynomenes*** (MFLU 22–0148, **new host record**) **a** *Shorea siamensis* with leaf spots, which the fungus was isolated from **b** Front colony on MEA **c** Reverse colony on MEA **d** Orange coloured spore masses on MEA **e–j** Conidiogenesis **k** Conidia fused by conidial anastomosis tubes **l–o** Conidia. Scale bar. **d** = 1000 µm, **e–o** = 10 µm

differs from *D. rostrata* in 10/ 826 bp (1.2%) for LSU and 42/ 857 bp (4.9%) for *tef1*, differs from *D. hydei* in 7/ 848 bp (0.8%) for LSU, and differs from *D. obpyriformis* in 6/ 790 bp (0.7%) for LSU and 40/ 838 bp (4.7%) for *tef1*. Thus, we consider *D. bambusicola* as a novel species in *Distoseptispora*.

Glomerellales Chadef. ex Réblová et al.

Réblová et al. (2011) validated *Glomerellales* to accommodate the families *Australiascaceae*, *Glomerellaceae* and *Reticulascaceae*. Maharachchikumbura et al. (2016) and Tibpromma et al. (2018) added *Plectosphaerellaceae* and *Malaysiascaceae* to this order.

Glomerellaceae Locq. ex Seifert & W. Gams, in Zhang et al., Mycologia 98(6): 1083 (2007) [2006].

The monotypic family is characterised by a *Colletotrichum* asexual morph and a *Glomerella* sexual morph (Hyde et al. 2020a, b, c).

Colletotrichum Corda, in Sturm, Deutschl. Fl., 3 Abt. (Pilze Deutschl.) 3(12): 41 (1831).

Colletotrichum comprises important plant pathogens, endophytes and saprobes as well as human and animal pathogens (Cannon et al. 2012; Jayawardena et al. 2021a; Talhinhas and Baroncelli 2021). Bhunjun et al. (2021) demonstrated that coalescent approaches and multi-locus phylogeny are vital in establishing species boundaries in *Colletotrichum*. Liu et al. (2022) accepted 280 species in 16 species complexes and 15 singleton species and established a genome tree comprising 94 species. Further 13 species were added by Alizadeh et al. (2022), Hassan et al. (2022) and Zheng et al. (2022).

Colletotrichum aeschynomenes B.S. Weir & P.R. Johnst., in Weir, Johnston & Damm, Stud. Mycol. 73: 135 (2012).

Index Fungorum number: IF563590; Facesofungi number: FoF11441; Fig. 86

Associated with leaf spots of *Shorea siamensis*. **Sexual morph:** Not observed. **Asexual morph:** *Vegetative hyphae* 1.5–4.5 µm diam. ($\bar{x}=3.4$, $n=15$), hyaline to pale brown, smooth-walled, septate, branched. *Pycnidia* forming on MEA, 500–1000 µm diam. solitary or aggregated, globose to irregular, releasing conidia in milk-orange, slimy, glistening masses. *Setae* not observed. *Conidiophores* 8.0–53.0 × 1.5–4.5 µm ($\bar{x}=25.1\times2.8$ µm, $n=20$), hyaline to light brown, cylindrical to clavate, smooth-walled, septate, sometimes branched or reduced to conidiogenous cells. *Conidiogenous cells* 1.5–16 × 1.5–4 µm ($\bar{x}=6.1\times3.0$ µm, $n=15$), hyaline to pale brown, solitary or aggregated, cylindrical, ovoid or ampulliform, smooth-walled. *Conidia* 17.0–24.5 × 5–7.5 µm ($\bar{x}=20.2\times6.0$ µm, $n=60$), aseptate, hyaline, cylindrical, clavate or ellipsoidal, with slightly curved basal end and mostly rounded apices, smooth-walled or slightly verruculose, guttulate, forming conidial anastomosis tubes. *Conidial anastomosis tubes* 2–10.5 × 2–3 µm ($\bar{x}=4.6\times2.4$ µm, $n=15$), hyaline to brown, smooth-walled, aseptate. *Appressoria* not observed.

Culture characteristics: Colonies on MEA flat or effuse with entire margin. Greyish white, reverse olivatious, grey towards the edge, reaching approximately 70 mm diam. in 5 days at 25 °C, with 20-days for sporulation. Aerial mycelium dense.

Material examined: Thailand, Chiang Mai Province, Omkoi, on leaf spots of *Shorea siamensis* (Dipterocarpaceae), 15 October 2019, D. Gomdola, MFLU22-0148; living culture MFLUCC 22-0086.

Known host and distribution: *Aeschynomene virginica* (USA), *Manihot esculenta* (Thailand), *Myrciaria dubia* (Brazil), *Platostoma palustre* (Taiwan), *Shorea siamensis* (Thailand, this study), *Theobroma cacao* (Brazil) (Farr and Rossman 2022).

GenBank numbers: OP278978 (ITS), OQ053325 (gapdh)

Notes: Weir et al. (2012) introduced *C. aeschynomenes* from a stem lesion of *Aeschynomene virginica*. *Colletotrichum aeschynomenes* is a common phytopathogen known to cause anthracnose in leaves. Listed chronologically, the pathogen has been found to infect cassava in central Thailand (Sangpueak et al. 2018), and cause anthracnose on *Theobroma cacao* in Brazil (Nascimento et al. 2019), *Myrciaria dubia* in Brazil (Matos et al. 2020) and *Ixora coccinea* in China (Li et al. 2021a, b). Herein, *C. aeschynomenes* is associated with leaf spots of *Shorea siamensis*. To delineate *C. aeschynomenes* from *C. fructicola*, *tub2* or *gapdh* gene regions are required (Weir et al. 2012). Phylogenetic analyses based on the concatenated ITS and *gapdh* sequence data depict our isolate as *C. aeschynomenes*. The latter is located in the *C. gloeosporioides* complex and clusters with the ex-type strain (ICMP 17673) with 71% MP, 84% ML and 0.91 BYPP (Fig. 87). We report our collection as a new host of *C. aeschynomenes* on living leaves of *Shorea siamensis*.

Colletotrichum flexuosum Damm, ***sp. nov.***

Index Fungorum number: IF558527; Facesoffungi number: FoF10680; Fig. 88

Etymology: The species epithet is derived from the shape of the setae that are often flexuous.

Holotype: CBS H-21899

Associated with leaf spots of *Xanthophyllum sylvestre*. **Asexual morph on synthetic nutrient-poor agar medium (SNA):** *Vegetative hyphae* 1.5–8 µm diam., hyaline to pale brown, smooth-walled, septate, branched. *Chlamydospores* not observed. *Conidiomata* absent, conidiophores and setae formed directly on hyphae. *Setae* medium brown, smooth-walled, verrucous (warts 1–2 mm

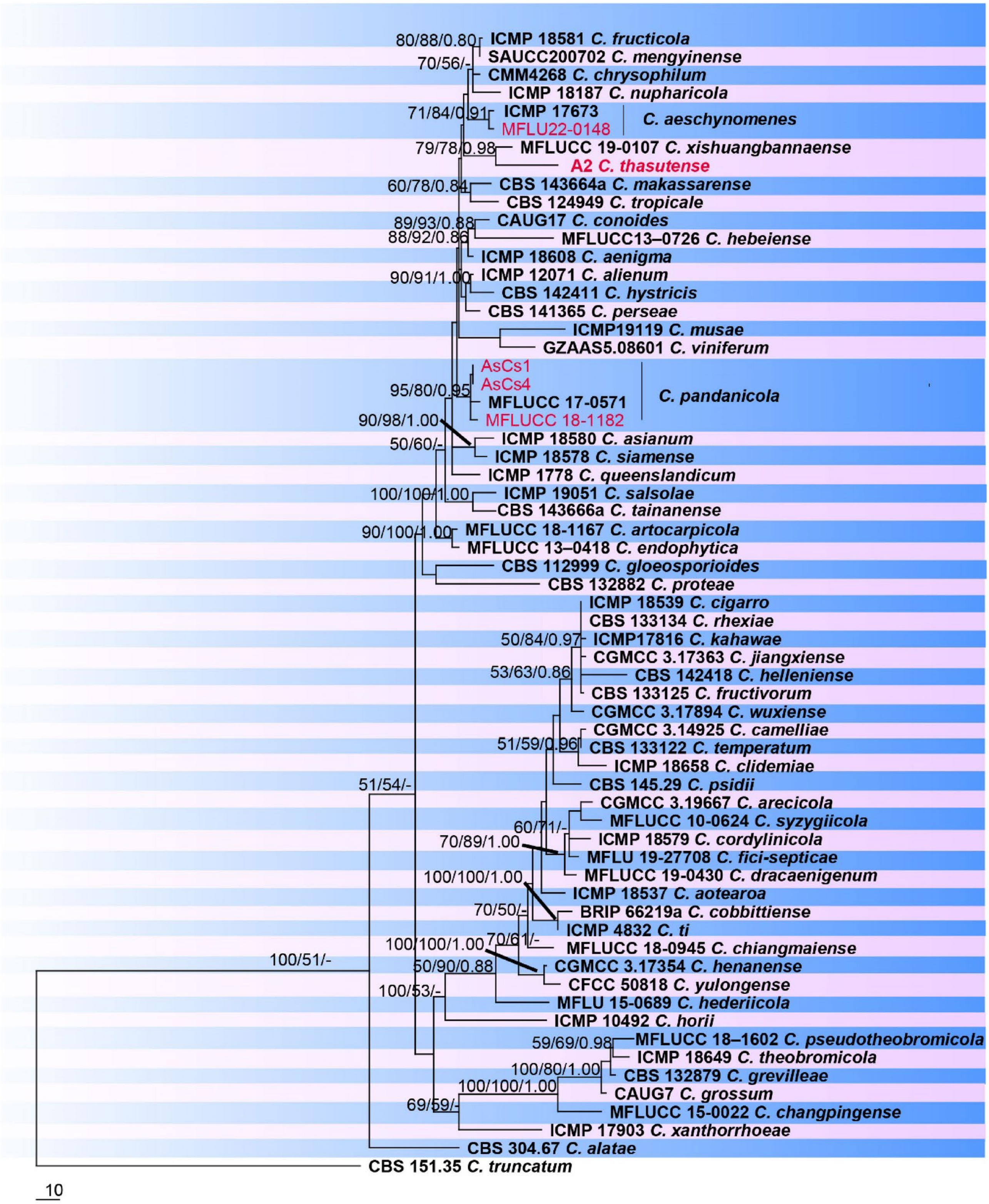


Fig. 87 One of two most parsimonious trees obtained with PAUP v. 4.0b10 (Swofford 2003) from a heuristic search of the combined sequence alignment of ITS, *gapdh*, *chs-1*, *act* and *tub2* of the *Colletotrichum gleosporioides* species complex, rooted with *C. truncatum* (CBS 151.35). Bootstrap support values of MP and ML ≥ 70% and BYPP values ≥ 0.90 are shown at the nodes. Ex-type and reference strains are in **bold**. New sequence data are in red

Fig. 88 ***Colletotrichum flexuosum*** (CBS 134419, **ex-type living culture**) **a–b.** Conidiomata. **c, h.** Tips of setae. **d, i.** Bases of setae. **e–g, j–k.** Conidiophores. **m–r.** Appressoria. **s–t.** Conidia. a, c–g, s. from *Anthriscus* stem. **b, h–r, t**. from SNA. **a–b**. Dissecting microscope (DM). **c–t**. Differential interference contrast illumination (DIC). Scale bars: **a** = 100 µm, **e** = 10 µm. Scale bar of a applies to **a–b**. Scale bar of e applies to **c–t**

diam.) close to the tip, 80–140 µm long, 3–4-septate, base inflated, 6–10 µm diam., tip ± acute to round, often strongly bent. *Conidiophores* pale brown, smooth-walled, simple or septate, to 20 µm long. *Conidiogenous cells* pale brown, smooth-walled, cylindrical to subglobose, 9–20(–26) × 5–9 µm, opening 2–2.5 µm diam., collarette 1 µm long, periclinal thickening conspicuous. *Conidia* hyaline, smooth-walled, aseptate (few septate conidia observed), straight, cylindrical, with both ends rounded, (14.5–)16.5–24(–21) × (6.5–)7–8.5(–9.5) µm, mean ± SD = 18.9 ± 2.3 × 7.8 ± 0.8 µm, L/W ratio = 2.4 (*n* = 30). *Appressoria* single, pale brown, smooth-walled, with a navicular to clavate outline and a lobate to crenate margin, (9–)12.5–18(–24) × (4–)5.5–8.5(–10) µm, mean ± SD = 15.1 ± 2.8 × 7.1 ± 1.4 µm, L/W ratio = 2.1 (*n* = 30). **Sexual morph:** not observed.

Asexual morph on *Anthriscus* stem: *Conidiomata*, conidiophores and setae formed on medium brown, smooth-walled, roundish to angular cells, 5–11 µm diam. *Setae* medium to dark brown, smooth-walled, 100–180 µm long, 3–4-septate, straight to ± flexuous, base cylindrical or restricted, 4–8 µm diam., tip ± round to acute. *Conidiophores* pale to medium brown, smooth-walled, septate, branched, to 90 µm long. *Conidiogenous cells* pale to medium brown, smooth-walled, cylindrical to clavate, 15–32 × 5–8 µm, opening 1.5–2 µm diam., collarette 0.5–1 µm long, periclinal thickening distinct. *Conidia* hyaline, smooth-walled, aseptate, cylindrical, with both ends rounded, sometimes a distinct membranous appendage remains at the base, (21–)23.5–28.5(–33.5) × (5–)6–7.5(–8) µm, mean ± SD = 25.9 ± 2.6 × 6.9 ± 0.8 µm, L/W ratio = 3.8 (*n* = 30). **Sexual morph:** not observed.

Culture characteristics: Colonies on SNA flat with entire margin, hyaline to honey, agar medium, filter paper and *Anthriscus* stem partly covered with grey acervuli and short floccose white aerial mycelium, reverse hyaline to honey, agar medium, filter paper and *Anthriscus* stem partly pale grey; growth 13.5–18 mm in 7 days at 20 °C under near UV light with 12 h photoperiod (21–28 mm in 10 days). Colonies on OA flat with entire margin; buff, grey olivaceous to olivaceous grey, partly covered with short floccose white aerial mycelium and dark grey to black spots, reverse

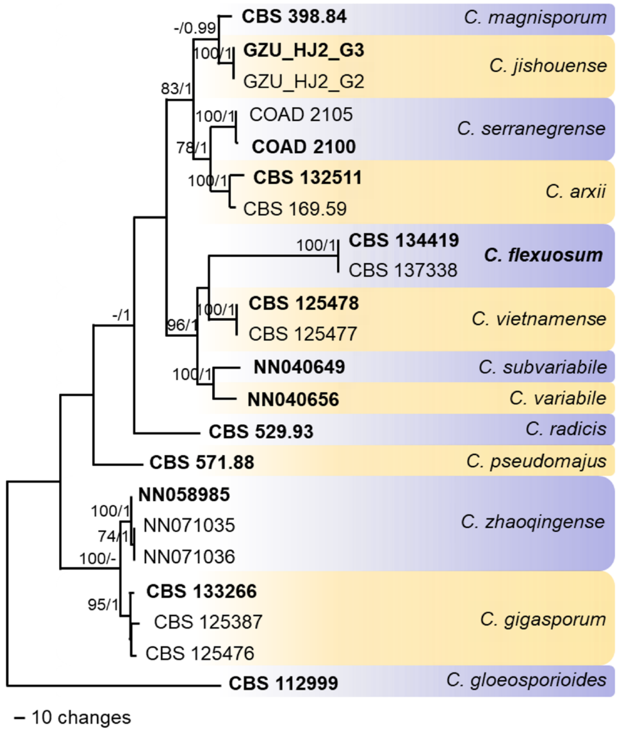


Fig. 89 One of two most parsimonious trees obtained with PAUP v. 4.0b10 (Swofford 2003) from a heuristic search of the combined sequence alignment (gene boundaries of ITS: 1–550, *tub2*: 551–1240, *gapdh*: 1241–1510, *act*: 1511–1756, *chs-1*: 1757–2007, *his3*: 2008–2385) of the *Colletotrichum gigasporum* species complex, rooted with *C. gloeosporioides* CBS 112999 (sequences from Damm et al. 2012; Rakotoniriana et al. 2013; Liu et al. 2014; Silva et al. 2018; Zhou et al. 2019; Liu et al. 2022). Bootstrap support values (BS) above 70% (bold) and Bayesian posterior probability (BYPP) values above 0.90 are shown at the nodes. Bootstrap support values have been calculated based on 10 000 replicates, and a Markov Chain Monte Carlo algorithm was used to generate phylogenetic trees with Bayesian probabilities using MrBayes v. 3.2.6 (Ronquist et al. 2012). Numbers of ex-type strains are in **bold**

olivaceous-grey, growth 20–21.5 mm in 7 days (30.5–32 mm in 10 days). *Conidia in mass* whitish.

Material examined: Vietnam, Ninh Bình Province, Cúc Phương National Park, rain forest, from leaf spots of *Xanthophyllum sylvestre* (*Polygalaceae*), 6 December 2012, Ulrike Damm (CBS H-21899, **holotype**); ex-holotype living culture, CBS 134419. Ninh Bình Province, Cúc Phương National Park, rain forest, from leaf spots of *Xanthophyllum sylvestre* (*Polygalaceae*), 6 December 2012, Ulrike Damm, living culture CBS 137338.

GenBank numbers: CBS 134419—MZ444580 (ITS), MZ444582 (*tub2*), MZ444584 (*gapdh*), MZ444586 (*act*), MZ444588 (*chs-1*), MZ444590 (*his3*).

CBS 137338—MZ444581 (ITS), MZ444583 (*tub2*), MZ444585 (*gapdh*), MZ444587 (*act*), MZ444589 (*chs-1*), MZ444591 (*his3*).

Notes: Colletotrichum flexuosum was isolated from leaves of *Xanthophyllum sylvestre*, a tree species native to Laos, Thailand and Vietnam (http://www.plantsoftheworldonline.org). Few fungi were previously reported from *Xanthophyllum*, including an unidentified *Colletotrichum* species on *X. octandrum* in Australia (Simmonds 1966; Farr and Rossman 2022). No *Colletotrichum* species was previously described or reported from *X. sylvestre*.

Based on blastn searches and sequence comparisons on NCBI GenBank, the closest neighbour of the strains from *Xanthophyllum* is *C. vietnamense*, belonging to the *C. gigasporum* complex. The ITS, *tub2*, *gapdh*, *act*, *chs-1* and *his3* sequences of this species were 80, 97, 91, 98, 98 and 96% identical (105, 23, 9, 4, 4and 15 nucleotides difference) with those of the ex-holotype strain of *C. vietnamense* (Liu et al. 2014). No strain was more than 82% identical with its ITS sequences. The closest match with the *act* sequences was *Colletotrichum* sp. gnqczg15 (KC293585, F. Huang, unpubl. study) with two nucleotides difference. In a phylogeny inferred from concatenated ITS, *tub2*, *gapdh*, *act*, *chs-1* and *his3* sequences of the *C. gigasporum* species complex (Fig. 89), the two strains formed a well-supported (BS 100%, BYPP 1) sister clade to *C. vietnamense* and a clade formed by two recently described species, *C. subvariabile* and *C. variabile* (Liu et al. 2022). *Colletotrichum flexuosum* can be identified with all loci included.

The species from *Xanthophyllum* is morphologically different from all previously described species of the *C. gigasporum* complex. Its conidia are shorter than those of *C. gigasporum* (22–32 × 6–9 µm on PDA), *C. magnisporum* (av. 34.3 × 9.7 µm on SNA, av. 33.8 × 9.9 µm on *Anthriscus* stem), *C. serranegrense* (24–37 × 7–9 µm on MEA) and *C. vietnamense* (av. 31.2 × 9.6 µm on SNA, av. 32.3 × 9.5 µm on *Anthriscus* stem) and larger than those of *C. jishouense* (av. 10.8 × 3.7 µm on PDA). In contrast to *C. arxii*, *C. jishouense*, *C. pseudomajus*, *C. radicis* and *C. vietnamense*, neither curved nor clavate conidia were formed, while conidia with membranous appendages and distinctly flexuous setae as formed by *C. flexuosum* were previously not observed in the *C. gigasporum* complex (Rakotoniriana et al. 2013; Liu et al. 2014, 2022; Silva et al. 2018; Zhou et al. 2019). Conidiogenous cells with a distinct periclinal thickening are typical for species of the *C. boninense* complex; within the *C. gigasporum* complex this was previously only observed with *C. zhaoqingense* (Liu et al. 2022). However, in contrast to *C. zhaoqingense*, conidial bases of *C. flexuosum* sometimes end with a membranous appendage, while most species of the *C. boninense* and the *C. dracaenophilum* complexes develop a prominent scar (Damm et al. 2012, 2019; Liu et al. 2022).

Colletotrichum pandanicola Tibpromma & K.D. Hyde, in Tibpromma et al., MycoKeys 33: 47 (2018).

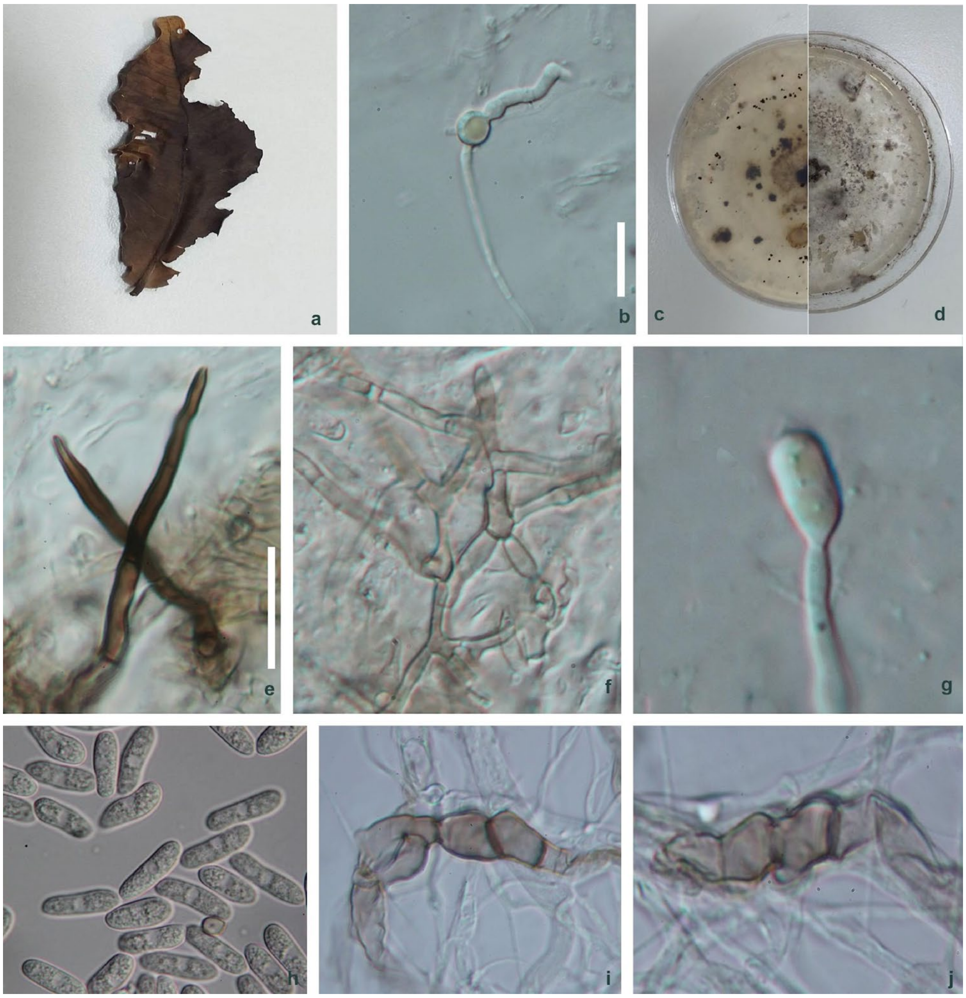


Fig. 90 ***Colletotrichum pandanicola*** (MFLU 18–1852, **new host record**) **a** Dead leaf of *Mangifera indica*. **b** Germinating spore. **c** Reverse view of the 7d old culture on PDA. **d** Upper view of the 7d old culture on PDA. **e** Setae. **f** Vegetative hyphae. **g** Conidiogenous cell. **h** Conidia. **i–j** Appressoria. Scale bars: **e** = 50 µm, **b** = 10 µm; scale bar of b applies to f–j

Index Fungorum number: IF823841; *Facesoffungi number*: *FoF05832; Figs.* 90, 91

Saprobic on *Mangifera indica* and pathogenic on *Alstonia scholaris*. **Sexual morph:** Not observed. **Asexual morph:** *On PDA vegetative hyphae* greyish white, dense, cottony. *Conidiomata* acervuli, black, circular to oval, submerged, solitary or aggregated. *Sporulation* abundant. *Setae* scattered, straight or ± bent, dark brown up to the tip, opaque, 2- to 4-septate, 50–80 µm long, smooth-walled, base cylindrical, 2–5 µm diam., tip acute. *Conidiophores* hyaline to light brown, cylindrical to clavate, smooth-walled, simple, occurring in densely arranged clusters. *Conidiogenous cells* enteroblastic, hyaline, smooth-walled, cylindrical to slightly inflated, periclinal thickening not visible. *Conidia* 7–12 × 2–6 µm ($\bar{x} = 7 \times 4$ µm, $n = 40$), hyaline, smooth-walled, aseptate, ovoid, cylindrical or clavate with rounded apices, guttulate. *Appressoria* 9–16 × 5–6 µm ($\bar{x} = 13 \times 5$ µm, $n = 10$), solitary to aggregated, in small groups or short chains, medium to dark brown, smooth-walled, irregular, rarely lobed.

Culture characteristics: *Colonies* grown from single conidia on PDA 50–70 mm diam. in 7 days, at first white becoming dark grey, reverse pale yellow.

Material Examined: Thailand, Chiang Rai Province, on leaf of *Mangifera indica* L. (Anacardiaceae), 19 May 2018, Ruvishika S. Jayawardena (MFLU 18-1852), living culture MFLUCC 18-1182. India, Karnataka, Mysuru on infected leaves of *Alstonia scholaris* (Apocyanaceae) as pathogen, May 2019, S. Mahadevakumar (UOM-IOE 19/15), living cultures (AsCs1, AsCs4).

GenBank numbers: MFLUCC 18-1182-MK629453 (ITS), MK639363 (*gapdh*), MK639357 (*chs-1*), MK639359 (*act*) and MK639361 (*tub2*)

AsCs1–OM912803 (ITS), OM934812 (*gapdh*), OM934814 (*tub2*)

AsCs4–OM912804 (ITS), OM934813(*gapdh*), OM934815 (*tub2*)

Notes: The species of the *C. gloeosporioides* species complex are mainly known as plant pathogens (Weir et al. 2012; Jayawardena et al. 2016, 2018, 2021a, b; Bhunjun et al. 2021), some species are also as endophytes or as

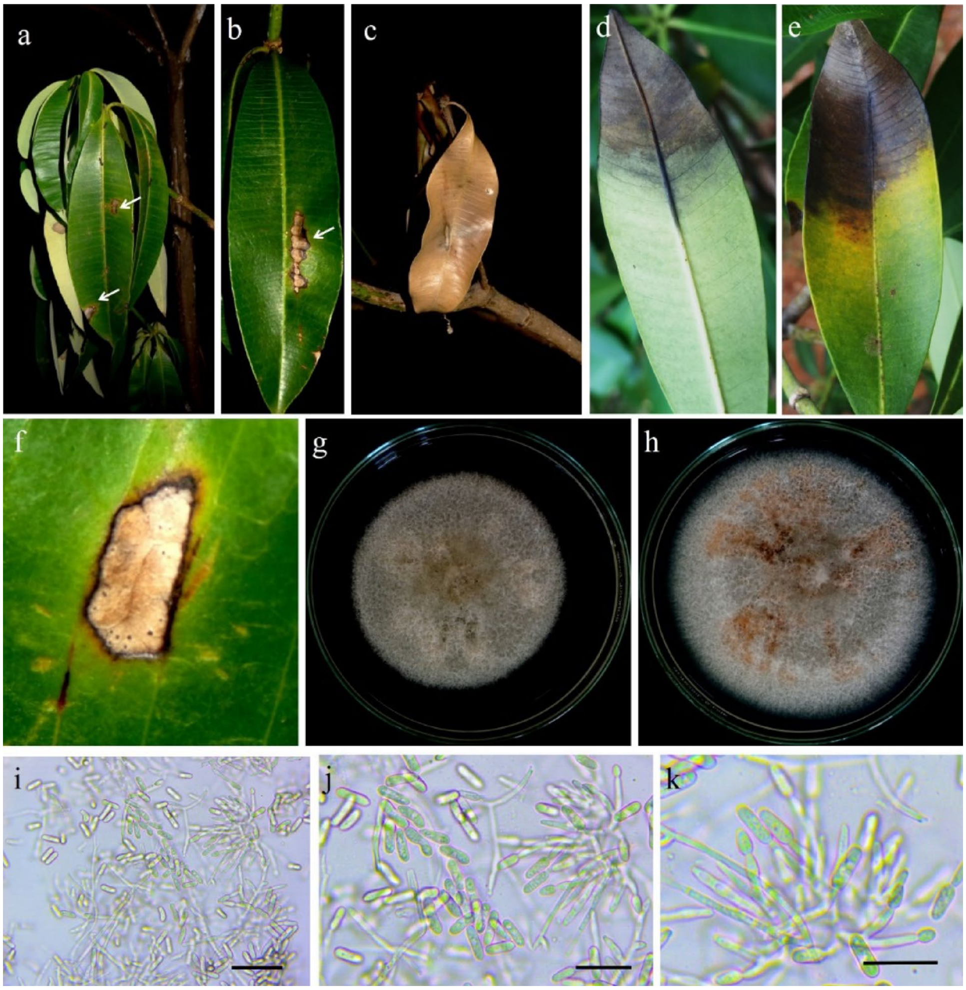


Fig. 91 **a**–**b** Leaf blight/early symptoms of anthracnose disease on *Alstonia scholaris*. **c** Complete death of infected branch due to anthracnose disease. **d**–**e** anthracnose symptoms appearing at the tip of the leaves caused necrosis. **f** a close view of anthracnose symptoms. **g** pure cultures of 10 days old *Colletotrichum siamense* on PDA. **i**–**k** Conidiogenous cells and conidia of *C. siamense* observed under a compound microscope (Scale bar: 10 µm)

saprobes (Jayawardena et al. 2021a, b). Strain MFLUCC 18-1182 belongs to the *Colletotrichum gloeosporioides* species complex and clusters with the ex-type of *C. pandanicola* (Fig. 87). However, strain MFLUCC 18–1182 differs from *C. pandanicola* by forming setae and appressoria, which were not observed in the ex-type strain of *C. pandanicola (*Tibpromma et al. 2018*)*. This represents the first report of *C. pandanicola* on Mango from Thailand.

Colletotrichum pandanicola was isolated from leaves of *Alstonia scholaris*, is an evergreen tropical tree and an important medicinal plant distributed throughout the Indian peninsula including Western Ghats regions of Karnataka. *Colletotrichum gleosporioides* has been reported as a pathogen on *A. scholaris* (Chandra 1974; Mathur 1979; Sarbhoy and Agarwal 1990; Sarbhoy et al. 1971). Pathogenicity tests were performed on healthy *A. scholaris* plants. After 10–12 days of pot inoculation, the initial necrotic spots developed on leaves were smaller and later coalesced to form larger necrotized lesions. The lesions developed on inoculated plants were fusiform and grayish brown. Phylogeny supports (Fig. 87) our strain to be *C. pandanicola*. This is a new report of *C. pandanicola* on *Alstonia scholaris* from India.

Colletotrichum thasutense Armand, K.D. Hyde and Jayaward., ***sp. nov.***

Index Fungorum number: IF900127; Faceoffungi number: FoF13361; Fig. 92

Etymology: Referring to the sub-district where the specimen was collected.

Holotype: MFLU 22-0206

Associated with leaf spot on *Syngonium* sp. **Sexual morph**: not observed. **Asexual morph**: On host: *Acervuli* present, setose, creamy to greyish white, subepidermal, produced solitary. *Conidiophores* rarely observed, hyaline, barrel shaped, 6.5–9 × 3–4 µm; *Conidiogenous cells* hyaline, cylindrical; 10.5–23 × 2.5–4 µm ($\bar{x}$ = 16 × 3 µm, $n = 20$). *Conidia* aseptate, hyaline, smooth-walled, cylindrical, straight to slightly curved, mostly rounded ends, rarely obtuse at one end, 13.5–17.5 × 3.5–5 µm ($\bar{x}$ = 15.5 × 4.5 µm, $n = 20$), *Appressoria* not observed.

On PDA: Acervuli, Setae and Sclerotia absent.

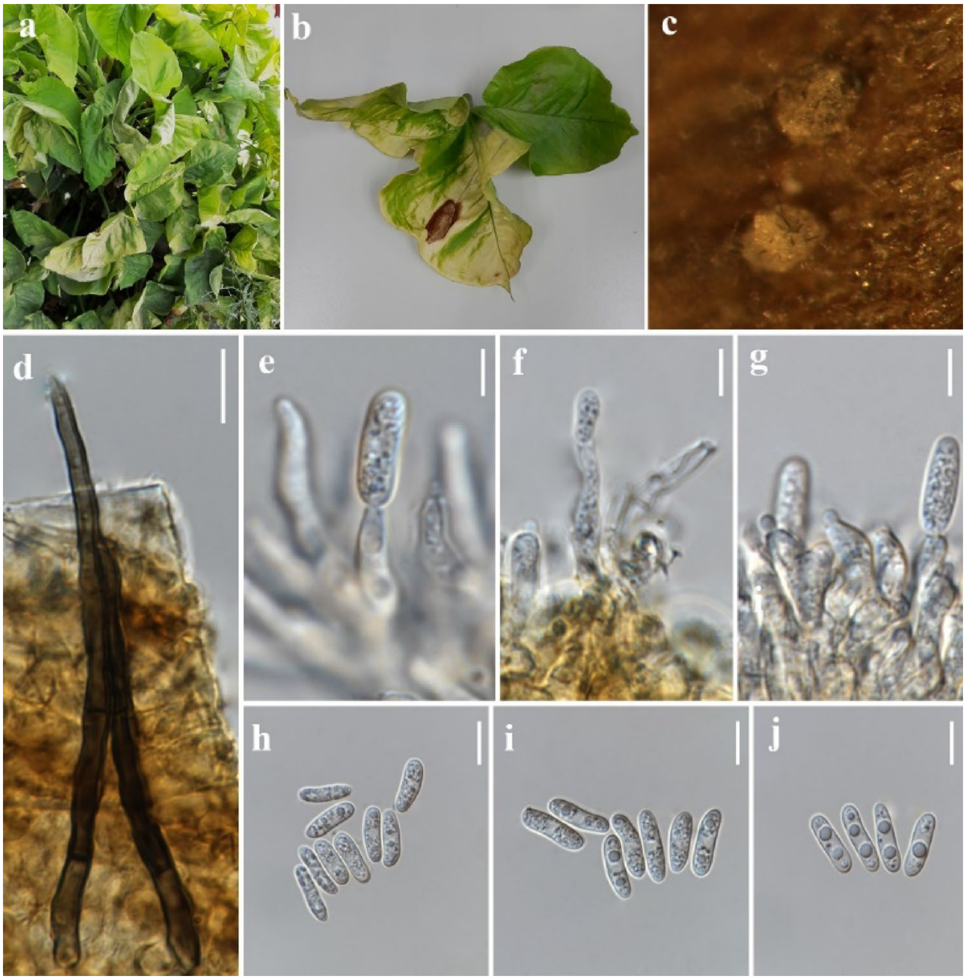


Fig. 92 ***Colletotrichum thasutense*** (MFLU 22–0206, **holotype**) **a** Host plant. **b** Host leaf with symptom. **c** Acervuli on the host. **d** setae. **e–g** Conidiogenous cells and conidia. **h–j** Conidia. Scale bars: **d** = 10 µm, **e–g** = 5 µm, **h-j** = 10 µm

Culture characteristics: Colonies on PDA white to pale yellow, reverse same color, reaching 70 mm diam. in 7 days at 28 °C. Colonies cottony, circular, slightly raised and depressed in the center, Aerial mycelia white and medium in dense.

Material examined: Thailand, Chiang Rai, Mueang, ThaSut, from *Syngonium* sp. (Araceae), associated with leaf spot; 16 October 2021, A. Armand, A2 (MFLU 22-0206, **holotype**), living ex-type living culture MFLUCC 22-0173.

GenBank numbers: OP821902 (ITS), OP831280 (*act*), OP831281 (*chs-1*),: OP831282 (*gapdh*), OP831283 (*tub2*).

Notes: Based on the phylogenetic analyses, *Colletotrichum thasutense* is closely related to *C. xishuangbannaense* (Fig. 87). Morphologically, *C. thasutense* differs from *C. xishuangbannaense* by producing longer and thicker conidia. *Colletotrichum xishuangbannaense* has 9–12 × 3–4 µm conidia (de Silva et al. 2021), whereas *C. thasutense* has 13.5–17.5 × 3.5–5 µm conidia. *Colletotrichum thasutense* can be differentiated from *C. xishuangbannaense* in having slightly curved conidia and obtuse at one end. However, *C. xishuangbannaense* produces straight conidia with rounded ends. Moreover, *C. thasutense* bears longer and thicker conidiogenous cells (10.5–23 × 2.5–4 µm) than *C. xishuangbannaense* (15–18 × 1.5–2 µm).

Hypocreales Lindau

Hypocreales includes 15 families, which are considered subtropical and tropical, namely Bionectriaceae, Calcarisporiaceae, Clavicipitaceae, Cocoonihabitaceae, Cordycipitaceae, Cylindriaceae, Flammocladiellaceae, Hypocreaceae, Myrotheciomycetaceae, Nectriaceae, Niessliaceae, Ophiocordycipitaceae, Sarocladiaceae, Stachybotryaceae, and Tilachlidiaceae, based on the basis of molecular evidence (Hyde et al. 2020a, b, c; Wijayawardene et al. 2022). These families differ in the presence of fleshy and colorful perithecial ascomata, ostiolate perithecia, varied ascospores, and pigment production. It has been estimated that Hypocreales diverged 229 million years ago (Hyde et al. 2020a, b, c).

Nectriaceae Tul. & C. Tul. [as 'Nectriei'], Select. fung. carpol. (Paris) 3: 3 (1865)

Nectriaceae was introduced by Tulasne and Tulasne (1865) and re-evaluated by Lombard et al. (2015) based on morphology and ten genes (*acl1*, *act*, *cmdA*, *his3*, ITS,

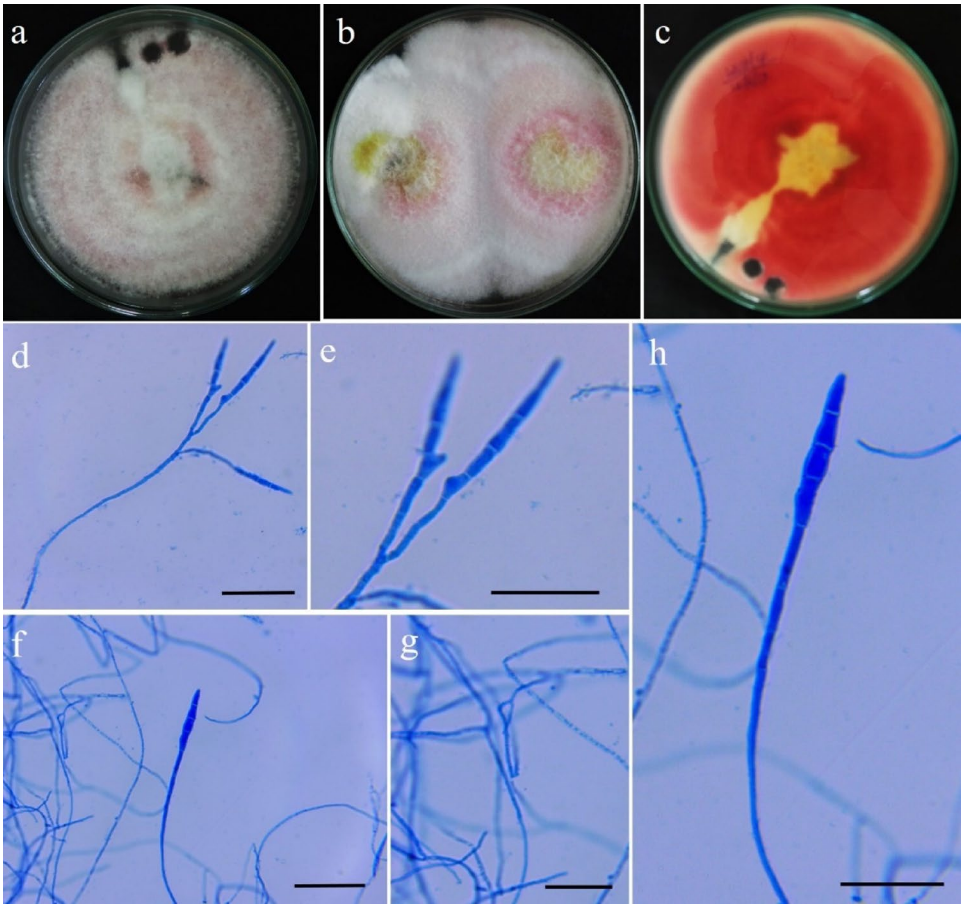


Fig. 93 Cultural and morphological features of *Fusarium brachygibbosum*: **a–c** pure cultures of *F. brachygibbosum* isolated on PDA medium (12 days old) (**a–b** Front view, **c**– reverse view); **d–h** Microscopic view of *F. brachyggibosum* conidia structures observed under compound microscope. Scale bar: **d–h** = 20 µm

LSU, *rpb1*, *rpb2*, *tef1* and *tub2*). This family includes 74 genera that are recognized by different perithecial pigments (Wijayawardene 2022; Lombard et al. 2015; Crous et al. 2021). The family contains a wide range of species, including plant pathogens, human pathogens, and industrial and commercial species (Rossman 1996; Luo and Zhuang 2008; Chaverri et al. 2011; Lechat et al. 2015; Lombard et al. 2015).

Fusarium Link, Mag. Gesell. naturf. Freunde, Berlin 3(1–2): 10 (1809).

Fusarium is famous for its difficulty in identification and pathogenicity. It has been extensively discussed in recent decades as one of the most taxonomically confusing genus within Nectriaceae (Gräfenhan et al. 2011; O'Donnell et al. 2013; Crous et al. 2021; Geiser et al. 2021). Crous et al. (2021) and Wang et al. (2022) have updated the taxonomy of this genus to include 19 species complexes. In addition, a variety of species within this genus contain virulent crop pathogens, such as *F. graminearum* and *F. oxysporun*, two of the top ten most economically damaging fungal pathogens (Dean et al. 2012; Leslie and Summerell 2006).

Fusarium brachygibbosum Padwick, Mycological Papers 12: 11 (1945).

Index Fungorum number: IF286508; Faceoffungi number: FoF11683; Figs. 93, 94

Pathogenic on roots of *Vigna unguiculata*. **Sexual morph**: Not observed. **Asexual morph:** *Conidiophores* 27–58 µm long, carried on aerial mycelium, unbranched or irregularly and/or sympodially branched bearing a terminal phialide. *Conidiogenous cells* 8–22 × 2–4 µm, polyphialide, subulate to subcylindical, smooth. *Macroconidia* 15.2–22 × 2–3 µm, hyaline, slightly curved with five distinct septa, wide central cells, slightly sharp apexes, basal cells with foot like shape. *Microconidia* rarely observed. *Chlamydospores* 6–24 µm diam. abundant, spherical o globose, smooth, slightly verrucose, formed terminally or intercalary in chains of two or three, wall 1–1.5 µm.

Culture characteristics: Colonies on PDA reaching 90 mm at 28 °C after 14 d in 12/12 dark, colonies appeared white to pink with abundant aerial mycelium.

Materials examined: India, Karnataka, Mysuru, Doddamaragowdanahally, diseased root of cowpea (*Vigna unguiculata* (L.) Walp. Fabaceae), May 2019, S. Mahadevakumar & Y.S. Deepika (UOM-IOE 19/16), living cultures CPFb1, CPFb2, CPFb3, CPFb4.

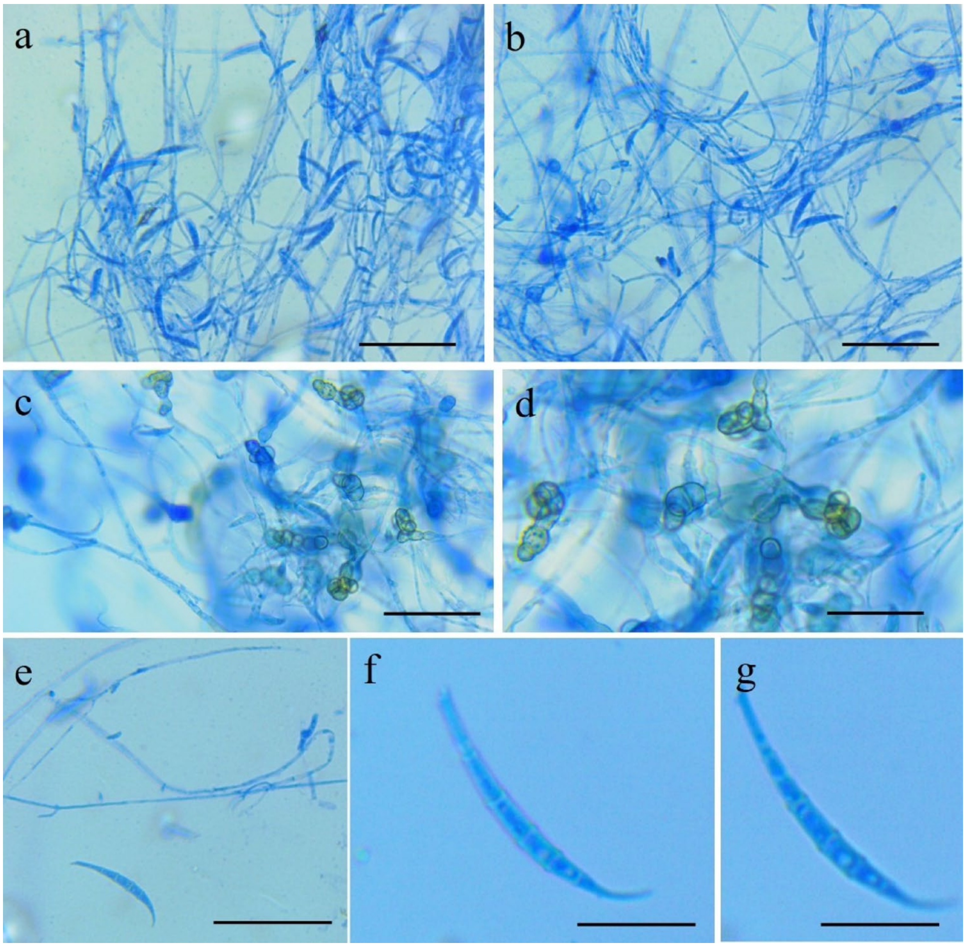


Fig. 94 Morphological features of *Fusarium brachygibbosum*: **a–b** Conidial morphology of *F. brachygibbosum* under compound microscope; **c–d** hyphal structures and chlamydospores of *F. brachygibbosum*; **e–f** a single macroconidium enlarged. Scale bar: **a–d** 50 µm; **e**–20 µm; **f– g** 10 µm

Hosts: Wide host range, including *Allium*, *Beta*, *Cannabis*, *Citrullus*, *Citrus*, *Euphorbia*, *Glycine*, *Gossypium*, *Helianthus*, *Nerium*, *Nicotiana*, *Phoenix*, *Plasmopara*, *Prunus*, *Sansevieria*, *Sorghum*, *Triticum*, *Vigna* and *Zea* (Farr and Rossman 2022; this study).

Distribution: Wide geographical range, including in Australia, Azerbaijan, China, India, Iran, Malaysia, Oman, Qatar, Soudi Arabia, Tunisia, Turkey and United States (Farr and Rossman 2022; this study).

GenBank numbers: CPFb1– MT804589 (ITS), OM938019 (*tef1*)

CPFb2– MT804590 (ITS), OM938020 (*tef1*)

CPFb3– MT804591 (ITS), OM938021(*tef1*)

CPFb4– MT804592 (ITS), OM938022 (*tef1*)

Notes: Fusarium brachygibbosum is known to associated with 19 host plants of which two records are represented from India (*Sorghum vulgare*, *Plasmopara viticola*) (Farr and Rossman 2022). This is the first record of *F. brachygibbosum* recorded on Cowpea (Fabaceae) from India (new host record) (Fig. 95).

Fusarium purpurea S.L. Han, M. Raza, W.J. Duan & L. Cai, ***sp. nov.***

Index Fungorum number: IF555883; Facesoffungi number: FoF10818; Fig. 96

Etymology: Refers to the pigment produced on PDA and OA, purpure.

Holotype: HMAS 351947.

Asexual morph: *Hyphae* 1.7–3.5 µm diam, hyaline, smooth-walled, septate, branched. *Conidiophores* arises on aerial mycelium, unbranched or irregularly branched, 11–29.5 × 2–4.5 µm ($\bar{x}$ = 19.9 × 3.0 µm, *n* = 35). *Phialides* mono- and polyphialide, subulate to subcylindrical, smooth- and thin-walled, 4.8–17.4 × 1.6–3.9 µm, periclinal thickening inconspicuous or absent. *Microconidia* hyaline, smooth- and thin-walled, two types, clavate with truncate base conidia (aseptate): 4.5–9.5 × 1.5–3.5 µm ($\bar{x}$ = 6.3 × 2.5 µm, *n* = 50); globose conidia (aseptate): 6.5–11 × 7–11.5 µm ($\bar{x}$ = 9.7 × 9.4 µm, *n* = 50). *Sporodochia* and *chlamydospores* not observed. **Sexual morph:** Not observed.

Culture characteristics: Colonies on PDA slow growing, reaching 52–57 mm diam in 7 d after incubation at 25 °C in the dark, colony flat, medium, filamentous, felted to velvety, rhizoid; colony from above; raised, dull, wrinkled folded, surface orchid purple (14C8) in the center, white (–A1) at the margin; reverse beetroot purple (13D8) in the center,

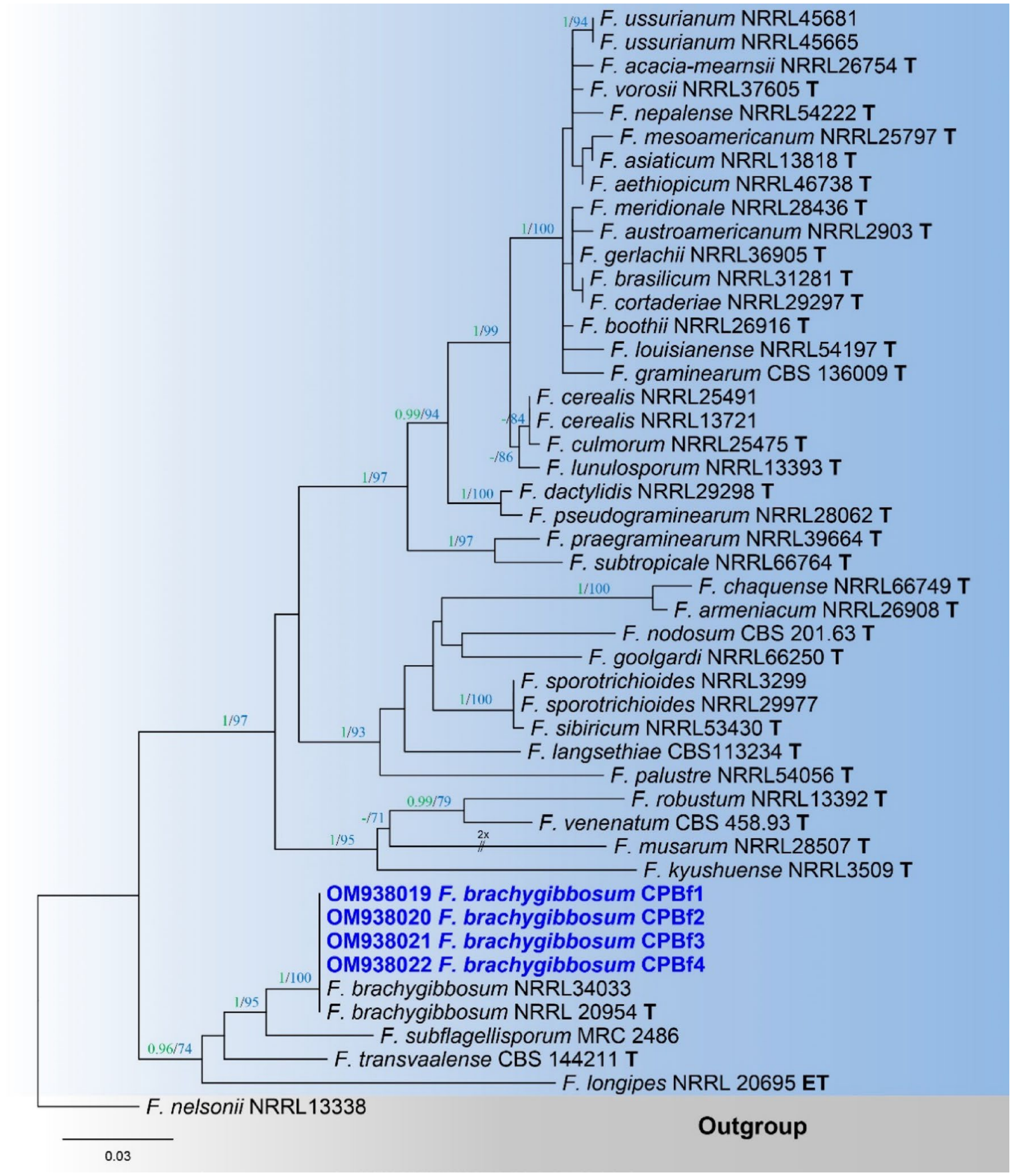


Fig. 95 RAxML phylogenetic tree generated from *tef*1 sequence data of *Fusarium sambucinum* species complex. Maximum likelihood bootstrap support ≥ 75% (in blue) and BYPP ≥ 0.95 (in green) are indicated on the branches. Ex-type and epi-type cultures are indicated in **bold** with 'T' and 'ET'

white (–A1) at the margin; odour absent, not producing pigment in PDA media. On OA reaching 41–49 mm in 7 d after incubation 25 °C in the dark; raised, felted to dusty, with abundant aerial mycelium, margin entire; surface amethyst (15C6) in the center, white (–A1) at the margin; reverse oak brown (5D6); odour absent.

Material examined: Kazakhstan, intercepted at Alashankou Port, isolated at Ningbo Customs, from seeds of *Triticum aestivum* imported to China, Jan. 2019, W.J. Duan & W.Z. Li (HMAS 351947, **holotype**), ex-type living culture, CGMCC 3.23515 = LC15871. *ibid*., LC15872; *ibid*., LC15873; *ibid*., LC15874.

GenBank numbers: CGMCC 3.23515 – ON365812 (*CaM*), ON365816 (*rpb1*), ON365820 (*rpb*2), ON365828 (*tef1*), ON365824 (*tub*2)

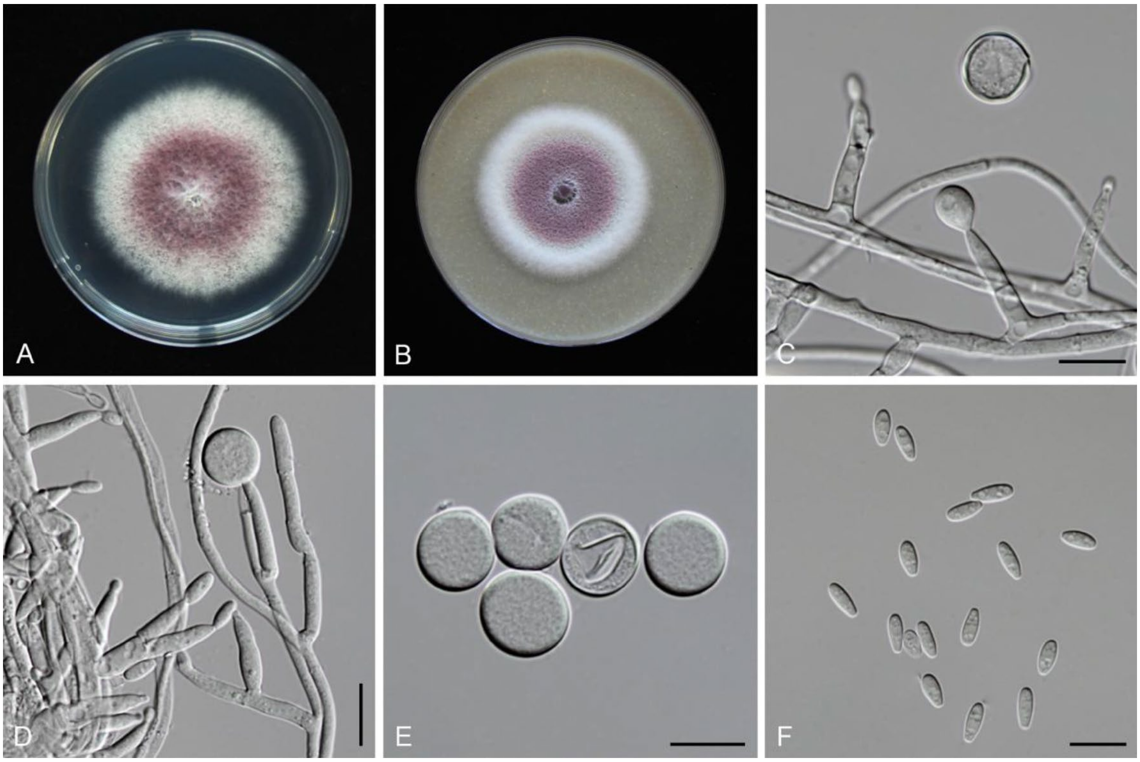


Fig. 96 ***Fusarium purpurea*** (CGMCC 3.23515, **ex-type living culture**). **a** Colony on PDA. **b** Colony on OA. **c-d** Aerial conidiophores and phialides. **e–f** Microconidia. Scale bars = 10 µm

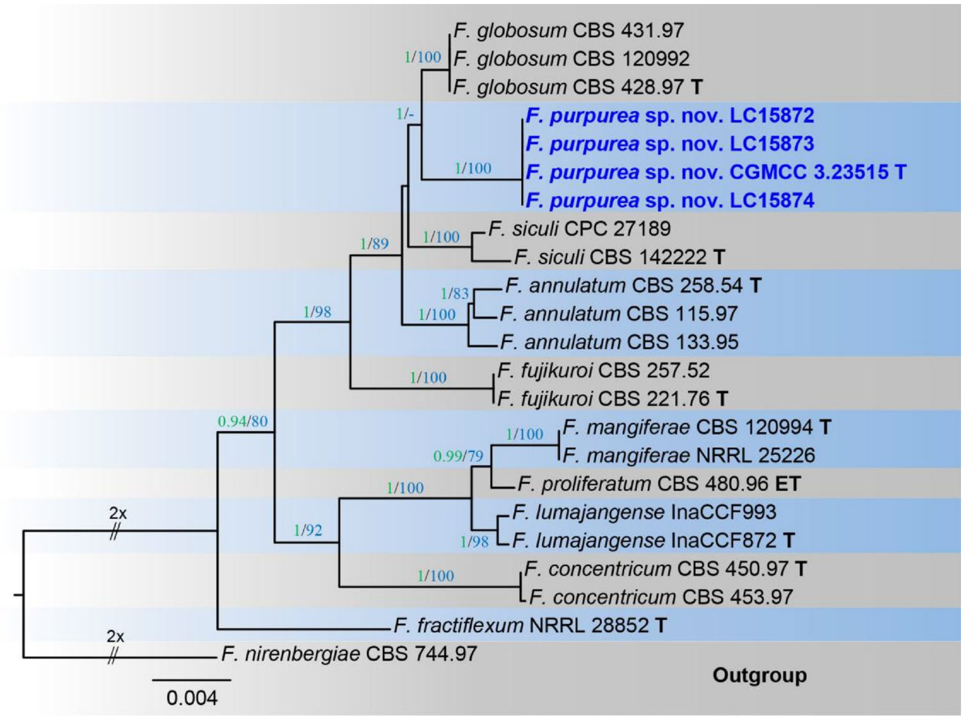


Fig. 97 RAxML phylogenetic tree generated from combined *CaM*, *rpb*1, *rpb*2, *tef*1 and *tub*2 sequence data of *Fusarium fujikuroi* species complex. Maximum likelihood bootstrap support values greater than 75% (in blue) and Bayesian posterior probabilities > 0.95 (in green) are indicated on the branches. Ex-type and epi-type cultures are indicated in **bold** with 'T' and 'ET'

LC15872 – ON365813 (*CaM*), ON365817 (*rpb1*), ON365821 (*rpb*2), ON365829 (*tef1*), ON365825 (*tub*2)

LC15873 – ON365814 (*CaM*), ON365818 (*rpb1*), ON365822 (*rpb*2), ON365830 (*tef1*), ON365826 (*tub*2)

LC15874 – ON365815 (*CaM*), ON365819 (*rpb1*), ON365823 (*rpb*2), ON365831 (*tef1*), ON365827 (*tub*2)

Notes: *Fusarium purpurea* formed a well-supported sister clade to *F. globosum* with 100% ML and 1.00 Bayesian posterior probabilities (BYPP) support (Fig. 96). *Fusarium purpurea* differs by 3 bp in the *CaM* gene, 16 bp in the *rpb*2 gene, 6 bp in the *tef*1 gene, and 1 bp in the *tub*2 gene compared to *F. globosum* (Proctor et al. 2013; Yilmaz et al. 2021). Morphologically, *F. purpurea* differs in the types of microconida production and its number of septation. For example, *F. purpurea* produces two types of microconidia: clavate with a truncate base (aseptate) and globose (aseptate) without papilla, while three types of microconidia were found in *F. globosum*: clavate with a truncate base (0- to 3-septate*)*, napiform/pyriform, and globose *(*0- to 1-septate) which often have a distinct papilla (Rheeder et al. 1996; Leslie and Summerell. 2006) (Fig. 97).

Microascales Luttr. ex Benny & R.K. Benj. (1980).

Microascales composed of seven families namely Ceratocystidaceae, Chadefaudiellaceae, Gondwanamycetaceae, Graphiaceae, Halosphaeriaceae, Microascaceae and Triadelphiaceae (Maharachchikumbura et al. 2016; Hyde et al. 2020a, b, c; Wijayawardene et al. 2022). A total of 109 genera were accepted under Microascales which were distributed in seven families (Wijayawardene et al. 2022).

Microascaceae Luttr. ex Malloch, Mycologia 62(4): 734 (1970)

Microascaceae was confined by Luttrell (1951) in Microascales and authenticated by Malloch (1970) (Maharachchikumbura et al. 2016). It includes saprobic, plant and opportunistic human pathogenic fungal genera (de Hoog et al. 2000; Sandoval-Denis et al. 2016; Maharachchikumbura et al. 2016). Currently this family is composed of 23 genera (Wijayawardene et al.2022).

Scedosporium Sacc. ex Castell. & Chalm., Manual of Tropical Medicine: 1122 (1919)

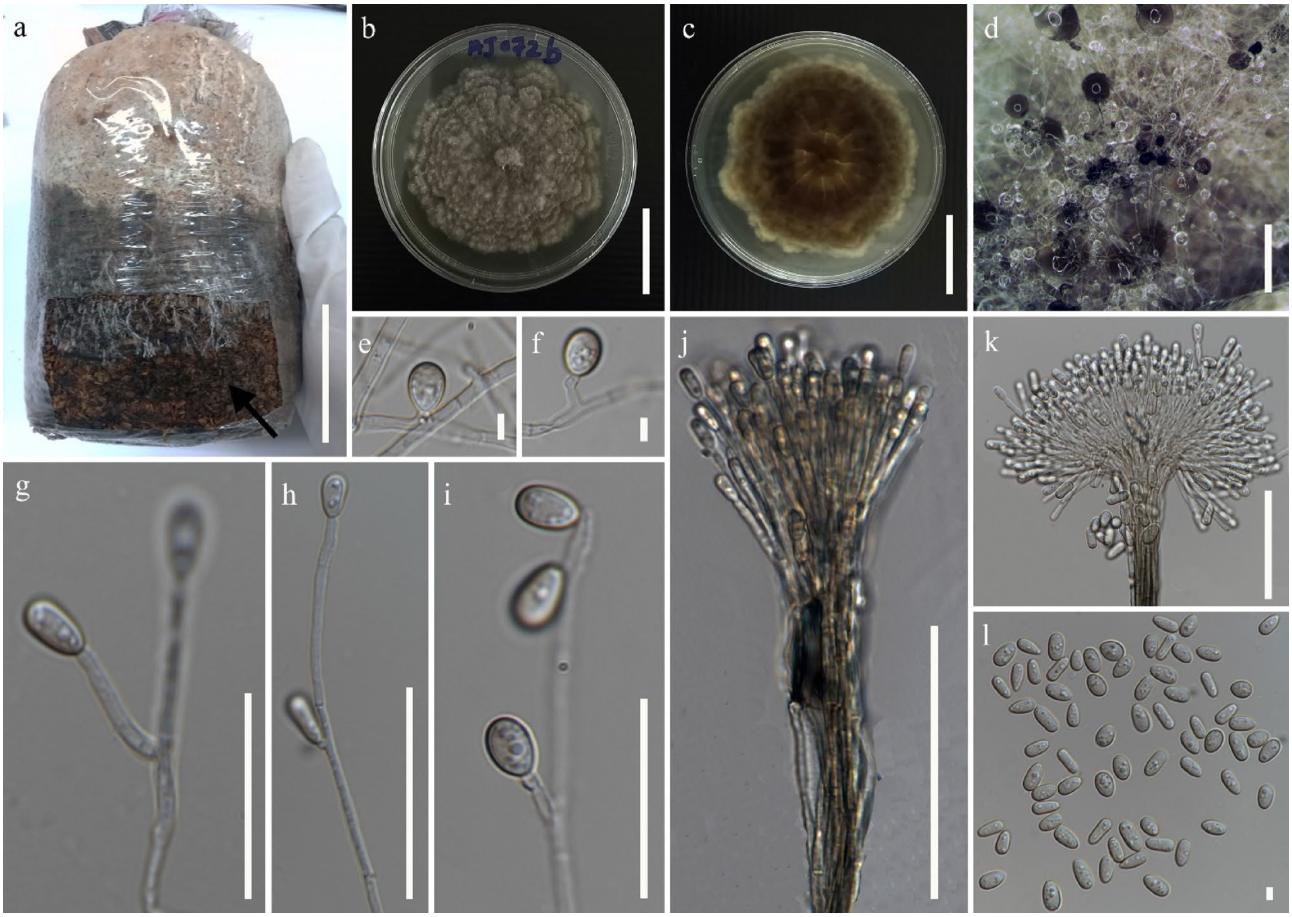
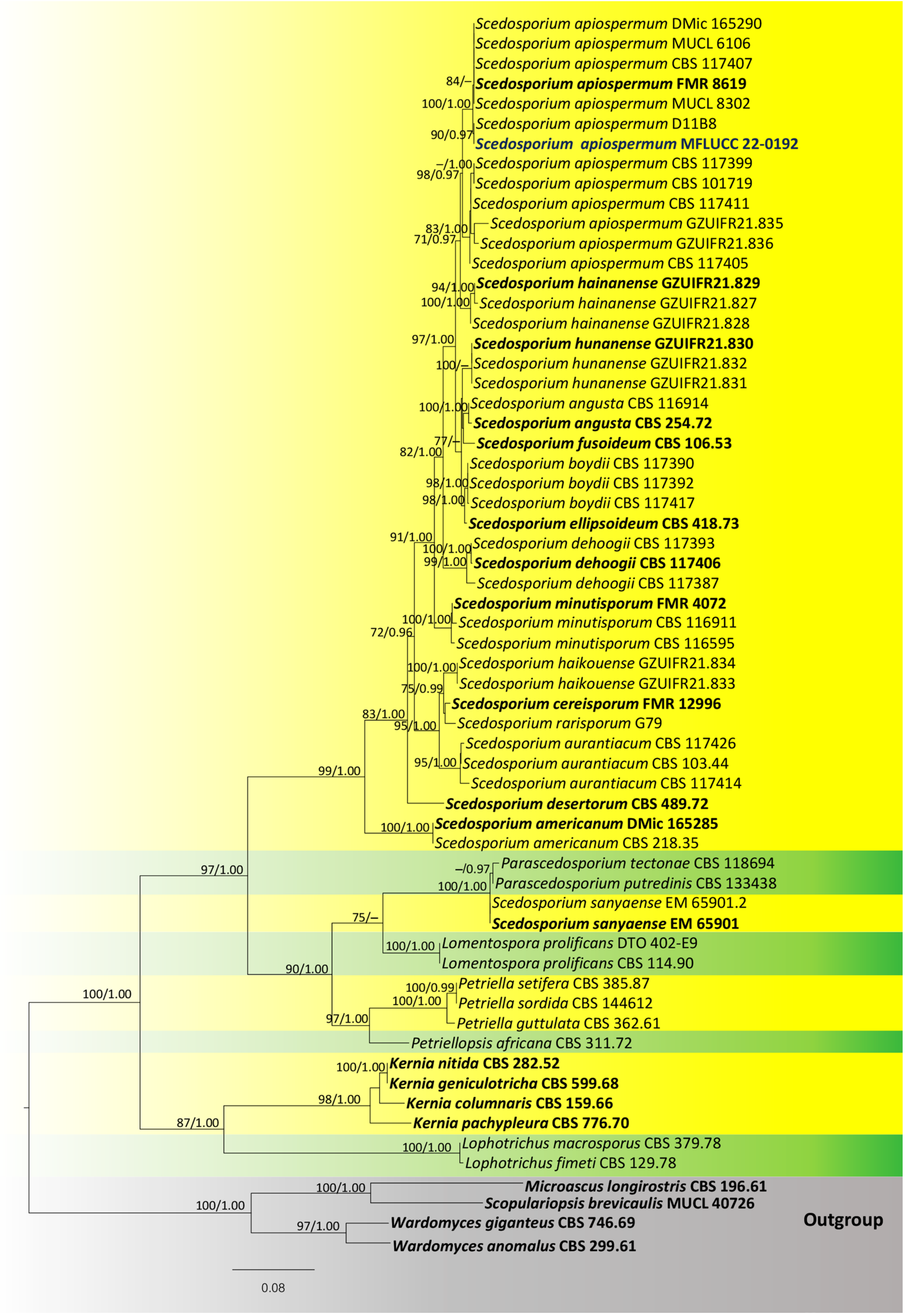


Fig. 98 ***Scedosporium apiospermum*** (MFLU 22-0160, **new record**) **a**. Contaminated oyster mushroom grow substrate. **b,c.** Colony on PDA. d. Sporulation of the colony on PDA. **e-i**. Conidial attachments and conidiogenous cells. **j,k**. Synnema with conidia. **l**. Conidia. Scale bars: **a** = 5 cm, **b,c** = 30 mm, **d** = 200 µm, **e,f,l** = 4 µm, **g** = 20 µm, **h** = 35 µm, **i** = 25 µm, **j** = 65 µm, **k** = 40 µm


Scedosporium apiospermum DMic 165290
Scedosporium apiospermum MUCL 6106
Scedosporium apiospermum CBS 117407
84/–
Scedosporium apiospermum FMR 8619
100/1.00
Scedosporium apiospermum MUCL 8302
Scedosporium apiospermum D11B8
90/0.97
Scedosporium apiospermum MFLUCC 22-0192
–/1.00
Scedosporium apiospermum CBS 117399
98/0.97
Scedosporium apiospermum CBS 101719
Scedosporium apiospermum CBS 117411
83/1.00
Scedosporium apiospermum GZUIFR21.835
71/0.97
Scedosporium apiospermum GZUIFR21.836
Scedosporium apiospermum CBS 117405
94/1.00
Scedosporium hainanense GZUIFR21.829
100/1.00
Scedosporium hainanense GZUIFR21.827
Scedosporium hainanense GZUIFR21.828
97/1.00
Scedosporium hunanense GZUIFR21.830
100/–
Scedosporium hunanense GZUIFR21.832
Scedosporium hunanense GZUIFR21.831
100/1.00
Scedosporium angusta CBS 116914
Scedosporium angusta CBS 254.72
77/–
Scedosporium fusoideum CBS 106.53
82/1.00
Scedosporium boydii CBS 117390
98/1.00
Scedosporium boydii CBS 117392
98/1.00
Scedosporium boydii CBS 117417
Scedosporium ellipsoideum CBS 418.73
91/1.00
100/1.00
Scedosporium dehoogii CBS 117393
99/1.00
Scedosporium dehoogii CBS 117406
Scedosporium dehoogii CBS 117387
Scedosporium minutisporum FMR 4072
100/1.00
Scedosporium minutisporum CBS 116911
72/0.96
Scedosporium minutisporum CBS 116595
100/1.00
Scedosporium haikouense GZUIFR21.834
Scedosporium haikouense GZUIFR21.833
75/0.99
Scedosporium cereisporum FMR 12996
83/1.00
95/1.00
Scedosporium rarisporum G79
Scedosporium aurantiacum CBS 117426
95/1.00
Scedosporium aurantiacum CBS 103.44
Scedosporium aurantiacum CBS 117414
99/1.00
Scedosporium desertorum CBS 489.72
100/1.00
Scedosporium americanum DMic 165285
Scedosporium americanum CBS 218.35
97/1.00
–/0.97
Parascedosporium tectonae CBS 118694
100/1.00
Parascedosporium putredinis CBS 133438
Scedosporium sanyaense EM 65901.2
75/–
Scedosporium sanyaense EM 65901
100/1.00
Lomentospora prolificans DTO 402-E9
90/1.00
Lomentospora prolificans CBS 114.90
100/1.00
100/0.99
Petriella setifera CBS 385.87
100/1.00
Petriella sordida CBS 144612
97/1.00
Petriella guttulata CBS 362.61
Petriellopsis africana CBS 311.72
100/1.00
Kernia nitida CBS 282.52
Kernia geniculotricha CBS 599.68
98/1.00
Kernia columnaris CBS 159.66
87/1.00
Kernia pachypleura CBS 776.70
100/1.00
Lophotrichus macrosporus CBS 379.78
Lophotrichus fimeti CBS 129.78
100/1.00
Microascus longirostris CBS 196.61
100/1.00
Scopulariopsis brevicaulis MUCL 40726
97/1.00
Wardomyces giganteus CBS 746.69
Outgroup
Wardomyces anomalus CBS 299.61
0.08

◂ **Fig. 99** Phylogram generated from maximum likelihood analysis based on combined ITS and *tub2* sequence data representing the species of *Scedosporium* and related genera. Related sequences are taken from Zhang et al. (2021). Sixty-two taxa are included in the combined analyses. *Microascus longirostris* (CBS 196.61), *Scopulariopsis brevicaulis* (MUCL 40,726), *Wardomyces anomalus* (CBS 299.61) and *Wardomyces giganteus* (CBS 746.69) are used as the outgroup taxa. Bootstrap support values for ML ≥ 70% and BYPP ≥ 0.95 are given near the nodes. The newly generated sequence is in blue. The type strains are indicated in black bold

Scedosporium is a ubiquitous filamentous fungus with a worldwide distribution. *Pseudallescharia boydii* is the sexual morph of *Scedosporium apiospermum*, which was first discovered in 1889 as a causative agent of human otitis (Siebenmann et al. 1899). Later *Monosporium apiospermum* was discovered as an anamorphic state of *P. bodydii* from a patient with human mycetoma in 1919 (Shear 1922).

This genus is typified by a sexual morph (*Pseudallescheria boydii*) characterized by closed ascomata (cleistothecia), a peridium (ascomata wall) of '*textura epidermoidea*', asci that are broadly clavate or spherical, and ascospores that are ellipsoidal or fusiform, which are symmetrical or nearly so (von Arx et al. 1988; De Hoog et al. 2000). The asexual morph includes: *Scedosporium*, characterized by hyaline, cylindrical conidiogenous cells arising from undifferentiated hyphae that produce obovoidal, hyaline, sticky conidia. Synnemata are characterized by large, erect bundles of hyphae terminating in a dense aggregate of conidiogenous cells. It produces conidia from a short extension of the conidiogenous cells with annellidic development (Gueho 1991; Lackner et al. 2014; Ramirez-Garcia et al. 2018).

Scedosporium species have been reported commonly from natural substrates such as soil, water anthropogenic influenced habitats, cattle dung and sewage (De Hoog et al. 2000; Ramirez-Garcia et al. 2018). Seventeen species are accepted under *Scedosporium* and these include: *S. americanum, S. angustum, S. apiospermum, S. aurantiacum, S. boydii, S. cereisporum, S. deficiens, S. dehoogii, S. desertorum, S. fusoideum, S. haikouense, S. hainanense, S. magalhaesii, S. minutisporum, S. multisporum, S. rarisporum* and *S. sclerotiale* (http://www.indexfungorum.org). The disease caused by *Scedosporium* species is termed as Scedosporosis. The occurrence of Scedosporium apiospermum associated with mushroom cultivation and *Scedosporium marina* and *S. dehoogii* from the marine environment are reported here.

Scedosporium apiospermum Sacc. ex Castell. & Chalm., Manual of tropical medicine (London): 1122 (1919).

Index Fungorum number: *IF432048*; *Facesoffungi number: FoF11704; Fig. 98*

Growing on Oyster mushroom grow substrate. **Sexual morph:** Not observed. **Asexual morph:** on host, *Mycelium* black powdery mass. *On PDA*, hyphomycetous, *Hyphae* 1.5–3.5 µm ($\bar{x}$ = 2.2 µm) wide, branched, septate, hyaline. *Conidiophores* solitary or synnematous, solitary conidiophores 75–128 × 1.8–3 µm ($\bar{x}$ = 102.5 × 2.6 µm, *n* = 10) hyaline, branched, forms 1–3 conidiogenous cells at the end. synnematous conidiophores 132–352 × 8.2–17.5 µm ($\bar{x}$ = 288.4 × 12.7 µm, *n* = 15) cylindrical stipe, erect, forms conidia at the end. *Conidiogenous cells* 4.8–25 × 1.2–2.5 µm ($\bar{x}$ = 15.2 × 1.3 µm, *n* = 10) lateral or terminal formation on solitary conidiophores, hyaline, cylindrical. *Conidia* hyaline, guttulate, conidia arising from conidiogenous cells 6.2–8.2 × 2–4.5 µm ($\bar{x}$ = 7.4 × 3.3 µm, *n* = 30) obvoid to ellipsoidal, conidia arising from synnematous conidiophores 6.4–9.2 × 1.7–3.5 µm ($\bar{x}$ = 7.5 × 2.8 µm, *n* = 35) cylindrical or claviform with a truncate base, conidia from undifferentiated hyphae 6–7.5 × 5.2–6.6 µm ($\bar{x}$ = 6.4 × 5.2 µm, *n* = 20) sessile, globose to subglobose.

Culture characteristics: colonies on PDA attaining 65–75 mm diameter after 14 days at 25 °C, cottony, dense, lanose, light gray to dark grey, margins fimbriate and irregular; reverse dark grey to brown, grey to white margins.

Material examined: Thailand, Phayao Province, growing on the oyster mushroom growing substrate, 06 June 2020, AJ. Gajanayake, AJ 072 (inactive dry culture, MFLU 22-0160, **new host record**), living culture, MFLUCC 22-0192.

GenBank numbers: ON714510 (ITS), ON714511(LSU), ON730889 (*tub2*).

Notes: Our isolate MFLUCC 22-0192, clusters within *Scedosporium apiospermum* with a 90% ML and 0.97 BYPP support (Fig. 99). Furthermore, the morphology of our isolate MFLUCC 22-0192 resembles the original description and illustrations for *Scedosporium apiospermum* by Saccarado in Castellani and Chalmers (1919) and the description and morphological illustrations by Gilgado et al. (2010). However, there are size differences of conidiophores, conidiogenous cells and conidia, when we compare our strain with the strains described in Castellani and Chalmers (1919) and Gilgado et al. (2010). The reason for this may be the differences in the media in which the colonies were grown.

Scedosporium apiospermum has been mainly identified as an opportunistic clinical pathogen relevant to many infections which commonly occur in the bones, central nervous system, lungs, paranasal sinuses, skin and soft tissues (Shinohara and George (2009); Goldman et al. 2016). Seephueak et al. (2017) isolated 21 fungal species from spent mushroom substrate of *Pleurotus* sp. collected from mushroom farms in southern Thailand. Among those 21 fungal species there were, *Alternaria* spp., *Aspergillus* spp., *Chaetomium* sp., *Cunninghamella* spp., *Fusarium* spp., *Lasiodiplodia* sp., *Neurospora* sp., *Penicillium* spp., *Rhizoctonia* sp. and *Trichoderma* spp. (Seephueak et al. 2017). Suada et al. (2015) have reported *Aspergillus* spp., *Fusarium* spp., *Gliocladium* sp., *Mucor* spp., *Neurospora* spp., *Paecilomyces* sp.,

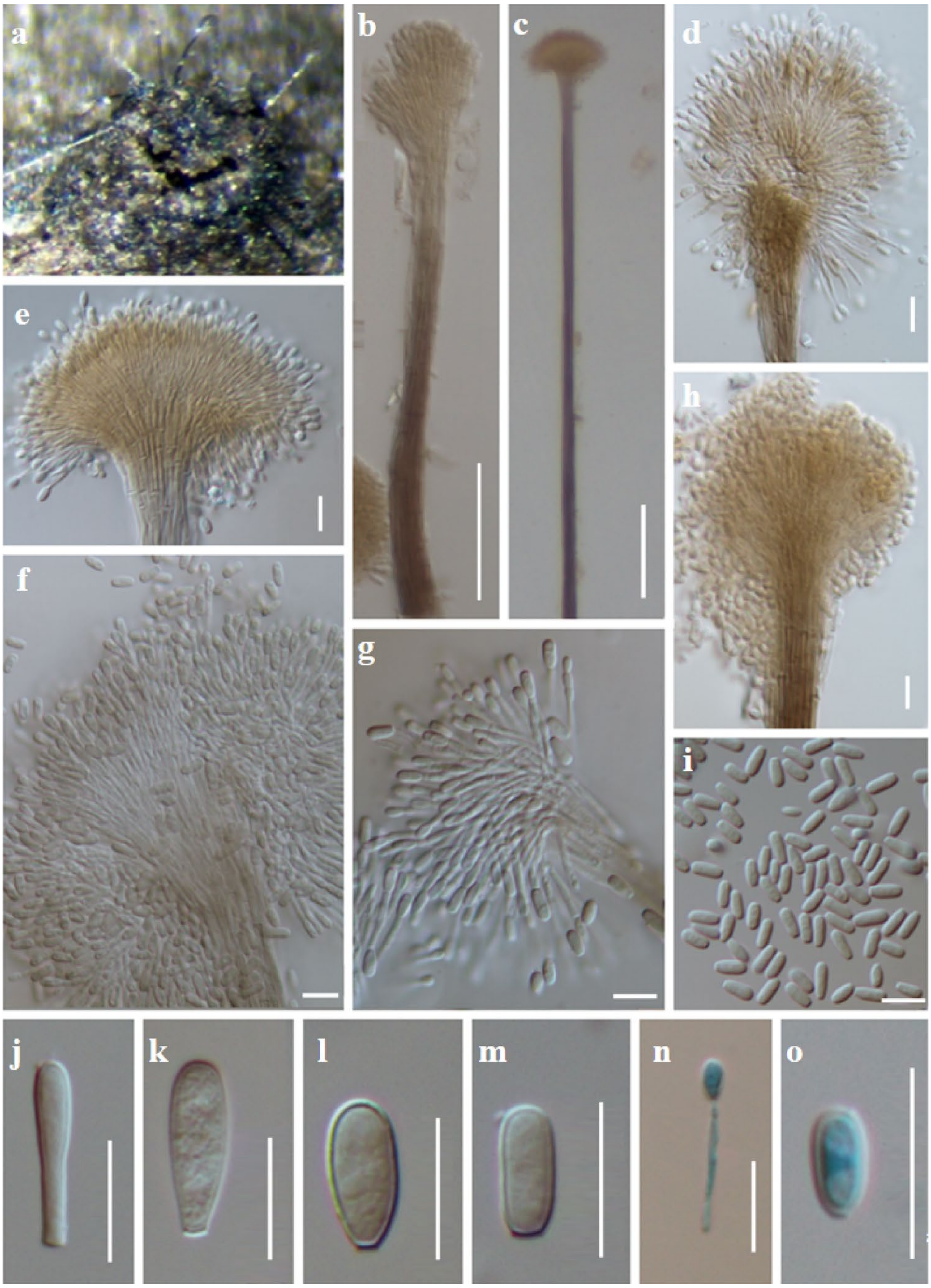


Fig. 100 ***Scedosporium marina*** on a twig (AMH-9946, **holotype**). **a**. Colonies on decaying woody stem of *Suaeda monoica*. **b – c** Synnemata. **d – e**, **h** Head and conidiophores. **f** Apical part of synnema producing conidia. **g** Conidiogenous cells with annellidic conidia. **i** Subcylindrical conidia. **k – l** Claviform conidia. **m – o** Obovoid conidia. Scale bars: b = 50 μm, c = 100 μm d – o = 10 μm

Penicillium spp., *Pythium* sp., *Stachybotrys* spp. and *Trichoderm*a spp. as contaminants from oyster mushroom growing substrate. According to best our knowledge this is the first report of *Scedosporium apiospermum* as a contaminant of oyster mushroom growing substrate.

Scedosporium marina Devadatha & V.V Sarma, ***sp. nov.***

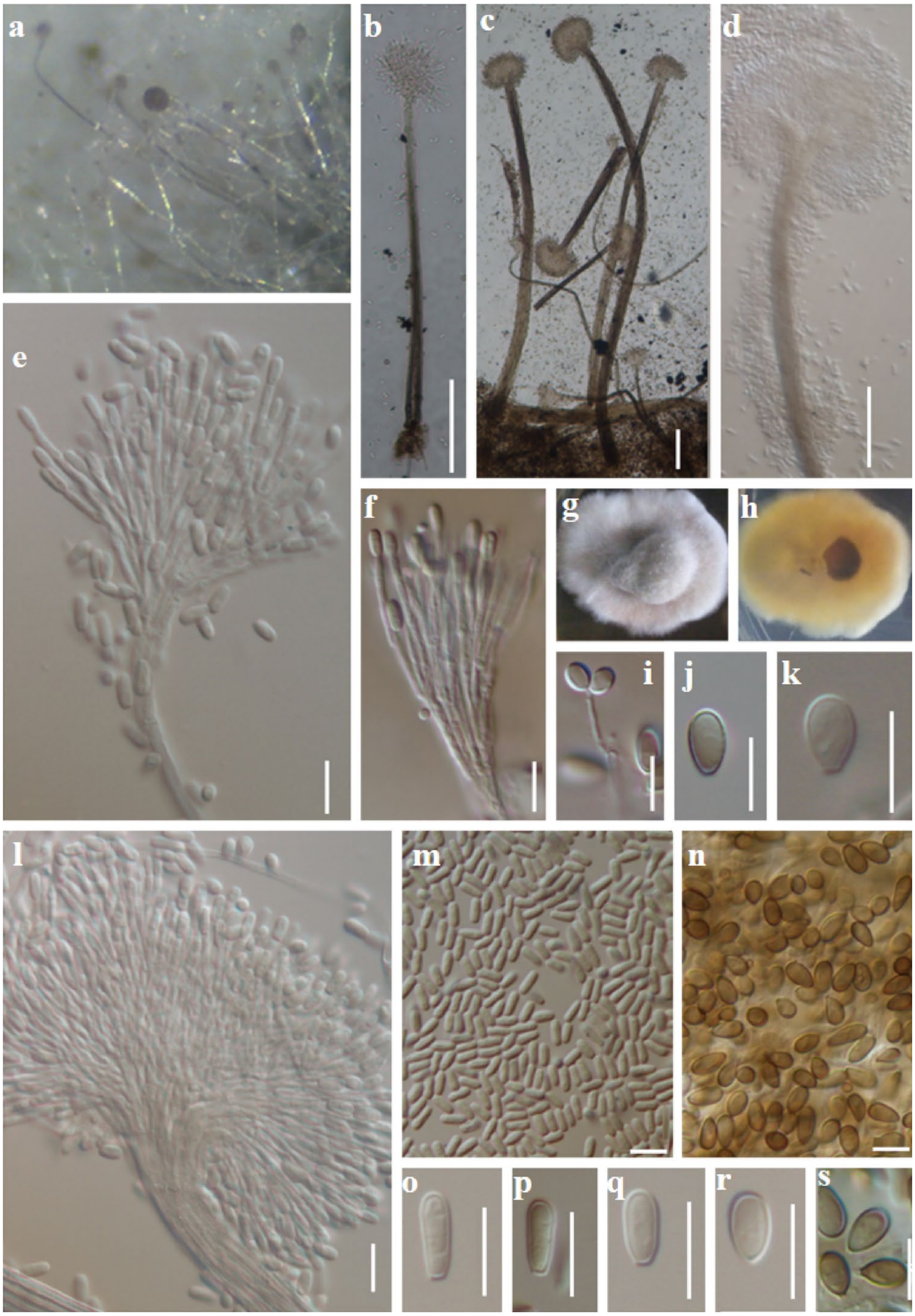
Index Fungorum number: *IF558432*, *Facesoffungi number*: *FoF05035; Figs.* 100, 101

Etymology: The specific epithet is in reference to the marine environment in which the fungus was collected.

Holotype: AMH-9946.

Saprobic on decaying woody stem of the halophyte *Suaeda monoica*. **Asexual morph:** *Colonies* effuse, light brown. *Mycelium* immersed, composed of septate, branched, smooth, pale brown to hyaline hyphae. *Synnemata* solitary to gregarious, erect, dark brown, 170–1110 *μm* tall with a cylindrical stipe, 10–25 μm wide ($\bar{x} = 642 \times 16$ μm, $n = 10$), dark gray, smooth-walled, terminate into a slimy head of conidia, slimy head 60–140 μm long and 60–165 μm wide ($\bar{x} = 86 \times 111$ μm, $n = 10$). *Hyphae* interwoven at the base, unbranched in the stipe,

Fig. 101 ***Scedosporium marina*** in culture (NFCCI-4273). **a** Synnemata on PDA **b – c** Synnemata. **g – h** Culture on PDA after 14 days. **d – e** Slimy head and Conidiophores. **f** Conidiogenous cells with annellidic conidia. **l** Apical part of synnema producing conidia. **m** Subcylindrical conidia. **n – r**, **s** Sessile obovoid conidia **o – q** Claviform Conidia. Scale bars: b – c = 100 µm d = 50 µm, e – f, i – s = 10 µm



branching at the apex to form *conidiophores*. *Conidiophores* synnematous, solitary, branched, *often* reduced to conidiogenous cells, growing laterally bearing a single verticil *conidiogenous cell. Conidiogenous* cells percurrent, terminal or lateral, hyaline, smooth-walled, cylindrical to slightly flask-shaped, 25–55 × 2–2.5 µm ($\bar{x}$ = 35 × 2.25 µm, *n* = 10). *Conidiogenous cell*s arising from undifferentiated hyphae are cylindrical to slightly flask-shaped, producing slimy heads of one-celled, smooth-walled, sub hyaline, obovoid or sub-cylindrical conidia. Three types of conidia are produced: (i) those produced on solitary conidiophores sub hyaline, smooth-walled, obovoid, or sub cylindrical 7–13 × 2.5–5.5 µm ($\bar{x}$ = 10 × 4 µm, *n* = 20); (ii) those produced on synnemata predominantly cylindrical or claviform, 5–13 × 1–3 µm ($\bar{x}$ = 9 × 2 µm, *n* = 20) with a wide truncate base; (iii) those developed mainly from the undifferentiated hyphae of the substrate, sessile or on short protrusions, solitary, lateral, brown, smooth, and thick-walled, mostly obovoid 2.5–10 × 2–2.5 µm ($\bar{x}$ = 9 × 2.3 µm, *n* = 20). **Sexual morph:** Not observed.

Culture characteristics: *Conidia* germinating on sea water agar within 24 h. Germ tubes produced from the conidial base. Colonies on PDA attaining 30–35 mm diameter after 14 days at 25 °C, circular, raised, light grayish at center and smoke gray at margins, cottony; yellow in reverse with entire margin. The optimum growth temperature was from 25 to 37 °C, and did not grow at 45 °C. *Hyphae* hyaline to pale brown, branched and septate, 3–7.5 µm wide. *Synnemata* developed after 30 days of incubation at 25 °C; synnemata solitary to gregarious, erect, dark brown, 190–1400 µm tall with a cylindrical stipe from 10 to 25 µm wide ($\bar{x}$ = 647 × 16.9 µm, *n* = 10), dark gray, smooth walled, terminated into a slimy head of conidia, 25–35 µm long and 35–50 µm wide ($\bar{x}$ = 30 × 36 µm, *n* = 10). *Conidiophores* solitary, branched, often reduced to conidiogenous cells growing laterally bearing single verticil of conidiogenous cells. *Conidiogenous cells* terminal or lateral, hyaline, smooth-walled, cylindrical to slightly flask-shaped, 25–50 × 2–3 µm ($\bar{x}$ = 35 × 16 µm, *n* = 10). *Conidiogenous cells* arising from undifferentiated hyphae, cylindrical to slightly flask-shaped, producing slimy heads of one-celled, smooth-walled, sub-hyaline, obovoid or sub-cylindrical conidia. There were three types of conidia: (i) those produced on solitary conidiophores subhyaline, smooth-walled, obovoid or subcylindrical 5–10 × 1.5–3 µm ($\bar{x}$ = 6.8 × 2.3 µm, *n* = 20); (ii) those produced on synnemata predominantly cylindrical or claviform, 7.5–10 × 2–3 µm ($\bar{x}$ = 8.7 × 2.4 µm, *n* = 20) with a wide truncate base; (iii) those developing mainly from the undifferentiated hyphae of the substrate, sessile or on short protrusions, solitary, lateral, brown, smooth, and thick-walled, mostly obovoid 5–10 × 2–2.5 µm ($\bar{x}$ = 9 × 2.4 µm, *n* = 20). Sexual state not observed after incubation for 2 months at 25 °C.

Material examined: India, Tamil Nadu, Tiruvarur, Muthupet mangroves (10.4° N 79.5° E), on decaying woody stem of the halophyte *Suaeda monoica* Forssk. ex J.F.Gmel. (Amaranthaceae) 28 November 2015, B. Devadatha (AMH-9946, **holotype**), ex-type living culture NFCCI-4273.

GenBank numbers: MF182397 (ITS), KY863508 (LSU), MH571780 (SSU), MF687078 (*tub2*), MF182399 (*tef1*)

Notes: Our present collection of *Scedosporium marina* (NFCCI-4273) has been assigned to *Scedosporium* based on its similar morphological characteristics in having *Graphium*-like synnemata and scattered, poorly differentiated, percurrent conidiogenous cells (Gueho 1991). The present taxon, *Scedosporium marina* (NFCCI-4273) and *S. aurantiacum* (FMR8630) share similar morphological characteristics in producing three different types of conidia like the obovoid, or sub cylindrical, cylindrical or claviform, sessile obovoid conidia with overlapping conidial dimensions and yellow diffusible pigments on PDA. However, combined multigene phylogenetic anlayses of combined datasets of ITS and *tub2* revealed that *Scedosporium marina* (NFCCI-4273) formed distinct lineage sharing a sister relation with *Scedosporium aurantiacum* with significant statistical support 100% ML, 97% MP (105). Morphologically *S. marina* (NFCCI-4273) is distinct from *S. aurantiacum* (FMR8630) in having long and wide synemmata (170–1110 × 10–25 *vs* 330–750 × 7.5–17.5), smaller heads (60–140 × 60–165 *vs* 60–70 × 140). The condiogenous cells of *S. marina* (NFCCI-4273) are percurrent and long in contrast to *S. aurantiacum* (FMR8630) (25–55 × 2–2.5 *vs* 10–37 × 1.5 2.5).

The optimum growth temperature of *S. marina* (NFCCI-4273) was from 25 to 37 °C and did not grow at 45 °C whereas *S. aurantiacum* (FMR8630) was from 37 to 40 °C and growth was also found at 45 °C but the fungus did not grow at 50 °C (Gilgado et al. 2005). The ITS sequence comparison revealed more than 30 nucleotide base pair differences between two taxa, which supports the establishment of a new species for our new taxon. Furthermore, *S. marina* is a saprobe on decaying woody stem of the halophyte *Suaeda monoica* from a marine habitat unlike other species of *Scedosporium* which are known to be human pathogens. *Scedosporium aurantiacum* is clearly distinguished from *S. marina* as an opportunistic human pathogen that is known to cause various infections in lungs, ears, respiratory sinuses and subcutaneous abscess in patients of diabetes and malignant lymphoma (Kondo et. al 2018). Hence, based on the above mentioned morphological, cultural, molecular and habitat differences we introduce a new species, *S. marina*, in *Scedosporium*.

Scedosporium dehoogii Gilgado, Cano, Gene´ Guarro in Journal of Clinical Microbiology 46: 2 (2008).

Index Fungorum number: *IF538388; Facesoffungi number: FoF04829; Fig. 102, 103*

Saprobic on decaying woody of *Avicennia marina*. **Asexual morph:** *Colonies* effuse, light brown. *Mycelium* mostly immersed, composed of septate, branched, smooth, pale brown to hyaline hyphae. *Synnemata* solitary to gregarious, erect, dark brown, 190–390 *µm* tall with a cylindrical stipe from 10 to 30 µm wide ($\bar{x}$ = 242 × 16 µm, *n* = 10), dark gray, smooth-walled, terminated into a slimy head of conidia, slimy head 45–75 µm long, 55–80 µm wide ($\bar{x}$ = 60 × 64 µm, *n* = 10). *Hyphae* interwoven at the base, unbranched in the stipe, branched at the apex to form *conidiophores. Conidiophores* synnematous, solitary, branched, often reduced to conidiogenous cells which were subhyaline. *Conidiogenous cells* terminal or lateral, hyaline, smooth-walled, cylindrical to slightly flask-shaped, 25–40 × 2–3 µm ($\bar{x}$ = 31 × 2.5 µm,

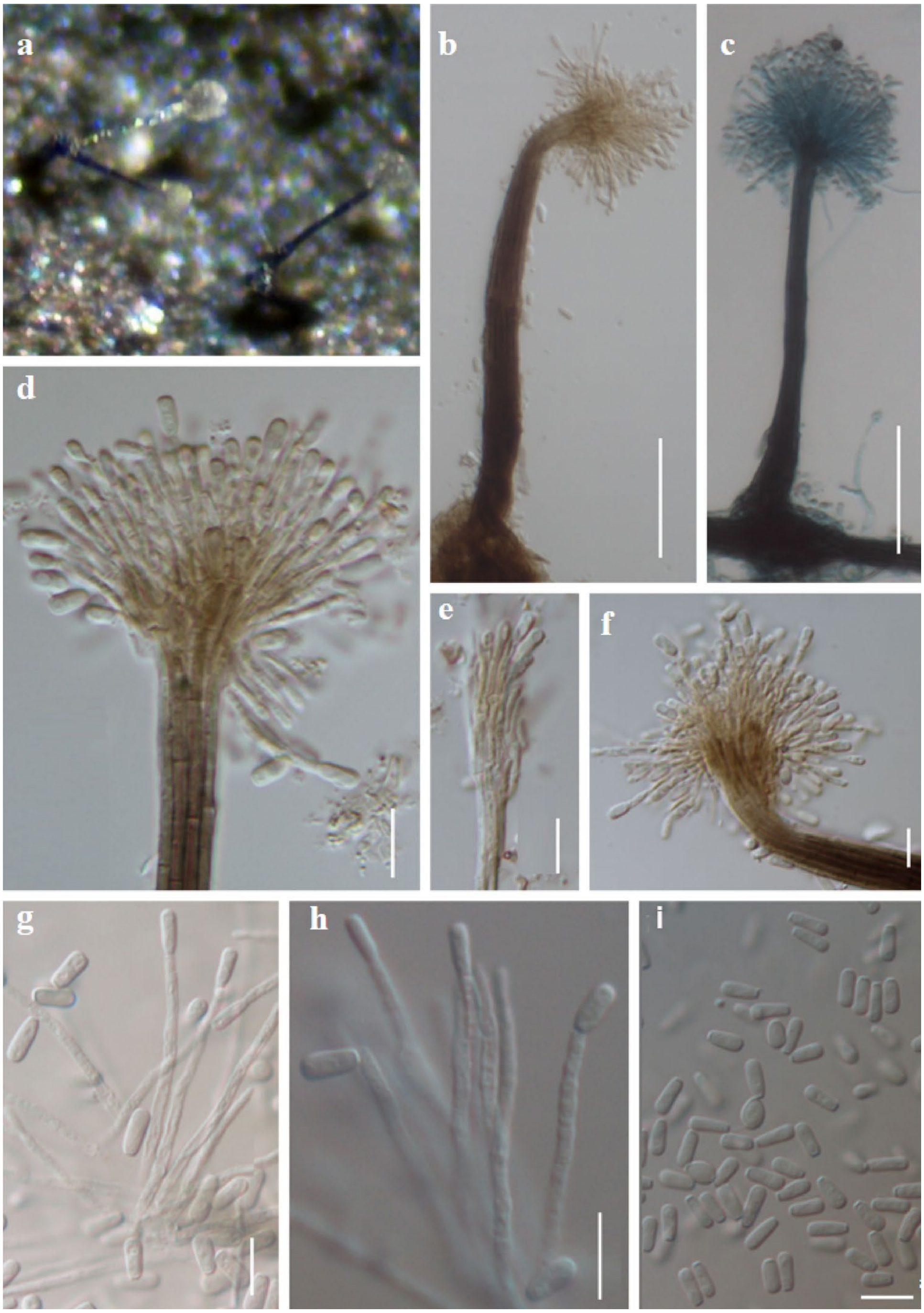


Fig. 102 ***Scedosporium dehoogii*** (AMH 9945, **new record**) **a** Colonies on decaying woody stem of *Suaeda monoica.* **b – c** Synnemata. **d – f** Slimy head and conidiophores. **g – h** Conidiogenous cells with annellidic conidia. **j** Cylindrical and obovoid conidia. Scale bars: **b** = 50 µm **c** = 100 µm, **d – j** = 10 µm

$n = 10$). *Conidiogenous cells* arise from undifferentiated hyphae, cylindrical to slightly flask-shaped, producing slimy heads of one-celled, smooth-walled, sub-hyaline, obovoid or sub-cylindrical conidia. *Conidia*: two types of conidia: (i) those produced on synnemata and solitary conidiophores were predominantly cylindrical or claviform, hyaline, 5–10 × 2–3 µm ($\bar{x} = 7.3 \times 2.7$ µm, $n = 20$) with a wide truncate base; (ii) those developed mainly from the undifferentiated hyphae of the substrate were sessile or on short protrusions, solitary, lateral, brown, smooth, and thick-walled, mostly obovoid 2.5–7.5 × 2–3 µm ($\bar{x} = 4.3 \times 2.4$ µm, $n = 20$). **Sexual morph:** Not observed.

Culture characteristics: *Conidia* germinating on Sea Water agar within 24 h. Germ tubes produced from the conidial base. Colonies on PDA fast growing, attaining 40–45 mm diameter after 14 days at 25 °C, circular, raised, with white to grey at centre and white to cream at margins, cottony; pale yellow in reverse with entire margin. The optimum growth temperature was from 25 to 37 °C. The fungus did not grow at 45 °C. *Hyphae* hyaline to pale brown,

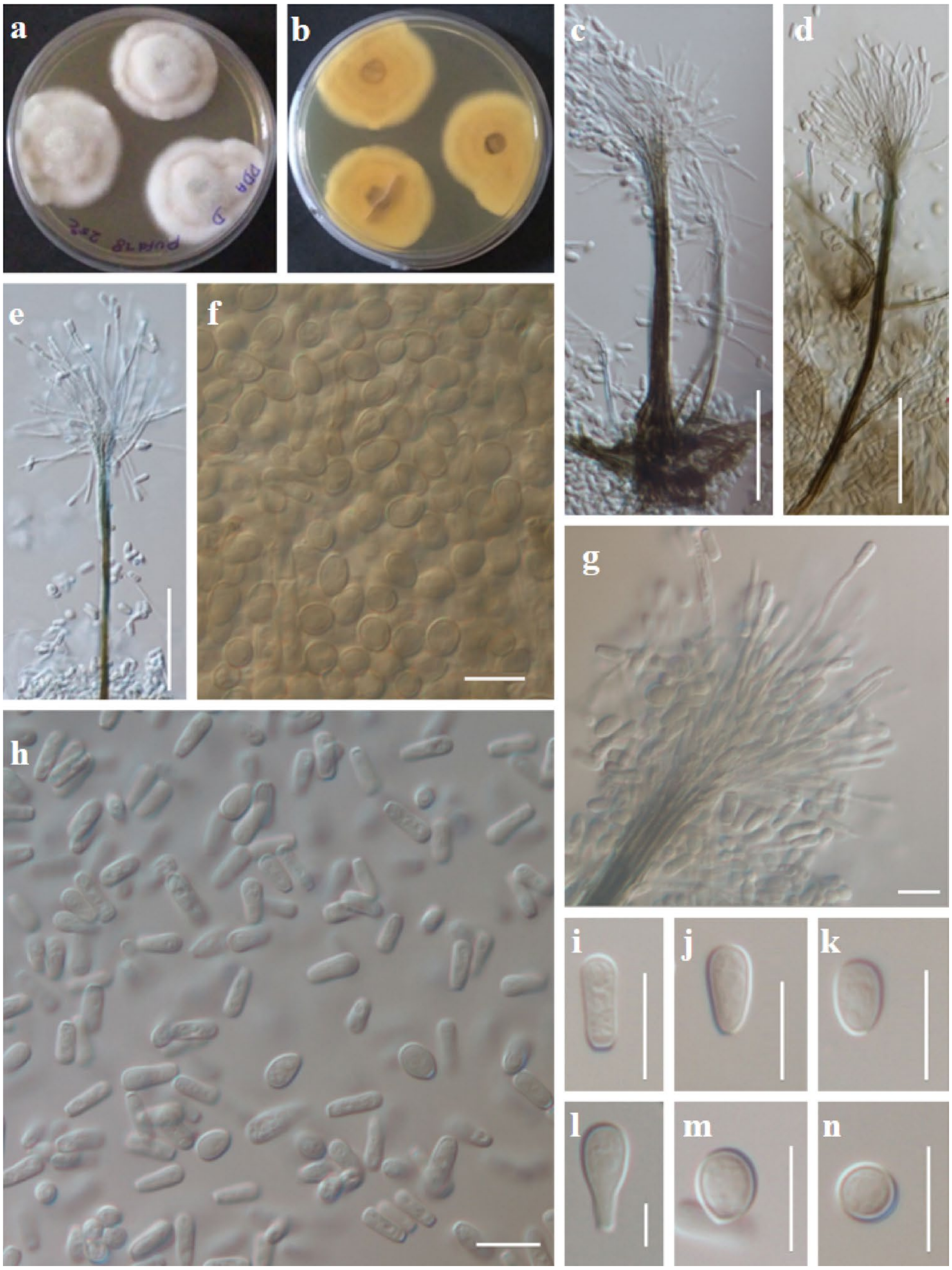


Fig. 103 ***Scedosporium dehoogii*** (NFCCI- 4274) **a – b** Cultures on PDA after 14 days. **c – d** Synnemata. **e** Slimy head and Conidiophores. **f** sessile obovoid conidia. **g** Conidiogenous cells with annellidic conidia. **h**. sub cylindrical conidia **i – n** Cylindrical and obovoid conidia and Scale bars: c = 50 μm d – n = 10 μm

branched and septate, 1–3 μm wide. *Conidiophores* synemmatous; synnemata solitary to gregarious, erect, dark brown, 180–255 μm tall with a cylindrical stipe from 10–30 μm wide ($\bar{x} = 223 \times 17$ μm, $n = 10$), dark gray, smooth walled, terminating into a slimy head of conidia, 45–85 μm long and 55–90 μm wide ($\bar{x} = 63 \times 66$ μm, $n = 10$). *Hyphae* interwoven at the base, unbranched in the stipe, branching at the apex to form conidiophores. *Conidiophores* solitary, branched often reduced to conidiogenous cells which were sub-hyaline. *Conidiogenous cells* terminal or lateral, hyaline smooth-walled, cylindrical to slightly flask-shaped, 30–45 × 2–3 μm ($\bar{x} = 35 \times 2.4$ μm, $n = 10$). *Conidiogenous* cells arising from undifferentiated hyphae, cylindrical to slightly flask-shaped, producing slimy heads of one-celled, smooth-walled, sub hyaline, obovoid or sub-cylindrical conidia. *Conidia*: two types: (i) those produced on synnemata and solitary conidiophores, predominantly cylindrical or claviform, hyaline, 5–15 × 2–5 μm ($\bar{x} = 10 \times 3$ μm, $n = 20$) with a wide truncate base; (ii) those developed mainly from the undifferentiated hyphae of the substrate were sessile or on short protrusions, solitary, lateral, brown, smooth, and thick-walled, mostly obovoid 2.5–9 × 2–5 μm ($\bar{x} = 5 \times 3.5$ μm, $n = 20$).

Material examined: India, Tamil Nadu, Tiruvarur, Muthupet mangroves (10.4° N 79.5° E), on decaying wood

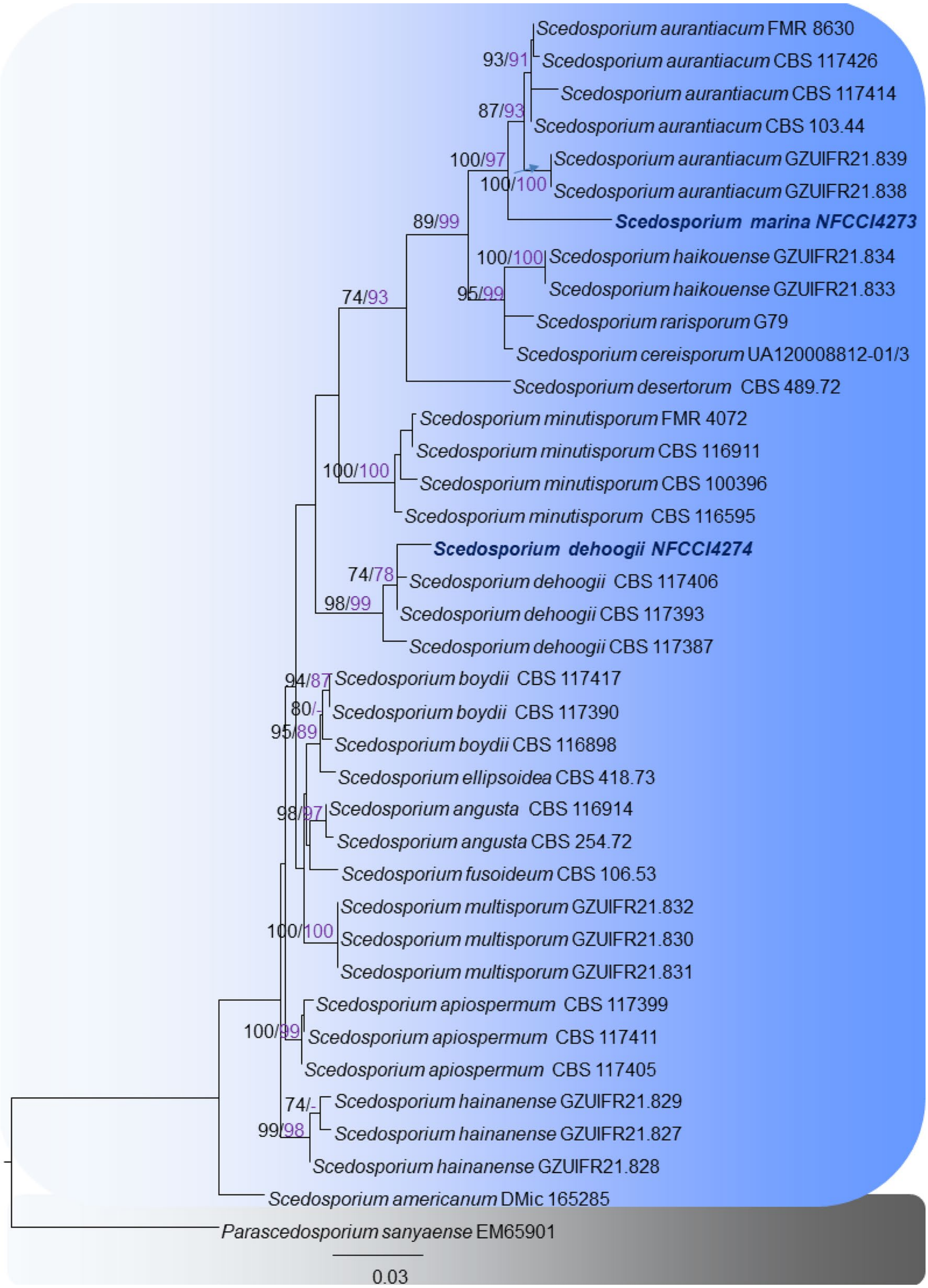


Fig. 104 Phylogram based on the RAxML analysis of a combined ITSrDNA and *tub2* sequence dataset. Bootstrap support values for ML and MP higher than 70% values are given above each branch respectively. The new isolates are represented in blue. The tree is rooted to *Parascedosporium sanyaense* EM65901. Thirty-eight sequences are included in the phylogenetic analyses with 1159 characters including gaps. The maximum parsimonious dataset consisted of 855 characters were constant, 166 parsimony-informative and 138 parsimony-uninformative. The parsimony analysis of the data matrix resulted in Two hundred and seventy equally parsimonious trees with a length of 486 steps (CI = 0.759, RI = 0.888, RC = 0.674, HI = 0.241)

of *Avicennia marina* (Forssk.) Vierh. (Acanthaceae), 28 November 2015, B. Devadatha (AMH 9945), living culture, NFCCI- 4274.

Hosts: Agricultural areas, playgrounds, riverbanks, Soil, Human infections (Rougeron et al. 2018)

Distribution: Australia, Austria, Chile, India, Netherlands, Spain, Thailand (Rougeron et al. 2018)

GenBank numbers: MH569493 (ITS), MH569492 (LSU), MH571777 (SSU)

Notes: Multigene phylogenetic anlayses of combined datasets of ITS sequence data revealed that *Scedosporium dehoogii* (NFCCI-4274) clustered together with the type and other existing strains of *S. dehoogii* with moderate statistical 74% ML and 78% MP support (Fig. 103). *Scedosporium dehoogii* (NFCCI-4274) from decaying wood of *Suaeda monoica* and *Avicennia marina* and colonies on PDA also share similar morphological characteristics with *S. dehoogii* (CBS-117406) reported from the soil (Gilgado et al. 2008). *Scedosporium dehoogii* is a common environmental species occurs on locations with high human activities like soil, water, agricultural areas and not involved in human infections (Kaltseis et al. 2009). However, this is the first report of *Scedosporium dehoogii* (NFCCI- 4274) from marine habitats. Earlier *Medicopsis romeroi* has been reported from mangroves (Devadatha et al. 2020). Also, Calabon et al. (2018) reported *S. aurantiacum* from Sponges in mangroves. With the present two species from mangroves totally three *Scedosporium* spp. are recorded from marine environments (Figs. 103, 104).

Hypocreomycetidae incertae sedis (***Rhexoacrodictys* and *Dematipyriforma* clade**)

Notes: In the current study, *Rhexoacrodictys* and *Dematipyriforma* form a distinct clade with a high statistical support (100/100/100 for ML/MP/BYPP, respectively) that is phylogenetically related to the orders Pleurotheciales and Savoryellales and might represent a new lineage (Fig. 105). The phylogenetic placement of *Rhexoacrodictys* is controversial in various studies. Shi et al. (2021) placed *Rhexoacrodictys* in Pleurotheciales, while Boonmee et al. (2021) placed the genus in Savoryellales. Sun et al. (2017) placed *Dematipyriforma* in Savoryellales where it forms a basal branch to representatives of the order.

Dematipyriforma L. Y. Sun, Hai-Yan Li, Xiang Sun & L.D. Guo.

Notes: *Dematipyriforma* is a monotypic genus typified by *D. aquilaria* L. Y. Sun, Hai-Yan Li, Xiang Sun & L.D. Guo that was isolated as an endophyte from a trunk of *Aquilaria crassna* in Laos (Sun et al. 2017). The genus is characterized by monoblastic, integrated, intercalary or terminal, pale brown to brown, determinate, cylindrical conidiogenous cells; solitary, pyriform conidia with transverse and often oblique or longitudinal, usually with a single small basal cell; produce variously shaped Chlamydospores in culture (Sun et al. 2017). During an ongoing study of freshwater fungi from River Nile in Egypt (e.g. Abdel-Aziz 2016a, b, c, 2020), three new species of *Dematipyriforma* were recorded on submerged wood and date palm rachis in the River Nile, Egypt that are described in this article based on morphology and their phylogenetic placement. Species of *Dematipyriforma* are phylogenetically related to *Rhexoacrodictys* species, both genera have rhexolytic conidial secession, however the later genus has macronematous conidiophores and percurrently extending conidiogenous cells vs. absent or micronematous conidiophores and determinate conidiogenous cells in *Dematipyriforma*. Boonmee et al. (2021) described *Rhexoacrodictys nigrospora* Boonmee, D.F. Bao & K.D. Hyde from decaying wood in Thailand with micronematous or semi-macronematous conidiophores and determinate conidiogenous cells. They did not include the sequences of *Dematipyriforma aquilaria*in their phylogenetic analyses and in our opinion *R. nigrospora* can be placed in *Dematipyriforma* based on morphology of the conidiophores (micronematous vs. macronematous with bulbous base) and conidiogenesis (determinate *vs*. percurrent proliferation in *Rhexoacrodictys erecta* (Ellis & Everh.) W.A. Baker & Morgan-Jones) and the phylogenetic analyses (Fig. 105).

Dematipyriforma aquatica Abdel-Aziz &Abdel-Wahab ***sp. nov.***

Index Fungorum number: IF900081; Facesoffungi number: FoF13400; Fig. 106

Etymology: Named after the aquatic habitat, where this fungus was collected.

Holotype: SUMCC H-12001 (Sohag University Microbial Culture Collection)

Saprobic on submerged wood in the River Nile. **Sexual morph**: Not observed. **Asexual morph**: *Mycelium* immersed and superficial, sub-hyaline to brown, septate, branched, smooth, 1.5–4 µm wide. *Conidiophores* absent or present, when present micronematous, mononematous, sub-hyaline to brown, flexuous, smooth, unicellular, 7–15 µm long, 1.5–4 µm wide. *Conidiogenous cells* holoblastic, integrated, intercalary or terminal, sub-hyaline to brown, determinate, ampulliform, clavate, subglobose, smooth, 5–8 µm long, 5–6 µm wide. *Conidial secession* rhexolytic. *Conidia* solitary or aggregated, effuse and heavily covered the surface of the wood, intercalary or terminal, smooth, pyriform or subglobose, rounded at the apex, black, with brown to dark-brown basal cell, muriform, 4–10 cells, 3–5 transverse septa and 0–2 longitudinal septa, not or slightly constricted at the septa, 27–38 × 15–26 µm ($\bar{x}$ = 32.2 × 20.9 µm, n = 50), apex and basal cells are singles. *Chlamydospores* intercalary

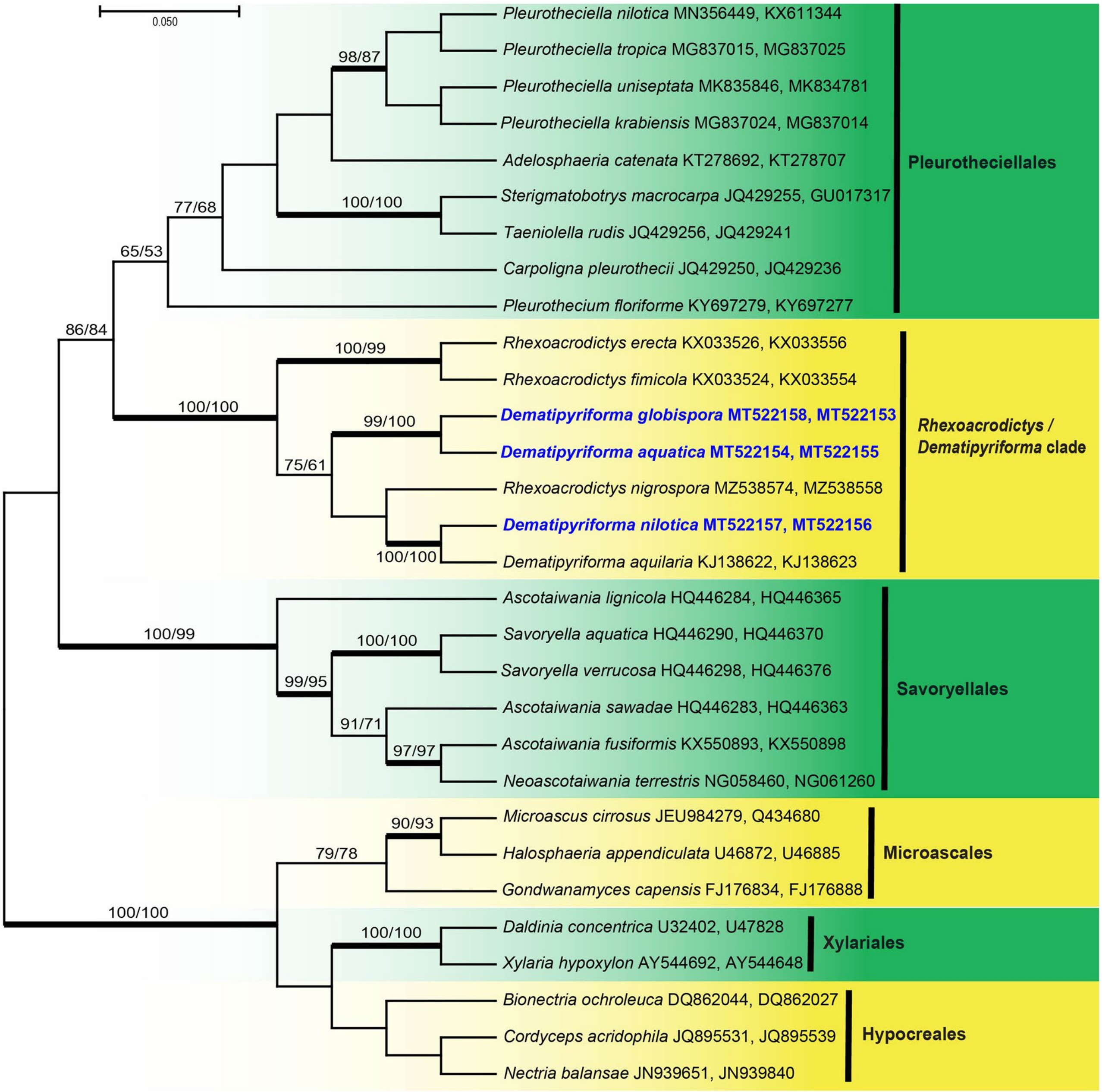


Fig. 105 Phylogenetic relationship of *Dematipyriforma* with related taxa based on the nucleotide sequences of the combined SSU and LSU rDNA. The maximum likelihood (ML) tree was constructed in MEGA X (Kumar et al. 2018). The maximum parsimonious data set of the combined genes consisted of 30 taxa with three representatives of Hypocreales used as outgroup. Phylogenetic trees obtained from ML, MP and BYPP were similar in topology. Bootstrap support on the nodes represents ML and MP ≥ 50%. Branches with a BYPP of ≥ 95% are in bold. The three new *Dematipyriforma* species are in blue

or terminal, catenated, straight, or curved, brown to dark brown, smooth, granulate, phragmoseptate.

Culture characteristics: Colonies on PDA reaching 25 mm diam after 3 weeks, at 25 °C, dark-brown to black, reverse dark-brown to black. Conidial dimensions and shapes are similar to those found on natural wood.

Material examined: Egypt, Sohag City, the River Nile, on submerged wood, 14 August 2012, F. A. Abdel-Aziz, SUMCC H-12001, **holotype**, ex-type living culture, SUMCC 12101.

GenBank numbers: MT522154 (SSU), MT522155 (LSU)

Notes: Combined phylogenetic analyses of SSU and LSU rDNA placed the three new species of *Dematipyriforma* with the type species *D. aquilaria* with high statistical support as distinct new taxa. The three new species differ from *D. aquilaria* in having black conidia *vs*. pale grey olivaceous to pale

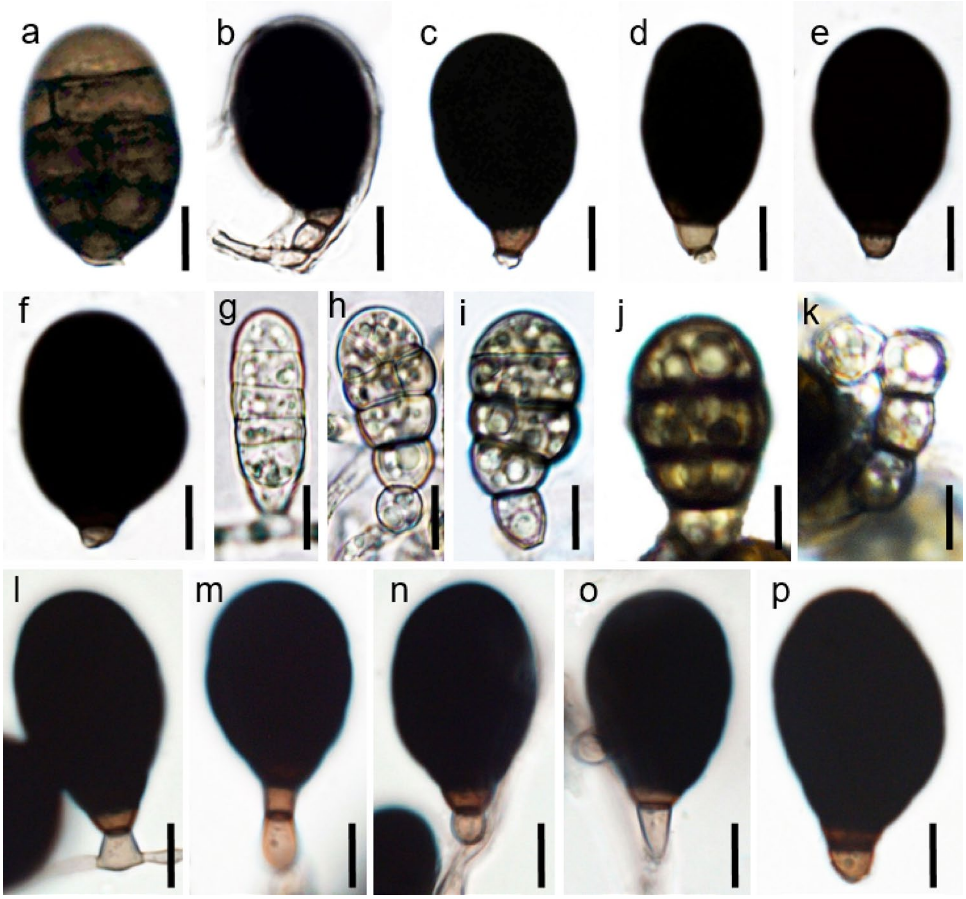


Fig. 106 ***Dematipyriforma aquatica*** (SUMCC H-12001, **holotype**).**a–j, l–p**Variously shaped conidia at different stages of maturity. **k** Chlamydospores in culture. **a–j** Conidia from natural wood. **g–j, l–p** Conidia from pure culture. Scale bars: **a–p** = 10 µm

brown in the latter species. *Dematipyriforma aquilaria* was isolated as an endophyte from a trunk of *Aquilaria crassna* in Laos (Sun et al. 2017), while the three new species are freshwater taxa. Conidia of *D. aquilaria* are evenly pigmented, while the three new species have black conidia with basal cells that are lighter. Chlamydospores of *D. aquilaria* have thick walls with axial perforative canals, these canals are absent in the three new species. A comparison of the 590 nucleotides of the D1/D2 region of the LSU rDNA of the three new species of *Dematipyriforma* with *D. aquilaria*s hows 14 base pair differences (2.37%) which justifies the erection of the three new species following the guidelines of Jeewon and Hyde (2016).

Dematipyriforma globispora Abdel-Aziz &Abdel-Wahab ***sp. nov.***

Index Fungorum number: IF900083; Facesoffungi number: FoF13865; Fig. 107

Etymology: Named after the shape of the globose shape of the conidia.

Holotype: SUMCC H-12002

Saprobic on submerged wood in the River Nile. **Sexual morph**: Not observed. **Asexual morph**: *Mycelium* immersed and superficial, sub-hyaline to brown, septate, branched, smooth, 2–4 µm wide. *Conidiophores* absent or present, when present micronematous, mononematous, sub-hyaline to brown, flexuous, smooth, unicellular, 6–12.5 µm long, 1.5–4.5 µm wide. *Conidiogenous cells* holoblastic, integrated, intercalary or terminal, sub-hyaline to brown, determinate, clavate, smooth, 4–6.5 µm long, 2.5–4.5 µm wide. *Conidial secession* rhexolytic. *Conidia* solitary or aggregated, effuse and heavily covered the surface of the wood, intercalary or terminal, smooth, globose or subglobose, rounded at the apex, black, with brown to dark-brown basal cell, muriform, with irregular transverse, longitudinal and oblique septa and form mass of cells, not constricted at the septa, sometimes surrounded by network of hyphae, 17–37 × 15–30 µm ($\bar{x}$ = 27.7 × 20.9 µm, n = 60), smaller buds are produced from conidia that are yellow–brown to brown in color, muriform, 11–19.2 × 7.1–14.5 µm. *Chlamydospores* intercalary or terminal, catenated, straight, or curved, brown to black, smooth, form large, black muriform masses similar to conidia but much larger in size 37–120 × 17–30 µm.

Culture characteristics: Colonies on PDA reaching 20 mm diam after 3 weeks, at 25 °C, dark-brown to black, reverse dark-brown to black. Conidial dimensions and shapes are similar to those found on natural wood.

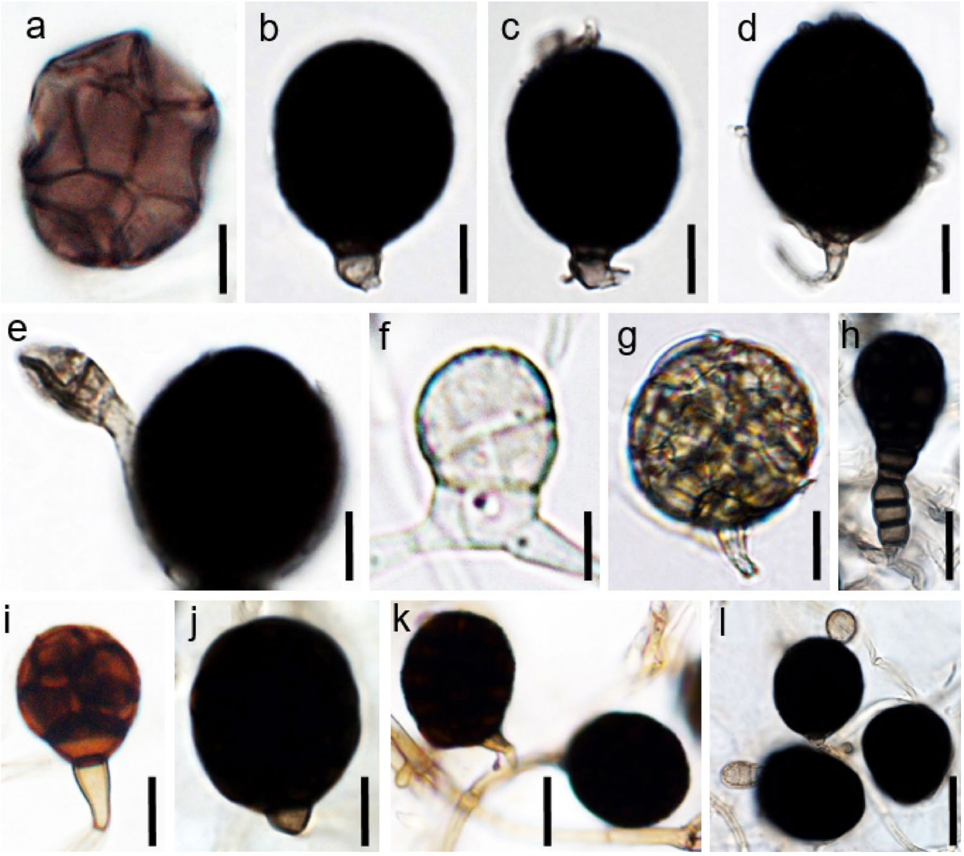


Fig. 107 ***Dematipyriforma globispora*** (SUMCC H-12002, **holotype**).**a–g, i–l**Variously shaped conidia at different stages of maturity. **h** Chlamydospores in culture. **a–e** Conidia from natural wood. **f–g, i–l** Conidia from pure culture. **c–d** Conidia are surrounded by network of hyphae. **e, l** Conidia with small buds. Scale bars: a–l = 10 µm

Material examined: Egypt, Sohag City, the River Nile, on submerged wood, 14 August 2012, F. A. Abdel-Aziz, SUMCC H-12002, **holotype**, ex-type living culture, SUMCC 12102.

GenBank numbers: MT522158 (SSU), MT522153 (LSU).

Notes: *Dematipyriforma globispora* differs from the other three species in having smaller conidia, that are mostly globose, sometimes surrounded by networks of hyphae and produce buds that are pale-brown to brown. *Dematipyriforma globispora* and *D. aquatica* are phylogenetically related, however, they differ in their morphology. Conidial cells in *D. globispora* are arranged irregularly and conidia are globose with small buds and surrounded by network of hyphae. Conidia in *D. aquatica* are pyriform or subglobose with 3 to 5 continuous transverse septa. *Rhexoacrodictys nigrospora* produce similar conidia with overlapping dimensions, however, conidia of *D. globispora* are surrounded by network of hyphae with brown buds. Mycelium in *R. nigrospora* are narrow (1–2 µm wide) with verruculose or finely echinulate-walled (Boonmee et al. 2021), while hyphae in *D. globispora* are 2–4 µm wide and smooth. A comparison of the 805 nucleotides of the LSU rDNA for *D. globispora* and *R. nigrospora*shows 11 base pair differences (1.36%) that confirm they are two different species.

Dematipyriforma nilotica Abdel-Aziz &Abdel-Wahab, ***sp. nov.***

Index Fungorum number: IF900084; Facesoffungi number: FoF13401; Fig. 108

Etymology: Named after the River Nile where the fungus was collected.

Holotype: SUMCC H-12003

Saprobic on submerged date palm rachis in the River Nile. **Sexual morph**: Not observed. **Asexual morph**: *Mycelium* immersed and superficial, sub-hyaline to brown, septate, branched, smooth, 1.5–3.5 µm wide. *Conidiophores* absent or present, when present micronematous, mononematous, sub-hyaline to reddish-brown, flexuous, smooth, unicellular, 7–13 µm long, 2.5–4.5 µm wide. *Conidiogenous cells* holoblastic, integrated, intercalary or terminal, sub-hyaline to brown, determinate, ampulliform, clavate, subglobose, cylindrical, smooth, 1.5–8.5 µm long, 4.5–6.5 µm wide. *Conidial secession* rhexolytic. *Conidia* solitary or aggregated, effuse and heavily covered the surface of the wood, intercalary or terminal, smooth, or surrounded by fine fibers, pyriform, globose or subglobose, rounded at the apex, conidial cells are filled gradually with black material, black when mature, with brown to dark-brown basal cell, muriform, 6–9 cells, 3–5 transverse septa and 0–2 longitudinal or oblique septa, not or slightly constricted at the septa, 31–45 × 21–37 µm

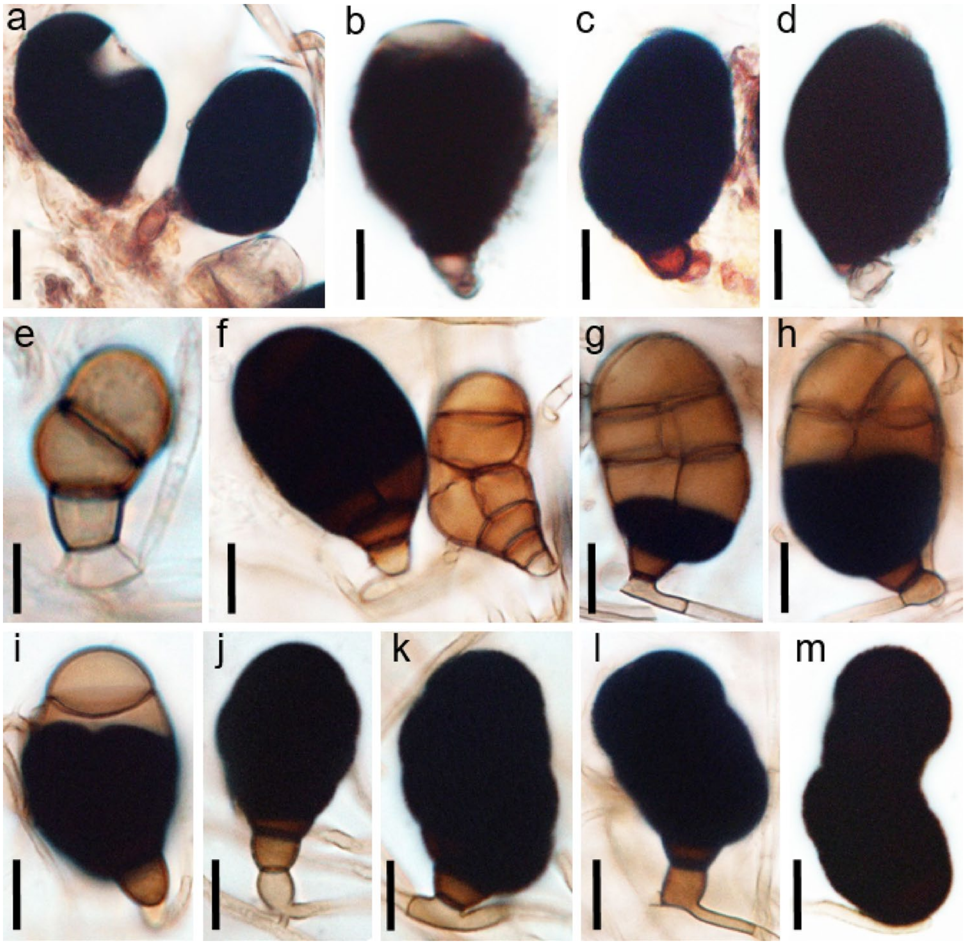


Fig. 108 ***Dematipyriforma nilotica*** (SUMCC H-12003, **holotype**). **a–l** Variously shaped conidia at different stages of maturity. **a–d** Conidia from natural date palm rachis. **e–l** Conidia from pure culture. **m** Chlamydospores in culture. **b,d** Conidia surrounded by fine fibers. **a–b, g–i** Gradual filling of the conidial rows by black material. Scale bars: a–m = 10 µm

($\bar{x} = 37 \times 26.3$ µm, $n = 50$), basal cells are singles. *Chlamydospores* intercalary or terminal, dark-brown to black, smooth, form large, black muriform masses with irregular shapes.

Culture characteristics: Colonies on PDA reaching 30 mm diam after 3 weeks, at 25 °C, brown to reddish dark-brown, reverse brown to dark-brown. Conidial dimensions and shapes are similar to those found on natural wood.

Material examined: Egypt, Sohag City, the River Nile, on submerged date palm rachis, 14 August 2012, F. A. Abdel-Aziz, SUMCC H-12003, **holotype**, ex-type living culture, SUMCC 12103.

GenBank numbers: MT522157 (SSU), MT522156 (LSU).

Notes: *Dematipyriforma nilotica* differs from the other three species in having larger conidial dimensions that sometimes surrounded by fine fibres. *Dematipyriforma nilotica* is phylogenetically related with *D. aquilaria*, however, the first species have black and larger conidia (31–45 × 21–37 µm *vs.* 25–37 × 15–22 µm in *D. nilotica* and *D. aquilaria* respectively) and grow on decaying date palm rachis in freshwater habitat, while the latter species produce brown conidia and live as an endophyte. Chlamdydospores in *D. aquilaria* have perforative canal that is absent in *D. nilotica*. Both *D. aquatica* and *D. nilotica* have 3–5 continuous transverse septa with 0–2 longitudinal septa, however, conidia in the latter species are surrounded by fine fibres and are larger in size (27–38 × 15–26 µm *vs.* 31–45 × 21–37 µm for *D. aquatica* and *D. nilotica* respectively). A comparison of the 800 nucleotides of the LSU rDNA for *D. aquatica* and *D. nilotica*shows 15 base pair differences (1.87%) that confirm they are two different species.

Key to *Dematipyriforma* species

1. Endophytic species, produce brown conidia……… ……………………………………………… *D. aquilaria*

1*.Saprobic species in freshwater habitat, produce black conidia………………………… ………………………2

2. Conidial cells arranged in rows with continuous transverse septa……………………………………………… 3

2*.Conidial cells arranged irregularly, globose conidia with small buds and surrounded by network of hyphae……………………………………*D. globispora.*

3. Conidial width less than 30 µm; smooth conidial wall…………………………………………*D. aquatica*

3*.Conidial width more than 30 µm; conidial wall with fine fibres ………………………………………*D. nilotica.*

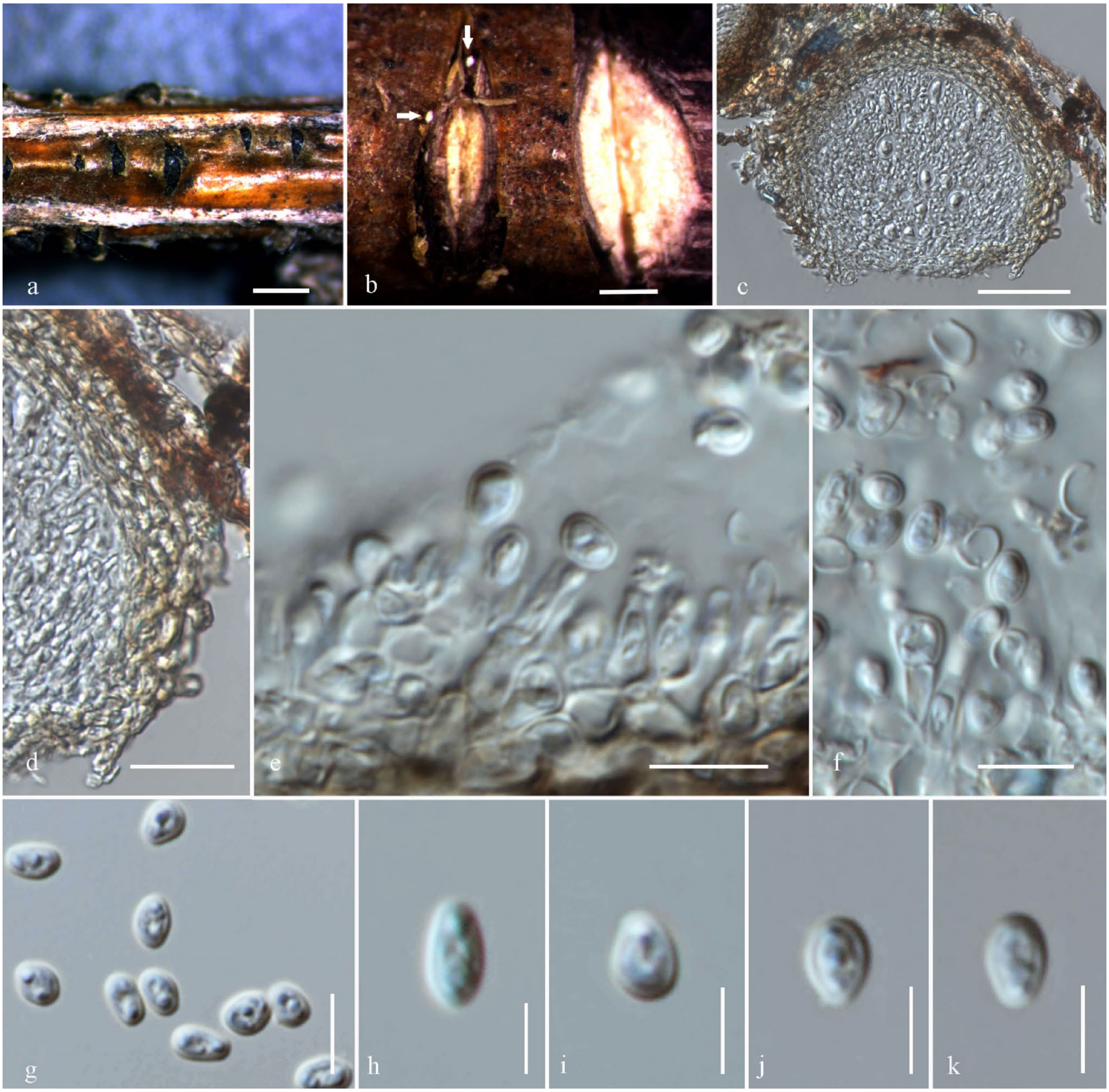


Fig. 109 ***Coniochaeta caraganae*** (MFLU 17–2500, **holotype**). **a, b**. Appearance of conidiomata on host surface. **c**. Vertical section through the conidioma. **d**. Peridium. **e, f**. Conidiogenesis**. g**–**k**. Conidia. Scale bars: a, b = 500 µm, c, d = 30 µm, e–k = 10 µm

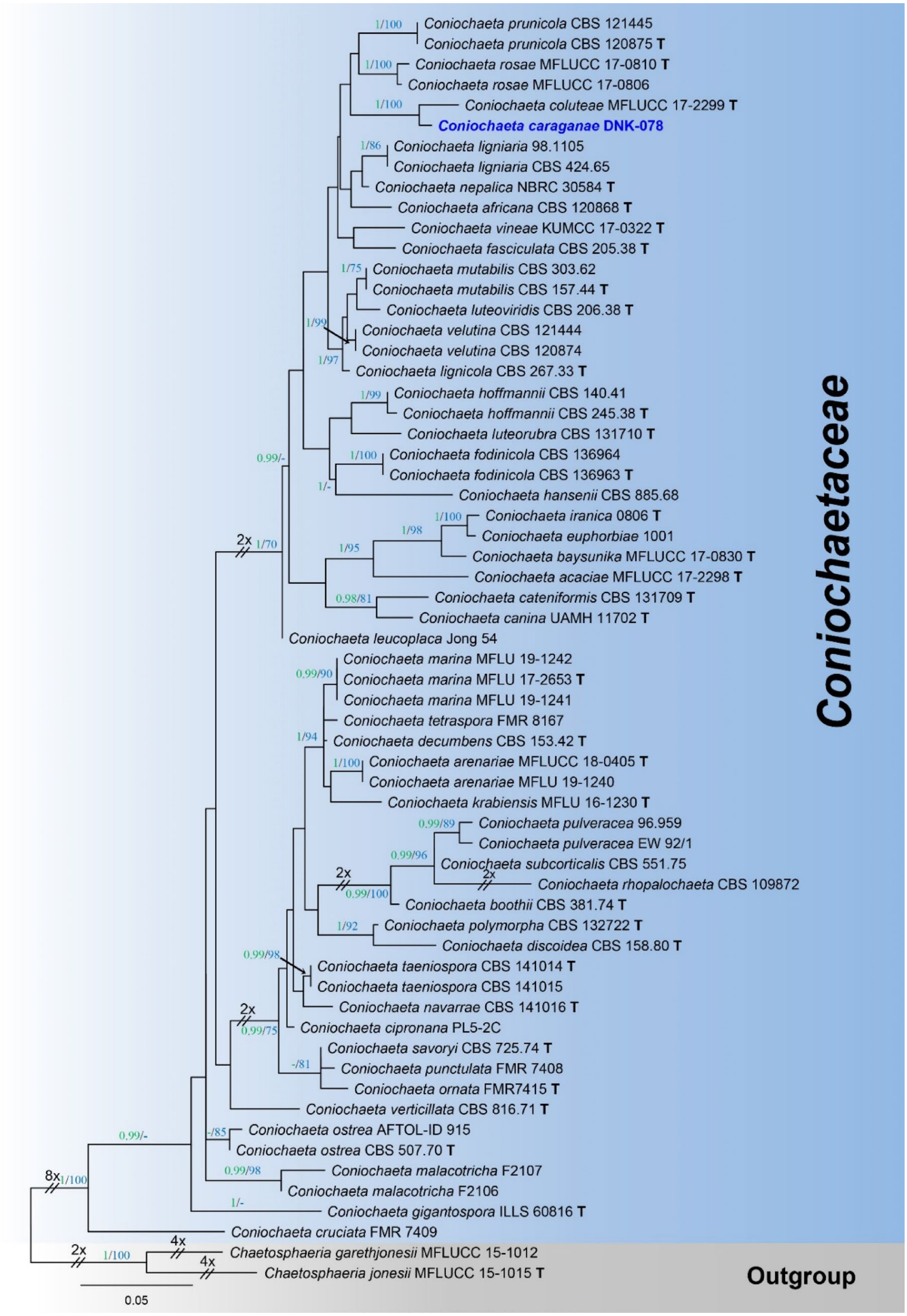
Subclass Savoryellomycetidae Hongsanan, K.D. Hyde & Maharachch.

Coniochaetales Huhndorf, A.N. Mill. & F.A. Fernández, Mycologia 96(2): 378 (2004).

Coniochaetales was introduced by Huhndorf et al. (2004) with Coniochaetaceae as the type family. Coniochaetales comprises two families namely Coniochaetaceae and Cordanaceae. Cordanaceae was previously accommodated in Cordanales. Hongsanan et al. (2017) treated Cordanales as a synonym of Coniochaetales based on molecular clock evidence. Hyde et al. (2020a, b, c) suggested the divergence time for Coniochaetales to be around 131 MYA. Coniochaetales comprises two families and five genera (Hyde et al. 2020a, b, c).

Coniochaetaceae Malloch and Cain (1971).

Coniochaetaceae was introduced by Malloch and Cain (1971) to accommodate two genera *Coniochaeta* and *Coniochaetidium* (Sacc.). Coniochaetaceae is typified by *Coniochaeta* and accommodates two genera *Barrina* A.W.


1/100
Coniochaeta prunicola CBS 121445
Coniochaeta prunicola CBS 120875 T
1/100
Coniochaeta rosae MFLUCC 17-0810 T
Coniochaeta rosae MFLUCC 17-0806
1/100
Coniochaeta coluteae MFLUCC 17-2299 T
Coniochaeta caraganae DNK-078
1/86
Coniochaeta ligniaria 98.1105
Coniochaeta ligniaria CBS 424.65
Coniochaeta nepalica NBRC 30584 T
Coniochaeta africana CBS 120868 T
Coniochaeta vineae KUMCC 17-0322 T
Coniochaeta fasciculata CBS 205.38 T
1/75
Coniochaeta mutabilis CBS 303.62
Coniochaeta mutabilis CBS 157.44 T
Coniochaeta luteoviridis CBS 206.38 T
1/99
Coniochaeta velutina CBS 121444
Coniochaeta velutina CBS 120874
1/97
Coniochaeta lignicola CBS 267.33 T
1/99
Coniochaeta hoffmannii CBS 140.41
Coniochaeta hoffmannii CBS 245.38 T
Coniochaeta luteorubra CBS 131710 T
0.99/-
1/100
Coniochaeta fodinicola CBS 136964
Coniochaeta fodinicola CBS 136963 T
1/-
Coniochaeta hansenii CBS 885.68
1/100
Coniochaeta iranica 0806 T
1/98
Coniochaeta euphorbiae 1001
2x 1/70
1/95
Coniochaeta baysunika MFLUCC 17-0830 T
Coniochaeta acaciae MFLUCC 17-2298 T
0.98/81
Coniochaeta cateniformis CBS 131709 T
Coniochaeta canina UAMH 11702 T
Coniochaeta leucoplaca Jong 54
Coniochaeta marina MFLU 19-1242
0.99/90
Coniochaeta marina MFLU 17-2653 T
Coniochaeta marina MFLU 19-1241
Coniochaeta tetraspora FMR 8167
1/94
Coniochaeta decumbens CBS 153.42 T
1/100
Coniochaeta arenariae MFLUCC 18-0405 T
Coniochaeta arenariae MFLU 19-1240
Coniochaeta krabiensis MFLU 16-1230 T
0.99/89
Coniochaeta pulveracea 96.959
Coniochaeta pulveracea EW 92/1
0.99/96
Coniochaeta subcorticalis CBS 551.75
2x
2x
Coniochaeta rhopalochaeta CBS 109872
0.99/100
Coniochaeta boothii CBS 381.74 T
1/92
Coniochaeta polymorpha CBS 132722 T
Coniochaeta discoidea CBS 158.80 T
0.99/98
Coniochaeta taeniospora CBS 141014 T
Coniochaeta taeniospora CBS 141015
Coniochaeta navarrae CBS 141016 T
2x
0.99/75
Coniochaeta cipronana PL5-2C
Coniochaeta savoryi CBS 725.74 T
-/81
Coniochaeta punctulata FMR 7408
Coniochaeta ornata FMR7415 T
Coniochaeta verticillata CBS 816.71 T
0.99/-
-/85
Coniochaeta ostrea AFTOL-ID 915
Coniochaeta ostrea CBS 507.70 T
0.99/98
Coniochaeta malacotricha F2107
Coniochaeta malacotricha F2106
8x 1/100
1/-
Coniochaeta gigantospora ILLS 60816 T
Coniochaeta cruciata FMR 7409
4x
2x 1/100
Chaetosphaeria garethjonesii MFLUCC 15-1012
4x
Chaetosphaeria jonesii MFLUCC 15-1015 T
0.05
Coniochaetaceae
Outgroup

◂ **Fig. 110** Phylogenetic tree generated from Maximum likelihood analysis (RAxML) based on combined ITS and LSU sequence data of *Coniochaetaceae* in the order Coniochaetales. Maximum likelihood bootstrap support values ≥ 70% (in blue) and Bayesian posterior probabilities ≥ 0.95 (in green) are indicated on the branches. The new isolate is in blue. The tree is rooted with *Chaetosphaeria jonesii* (MFLUCC 15–1015) and *Chaetosphaeria garethjonesii* (MFLUCC 15–1012)

Ramaley and *Coniochaeta* (Sacc.) Cooke (Wijayawardene et al. 2020) based on multi gene phylogeny (Maharachchikumbura et al. 2015a, b; Samarakoon et al. 2018). Species belonging to this family are saprobes and pathogenic on various decaying wood and plants or animals, respectively (Khan et al. 2013; Maharachchikumbura et al. 2015a, b, 2016; Wijayawardene et al. 2017a, b; Samarakoon et al. 2018).

Coniochaeta (Sacc.) Cooke, Grevillea 16(no. 77): 16 (1887)

Coniochaeta was introduced by (Sacc.) Cooke (1887a, b) and is typified by *Coniochaeta ligniaria* (Grev.) Cooke. *Coniochaeta* is characterized by solitary or aggregated, typically setose, dark brown to black, pyriform to globose ascomata, membranaceous to pseudoparenchymatous or coriaceous peridium, paraphysate hamathecium, unitunicate and thin-walled asci with a small non-amyloid apical ring and one-celled, usually dark brown and often laterally compressed with a germ slit ascospores (Greville 1823–1824, Cooke 1887a, b). The hyphomycetous asexual morph is characterized by phialidic conidiogenous cells, previously described in *Lecythophora* (Weber 2002; Khan et al. 2013). In this study, we introduce a new species *C. caraganae* collected on dead twigs of *Caragana frutex* in Russia based on morphology and phylogenetic evidence.

Coniochaeta caraganae D. Pem, Bulgakov & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF559528, Facesoffungi number: FoF08686; Fig. 109

Etymology: "*caraganae*" refers to the host plant from which the fungus was isolated.

Holotype: MFLU 17-2500

Saprobic on dead branch of *Caragana frutex*. **Sexual morph**: Not observed. **Asexual morph**: *Coelomycetous*. *Conidiomata* 106–114 µm diam., 4–7 µm high ($\bar{x} = 110.7 \times 6.2$ µm, $n = 20$), small, pycnidial, solitary, scattered, immersed, uniloculate, globose to subglobose, thin-walled. *Peridium* 26–32 µm composed of two layers. Inner layer consisting cells of *textura prismatica*, hyaline to subhyaline, strongly compressed. Outer layer consisting of densely packed, moderately thick-walled, brown cells of *textura angularis*, tending to be darker and more isodiametric towards the outside. *Conidiophores* 7–10 × 2–3 µm ($\bar{x} = 6.5 \times 2.3$ µm, $n = 20$), hyaline, straight or irregularly bent, reduced to conidiogenous cells. *Conidiogenous cells* 2–3 × 4–6 µm ($\bar{x} = 3.1 \times 5.1$ µm, $n = 20$), holoblastic, annellidic, simple, determinate, hyaline, doliiform to cylindrical, smooth-walled. *Conidia* 3–4 × 5–6 µm ($\bar{x} = 4.1 \times 5.8$ µm, $n = 20$) oblong to ovoid, straight, rounded at both ends, sometimes truncate at base, cylindrical, aseptate, smooth and thick-walled, eguttulate.

Culture characteristics: colonies on MEA, reaching 25–35 mm diam. after 4 weeks at 25 °C, grey whitish, dense, effuse, with white hyphal stands towards the edge, rough surface towards centre, diffuse margin; reverse dark grey with whitish edges, grayish orange at the center, radiating, effuse and zonate.

Material examined: Russia, Donetsk People's Republic, Shakhtersk district, regional landscape park «Donetsk ridge» (Rus. «Donetsky kryazh»), steppe near Leontievsky forest, on dead twigs of *Caragana frutex* (L.) K. Koch (Fabaceae), 19 May 2017, Timur S. Bulgakov (MFLU 17-2500, **holotype**); ex-type living culture MFLUCC 18-0780.

GenBank numbers: MT573224 (ITS), MT573223 (LSU).

Notes: Based on phylogenetic analyses, the new asexual species *Coniochaeta caraganae* is closely related with *C. coluteae* (Samarakoon et al. 2018; Fig. 110). The asexual morph of *C. coluteae* is hyphomycetous and has been obtained from culture. It is characterized by hyaline vegetative hyphae, hyphoide conidiophores, phialidic conidiogenous cells and one celled hyaline conidia. Our new species *C. caraganae* has been obtained from dead branch of *Caragana frutex* and is characterized by pycnidial conidiomata, hyaline conidiophores and oblong to ovoid conidia. In a comparison of the 565 ITS (+ 5.8S) nucleotides of these two strains *C. coluteae* MFLUCC 17-2299 to that of *C. caraganae* reveals 11 (1.9%) nucleotide differences which justifies these two isolates as two distinct taxa (Jeewon and Hyde 2016). Therefore, *C. caraganae* is introduced herein as a new species.

Pleurotheciales Réblová & Seifert

Notes: Pleurotheciales was introduced by Réblová et al. (2016) with Pleurotheciaceae as the type family. Wijayawardene et al. (2020, 2022) listed Pleurotheciales as a monotypic order and new taxa have been included in it (Boonmee et al. 2021; Crous et al. 2021; Dong et al. 2021).

Pleurotheciaceae Réblová & Seifert, in Réblová, Seifert, Fournier & Štěpánek, Persoonia 37: 63 (2015) [2016]

Notes: Wijayawardene et al. (2022) listed 14 genera in Pleurotheciaceae. Recently, *Saprodesmium* was introduced in this family for a saprobic fungus found on decaying wood submerged in freshwater in China (Dong et al. 2021). Pleurotheciaceae was introduced by Réblová et al. (2016) with *Pleurothecium recurvatum* as the type species. Fourteen genera *viz*. *Adelosphaeria*, *Anapleurothecium*,

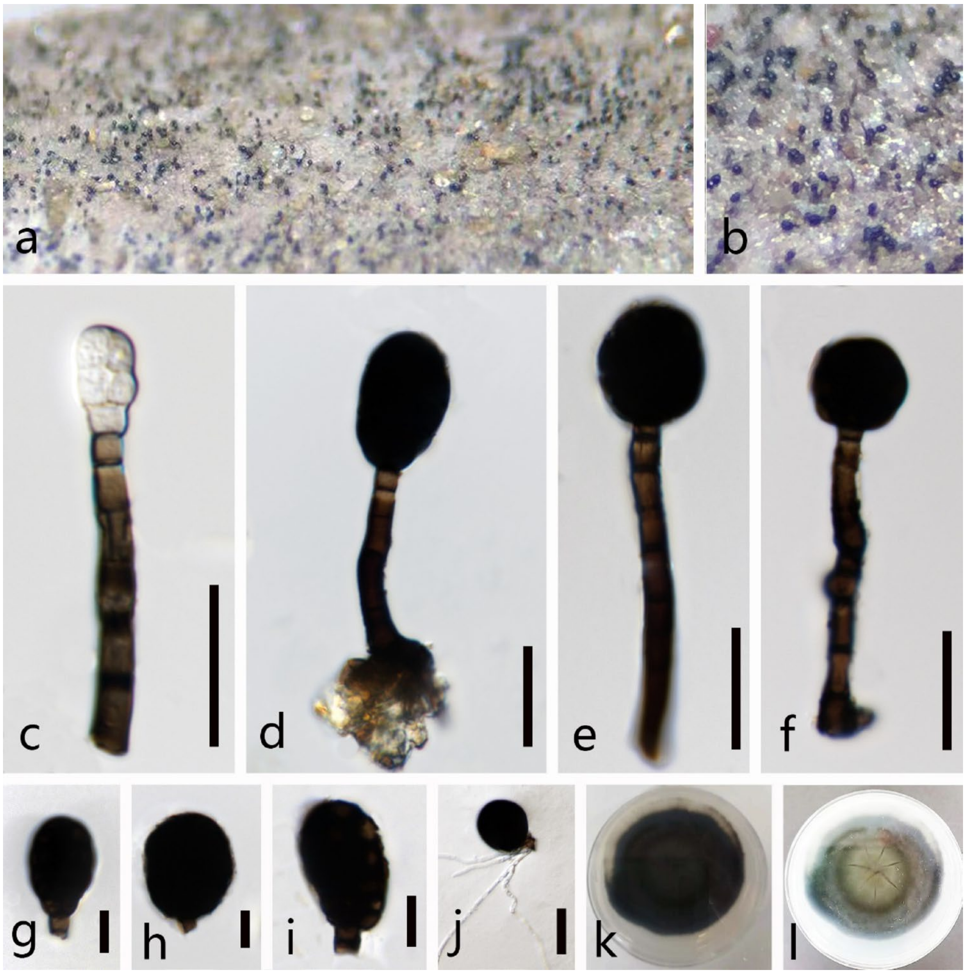


Fig. 111 ***Rhexoacrodictys erecta*** (MFLU 21–0277, **new record**). **a, b** Colonies on wood. **c–f** Conidiophore with conidia. **g–i** Conidia. **j** Germinating conidia. **k, l** Culture on PDA from surface and reverse. Scale bars: c–f, j = 20 µm, g–i = 10 µm

Coleodictyospora, *Dematipyriforma*, *Helicoascotaiwania*, *Melanotrigonum*, *Monotosporella*, *Neomonodictys*, *Phaeoisaria*, *Phragmocephala*, *Pleurotheciella*, *Pleurothecium*, *Saprodesmium*, and *Sterigmatobotrys* are accepted in the family (Hyde et al. 2020a, b, c; Boonmee et al. 2021; Dong et al. 2021; Bao et al. 2022). Species in Pleurotheciaceae are cosmopolitan with a wide range of hosts and substrates from terrestrial and freshwater habitats (Hyde et al. 2020a, b, c; Dong et al. 2021; Boonmee et al. 2021; Bao et al. 2022).

The sexual morphs of Pleurotheciaceae share perithecial, immersed to superficial, papillate ascomata, leathery to fragile, carbonaceous peridial walls, unitunicate, cylindrical, 8-spored, asci with a distinct non-amyloid apical annulus, abundant paraphyses and ellipsoidal to fusiform, septate, hyaline or versicolorous ascospores (Réblová et al. 2016; Luo et al. 2018a, b; Hyde et al. 2020a, b, c). The asexual morphs of Pleurotheciaceae have been reported as hyphomycetes forming indeterminate synnemata or loose fascicles. Conidiophores are macronematous or semi-macronematous. Conidiogenous cells produce holoblastic conidia, with rhexolytic conidial secession on short denticles or extending polyblastically on a sympodial rachis. Conidia are hyaline to brown, varied in shape, septate or aseptate (Hyde et al. 2020a, b, c, Dong et al. 2021, Boonmee et al. 2021, Bao et al. 2022).

Rhexoacrodictys W.A. Baker & Morgan-Jones, Mycotaxon 82: 98 (2002)

Rhexoacrodictys was introduced by Baker et al. (2002) to accommodate species previously identified as *Acorcdictys* (i.e., *A. erecta*, *A. fimicola*, *A. fuliginosa* and *A. queenslandica*) and wherein *Rhexoacrodictys erecta* was designated as the type. Two additional species *R. martini* and *R. broussonetiae* were subsequently added to the genus based on morphological characteristics (Delgado 2009; Xiao et al. 2018). While R. *martini* and R. *queenslandica* were transferred to *Distoseptispora* and *Junewangia* based on phylogenetic analysis (Xia et al. 2017). Currently, four species are accepted in *Rhexoacrodictys* (*R. broussonetiae*, *R. erecta*, *R. fimicola*, and *R. fuliginosa*).

Rhexoacrodictys erecta (Ellis & Everh.) W.A. Baker & Morgan-Jones, in Baker, Partridge & Morgan-Jones, Mycotaxon 82: 99 (2002)

Refer to Species Fungorum (2022a, b) for synonyms.

Index Fungorum number: IF381123; Facesoffungi number: FoF13392; Fig. 111

Saprobic on dead culms of bamboo. **Sexual morph:** Not observed. **Asexual morph:** *Colonies* on the substratum superficial, hairy, effuse, blackish, shining. *Mycelium* mostly immersed, cylindrical, brown to dark brown hyphae. *Conidiophores* 28–57 × 4–5 µm ($\bar{x}$ = 42.5 × 4.5 µm, *n* = 15), macronematous, mononematous, erect, single, straight or somewhat flexuous, cylindrical, smooth-walled, brown to dark brown, septate. *Conidiogenous cells* monoblastic, pale brown to brown, integrated, terminal. *Conidia* 19–27.5 × 15–19 µm ($\bar{x}$ = 23.5 × 17 µm, *n* = 30), holoblastic, solitary, dry, broad oval to subglobose, muriform, acrogenous, transversely and longitudinally septate, dark brown to black, smooth-walled, narrowly truncate at the base.

Culture characteristics: Colonies on PDA, 30 mm diam after two weeks at 28 °C, brown to blackish at the front and reverse sides, mycelium sparse; reverse blackish.

Material examined: Thailand, Chiang Rai Province, Muang District, on dead culms of *Bambusa* sp. (Poaceae), 11 November 2020, X. G. Tian U–2–3 (MFLU 21–0277), living culture, MFLUCC 21–0157.

Habitat: on submerged wood, *Arundo donax*, *Bambusa multiplex*, *Bambusa* sp., *Fagus crenata*, palm tree, *Saccharum officinarum*, *Sorghum bicolor*, *Sporoschisma saccardoi* and *Zea mays* (Ellis 1961; Baker et al. 2002; Zhao et al. 2011; Xia et al. 2017; Shi et al. 2021).

Distribution: Known from China, India, Japan, Sierra Leone, South Africa, Thailand, USA and Venezuela (Ellis 1961; Baker et al. 2002; Zhao et al. 2011; Xia et al. 2017; Shi et al. 2021; This study).

GenBank numbers: OL606411 (ITS), OL606151 (LSU), OL606015 (SSU).

Notes: This species was reported as *Acrodictys erecta* on *Arundo donax* in Venezuela and on *Zea mays* in USA by Ellis (1961). Baker et al. (2002) examined several type specimens of synonyms of this species and erected *Rhexoacrodictys* based on morphological analysis. Our new isolate (MFLUCC 21-0157) clustered with the strains of *Rhexoacrodictys erecta* (HMAS 245615, IFRD500–016 and HMAS 245616; Fig. 112). Morphologically, our new collection is similar to those of *Rhexoacrodictys erecta* (Ellis 1961; Baker et al. 2002).

Based on nucleotide comparisons of ITS, LSU and SSU, our new strain (MFLUCC 21–0157) and three of *Rhexoacrodictys erecta* (HMAS 245615, IFRD500–016 and HMAS 245616) show no differences; however, the new strain (MFLUCC 21–0157) is different from *Monotosporella setosa* (HKUCC 3712) in 14/516 bp (2.71%) of the LSU (data contains 6 gaps). Based on both phylogeny and morphology showed that our strain (MFLUCC 21-0157) is identical to *Rhexoacrodictys erecta*.

Phaeoisaria Höhn., Sber. Akad. Wiss. Wien, Math.-naturw. Kl., Abt. 1 118: 330 (1909).

Notes: Phaeoisaria is a genus of hyphomycetes (von Höhnel 1909) having morphological features mainly characterized by 'indeterminate synnemata with aseptate or septate ellipsoidal, obovoidal, fusiform-cylindrical to falcate, hyaline conidia' (Boonmee et al. 2021). We follow Crous et al. (2021), Boonmee et al. (2021) and Wijayawardene et al. (2022) for the classification and updated account of *Phaeoisaria* species.

Phaeoisaria goiasensis H.M. Silva, A.D. Cavalcanti & J.D.P. Bezerra, ***sp. nov.***

MycoBank number: MB840294, Facesoffungi number: FoF09975, Fig. 113

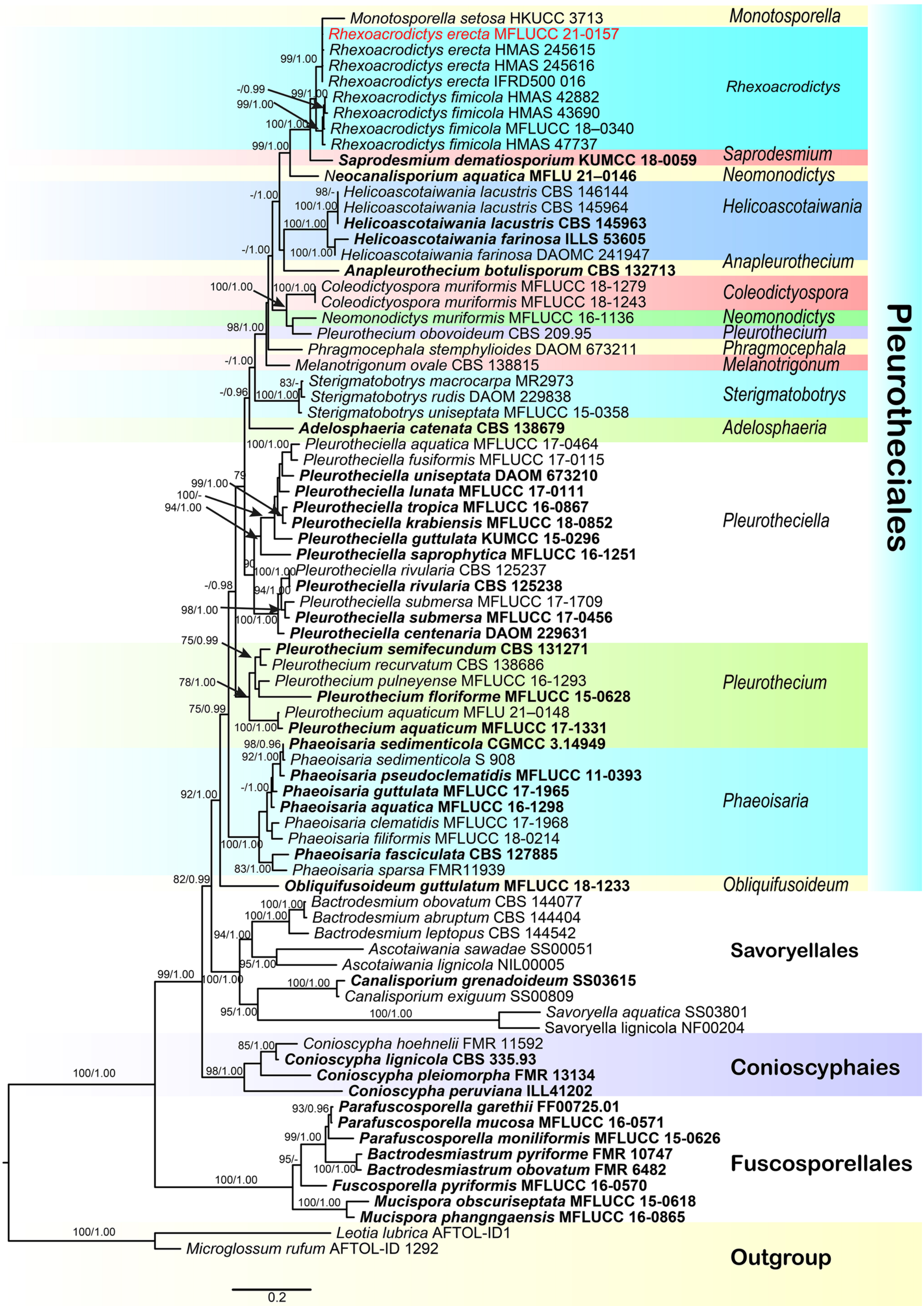
Etymology: The name refers to the Brazilian state, Goiás, where the fungus was isolated.

Holotypus: UFG 71083.

Isolated from a Petri-dish with culture medium storage in a fridge. **Asexual morph:** *Hyphae* hyaline to pale brown with age, smooth wall, septate, 1.5–2.5(–3) µm wide. *Synnemata* erect, brown, smooth, indeterminate, composed of compactly and parallels conidiophores and commonly with conidiogenous cells in the above half, 93–147 × 3.5–4.5 µm. *Conidiophores* straight or slightly curved, septate, reduced to conidiogenous cell, cylindrical, hyaline to pale brown, smooth wall, (10–)15–49(–72) × (1.5–)2–2.5(–3.5) µm. *Conidiogenous cells* polyblastic, integrated, terminal or intercalary, cylindrical, hyaline, smooth wall, (3–)3.5–9.5(–15.5) × (1.5–)2–3(–3.5) µm, forming conidia on denticles, 1–2 µm long, 0.5–1 µm wide, scattered or clustered in the apical region. *Conidia* ellipsoidal to obovoid, straight or slightly curved, rounded at the ends or occasionally tapering toward the base, hyaline, aseptate, guttulate, smooth wall, (4.5–)7.5–9(–10.5) × (2–)2.5–3(–4) µm. *Chlamydospores* terminal, globose, pyriform, first hyaline and becoming brown to dark brown with age, (8–)8.5–10.5(–17) × (2–)7–8(–8.5) µm. **Sexual morph:** Not observed.

Culture Charactersistics: Colonies grew in the dark for 7 days at 25 °C. On PDA, colonies elevated, aerial mycelium absent, irregular, greyish to dark grey with edge whitish, up to 15 mm. On MEA, colonies plane, aerial mycelium absent, greyish to dark grey with edge brown to dark brown, up to 10 mm. On oatmeal agar (OA), colonies growing up to 18 mm. At 36 °C, colonies are similar to at 25 °C, growing up to 8 mm on PDA, 9 mm on MEA, and 6 mm on AO. No growth at 10 °C.

Material examined: Brazil, Goiás state, Goiânia City, Universidade Federal de Goiás (UFG), Instituto de Patologia Tropical e Saúde Pública (IPTSP), Laboratório de Micologia


Monotosporella setosa HKUCC 3713
Rhexoacrodictys erecta MFLUCC 21-0157
99/1.00
Rhexoacrodictys erecta HMAS 245615
Rhexoacrodictys erecta HMAS 245616
Rhexoacrodictys erecta IFRD500 016
-/0.99
99/1.00
Rhexoacrodictys fimicola HMAS 42882
99/1.00
Rhexoacrodictys fimicola HMAS 43690
100/1.00
Rhexoacrodictys fimicola MFLUCC 18–0340
99/1.00
Rhexoacrodictys fimicola HMAS 47737
Saprodesmium dematiosporium KUMCC 18-0059
Neocanalisporium aquatica MFLU 21–0146
-/1.00
98/-
Helicoascotaiwania lacustris CBS 146144
100/1.00
Helicoascotaiwania lacustris CBS 145964
100/1.00
Helicoascotaiwania lacustris CBS 145963
Helicoascotaiwania farinosa ILLS 53605
-/1.00
100/1.00
Helicoascotaiwania farinosa DAOMC 241947
Anapleurothecium botulisporum CBS 132713
100/1.00
100/1.00
Coleodictyospora muriformis MFLUCC 18-1279
Coleodictyospora muriformis MFLUCC 18-1243
Neomonodictys muriformis MFLUCC 16-1136
98/1.00
Pleurothecium obovoideum CBS 209.95
Phragmocephala stemphylioides DAOM 673211
-/1.00
Melanotrigonum ovale CBS 138815
83/-
Sterigmatobotrys macrocarpa MR2973
-/0.96
100/1.00
Sterigmatobotrys rudis DAOM 229838
Sterigmatobotrys uniseptata MFLUCC 15-0358
Adelosphaeria catenata CBS 138679
100/1.00
Pleurotheciella aquatica MFLUCC 17-0464
Pleurotheciella fusiformis MFLUCC 17-0115
79
Pleurotheciella uniseptata DAOM 673210
99/1.00
Pleurotheciella lunata MFLUCC 17-0111
100/-
Pleurotheciella tropica MFLUCC 16-0867
94/1.00
Pleurotheciella krabiensis MFLUCC 18-0852
Pleurotheciella guttulata KUMCC 15-0296
Pleurotheciella saprophytica MFLUCC 16-1251
90
100/1.00
Pleurotheciella rivularia CBS 125237
-/0.98
Pleurotheciella rivularia CBS 125238
94/1.00
Pleurotheciella submersa MFLUCC 17-1709
98/1.00
100/1.00
Pleurotheciella submersa MFLUCC 17-0456
Pleurotheciella centenaria DAOM 229631
75/0.99
Pleurothecium semifecundum CBS 131271
Pleurothecium recurvatum CBS 138686
Pleurothecium pulneyense MFLUCC 16-1293
78/1.00
Pleurothecium floriforme MFLUCC 15-0628
75/0.99
Pleurothecium aquaticum MFLU 21–0148
100/1.00
Pleurothecium aquaticum MFLUCC 17-1331
98/0.96
Phaeoisaria sedimenticola CGMCC 3.14949
92/1.00
Phaeoisaria sedimenticola S 908
Phaeoisaria pseudoclematidis MFLUCC 11-0393
-/1.00
Phaeoisaria guttulata MFLUCC 17-1965
92/1.00
Phaeoisaria aquatica MFLUCC 16-1298
Phaeoisaria clematidis MFLUCC 17-1968
Phaeoisaria filiformis MFLUCC 18-0214
100/1.00
Phaeoisaria fasciculata CBS 127885
83/1.00
Phaeoisaria sparsa FMR11939
82/0.99
Obliquifusoideum guttulatum MFLUCC 18-1233
100/1.00
Bactrodesmium obovatum CBS 144077
100/1.00
Bactrodesmium abruptum CBS 144404
Bactrodesmium leptopus CBS 144542
94/1.00
Ascotaiwania sawadae SS00051
95/1.00
Ascotaiwania lignicola NIL00005
99/1.00
100/1.00
100/1.00
Canalisporium grenadoideum SS03615
Canalisporium exiguum SS00809
95/1.00
100/1.00
Savoryella aquatica SS03801
Savoryella lignicola NF00204
85/1.00
Conioscypha hoehnelii FMR 11592
Conioscypha lignicola CBS 335.93
98/1.00
Conioscypha pleiomorpha FMR 13134
100/1.00
Conioscypha peruviana ILL41202
93/0.96
Parafuscosporella garethii FF00725.01
Parafuscosporella mucosa MFLUCC 16-0571
99/1.00
Parafuscosporella moniliformis MFLUCC 15-0626
95/-
Bactrodesmiastrum pyriforme FMR 10747
100/1.00
Bactrodesmiastrum obovatum FMR 6482
100/1.00
Fuscosporella pyriformis MFLUCC 16-0570
100/1.00
Mucispora obscuriseptata MFLUCC 15-0618
Mucispora phangngaensis MFLUCC 16-0865
100/1.00
Leotia lubrica AFTOL-ID1
Microglossum rufum AFTOL-ID 1292
0.2
Monotosporella
Rhexoacrodictys
Saprodesmium
Neomonodictys
Helicoascotaiwania
Anapleurothecium
Coleodictyospora
Neomonodictys
Pleurothecium
Phragmocephala
Melanotrigonum
Sterigmatobotrys
Adelosphaeria
Pleurotheciella
Pleurothecium
Phaeoisaria
Obliquifusoideum
Pleurotheciales
Savoryellales
Conioscyphaies
Fuscosporellales
Outgroup

◂ **Fig. 112** Combined phylogeny using ITS, LSU SSU, *rpb2* and *tef1* of selected members of four orders of the Hypocreomycetidae. The dataset of combined ITS, LSU, SSU, *rpb2* and *tef1* sequence data comprise 79 strains with 4413 characters including gaps (*rpb2*: 1–1051 bp, *tef1*: 1052–2046 bp, ITS: 2047–2623 bp, LSU: 2624–3413 bp, SSU: 3414–4413 bp). *Leotia lubrica* (AFTOL-ID1) and *Microglossum rufum* (AFTOL-ID 1292) were used as outgroup taxa. RAxML and Bayesian analyses were conducted and resulted in generally congruent topologies. Bootstrap support values for ML ≥75% and BYPP ≥0.95 are given as ML/BYPPP above the nodes. Newly obtained sequences are indicated in red and ex-type strains are in **bold**

(LabMicol), isolated from a Petri dish with culture medium storage in a fridge, 19 November 2019, J.D.P. Bezerra & H.M. Silva (UFG 71083, **holotype**); ex-type living culture URM 8387 = FCCUFG 02; *ibid.* living culture FCCUFG 03.

GenBank numbers: URM 8387 = FCCUFG 02 –MT210320 (ITS), MT375865 (LSU), MT384422 (*tub2*), MT384424 (*tef1*)

FCCUFG 03 – MT210321 (ITS), MT375866 (LSU), MT384423 (*tub2*), MT384425 (*tef1*)

Notes: *Phaeoisaria* was described by von Höhnel (1909) and has 32 records in the Index Fungorum and MycoBank databases (8 June 2022). Based on our phylogenetic analysis (Fig. 114), our isolates here are proposed for the new species *P. goiasensis*. *Phaeoisaria goiasensis* differs from *P. annesophieae*, which was isolated from soil in The Netherlands, by the presence of synnemata in old cultures (after 30 days) and defined conidiophores in *P. goiasensis*, and by the size of conidiogenous cells (12–39 × 1–3.5 µm), conidia (4.5–9 × 2–3.5 µm), and chlamydospores (9–18 × 7–9.5 µm) of *P. annesophieae* (Crous et al. 2017). The BLASTn searches (8 June 2022) using ITS sequences of *P. goiasensis* demonstrated that they are identical to sequences deposited as *Phaeoisaria* sp. INBio 4514E, which was isolated from substrate related to *Passalidae galleries* in decayed trunks (Vargas-Asensio et al. 2014), and to sequences obtained from submerged wood and deposited as Ascomycota (Brown et al. 2016). The ITS sequences from *P. goiasensis* also had highest similarity to *P. annesophieae* (strain CBS 143235, GenBank MG022180.1; Identities = 500/511 (98%), 0 gap (0%)). The LSU sequences had high identity to *Phaeoisaria* sp. INBio 4514E and *P. annesophieae* MFLU 19–0531, amongst other sequences deposited as *Phaeoisaria* species/isolates. The *tef1* sequences had high similarity to *P. filiformis* MFLU 18-1462 and it was also 96.59% identical to *P. sedimenticola* S-908. The *tub2* sequences had low identity to Sordariomycetes species.

Pleurothecium Höhn., Ber. dt. bot. Ges. 37: 154 (1919).

Notes: *Pleurothecium* was introduced by Höhnel (1919) with *Pleurothecium recurvatum* (Morgan) Höhn as the type species. There are 11 species listed in Index Fungorum (June, 2022), and a new species, *P. aquisubtropicum*, is described and illustrated here (Fig. 5).

Pleurothecium aquisubtropicum J. Ma, Y.Z. Lu & K.D. Hyde, ***sp. nov***.

Index Fungorum number: *IF559508*, *Facesoffungi number*: *FoF08709; Fig. 115*

Etymology: Referring to the aquatic habitat and collecting site in subtropical country, China.

Holotype: GZAAS 21–0384

Saprobic on decaying wood in a freshwater stream. **Asexual morph:** Colonies on natural substrate superficial, effuse, brown or dark brown, smooth. *Mycelium* immersed or superficial, smooth. *Conidiophores* 82–177 × 3.5–5.5 µm ($\bar{x}$ = 121.3 × 4.3 µm, *n* = 20), macronematous, mononematous, sucylindrical, straight, unbranched, smooth, septate, brown, paler towards the apex. Conidiogenous cells 25–38 × 2.7–3.8 µm ($\bar{x}$ = 29.6 × 3.2 µm, *n* = 15), holoblastic, polyblastic, integrated, terminal, subhyaline to pale brown, subcylindrical. *Conidia* 13.4–15.5 × 3.4–5.5 µm ($\bar{x}$ = 14.4 × 4.4 µm, *n* = 21), acrogenous, solitary, aseptate, pale brown, straight, guttulate, hyaline or pale green, smooth. **Sexual morph:** Not observed.

Culture Characters: Colonies growing slowly on PDA, reaching 37 mm in 35 days at 25 °C, flat, filiform, round, gray or white, smooth; In reverse, milky at the center, brown or dark brown at the margin.

Material examined: China, Guizhou Province, Xishui County, on decaying wood submerged in a freshwater stream, 13 February 2021, Jian Ma, TL2(GZAAS 21–0384, **holotype**); ex–type living culture, GZCC 21–0670.

GenBank numbers: OM339436 (ITS), OM339433 (LSU)

Notes: Our new collection fits well with the generic concept of *Pleurothecium* in having macronematous, mononematous, brown conidiophores, polyblastic, integrated conidiogenous cells and septate, smooth allantoid or fusiformis conidia. In our phylogenetic analyses, our new collection of *Pleurothecium aquisubtropicum* was placed within *Pleurothecium* and is basal to other *Pleurothecium* species (Fig. 116). *Pleurothecium aquisubtropicum* resembles ***P.*** *aquaticum* in the shape of the conidiophores, and conidia (Luo et al. 2018a, b). However, *Pleurothecium aquisubtropicum* differs from *P. aquaticum* by its darker and longer conidiophores (82–177 µm *vs* 53–65 µm) and smaller conidia (13.5–15.5 × 3–5.5 µm *vs* 19–21 × 4.5–5.5 µm). Hence, based on both morphology and phylogeny, we introduce our collection as a new species of *Pleurothecium aquisubtropicum*.

Subclass Xylariomycetidae O.E. Erikss & Winka.

Amphisphaeriales D Hawksw & OE Erikss.

Amphisphaeriales was introduced by Eriksson and Hawksworth (1986). However, Amphisphaeriales was synonymized with Xylariales by Eriksson and Hawksworth (1987). Based on morphological and molecular data, these two orders were separated and Amphisphaeriales

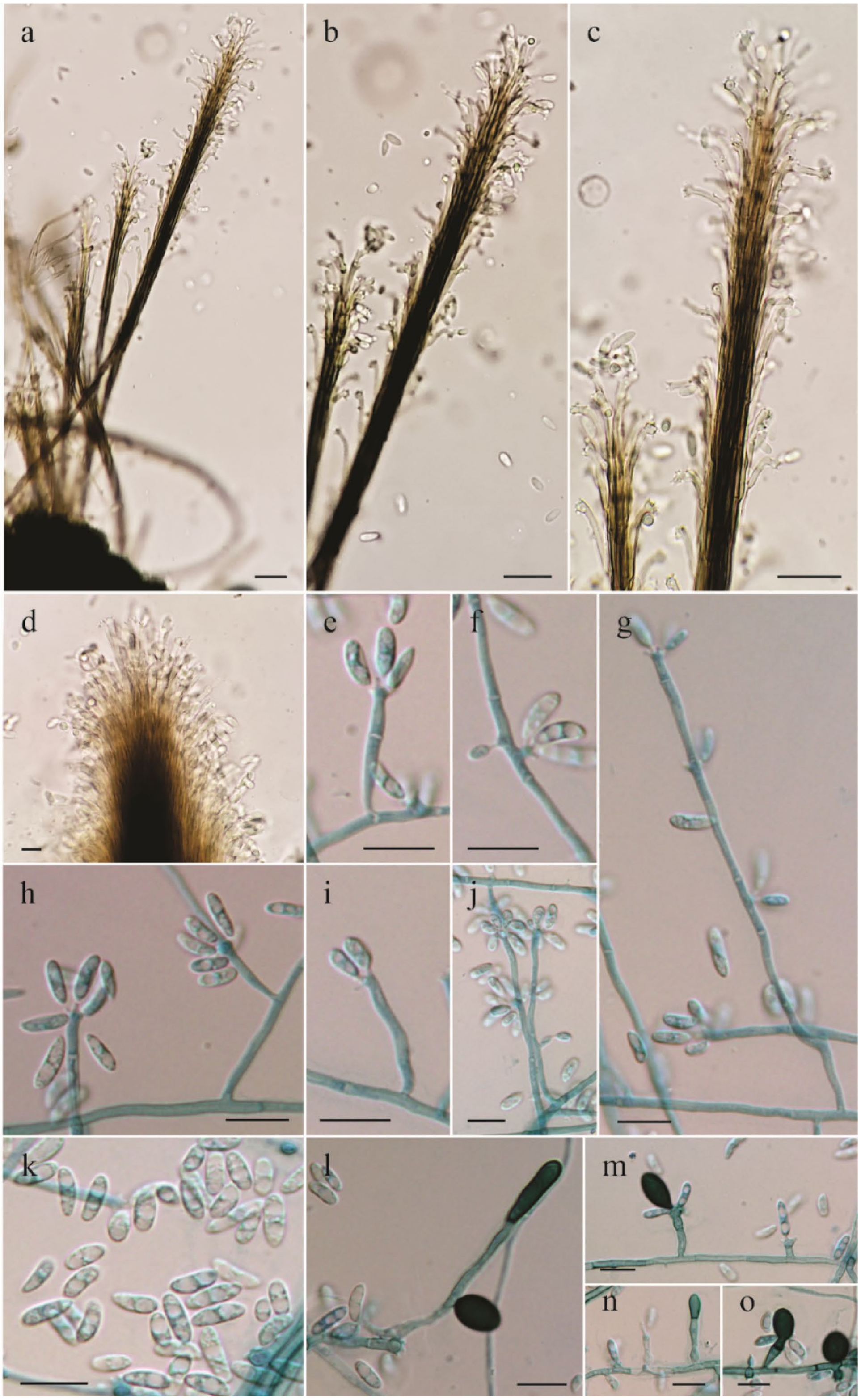


Fig. 113 ***Phaeoisaria goiasensis*** **(UFG 71083, holotype)** **a–c** Synnemata **d** Details of a synnema **e–j** Conidiophores and conidia **k** Conidia **l–o** Chlamydospores and conidia. Scale bars: 10 µm

was resurrected (Senanayake et al. 2015). The evidence for the continuation of Amphisphaeriales and Xylariales as distinct orders in Xylariomycetidae is also provided in Maharachchikumbura et al. (2016), Samarakoon et al. (2016a, b), Hongsanan et al. (2017) and Daranagama et al. (2018). Amphisphaeriales comprises with 17 families *viz* Amphisphaeriaceae, Apiosporaceae, Beltraniaceae, Castanediellaceae, Clypeophysalosporaceae, Cylindriaceae,

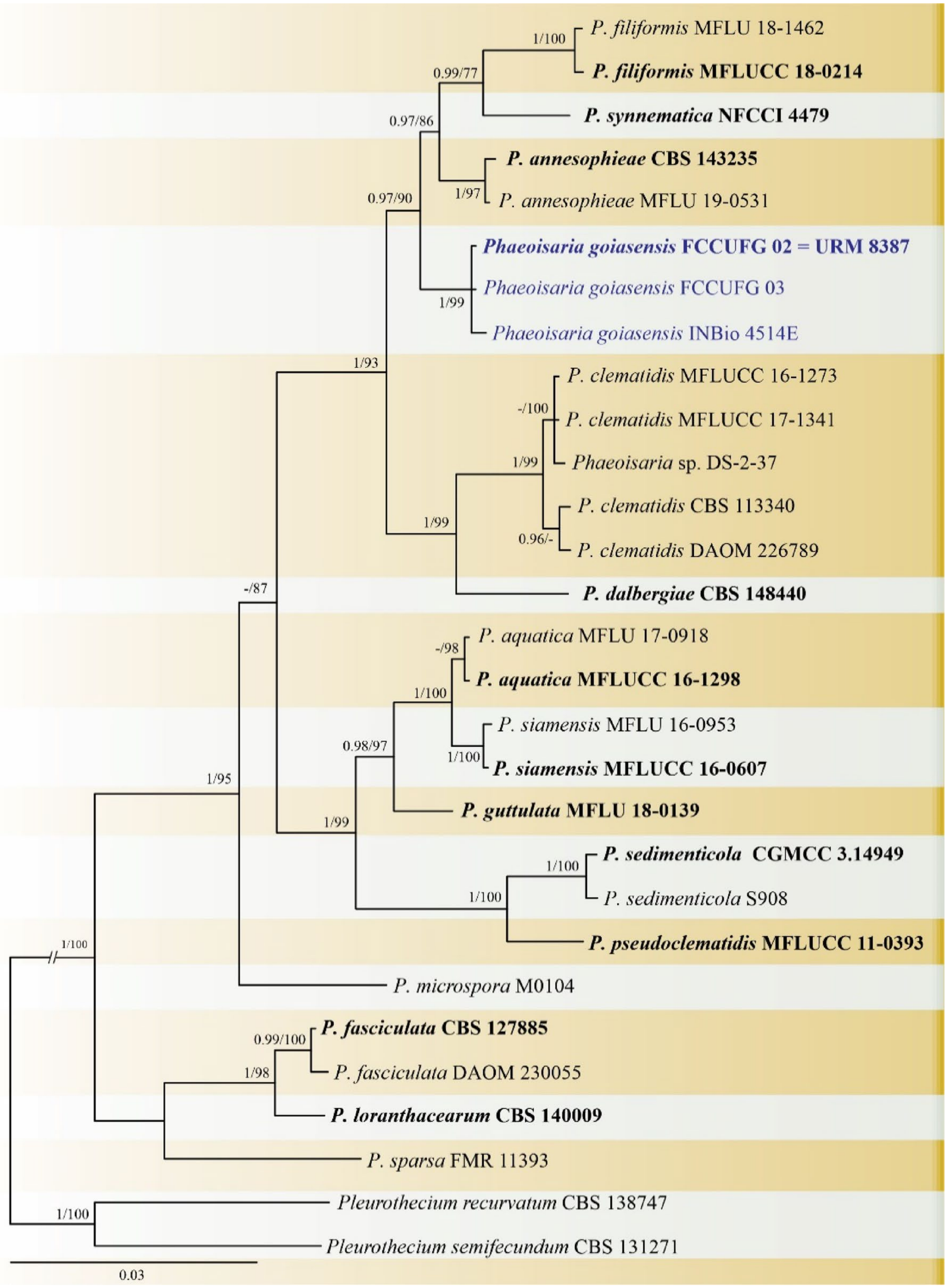


Fig. 114 Phylogram generated from Bayesian analysis based on combined ITS and LSU rDNA sequence data of *Phaeoisaria* conducted in MrBayes on XSEDE in the CIPRES science gateway. Twenty-nine strains/isolates are included in the combined analysis, which comprised a total of 1435 characters (ITS = 591 and LSU = 844), including gaps. The substitution model GTR + I + G was used for ITS and LSU alignments. The tree is rooted with *Pleurothecium semifecundum* CBS 131271 and *Pleurothecium recurvatum* CBS 138747 and the scale bar indicates the number of changes. The ex-types (reference strains) are in **bold** and the new isolates are in blue. Maximum likelihood bootstrap (ML-BS) support values obtained with RAxML using 1000 replicates greater than 70% and Bayesian posterior probabilities (BYPP) greater than 0.95 are indicated near nodes

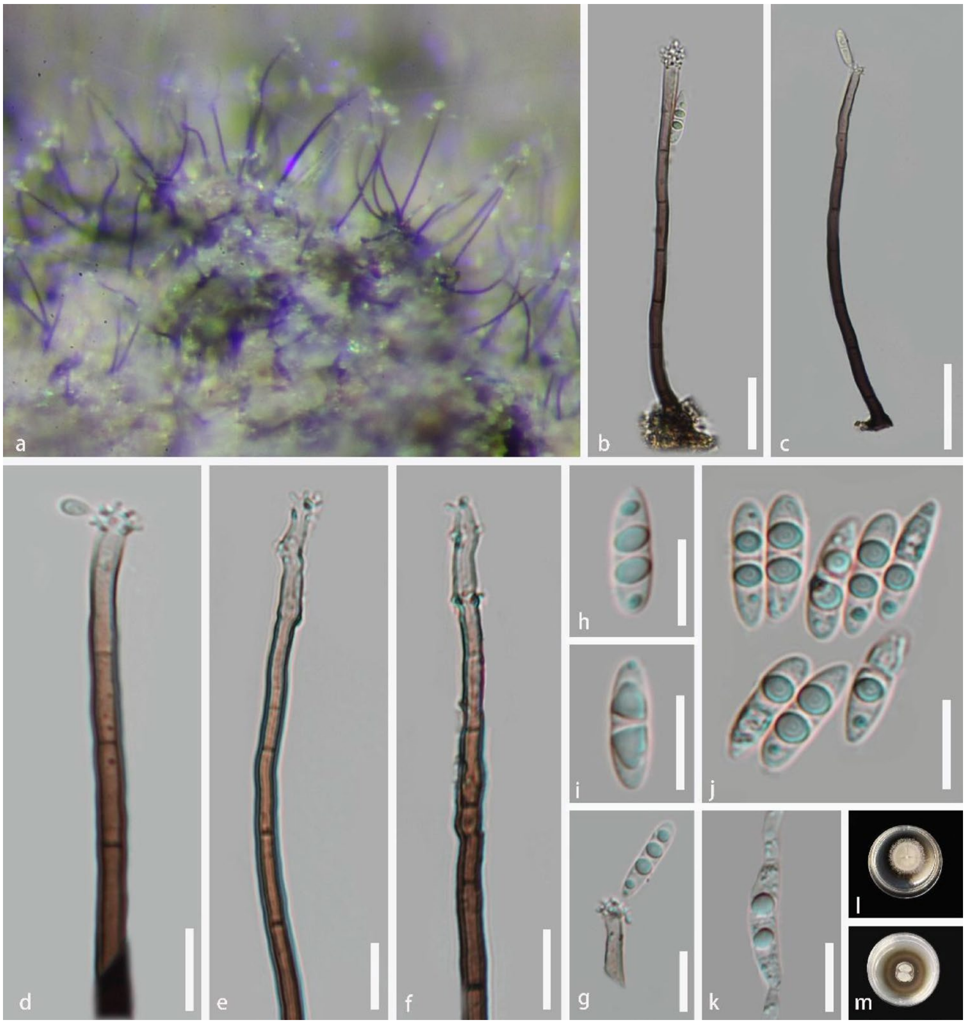


Fig. 115 *Pleurothecium aquisubtropicum* (GZAAS 21–0384, **holotype**) **a** Colony on decaying wood **b–c** Conidiophores with attached conidia **d–g** Conidiogenous cells and conidia **h–j** Conidia **k** Germinating condium **l–m** Colony on PDA from above and below. Scale bars: **b, c** = 20 µm, **d–k** = 10 µm

Hyponectriaceae, Iodosphaeriaceae, Melogrammataceae, Oxydothidaceae, Phlogicylindriaceae, Pseudomassariaceae, Pseudosporidesmiaceae, Pseudotruncatellaceae, Sporocadaceae, Vialaeaceae, and Xyladictyochaetaceae (Hyde et al. 2020a, b, c; Wijayawardena et al. 2020).

Sporocadaceae Corda, [as 'Sporocadeae'], Icon. fung. (Prague) 5: 34 (1842).

Sporpcadaceae was first established by Corda (1842) and typified by *Sporodocadus* Corda (1839). The members of Sporocadaceae can be found as saprobes, pathogens, and endophytes in a variety of habitats (Nag Raj, 2993, Tanaka et al. 2011, Hyde et al. 2020a, b, c). The family contains 32 genera *viz Allelochaeta*, *Annellolacinia*, *Bartalinia*, *Broomella*, *Ciliochorella*, *Diploceras*, *Disaeta*, *Discosia*, *Distononappendiculata*, *Diversimediispora*, *Doliomyces*, *Heterotruncatella*, *Hyalotiella*, *Hymenopleella*, *Immersidiscosia*, *Monochaetia*, *Morinia*, *Neopestalotiopsis*, *Nonappendiculata*, *Parabartalinia*, *Pestalotiopsis*, *Pseudopestalotiopsis*, *Pseudosarcostroma*, *Robillarda*, *Sarcostroma*, *Seimatosporium*, *Seiridium*, *Sporocadus*, *Strickeria*, *Synnemapestaloides*, *Truncatella*, *Xenoseimatosporium* (Hyde et al. 2020a, b, c; Tibproma et al. 2020; Wijayawardene et al. 2020).

Bartalinia Tassi, Bulletin Labor. Orto Bot. de R. Univ. Siena 3: 4 (1900)

Bartalinia was introduced by Tassi (1900) and belongs to *Sporocadaceae*, (Hyde et al. 2020a, b, c; Wijayawardene et al. 2020). *Bartalinia* is morphologically similar to *Heterotruncatella*, *Hymenopleella*, *Morinia*, *Parabartalinia*, *Pestalotiopsis*, *Pseudosarcostroma*, and *Truncatella*. The characteristic features of *Bartalinia* are pycnidial conidiomata and fusiform, 3–4-septate, appendage bearing conidia with an acute or blunt apex (Senanayake et al. 2015). There are 22 *Bartalinia* species in the Species Fungorum (2022a, b) and a new species *B. kevinhydei* was introduced by Tibprommа et al. (2021). The generic and species boundaries of *Bartalinia*-like taxa are complicated

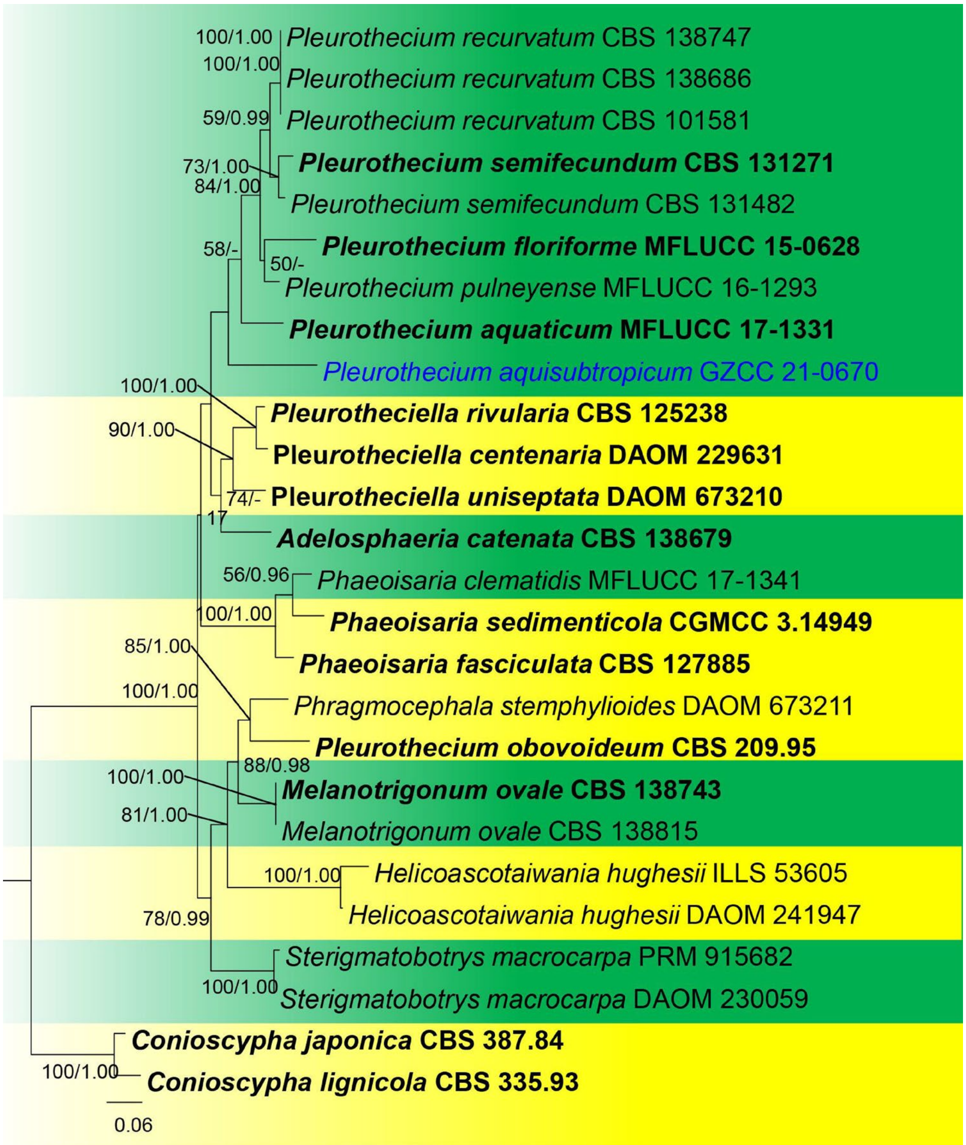


Fig. 116 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Twenty–six taxa were included in the combined analyses, which comprised 1420 characters (LSU: 910, ITS: 510) after alignment. The best scoring RA × ML tree with a final likelihood value of is presented. Bootstrap support values for ML ≥ 50% and BYPP ≥ 0.95 are given above the nodes. The tree is rooted with *Conioscypha lignicola* CBS 335.93 and *C. japonica* CBS 387.84

due to overlapping morphological characteristics. Liu et al. (2019a, b, c, d) has revised the taxa with appendage-bearing conidia in *Sporocadaceae* based on morphology and multigene phylogeny. A new genus *Parabartalinia* was introduced based on *Bartalinia*-like taxon.

Bartalinia bidenticola Htet, Mapook & K.D. Hyde, ***sp.nov.***

Index Fungorum number: *IF559553*; *Facesoffungi number: FoF10766; Fig. 117*

Etymology: The name refers to the host plant from which it was collected *Bidens pilosa*.

Holotype: MFLU 22-0103

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 120–130 × 190–200 μm ($\bar{x}$ = 123 × 196 μm, n = 5), uniloculate, solitary, immersed to semi-immersed, globose to subglobose. *Ostiole* absent. *Peridium* 23–30 μm wide, 3–4 layered, comprised of brown cells of *textura globulosa. Conidiogenous cells* 1–2 μm wide, filiform, hyaline. *Conidia* 23–27 × 4–6 μm, ($\bar{x}$ ± SD = 24.9 ± 0.8 × 4.9 ± 0.3 μm), fusoid to ellipsoid, straight to slightly curved at the apex, 4-septate, constricted ate the septa, brown in three middle cells and hyaline at the basal and apical cells; basal cells 2–4 μm long, hyaline, obconic to conic with a truncate base, thin-walled; three median cells 14–18 μm long, ($\bar{x}$ ± SD = 15.8 ± 0.8 μm), (second cell from the base pale brown, 6–7 μm long; third cell pale brown, 4–6 μm long; fourth cell pale brown, 4–7 μm long), doliiform, wall rugose, versicoloured; apical cells 3–6 μm long, hyaline, subcylindrical, smooth-walled; with 2–3 tubular appendages (mostly 2), unbranched, filliform (13–)17–24(–24) μm long, ($\bar{x}$ ± SD = 22.7 ± 2.7 μm); basal appendage single, tubular, unbranched, centric 4–8(–10) μm long.

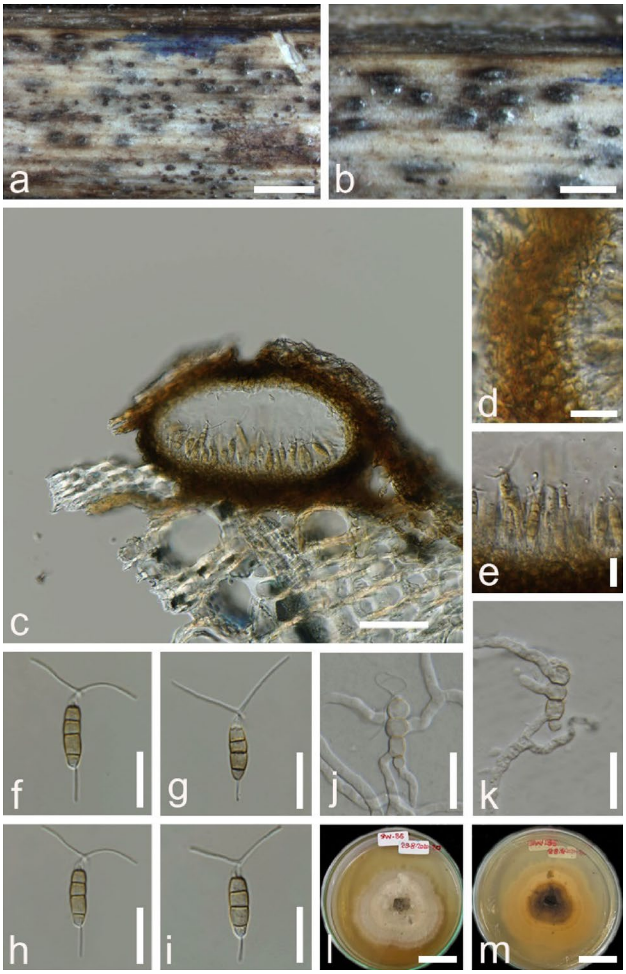


Fig. 117 ***Bartalinia bidenticola*** (MFLU 22–0103**, holotype). a,b** Appearance of conidiomata on host substrate. **c** Section through conidioma. **d** Peridium. **e** Conidia on the conidiogenous cells. **f–i** Conidia. **J–k** Germinating conidia. l–m Culture on MEA from surface and reverse. Scale bar **a = 300** μm**, b** = 200 μm, **c** = 50 μm, **d** = 20 μm, **e = 10** μm**, f,g,h,I,j,k,l,m** = 20 μm

Culture characteristics: Spores germinating on MEA within 24 h, reaching 50 mm after 7 days at room temperature, irregular, undulate, concentric, flat, leathery surface, grey.

Material examined: Thailand, Chiang Rai Province, Doi Pui, on the dead stems of *Bidens pilosa* Linn var *radiata* (Asteraceae), 10 July 2020, Zin Hnin Htet SW35 (MFLU 22-0103, **holotype**), ex-type living culture (MFLUCC 22-0008).

GenBank numbers: ON715467(LSU), ON715520(ITS).

Notes: *Bartalinia bidenticola* (MFLUCC 22-0008) resembles *Bartalinia* in having subcylindrical to fusoid, pale yellow septate conidia, with an apical cell modified into branched appendages. According to the BLASTn results, the closest match for the LSU sequence of *Bartalinia bidenticola* (MFLUCC 22-0008) was *Bartalinia kevinhydei* (MFLUCC 12-0384) with 97.32% similarity and the closest match for ITS sequence was *Bartalinia pondoensis* (CCTU 459) with 98.85% similarity. Phylogenetic analyses of a combined ITS and LSU sequence dataset (Fig. 118) show that *Bartalinia bidenticola* (MFLUCC 22-0008) is phylogenetically well distinguished and branched off from all other species in *Bartalinia* with ML = 100% and BYPP = 1.00 support. We, therefore, identify our isolate as a new species which was found from *Bidens pilosa*.

Bartalinia caryotae Senan., Kular. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558407; Facesoffungi number: FoF10699; Fig. 119

Etymology: Species epithet refers to the host genus.

Holotype: HKAS115853

Associated with leaf-tip spots of *Caryota* sp. **Sexual morph:** Not observed. **Asexual morph**: *Coelomycetous*. *Conidiomata* 55–75 × 115–140 μm ($\bar{x} = 62 \times 120$ μm, $n = 15$), pycnidial, superficial or rarely erumpent, solitary, scattered, dark brown, uniloculate, conical, glabrous, ostiolate, without a papilla. *Conidiomata wall* 3–8 μm wide ($\bar{x} = 6$ μm, $n = 5$), comprising several layers of brown, pseudoparenchymatous cells of *textura angularis*, paler towards the inner layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–7 × 1.5–4 μm ($\bar{x} = 5 \times 3$ μm, $n = 10$), enteroblastic, annellidic, integrated, hyaline to subhyaline, ampulliform to subcylindrical, or obclavate, aseptate, thin- and smooth-walled. *Conidia* 17.5–19 × 5–7 μm ($\bar{x} = 18 \times 6$ μm, $n = 20$), subcylindrical, hyaline when immature, olivaceous when mature, straight to slightly curved, 4-septate, constricted at septa, smooth, with longest cell second from base, bearing appendages at both ends; basal cell 2–4 μm long, conical, hyaline, to pale brown, paler than middle cells; second cell from base 5–8 μm long, pale brown; third cell 3–5 μm long, pale brown; fourth cell 3–5 μm long, pale brown; apical cell 2–3 μm long, conical, hyaline, smooth-walled with a tubular, flexuous, divergently 3–4, unbranched, 20–30 μm long, tubular appendages arising from the tip of apical cell, with a basal 10–25 μm long, centric to eccentrically located, unbranched, flexuous, tubular to filiform appendage.

Culture characteristics: Colonies on PDA reaching 2 cm diam. after 5 days at 16 °C, flattened, circular, smooth margin, white with off-white aerial mycelia; reverse cream.

Material examined: China, Guangdong Province, Shenzhen, Nanshan District, Mountain Yangtai Forest Park, 22° 39′ 21.26″ N 113° 57′ 18.53″ E, living leaves of *Caryota* sp (*Arecaceae*), 4 October 2019, ND Kularathnage, NDK 24, (HKAS115853, **holotype**), ex-type living culture, ZHKUCC 21–0093; China, Guangdong Province, Shenzhen, Nanshan District, Mountain Yangtai Forest Park, 22° 39′ 21.26″ N 113° 57′ 18.53″ E, living leaves of *Caryota* sp

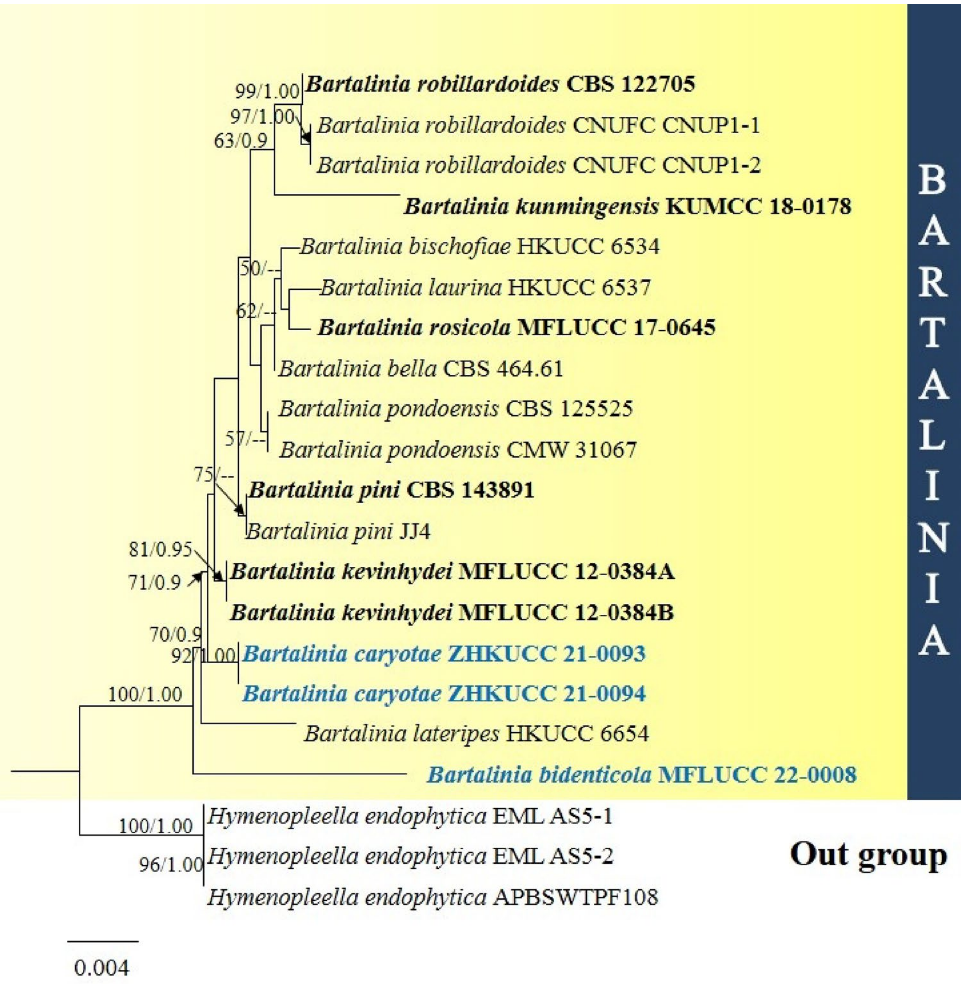


Fig. 118 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data for *Bartalinia*. Twenty taxa were included in the combined analyses, which comprised 1479 characters (LSU = 897 bp, ITS = 582 bp) after alignment. Bootstrap support values for maximum likelihood (ML) ≥ 50% and clade credibility values ≥ 0.90 from Bayesian inference analysis are labelled at each node. Ex-type strains are in bold and the new isolate is indicated in blue bold. *Hymenopleella endophytica* (APBSWTPF108, EML AS5-1, EML AS5-2) were used as the outgroup taxa

(*Arecaceae*), 15 September 2018, IC. Senanayake, SI 43, (ZHKU 21–0005, **paratype**), ex-paratype living culture, ZHKUCC 21–0094.

GenBank numbers: ZHKUCC 21–0093 – MZ520792(ITS), MZ520794 (LSU).

ZHKUCC 21–0094 –MZ520793(ITS), MZ520795 (LSU)

Notes: In the combined ITS and LSU gene analysis, *Bartalinia caryotae* formed a distinct clade with (MP = 100 and BYPP = 1.00) support, basal to *B. kevinhydei* (Fig. 118). The comparison of the DNA sequence of ITS and LSU loci of *Bartalinia caryotae* with *B. kevinhydei* revealed base pair differences of 0.3% and 0.4% respectively. However, *Bartalinia caryotae* is morphologically different from *Bartalinia kevinhydei* in having small, conical conidiomata with large, 3–4 unbranched apical appendages (Liu et al. 2019a, b, c, d). Therefore, we introduce *Bartalinia caryotae* as a novel taxon from leaves of *Caryota* species and *Bartalinia* species are rarely reported on monocotyledon plants. Our species forms superficial to erumpent conidiomata on leaves.

Pestalotiopsis Steyaert, Bull. Jard. bot. État Brux. 19: 300 (1949).

Notes: Steyaert (1949), based on the conidial features, divided *Pestalotia* into three genera, namely *Pestalotia*, *Pestalotiopsis* and *Truncatella*. Species with 5-celled conidia (4-septate) were grouped within *Pestalotiopsis*. Based on multilocus phylogenetic and morphological analyses of *Pestalotiopsis*-like species, Maharachchikumbura et al. (2014) divided the complex into three genera: *Pestalotiopsis*, *Neopestalotiopsis* and *Pseudopestalotiopsis*. *Pestalotiopsis* is characterized by median cells concolourous, i.e. three pale-pigmented median cells. *Pestalotiopsis* is a complex genus and has considerable phenotypic diversity (Maharachchikumbura et al. 2014). Thus, the identification is complemented with DNA sequence data and phylogenetic analyses based on the combination of three gene regions (ITS, *tub2* and *tef1*) (Jeewon et al. 2003; Maharachchikumbura et al. 2011, 2012, 2013; Geng et al. 2013).

Pestalotiopsis piraubensis V.P. Abreu & O.L. Pereira, ***sp. nov.***

Index Fungorum number: *IF556023*; *Facesoffungi number*: *FoF04861*; *Fig. 120*

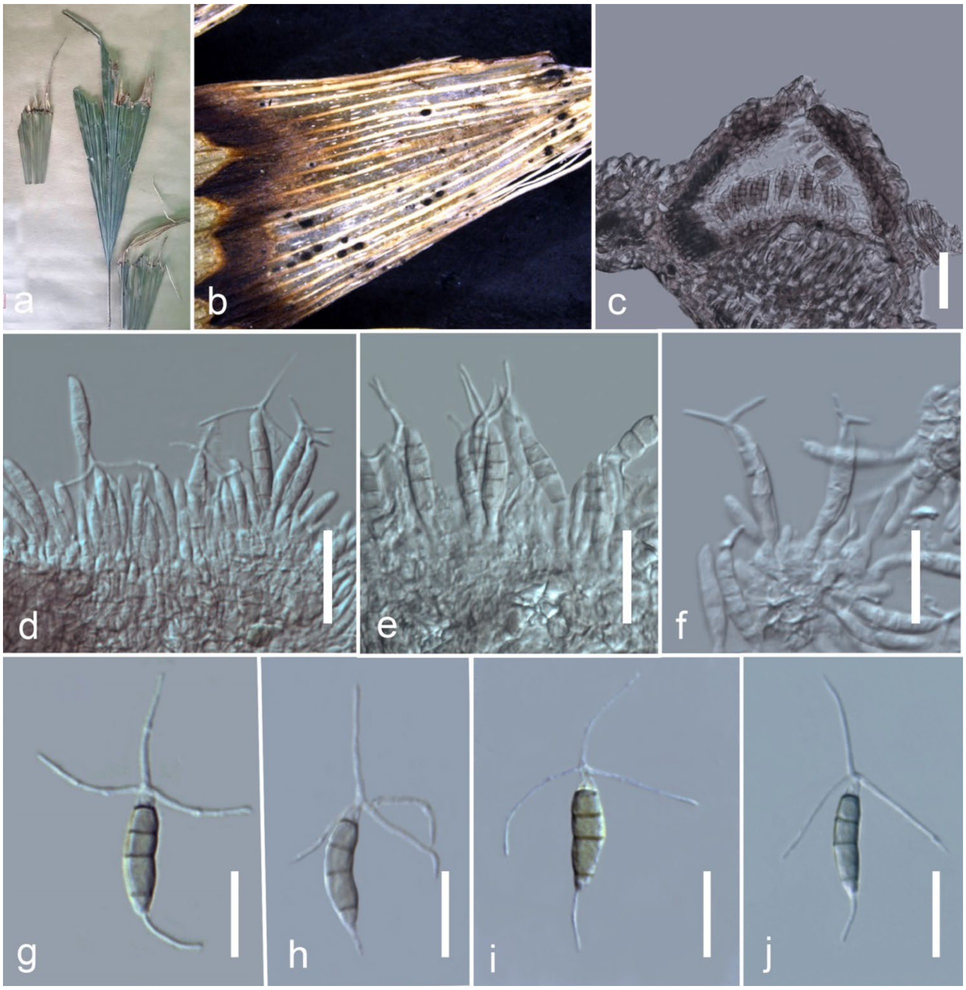


Fig. 119 ***Bartalinia caryotae*** (HKAS115853, **holotype**). **a** Specimen. **b** Conidiomata on substrate. **c** Cross section of conidiomata. **d-f** Conidia attached to conidiogenous cells. **g-j** Conidia. Scale bars: **c** = 30 µm, **d-f** = 20 µm, **g-j** = 15 µm

Etymology: Name refers to the city of Piraúba, state of Minas Gerais, Brazil, where the fungus was collected.

Holotype: VIC 44199

Asexual morph: Culture obtained by direct isolation from diseased guava fruits (Fig. 120a). On MEA, *conidiomata* sporodochial, globose, solitary, semi-immersed, black, exuding globose, dark brown to black conidial masses (Fig. 120d–e). *Conidiophores* indistinct, reduced to conidiogenous cells. *Conidiogenous cells* discrete, cylindrical or spathulate, hyaline, smooth-walled, 4–10 × 1.5–3 µm. *Conidia* fusoid, ellipsoid, straight to slightly curved, 4-septate, 25–33.5 × 5–7.5 µm, basal cell conic, hyaline, smooth and thin-walled, 4.5–7.5 µm long; three median cells doliiform, 15.5–20.5 µm long, minutely verruculose, concolourous, pale brown, septa darker than the rest of the cell (second cell from the base 5–7.5 µm long; third cell 4.5–6.5 µm long; fourth cell 5–7 µm long); apical cell 3.5–6 µm long, hyaline, cylindrical to subcylindrical, thin- and smooth-walled; with 1–3 tubular apical appendages, arising from the apical crest, unbranched, filiform, flexuous 12–25.5 µm long; basal appendage single, tubular, unbranched, centric, 2–6.5 µm long (Fig. 120f–h). **Sexual morph:** Not observed.

Culture characteristics: Colonies on MEA attaining 43 mm diam after 7 days at 25 °C, with a regular edge, whitish to pale yellow-coloured, with dense aerial mycelium and dark brown to black conidial masses (Fig. 120b). Colonies on PDA attaining 68 mm diam after 7 days at 25 °C, with irregular edge, whitish to pale yellow-coloured, with sparse aerial mycelium on the central surface and dark brown to black conidial masses (Fig. 120c).

Pathogenicity test: The inoculation method used consisted of the wounding of the detached fruits and on these, the mycelium plug, with the mycelial part facing the surface of the fruit was added. Causing fruit rot disease, seven days after the inoculation of healthy ripe guava fruits.

Material examined: Brazil, Minas Gerais, Piraúba, in a commercial orchard, on fruits of *Psidium guajava* L. (*Myrtaceae*), 20 January 2014, V.P. Abreu & O.L. Pereira (VIC 44199, **holotype**), ex-type living culture COAD 2165.

GenBank numbers: MH627381 (ITS), MH643773 (*tub2*), MH643774 (*tef1*-α).

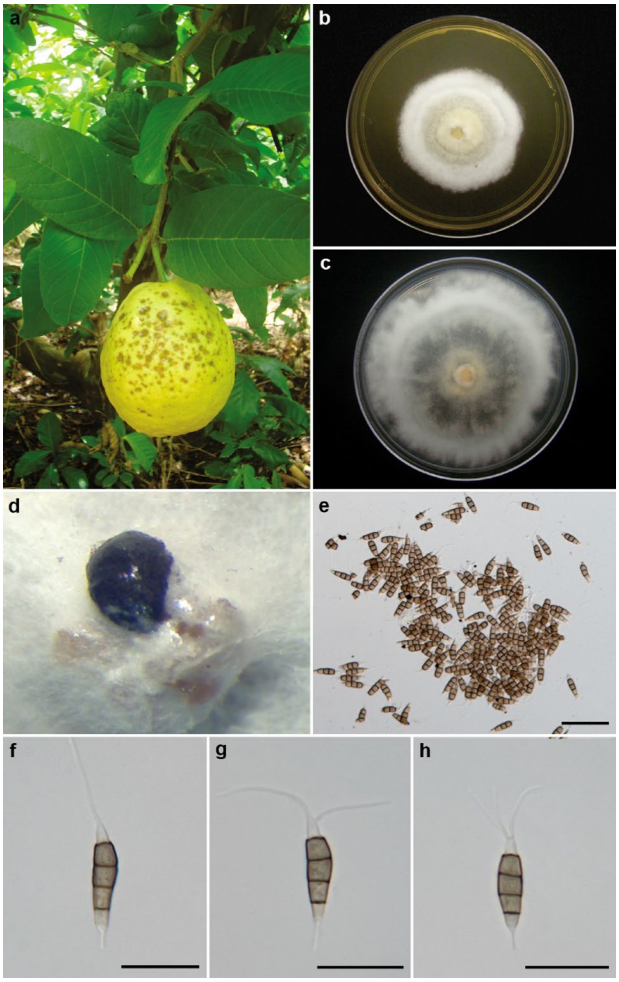


Fig. 120 ***Pestalotiopsis piraubensis*** (VIC 44,199, **holotype**) **a** disease symptom on the fruit of *Psidium guajava* in a commercial orchard in the city of Piraúba, state of Minas Gerais, Brazil. **b** Colony on MEA (Malt Extract Agar) after 7 d at 25 °C with a photoperiod of 12 h in the dark in Petri dishes (90 × 15 mm) (COAD 2165). **c** Colony on PDA (Potato Dextrose Agar) after 7 d at 25 °C with a photoperiod of 12 h in the dark in Petri dishes (90 × 15 mm) (COAD 2165). **d** Conidioma sporulating on PDA. **e** Conidial masses. **f** Conidia (1–3 apical appendages). Scale bars: **e** = 50 µm, **f–h** = 20 µm

Notes: *Pestalotiopsis* spp. were previously considered opportunistic pathogens that affect stressed plants (Coyier and Roane 1987). Pirone (1978) reported different species of *Pestalotiopsis* causing leaf spots on a range of ornamentals. However, in recent years, there has been an increase in reports of these pathogens causing widespread damage to several economically important crops (Keith et al. 2006; Ko et al. 2007; Rodrigues et al. 2014; Rosado et al. 2015; Solarte et al. 2018). Therefore, the increase of guava planting areas has contributed to the emergence of several diseases, and there is no data on the environmental requirements of *Pestalotiopsis* infection on guavas in Brazil, nor any studies on field epidemiology for these diseases or post-harvest management. The topology of the concatenated tree was similar to that of individual trees, thus, only the concatenated tree is presented here (Fig. 121). Molecular data showed that *Pestalotiopsis piraubensis* COAD 2165 did not group with any other species reported in the literature. Morphologically, *P. piraubensis* differs from *P. trachicarpicola* for presenting larger conidia. *Pestalotiopsis piraubensis* has 1–3 apical appendages and the other species have 2–4 (mostly 3). *Pestalotiopsis kenyana* and *P. biciliata* differ from *P. piraubensis* by having conidiomata pycnidial in culture on PDA. *P. photinicola* presents smaller conidia (18–24 × 4–5 µm) than *P. piraubensis*. Although most of the morphological characteristics did not differ so much, the most striking feature of *P. piraubensis* was the size of the conidiogenous cells, which was much smaller (4–10 × 1.5–3 µm diam), when compared to the other species. Phylogenetic analyses and morphological comparisons support the introduction of *P. piraubensis* as a new species within this genus. Besides that, this study may be helpful for further studies on the management of guava diseases.

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr, in Hyde, Fröhlich & Taylor, Sydowia 50(1): 23 (1998).

Notes: *Apiosporaceae* was introduced by Hyde et al. (1998), with *Apiospora* as the type genus. Description of *Apiosporaceae* has been provided in Hyde et al. (2020a, b, c), wherein the authors listed five genera in this family, *Appendicospora*, *Arthrinium*, *Dictyoarthrinium* and *Endocalyx*, *Nigrospora*. However, phylogenetic analysis resulted in the transfer of *Dictyoarthrinium* and *Spegazzinia* to Didymosphaeriaceae (Pleosporales) (Tanaka et al. 2015; Samarakoon et al. 2020).

Apiospora Sacc., Atti Soc. Veneto-Trent. Sci. Nat., Padova, Sér. 4 4: 85 (1875).

Notes: *Apiospora* is characterized by densely arranged perithecia arranged in a longitudinal stroma, clavate to broadly cylindrical asci and apiospores in the sexual morph and *Arthrinium*-like asexual morph (Hyde et al. 2020a, b, c). Species of this genus commonly live as endophytes, epiphytes, saprobes on grass in Poaceae (Samarakoon et al. 2022). *Apiospora* and *Arthrinium* has no clear boundary as to the morphological characteristics. However, *Apiospora* and *Arthrinium* sensu stricto were recognized in *Apiosporaceae* as two independent lineages in this family (Pintos and Alvarado 2021).

Apiospora guiyangensis Samarak., Jian K. Liu & K.D. Hyde, in Samarakoonet al., Fungal Diversity 112: 19 (2022).

Index Fungorum number: IF558711; Facesoffungi number: FoF10187; Fig. 122

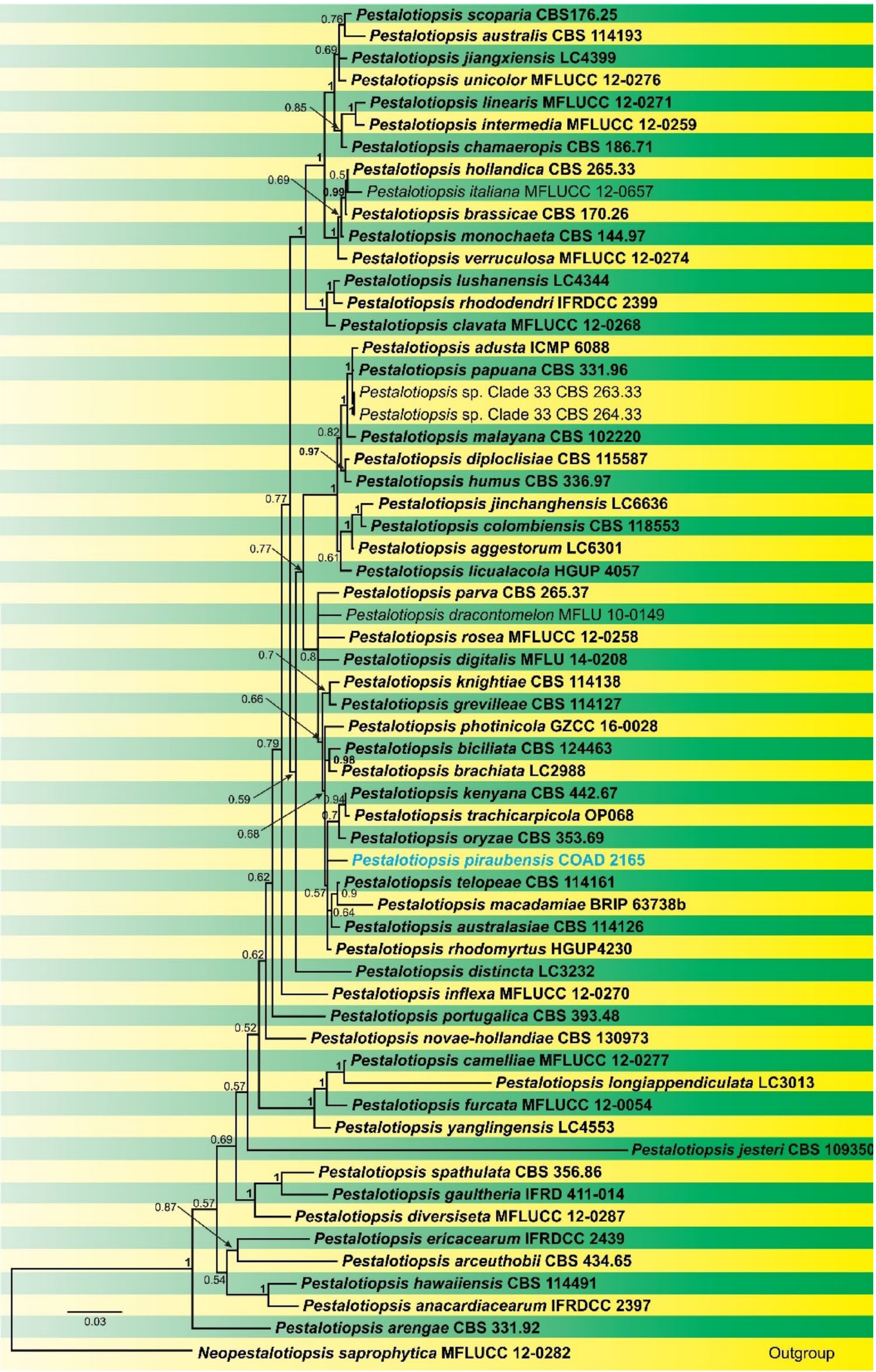


Fig. 121 Phylogram generated from Bayesian Inference analysis based on combined ITS, *tub2* and *tef1* sequence data for several closely related species in *Sporocadaceae*. Sequence data of type cultures, ex-type or ex-epitype obtained from Maharachchikumbura et al. (2014), Chen et al. (2017a, b), Akinsanmi et al. (2017), Liu et al. (2017) were included in this study. The combined genes sequence analysis included 61 taxa, which comprise total 1994 characters (557 characters for ITS, 830 characters for *tub2*, 607 characters for *tef1*-α), and outgroup taxon *Neopestalotiopsis saprophytica* MFLUCC 12–0282. Bayesian posterior probability are indicated at the nodes, and values ≥ 0.95 are in bold. Isolate numbers are indicated after species names. The ex-type or ex-epitype strains are in **bold** and black. The newly generated sequence is indicated in **bold** and blue

Saprobic on a dead twig of *Bothriochloa ischaemum*. **Sexual morph:** Stromata visible as fusiform, black, erumpent pustules with alongitudinal slit on the top. *Ascomata* 123–165 × 109–185 ($\bar{x}$ = 140 × 130, *n* = 10) µm, subglobose, unilocular, immersed, papillate, arranged in a linear row along with the thelongitudinal slit. *Peridium* 11–15 ($\bar{x}$ = 13, *n* = 10) µm in width, consisting of dark brown cell *of textura angularis,* thin at base, becoming thicker near the ostioles, with a pseudoparenchymatous wall at the most inner layer. *Paraphyses* 3.6–7.6 ($\bar{x}$ = 5.2, *n* = 10) µm, hyaline, cylindrical, septate, guttulate. *Asci* 60–84 × 9.3–13 ($\bar{x}$ = 70 × 11, *n* = 20) µm, fusiform, unitunicate, 8-spored, apex lacking

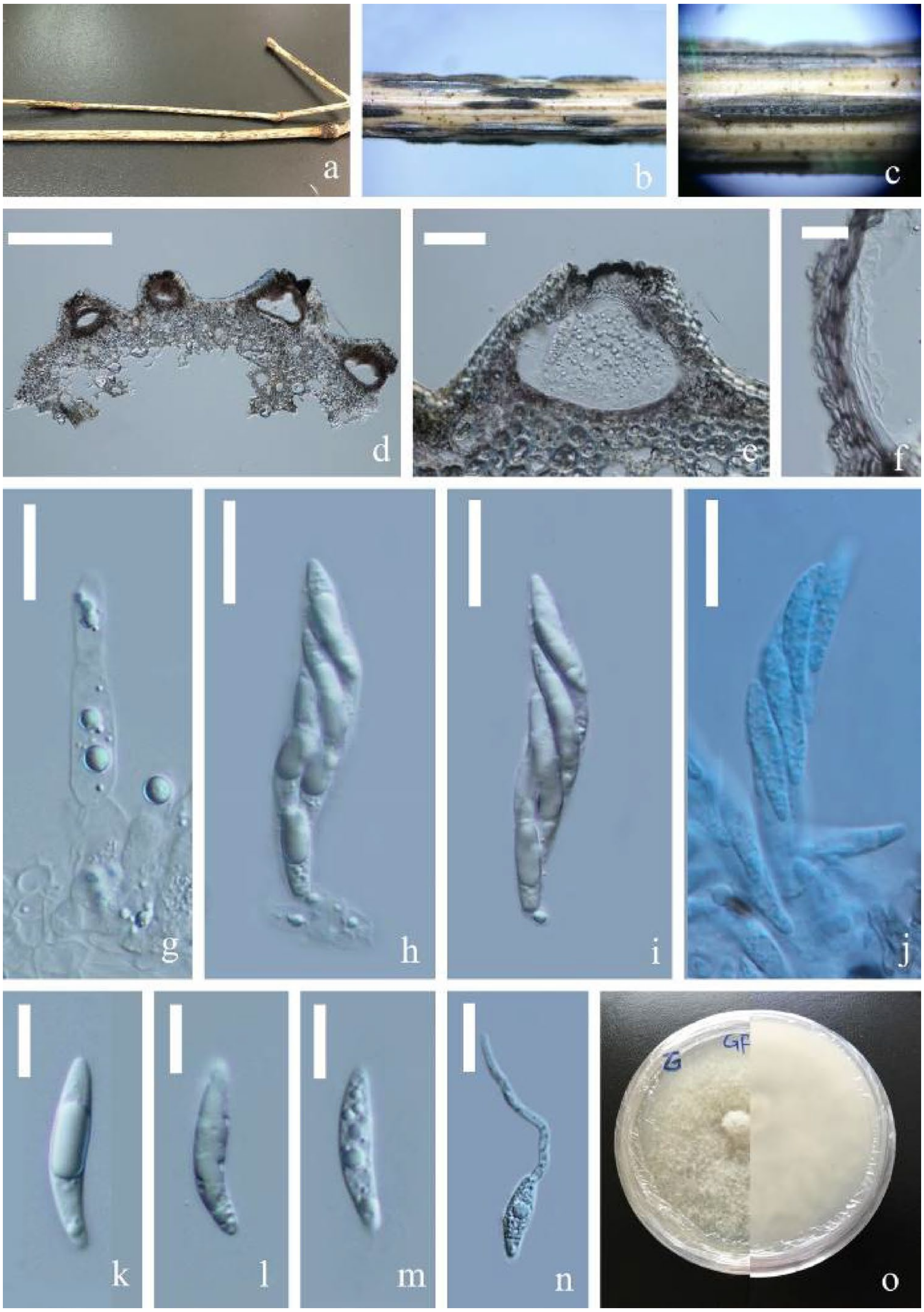


Fig. 122 ***Apiospora guiyangensis*** (KUN-HKAS 125898, **new host record**)**a** Host. **b, c** Appearance of ascostroma on host. **d, e** Section through ascomata**. f** Peridium. **g** Paraphysis. **h**–**j** Asci (j is stained in cotton blue). **k**–**m** Ascospores. **n** Germinal spore. **o** Upper and reverse view of cultures on PDA at 8 days incubation. Scale bars**: d** = 300 µm, **e** = 50 µm**, f, h**–**j, n** = 20 µm, **k**–**m** = 10 µm

apical mechanism, with a short basal pedicel. *Ascospores* 22–28 × 4.6–6.7 ($\bar{x}$ = 25 × 5.4, *n* = 30) µm, hyaline, ellipsoid to reniform, slightly curve, smooth-walled, aseptate, guttulate. **Asexual morph:** see description in Samarakoon et al. (2022).

Culture characteristics: Colonies on PDA rapid growing, reaching 45 mm diam. after 8 days at 20–25 °C, colonies medium dense, circular, mycelium superficial in media, cottony, round aspect, white from above and reverse.

Material examined: China, Guizhou Province, Qianxinan Buyei and Miao Autonomous Prefecture, Ceheng County, Gaofeng Village, on dead culms of *Bothriochloa ischaemum* (Poaceae), 8 August 2018, D. P. Wei, GFC613 (KUN-HKAS 125898), living culture KUNCC22-12539.

Known hosts and distribution: Poaceae (Guizhou, China) (Samarakoon et al. 2022).

GenBank numbers: OQ029540 (*ITS*), OQ029613(*LSU*), OQ061263(*SSU*), OQ186444(*tef1*), OQ186446 (*tub2*).

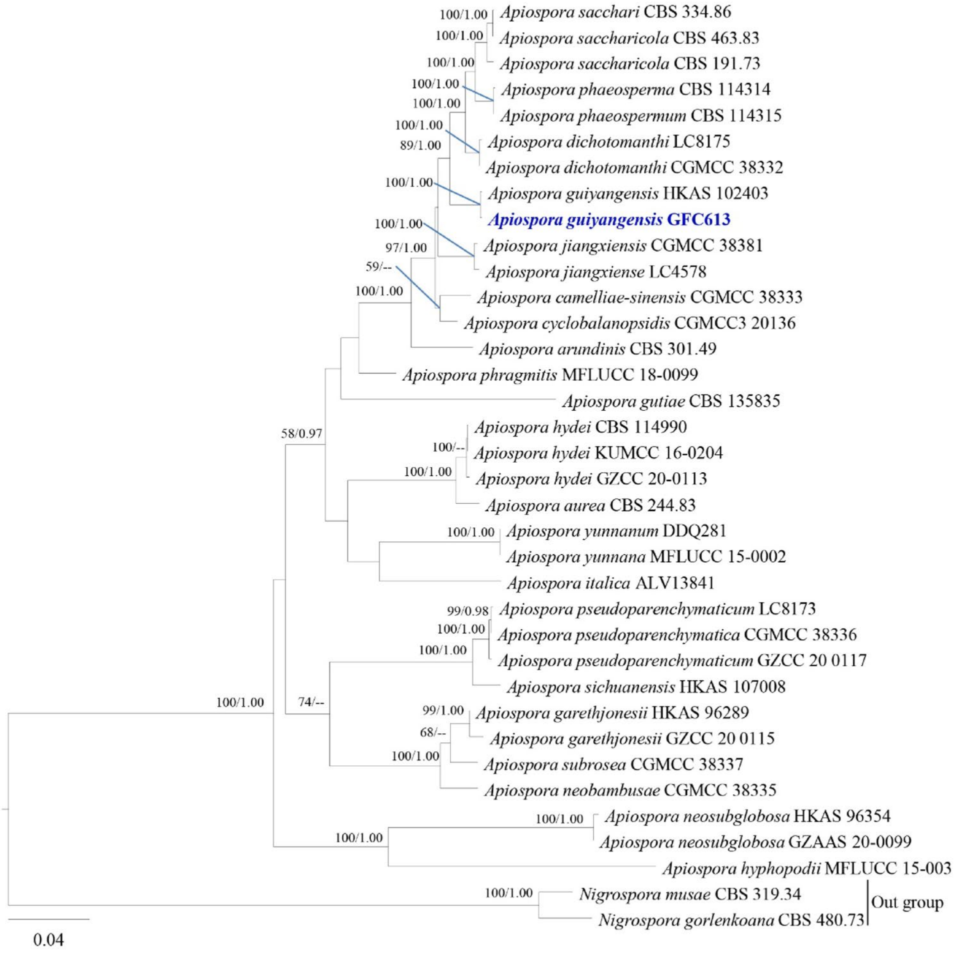


Fig. 123 RAxML tree inferred from combined ITS, LSU, *rpb2* and *tub2* sequence. Bootstrap support for maximum likelihood analysis ≥ 50% and Bayesian posterior probabilities ≥ 0.95 are denoted next to the notes in this order. The new collection is marked in blue bold font

Notes: *Apiospora guiyangensis* was introduced by Samarakoon et al. (2022) from an unidentified Poaceae species in Guizhou, China. Our species colonizing on dead column of *Bothriochloa ischaemum* (Poaceae) was collected from the same province of type strains of *A. guiyangensis*. Its sexual morph fits well to the description of *A. guiyangensis* in the linear stromata with a slit-like opening, immersed, subglobose, gregarious, ascomata and ellipsoid to reniform ascospores. Additionally, the phylogenetic analysis of a combination of ITS-LSU-*tef1* -*tub2* shows our isolate sisters to *A. guiyangensis* with ML = 100% and BYPP = 1.00 support (Fig. 123). Thus, we determine our isolate as a new collection of *A. guiyangensis* and this finding indicates that *A. guiyangensis* probably specific to Poaceae.

Xylariales Nannf.

Notes: Xylariales belongs to subclass Xylariomycetidae and the placement is confirmed by different phylogenetic and evolutionary studies (Maharachchikumbura et al. 2016; Samarakoon et al. 2016a, b; Hongsanan et al. 2017). The continuous taxonomic studies expand the number of families and genera in *Xylariales*. Twenty-one families and 183 genera are listed in this order (Konta et al. 2016; Dayarathne et al. 2017; Wijayawardene et al. 2022; Hyde et al. 2020a, b, c).

Diatrypaceae Nitschke, [as 'Diatrypeae'], Verh. naturh. Ver. preuss. Rheinl. 26: 73 (1869).

Notes: *Diatrypaceae* is a significant family in Xylariales introduced by Nitschke (1869) with the generic type *Diatrype* (Augusto et al. 2016; Hyde et al. 2020a, b, c; Boonmee et al. 2021). Numerous saprobic, endopytic and pathogenic diatrypaceaous taxa are available in both terrestrial and aquatic habitats worldwide (Dissanayake et al. 2021a, b; Zhu et al. 2021; Wijayawardene et al. 2020). The family is characterized by erumpent or immersed ascostromata that contain 8-spored or polysporous, long pedicel asci with allantoid ascospores in the sexual morph and coelomycetous or hyphomycetous asexual morphs (Konta et al. 2020; Carpouron et al. 2021; Dissanayake et al. 2021a, b). The early identification of Diatrypaceae species were based only on morphology. Currently most studies are performed by

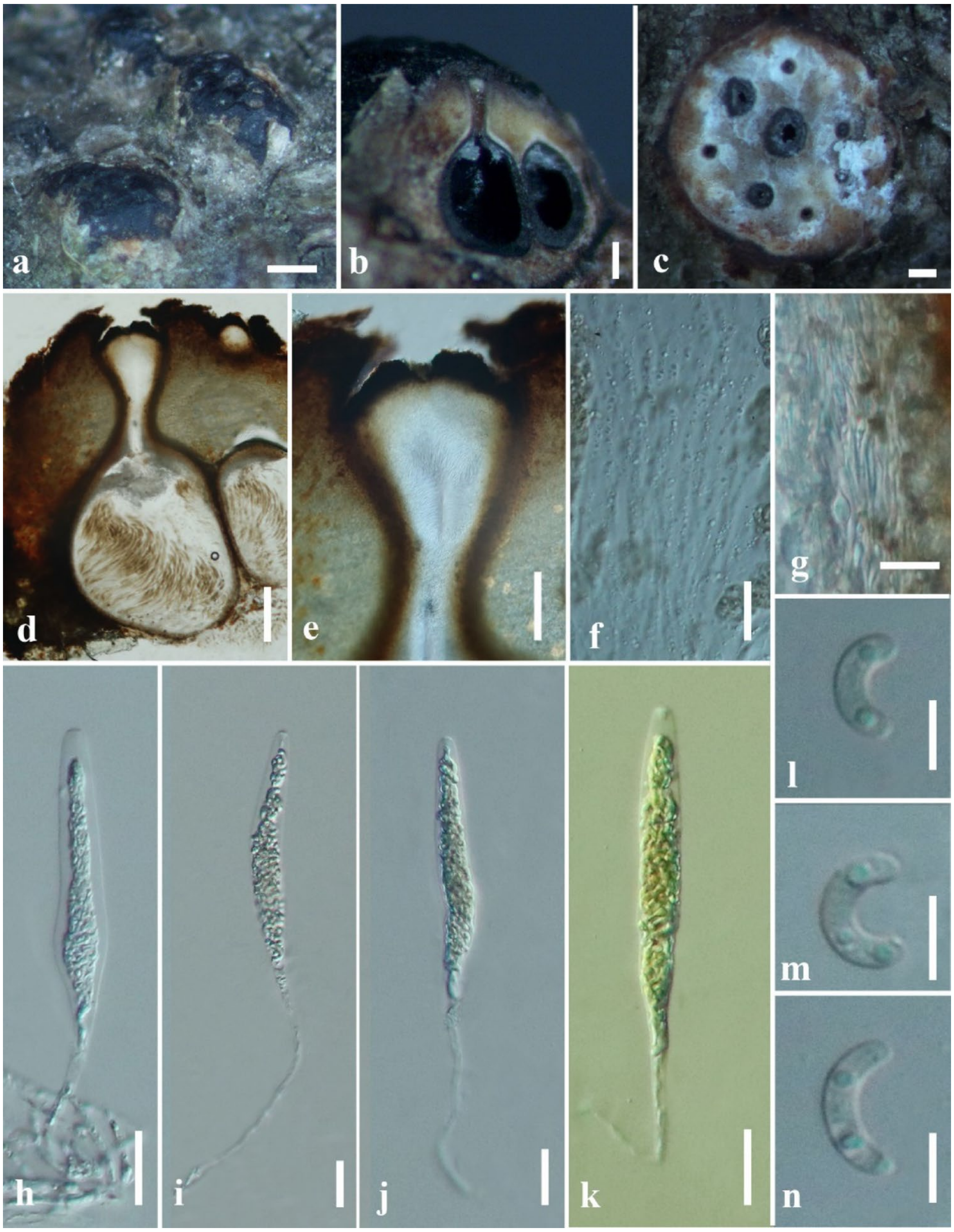


Fig. 124 ***Diatrypella quercina*** (MFLU 18–1865, **new host record**). **a-c**. Appearance of ascostromata on a twig of *Quercus petraea* subsp. *polycarpa* host. **d**. Longitudinal section of an ascoma. **e**. Ostiole. **f**. Paraphyses. **g**. Peridium **h–k**. Asci **l-n**. Ascospores. **a** = 500 µm **b-c**, **f** = 200 µm, **d-e** = 100 µm, **h–k** = 20 µm, **g** = 10 µm, **l-n** = 5 µm

using both morphological observations with ITS and *tub*2 sequence data analyses (Konta et al. 2020; Dissanayake et al. 2021a, b; Wijayawardene et al. 2022). However, many genera of the family are polyphyletic and further taxonomic studies still need to be performed for resolving diatrypaceous taxa (Dissanayake et al. 2021a, b). There are 22 genera in Diatrypaceae with more than 1500 species (Carpouron et al. 2021; Wijayawardene et al. 2020). In this study we discuss a novel host record of *Diatrypella* species collected from Russia.

Diatrypella (Ces. & De Not.) De Not., Sfer. Ital.: 29 (1863)

Diatrypella was established to constitute stromatic *Sphaeriales* with ovoid and multi spored asci (Croxall 1950, Carpouron et al. 2021). *Diatrypella* was introduced by Cesati and De Notaris (1863) and typified *D. verruciformis*. The genus is characterized by a libertella-like coelomycetous asexual morph. In the sexual morph, conical to truncate and discoid, cushion-like stromata are delimited by black zones on the substrates, umbilicate or sulcate ostiolar necks, long-stalked, cylindrical and polysporous asci with allantoid, hyaline or yellowish ascospores (Kirk et al. 2008; Dissanayake et al. 2020; Hyde et al. 2020a, b, c). Recently several *Diatrypella* species were introduced by different authors from different hosts (Dissanayake et al. 2020; Hyde et al. 2020a, b, c; Zhu et al. 2021). There are 84 records under *Diatrypella* in Species Fungorum (2022a, b) while, only 24 taxa have molecular data in GenBank. We follow the latest treatment for *Diatrypaceae* in Boonmee et al. (2021) to resolve the taxonomic placements of our strain and updated phylogenetic tree is presented in Fig. 124. In this study, we discuss a new collection of *Diatrypella quercina* from Russia.

Diatrypella quercina (Pers.) Cooke, J. Bot., Lond. 4: 99 (1866).

Index Fungorum number: IF215896; Facesoffungi number: FoF11778; Fig. 124

Saprobic on dead twigs on *Quercus robur*. **Sexual morph**: *Stromata* 1.0–1.5 mm in diam., well-developed, solitary to gregarious, immersed to semi immersed, erumpent at the maturity, globose to subglobose, black. *Ascomata* 610–660 µm high, 550–600 µm diam. ($\bar{x}=650\times580$ µm, $n=10$), perithecial, surrounded by white entostroma, 6–8 perithecia arranged in a valsoid configuration, conical, individual ostiole with a long neck. Neck 450–490 µm long ($\bar{x}=480$ µm, $n=10$), cylindrical, with periphyses. *Peridium* 20–30 µm wide ($\bar{x}=26$ µm, $n=10$), composed outermost layers of brown, thick-walled cells in *textura angularis*, inner layers hyaline, cells forming of *textura prismatica*. *Hamathecium* comprises 1–2 µm wide ($\bar{x}=1.5$ µm, $n=20$) paraphyses arising from base of perithecia, hyaline, long, narrow, unbranched, septate, guttulate, narrowing and tapering towards apex. *Asci* 70–120 × 10–15 µm ($\bar{x}=100\times14$ µm, $n=30$), polysporous, unitunicate, strongly curved, apically round, with a J-apical ring, long pedicellate (50–70 µm). *Ascospores* 6–9 × 1.8–2.3 µm ($\bar{x}=7.5\times2.0$ µm, $n=30$), overlapping, hyaline, yellowish in mass, allantoid, aseptate, guttulate, guttules conspicuous near to apex, smooth-walled. **Asexual morph**: see Adamčíková et al. (2013).

Material examined: Russia, Sochi, Khostinsky City District, the territory of Subtropic Scientific Centre of Russia Academy of on a dead branch of *Quercus petraea* subsp. *polycarpa* (Schur) Soó (syn. *Q. colchica* Czeczott, *Q. iberica* Steven ex M. Bieb.) (Fagaceae), Timur S. Bulgakov, 4 August 2018, T-7330 (MFLU 18–1865).

GenBank number: ON705330 (ITS), ON713468 (*tub2*).

Notes: Ruhland (1900) considered *Diatrypella quercina* as a species in *Diatrype* because of strongly developed ectostromata. Later, Wehmeyer (1926) discussed the possibility of including this taxon in *Diatrype*. Croxall (1950) distinguished *D. quercina* from other *Diatrypella* species because of its strongly curved ascospores. *Cryptovalsa* and *Diatrypella* also have polysporous asci and cannot easily be distinguished, based on morphological comparisons (Acero et al. 2004; Vasilyeva and Stephenson 2005; Dissanayake et al. 2021a, b). A number of taxonomic studies have been done for *D. quercina* species based on morphological observations from different countries in the world (Farr and Rossman 2022). Adamčíková et al. (2011) reported the records of *Libertella quercina* based on their morphology on *Castanea sativa* from Slovakia. *Libertella quercina* was also reported on bark of *Quercus* in England and France (Grove 1937; Adamčíková et al. 2011). Saccardo (1906) described *Cytosporina quercina* (basionym *Libertella quercina*) on branches of *Quercus* and *Castanea* in Italy, France, and Germany and later, the taxon was identified as the asexual morph of *Diatrypella quercina* (Grove 1937). Popov et al. (2008) reported *D. quercina* on *Quercus robur* from Russia based on morphology while our strain MFLU 18–1865, was from *Q. petraea* subsp. *polycarpa* is also known as Georgian, or Colchician oak—the native oak species for western Caucasus. However, no genetic studies were reported from Russia for this taxon. There were only two studies providing molecular data for the species from Spain (on *Quercus faginea*) (Acero et al. 2004; Vu et al. 2019 taken from GenBank 2022). We provided a comprehensive taxonomic study for *D. quercina* based on their morpho-molecular and phylogenetic analyses. In our phylogenetic analyses our strain (MFLU 18–1865) grouped with other isolates of *D. quercina* (CBS 108.18 and DL30M) in Clade B, with 85% MLBS, 0.95 BYPP support. Also, our strain forms a sister lineage to CBS 108.18 and grouped with high bootstrap support (95% ML). In comparison of base pair differences between CBS 108.18 and DL30M (*D. quercina*), 6 bp differences (1.16%) have revealed by 513 nucleotides in ITS region while *tub*2 regions are not available. However, we provided *tub*2 sequence data for *D. quercina* in this study. We revealed 1 and 5 pb differences from 515 nucleotides (0.19% and 0.97%) in ITS regions when comparing our strain (MFLU 18–1865) with CBS 108.18 and DL30M respectively. Trimen et al. (1866, https://www.biodiversitylibrary.org/page/16233050) provided incomplete morphology for the taxa and these characters are matched with the morphology of our strain. Based on referred morpho-molecular data we conclude that our stain should be another collection of *D. quercina* from Russia. This is the first genetic study on *D. quercina* in Russia with detailed morphology and it is also the new host record on *Q. petraea* subsp. *polycarpa*. However, detailed morphological studies are suggested in future for this taxon (Figs. 124, 125).

Hypoxylaceae DC., in Lamarck & de Candolle, Fl. franç., Edn 3 (Paris) 2: 280 (1805)

Xylariales comprises with 26 families. Xylariaceae and Hypoxylaceae are two of the most diverse families in this order. Hypoxylaceae is represented by 16 genera including which comprises sexual morphs 16 and asexual morphs 11 genera (Wijayawardene et al. 2022). Hypoxylaceae are distributed in tropical, subtropical regions (Lambert et al. 2019), known for its huge species diversity and abundant bioactive secondary metabolites (Helaly et al. 2018) and plays an important ecological role in protecting host plants from pathogens (Song et al. 2022). The family is

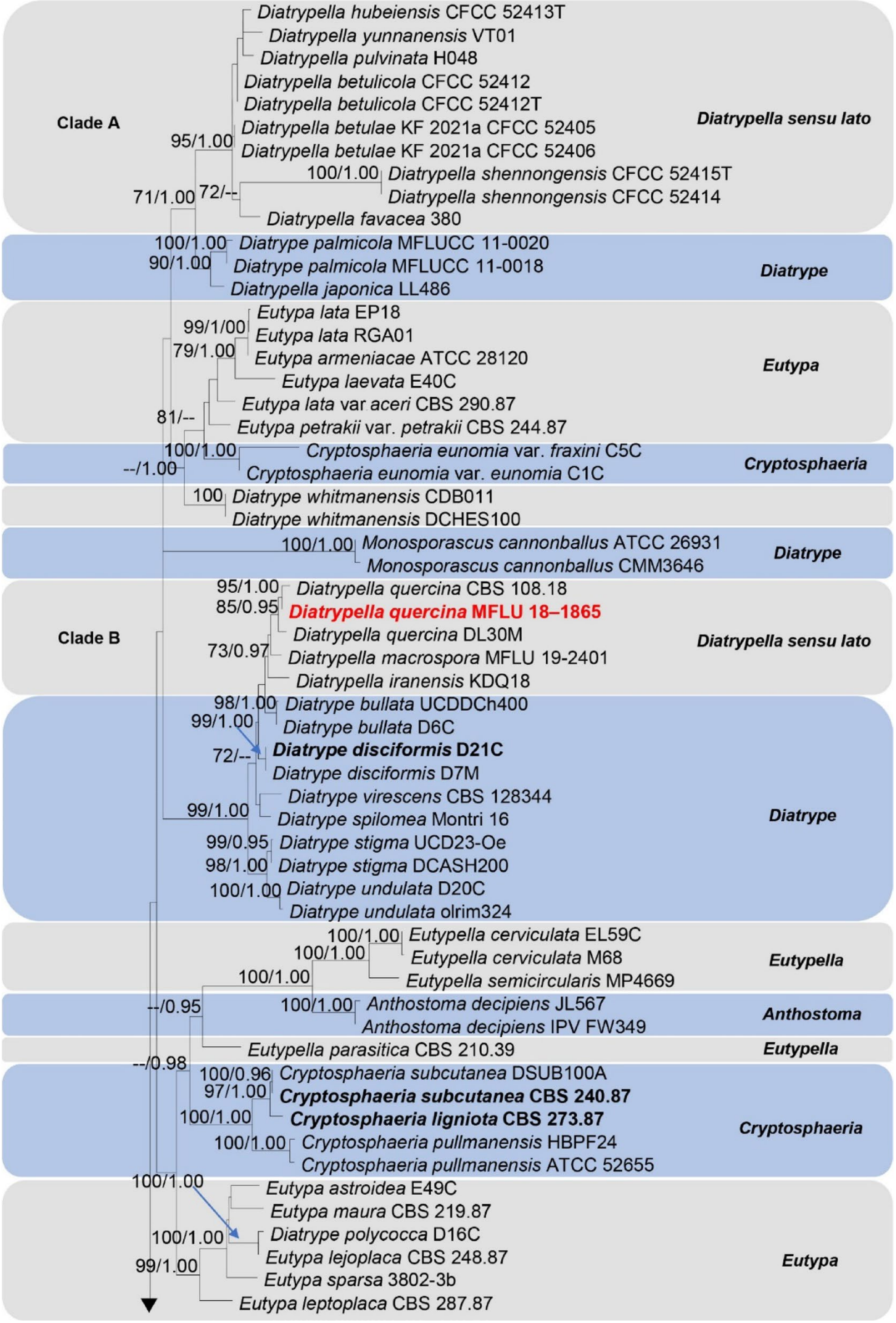


Fig. 125 Phylogram generated from maximum likelihood analysis based on combined ITS and *tub*2 sequence data representing *Diatrypaceae* in Xylariales. Related sequences are taken from Boonmee et al. (2021) and additions according to the BLAST searches in NCBI. Hundred and thirty-five strains are included in the combined analyses which comprised 912 characters (517 characters for ITS and 395 characters for *tub*2) after alignment. *Kretzschmaria deusta* (CBS 826.72) and *Xylaria hypoxylon* (CBS 122,620) in *Xylariaceae* (Xylariales) were used as the outgroup taxa. Bootstrap support values for ML ≥ 75% are given above the nodes (left side). Bayesian posterior probabilities (BYPP) ≥ 0.95 are given above the nodes (right side). Ex-type strains are in **bold** and newly generated sequence is in red

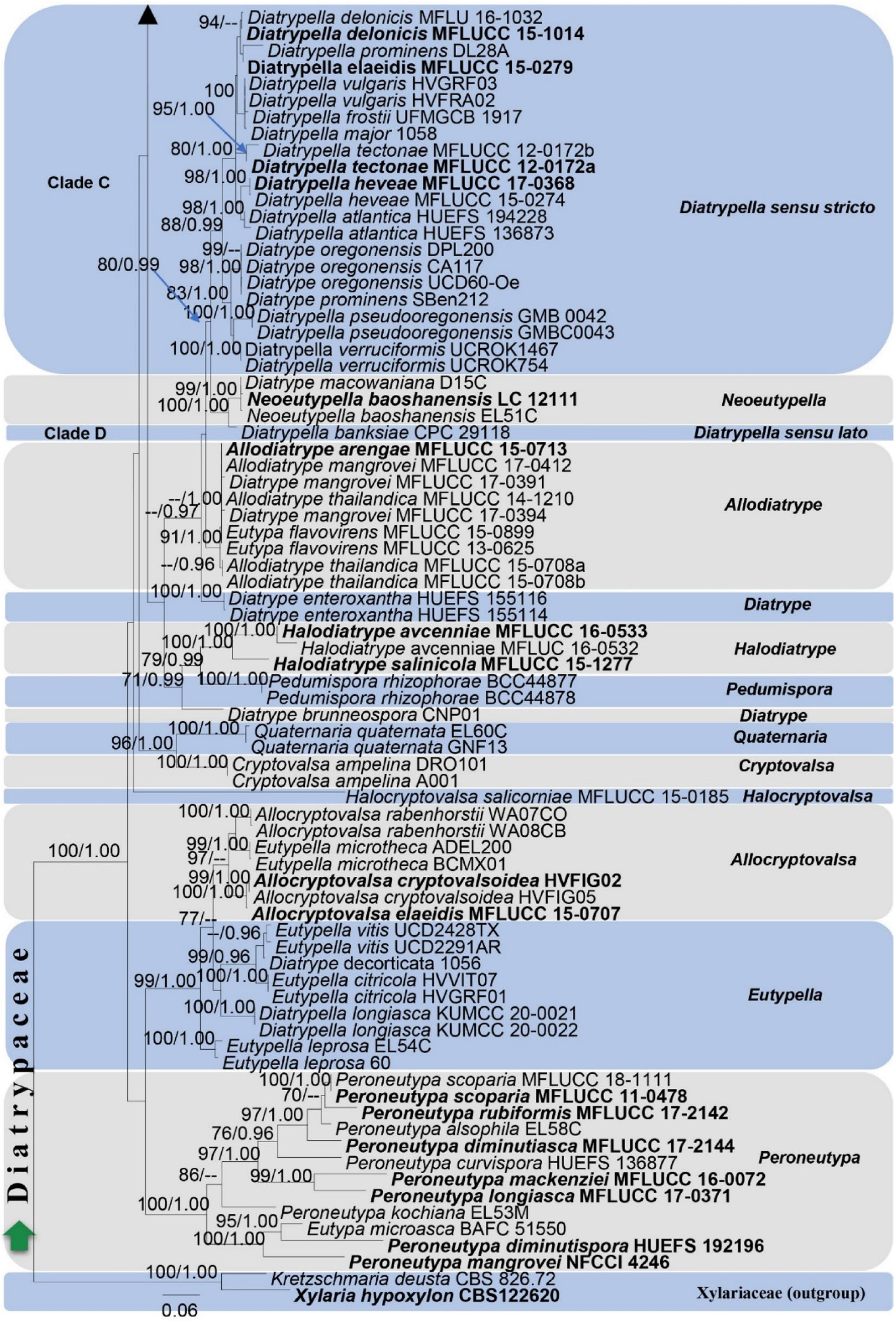


Fig. 125 (continued)

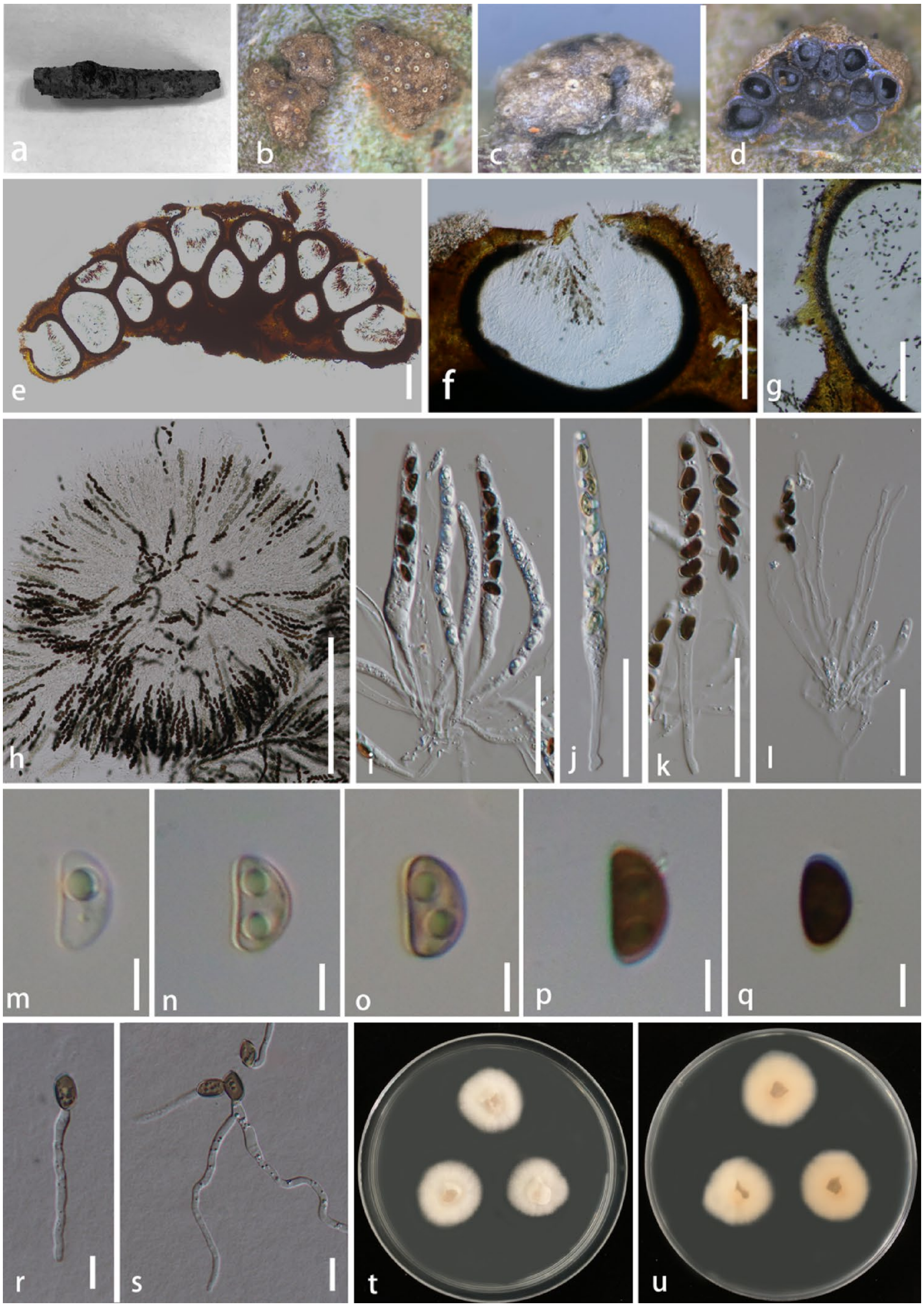


Fig. 126 ***Hypoxylon inaequale***. (HKAS123207, **holotype**) **a** Substrate. **b, c** Stromata showing ostioles. d, e Vertical section through stromata. **f** Perithecium. **g** Peridium. **h–k** asci. **l** paraphyses. **m–q** Immature to mature ascospores. **r**, **s** Germinating ascospores. **t**, **u** Culture on PDA. Scale bars: **e–f**, **h** = 200 µm, **g** = 100 µm **i–l** = 50 µm, **m–s** = 5 µm

characterised by carbonised stromatal tissue. Stromata surface is usually blackened when mature, olivaceous, with %10 KOH are purplish or orange. Ostioles that are always higher than the level of stromatal surface (Cruz et al. 2021).

Hypoxylon Bull., Hist. Champ. Fr. (Paris) 1(1): 168 (1791)

Hypoxylon was introduced by Bulliard, that contains primarily saprotrophs and endophytes of angiospermous plants. The type genus *Hypoxylon* is the largest genus in the Hypoxylaceae, with more than 200 species (Pourmoghaddam et al. 2020). Members of the genus have a worldwide distribution, but they display a higher diversity in the tropics and subtropics (Kuhnert et al. 2014). In the twentieth century, the generic concept of *Hypoxylon* was based only on morphological characteristics (Ju and Rogers 1996). Currently, morphological, phylogenetic, and chemotaxonomic evidence, has also been used to infer species limits in inter- and intragenera in Hypoxylaceae (Sir et al. 2016). *Hypoxylon* is quite common in China; however, the occurrence of the species in China has not been confirmed by molecular phylogenetic

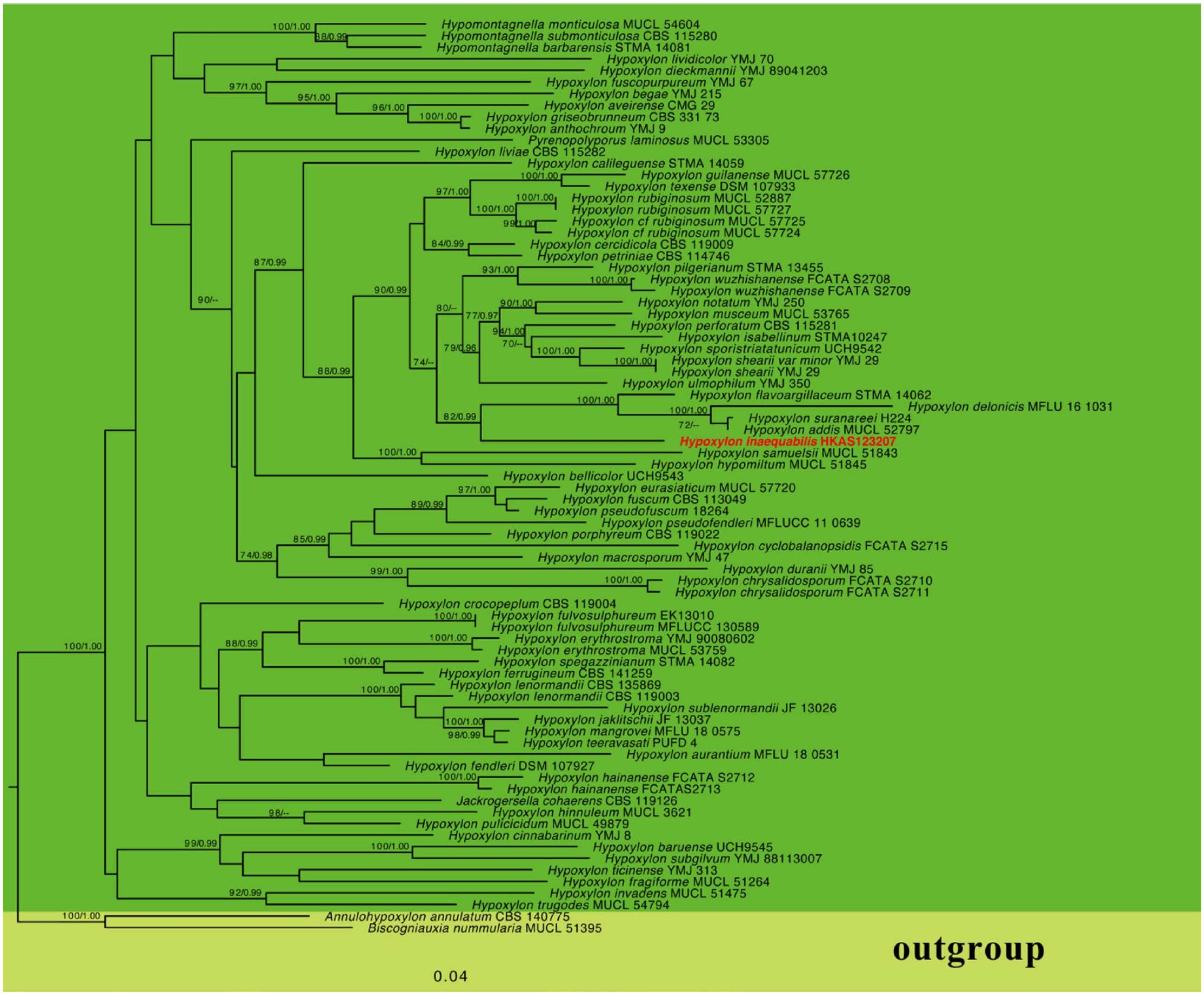


Fig. 127 Phylogram generated from maximum likelihood analysis based on combined ITS, *tub2* sequence data representing Hypoxylaceae in Xylariales. Related sequences are taken from (Cedeño–Sanchez 2020) and additions according to the BLAST searches in NCBI. Seventy-two strains are included in the combined analyses which comprised 1654 characters (532 characters for ITS,1122 characters for *tub2*) after alignment. *Biscogniauxia nummularia* (MUCL 51,395) and *Annulohypoxylon annulatum* (CBS 140775) in *Xylariales* were used as the outgroup taxa. Bootstrap support values for ML ≥ 70% are given above the nodes (left side). Bayesian posterior probabilities ≥ 0.95 are given above the nodes (right side). Ex-type strains are in **bold** and newly generated species is in red

analyses, and the species diversity and distribution of the genus in China are unclear (Hyde et al. 2020a, b, c). The aims of this study were to confirm the taxonomic status of the new species, explore the species diversity of *Hypoxylon*, and infer the evolutionary relationships of *Hypoxylon*.

Hypoxylon inaequale S.C. He & Jayaward., ***sp. nov.***

Index Fungorum number: *IF900071; Facesoffungi number*:*FoF13393*; *Fig. 126*

Etymology: Based on the inequilateral spore character.

Holotypus: HKAS123207.

Saprobic on dead stem plant from *Itoa orientalis*. **Sexual morph:** *Stromata* 40–50 × 20–30 mm (M = 45 × 25 mm, $n = 15$), glomerate, fawn, sessile, gregarious or solitary, with white ostioles. *Perithecia* 250–300 × 260–450 µm ($\bar{x} = 275 \times 365$ µm, $n = 15$), spherical to obovoid, completely immersed in stromata. *Ostioles* 90–120 µm diam, umbilicate, white. *Paraphyses* 2.5 × 3.1 µm wide, copious, filiform, aseptate, unbranched. *Asci* 132 – 153 × 9–11 µm ($\bar{x} = 142 \times 10$ µm, $n = 10$), cylindrical, 8-spored, uniseriate, stipitate, with apical apparatus colorless in Melzer's reagent. stipe 40–112 µm ($n = 10$). *Ascospores* 9.8–11.8 × 5.0–5.9 µm ($\bar{x} = 10.45 \times 5.45$ µm $n = 20$), pale dark brown when immature, becoming dark brown with age, ellipsoid-inequilateral with round ends, unicellular, with two round guttulae, obliquely arranged. **Asexual morph**: Not observed.

Fig. 128 Astrocystis bambusicola (KUN-HKAS 125897, **new record**) **a** Substrate. **b**, **c**. Ascomata. **d** Section through ascoma. **e–h** Asci. **i** Paraphysis. **j** Asci with J.+ apical ring. **k** Ascospore. **l**, **m** Upper and reverse view of cultures on PDA at 8 days incubation. **n** Germinating spore. Scale bars: **d**, **e** = 50 µm, **f–j** = 30 µm, **k**, **n** = 10 µm. (j stained in Melzer's reagent)

Culture characteristics: Culture was made from germinating ascospores and was incubated with PDA media at 25 ℃, reaching 2.2–2.4 cm in 24 days. The colony white, occasionally raised, fluffy, with dense mycelia, umbonate margin, reverse chrome yellow.

Material Examined: China, Yunnan Province, Kunming City, Kunming Institute of Botany, Chinese Academy of Sciences, on Itoa orientalis Hemsl. (*Salicaceae*), 30 August 2021,Shu-Cheng He, HSC20B (HKAS123207, **holotype**); ex-type living culture, KUNCC22-10798.

GenBank numbers: ON329812 (ITS).

Notes: Based on the multi-gene phylogenetic results, our specimen is closely related to *Hypoxylon delonicis* (Perera et al. 2020). Based on morphology, our strain differes from *Hypoxylon delonicis* by having wider asci and shorter and woder ascospores. Based on a megablast search of the NCBIs nucleotide database using the multi-gene sequence, the highest similarities ITS (GenBank KU683766; Identities = 480/541(89%), Gaps = 17/541(3%)), *tub2* (GenBank AY951740; Identities = 1126/1265(89%), other species of

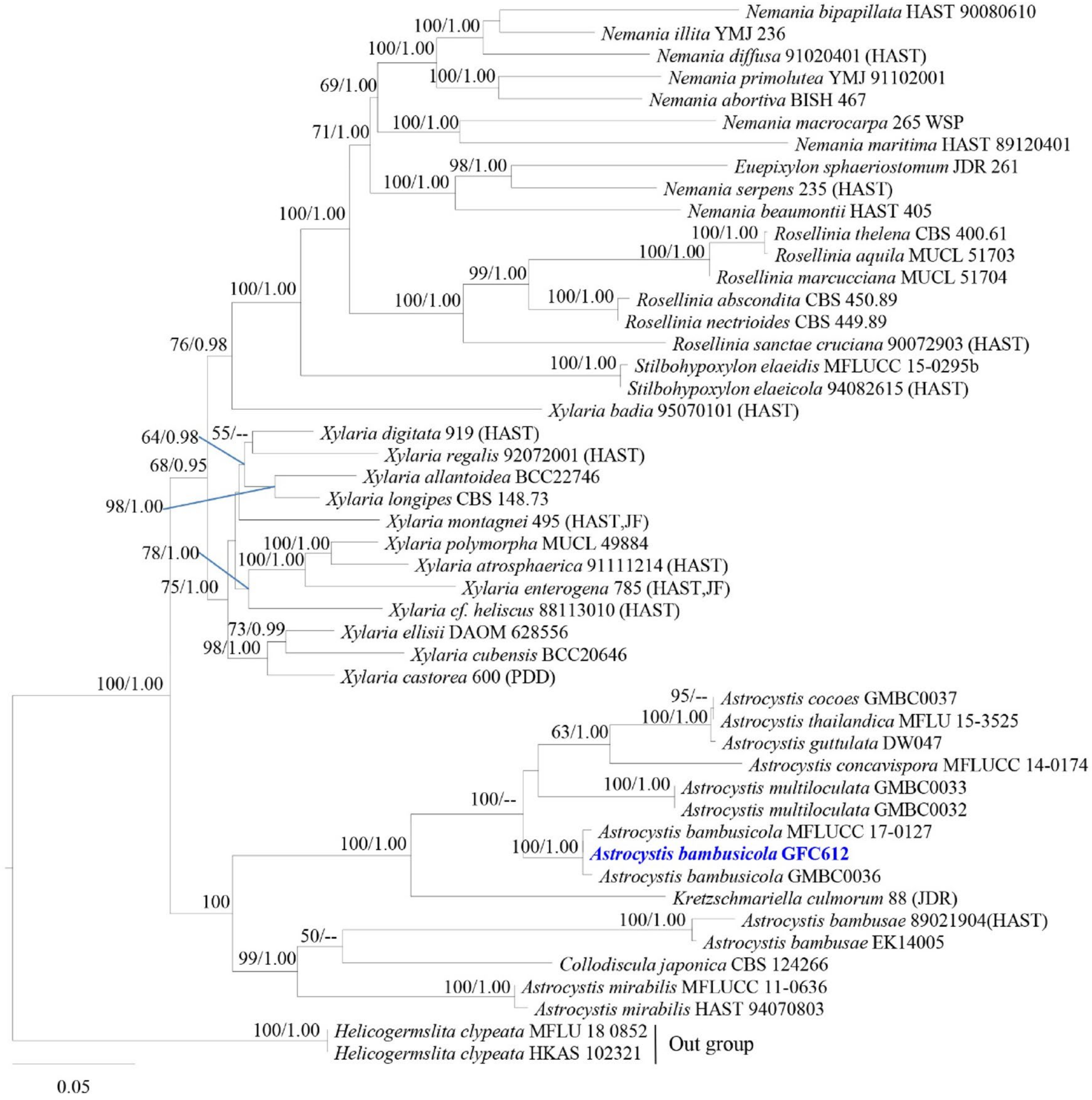


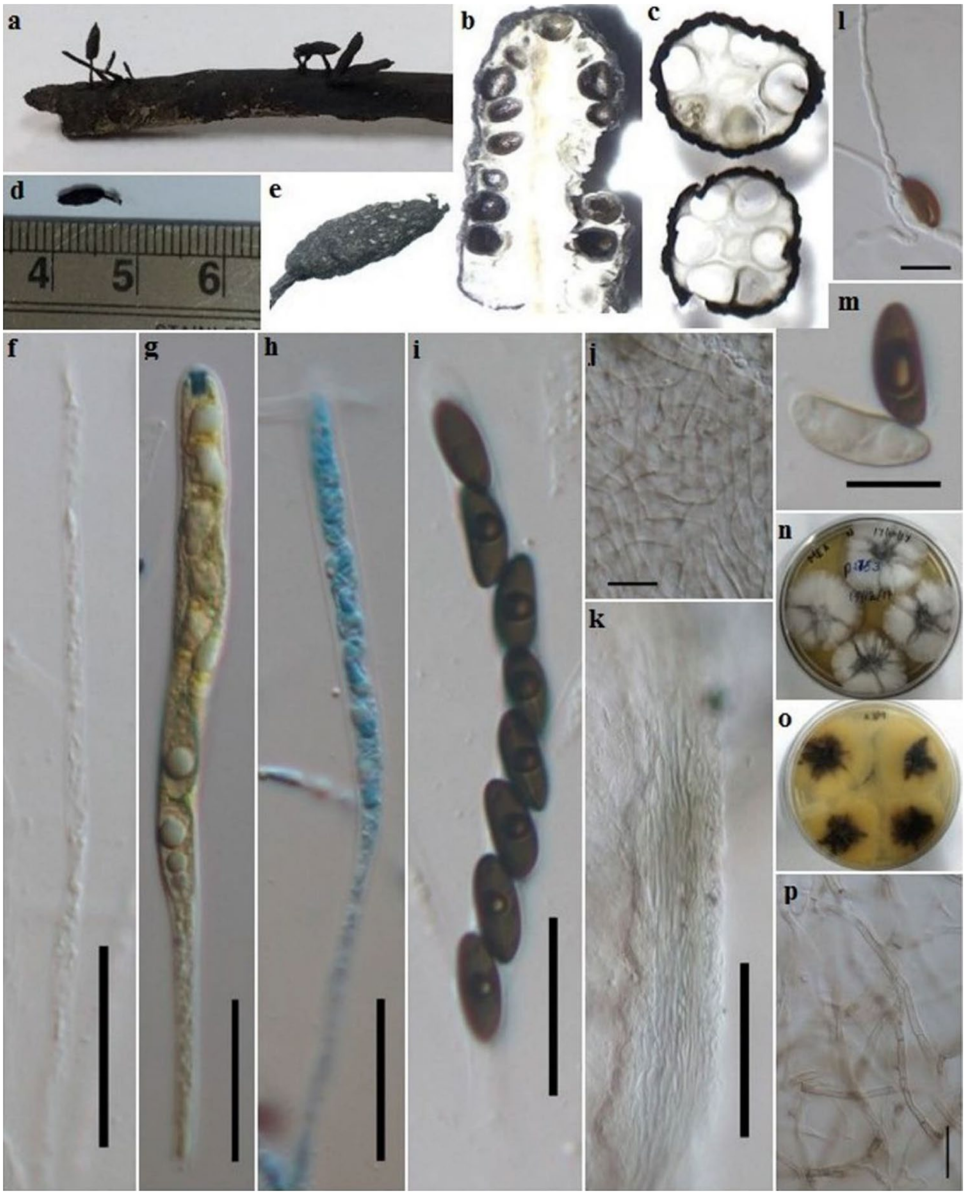
Fig. 129 RAxML tree inferred from combined ITS, LSU, *rpb2* and *tub2* sequence. Bootstrap support for maximum likelihood analysis ≥ 50% and Bayesian posterior probabilities ≥ 0.95 are denoted next to the notes in this order. The new collection is marked in blue bold font

Hypoxylon delonicis with strong bootstrap support (82/0.99, Fig. 127). We identified *Hypoxylon inaequale* as a new species of *Hypoxylon*.

Xylariaceae Tul. & C. Tul. [as 'Xylariei'], Select. fung. carpol. (Paris) 2: 3 (1863).

Notes: Xylariaceae is the type and largest family of Xylariales (Hyde et al. 2020a, b, c). Number of genera in this family has been subjected to multiple revision in different articles. Kirk et al. (2001) and Eriksson (2007) estimated that there are 75 genera and about 800 species in Xylariaceae. Hyde et al. (2020a, b, c) counted 32 genera in this family and provided notes for each accepted genus. Wijayawardene et al. (2022) listed 38 genera in Xylariaceae, without giving supported annotation. Xylariaceae can live as saprobes, pathogens, or endophytes, habiting wood, leaves and fruits (Hyde et al. 2020a, b, c). Xylariaceae is characterized by perithecia embedded in erect, applanate or effuse-pulvinate, dark-coloured stromata, cylindrical asci with an amyloid apical ring, brown to black, 1–2-celled, ellipsoidal, subglobose or reniform, with with germ slits or pores (Tang et al. 2009; Maharachchikumbura et al. 2016; Hyde et al. 2020). Xylariaceae was divided into two subfamilies including Xylaroideae and Hypoxyloideae based on their respective anamorphic types, their stromatal pigments and secondary metabolites. Xylaroideae generally is considered to comprise species with *Nodulisporium*-type anamorph and KOH+ stromatal

Fig. 130 *Xylaria venosula* (Herbarium AMH-10068, **new record**) **a, d, e** Stromata on decaying host, **b** Vertical section of stromata **c** Horizontal section of stromata **f** Paraphyses, **g-i** Asci **j** *Textura intricata* **k** Peridium**, l m** Germinating spore **n, o** Culture on MEA plates, **p** Hypha. Scale bars: **k** = 50 µm, **f-i** = 20 µm. **j, m, n, p** = 10 µm



pigments, while it is Geniculosporium-type and KOH^{-} in Hypoxyloideae. Multigene phylogenetic analysis based on LSU, SSU and *rpb2* sequence well reflect these two subfamilies (Samarakoon et al. 2016a, b).

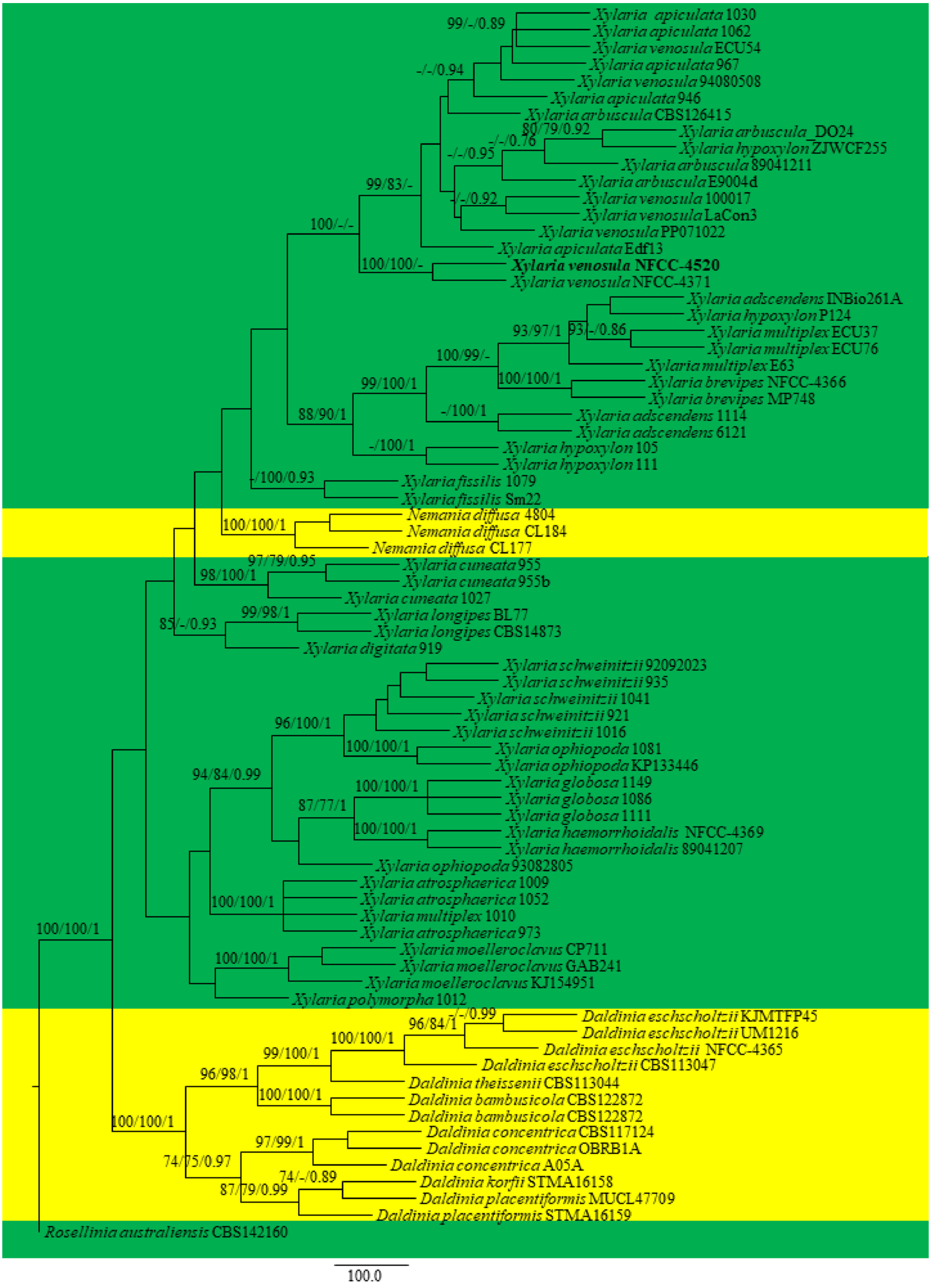
Astrocystis Berk. & Broome, J. Linn. Soc., Bot. 14(no. 74): 123 (1873) [1875].

Notes: *Astrocystis* was introduced by Berkeley and Broome (1850) and typified by *Astrocystis mirabilis*. Index fungorum (2022a, b) lists 28 epithets in *Astrocystis*, while four of them have been excluded from this genus. Species of this genus mainly exist in saprobes on monocotyledonous substrates, such as bamboo, palm and Smilax (Laessøe and Spooner 1993). *Astrocystis* is characterized by uni- to multi-peritheciate stromata, carbonaceous peridium, asci with a relatively short stipe and small, amyloid, stopper-shaped ascal ring (Pinnoi et al. 2010). It is widely accepted that *Astrocystis* bear similar morphology with *Rosellinia*, while the former genus can be distinguished from the latter by small and cylindrical or funnel-shaped apical ring of asci. *Rosellinia* has conspicous, barrel-shaped apical apparatus (Dulymamode et al. 1998).

Astrocystis bambusicola R.H. Perera & K.D. Hyde, in Hyde et al., Fungal Diversity 87: 173 (2017).

Index Fungorum: IF553799; *Facesoffungi number: FoF10187*; *Fig. 128*

Saprobic on dead culms of *Microstegium* sp. appearing as black raised spots on the host. **Sexual morph:** *Ascomata* up to 173 µm in width and 135 µm in high, subglobose,


99/-/0.89
Xylaria apiculata 1030
Xylaria apiculata 1062
Xylaria venosula ECU54
-/-/0.94
Xylaria apiculata 967
Xylaria venosula 94080508
Xylaria apiculata 946
Xylaria arbuscula CBS126415
80/79/0.92
-/-/0.76
Xylaria arbuscula_DO24
-/-/0.95
Xylaria hypoxylon ZJWCF255
Xylaria arbuscula 89041211
99/83/-
Xylaria arbuscula E9004d
-/-/0.92
Xylaria venosula 100017
Xylaria venosula LaCon3
100/-/-
Xylaria venosula PP071022
Xylaria apiculata Edf13
100/100/-
Xylaria venosula NFCC-4520
Xylaria venosula NFCC-4371
Xylaria adscendens INBio261A
Xylaria hypoxylon P124
93/97/1
93/-/0.86
Xylaria multiplex ECU37
100/99/-
Xylaria multiplex ECU76
Xylaria multiplex E63
99/100/1
100/100/1
Xylaria brevipes NFCC-4366
Xylaria brevipes MP748
88/90/1
-/100/1
Xylaria adscendens 1114
Xylaria adscendens 6121
-/100/1
Xylaria hypoxylon 105
Xylaria hypoxylon 111
-/100/0.93
Xylaria fissilis 1079
Xylaria fissilis Sm22
Nemania diffusa 4804
100/100/1
Nemania diffusa CL184
Nemania diffusa CL177
97/79/0.95
Xylaria cuneata 955
98/100/1
Xylaria cuneata 955b
Xylaria cuneata 1027
99/98/1
Xylaria longipes BL77
85/-/0.93
Xylaria longipes CBS14873
Xylaria digitata 919
Xylaria schweinitzii 92092023
Xylaria schweinitzii 935
Xylaria schweinitzii 1041
96/100/1
Xylaria schweinitzii 921
Xylaria schweinitzii 1016
100/100/1
Xylaria ophiopoda 1081
Xylaria ophiopoda KP133446
94/84/0.99
100/100/1
Xylaria globosa 1149
87/77/1
Xylaria globosa 1086
Xylaria globosa 1111
100/100/1
Xylaria haemorrhoidalis NFCC-4369
Xylaria haemorrhoidalis 89041207
Xylaria ophiopoda 93082805
Xylaria atrosphaerica 1009
100/100/1
Xylaria atrosphaerica 1052
Xylaria multiplex 1010
100/100/1
Xylaria atrosphaerica 973
100/100/1
Xylaria moelleroclavus CP711
Xylaria moelleroclavus GAB241
Xylaria moelleroclavus KJ154951
Xylaria polymorpha 1012
-/-/0.99
96/84/1
Daldinia eschscholtzii KJMTFP45
Daldinia eschscholtzii UM1216
100/100/1
Daldinia eschscholtzii NFCC-4365
99/100/1
Daldinia eschscholtzii CBS113047
96/98/1
Daldinia theissenii CBS113044
100/100/1
Daldinia bambusicola CBS122872
100/100/1
Daldinia bambusicola CBS122872
97/99/1
Daldinia concentrica CBS117124
74/75/0.97
Daldinia concentrica OBRB1A
Daldinia concentrica A05A
74/-/0.89
Daldinia korfii STMA16158
87/79/0.99
Daldinia placentiformis MUCL47709
Daldinia placentiformis STMA16159
Rosellinia australiensis CBS142160
100.0

◂ **Fig. 131** Maximum parsimony tree generated from by using the ITS sequences belongs to Xylariaceae species. The tree includes the ML, MP and BYPP values. In the phylogenetic tree the sequence analysis of *Xylaria venosula* NFCC-4520 (black bold letters) is shown with other species of *Xylaria* and *Rosellinia australiensis* as out-group

black, perithecial, gregarious, superficial, 1–2-loculate, with flattened top and projecting papillas. *Peridium* 43–60 ($\bar{x}=50$, $n=10$) µm, composed of membranous inner wall and black, fragile, carbonaceous outer wall. *Paraphyses* 3.8–8.3 ($\bar{x}=6.2$, $n=25$) µm, septate, cylindrical, hyaline, unbranched, guttulate. *Asci* 84–121 × 6.8–11 ($\bar{x}=99\times8.8$, $n=30$) µm, 8-spored, unitunicate, cylindrical, with a short pedicel and J^+ apical ring. *Ascospores*12–15 × 5.7–8 ($\bar{x}=14\times6.5$, $n=50$) µm, reniform, dark brown to black, uniseriate, aseptate, guttulate, smooth-walled, with a germ-slit, without a gelatinous sheath. **Asexual morph:** Not observed.

Culture characteristics: Culture was made from germinal ascospores that germinated on PDA within 24 h, at 23–25 °C. Colonies rapidly growing on PDA, reaching 30 mm at 8 days, white from above and reverse, cottony, circular, umbonate, edge irregular.

Material examined: China, Guizhou Province, Qianxinan Buyei and Miao Autonomous Prefecture, Ceheng County, Gaofeng Village, on dead culms of *Microstegium* sp. (Poaceae), 8 August 2018, D. P. Wei, GFC612 (KUN-HKAS 125898), living culture KUNCC 22-12539.

Known hosts and distribution: Bamboo (Yunnan, China; Thailand) (Hyde et al. 2017, 2020a, b, c).

Genbank numbers: OQ029540 (ITS), OQ029613 (LSU), OQ061263 (SSU), OQ186444 (*tef1*), OQ186446 (*tub2*).

Notes: *Astrocystis bambusicola* has been reported on bamboo column from China and Thailand (Hyde et al. 2017, 2020a, b, c). Our isolate phylogenetically groups with *Astrocystis bambusicola* with great support (100% ML/1.00 BYPP, Fig. 129). Morphologically our isolate bears resemblance with *Astrocystis bambusicola* in the subglobose, black, superficial ascomata, carbonaceous peridium, cylindrical asci with J^+ apical ring and reniform, dark brown to black ascospores with a germ-slit. We introduce our isolate as a new host record species of *Astrocystis bambusicola* from *Microstegium* sp. in Guizhou Province, China.

Xylaria Hill ex Schrank, Baier. Fl. (München) 1: 200 (1786).

Notes: *Xylaria* is one of the largest genera in Xylariaceae and it includes more than 600 species *(*Hyde et al. 2020a, b, c; Boonmee et al. 2021). Its occurrence in diverse environments shows its unique role as saprobes, endophytes and as plant pathogens (Edwards et al. 2003; Ju et al. 2018; Hyde et al. 2020a, b, c). *Xylaria* species mostly have long stalked thread-like macro structures. A few species of this genus coexist with plants as endophytes (Chen et al.2013), which may later turn into saprobes (Promputtha et al. 2007) when plants die. They also extend their habits as coprophilous and endolichenic (Piasai and Manoch 2009; Cañón et al. 2019). Most *Xylaria* species also serve as economically important compound producers (Ratnaweera et al. 2014; Adeleke and Babalola 2021; Wangsawat et al. 2021; Becker and Stadler 2021), which act as antibacterial, antifungal and/or biocontrol agents. Therefore, there is a need for the discovery of novel species and new geographical records of this genus. Annually ten or more, new species are introduced to this genus. For instance, in 2020, ten new species were discovered and in the next year, 15 species were discovered (Index Fungorum 2022a, b) by morphology and molecular data.

Xylaria venosula Speg. Boletín de la Academia Nacional de Ciencias en Córdoba 11 (4): 511 (1889).

Index Fungorum number: IF 247711; *Facesoffungi number*: *FoF09866; Fig. 130*

Saprobic on decaying twig. **Sexual morph:** *Ascostromata* 1 cm long, superficial, aggregated in clusters, surface undulated, rarely with parallel cracks, with acute apices. Ascomata 340–385 × 370–450 µm ($\bar{x}=362\times406$ µm, $n=5$), globose, erumpent, pulvinate, with central periphysate necks 90–120 × 60–100 µm ($\bar{x}=101\times75$ µm, $n=5$). Peridium 32 µm wide, with brown to hyaline, *textura porrecta* cell layers. *Hamathecium*: paraphyses septate, branched, 2.8 µm wide, longer than asci, sparsely present. *Asci* 110 –132 × 5.6–8 µm ($\bar{x}=117.5\times6.6$ µm, $n=25$), unitunicate, 8–spored, cylindrical, apically rounded with J + apical rings, rings 2.6–3.6 × 1.7–2.3 µm ($\bar{x}=3.2\times2$ µm, $n=25$), long-pedicellate, persistent. *Ascospores* 12.5 –15.5 × 4.7–7 µm ($\bar{x}=13.6\times5.7$ µm, $n=25$), overlapping uniseriate, hyaline to brown at maturity, oblong to navicular, with straight germ slits, uni-guttulate, obtuse ends, smooth-walled. **Asexual morph:** Not observed.

Distribution: Brazil, China, Ecuador, India and USA.

GenBank numbers: MZ292933 (ITS).

Material examined: India, Andaman and Nicobar Islands, South Andaman, Mount Harriet, (11° 71′ 09.8″ N 92° 73′ 30.6″ E), recorded on an unidentified decaying log, 7 December, 2017, M. Niranjan and V. V. Sarma (PUFNI 1763). Herbarium submitted in Ajrekar Mycological Herbarium-AMH (AMH-10068) and Living culture (NFCC-4520) deposited in National Fungal Culture Collection of India (NFCCI), Pune.

Notes: The references for descriptions of *X. venosula* could be found in Index Fungorum (https://www.biodiversitylibrary.org/page/2937143#page/534/mode/1up) and the global fungal red list (http://iucn.ekoo.se/iucn/species_view/247711). The present taxon has morphological characteristics that are similar to the type and other with slight differences. The present collection consists of paraphyses, smaller asci (109 –132 × 5.6–8 *vs*. 90–400 × 7–9) and oblong to navicular, smaller ascospores

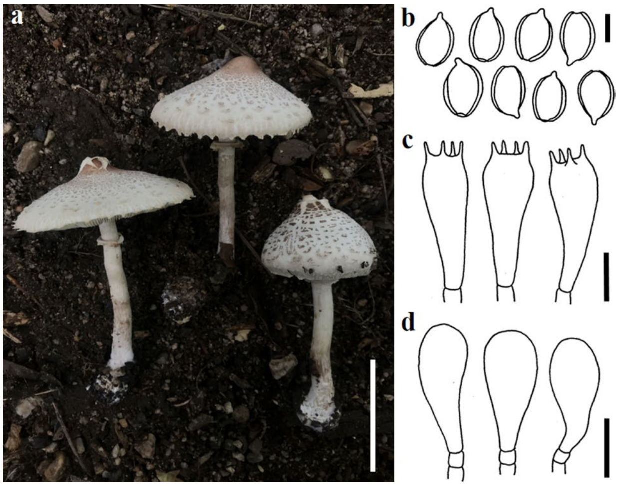


Fig. 132 ***Chlorophyllum squamulosum*** (SDBR-CMUNK0585, **new record**). **a**. Basidiomata. **b**. Basidiospores. **c**. Basidia. **d**. Cheilocystidia. Scale bars: a = 50 mm; b = 5 µm; c, d = 10 µm

(12.5 –15.5 × 4.7–7 *vs*. 14 –18 × 6–7 µm). Geographical distribution of *X. venosula* in five countries mentioned in distribution (https://www.gbif.org/occurrence/search?q=Xylaria%20venosula&taxon_key=5487903) and this is the first report of *X. venosula* from the Andaman Islands, India and as such the present collection extends the geographical distribution and range of this taxon globally (Fig. 131).

Basidiomycota R.T. Moore.

We follow the latest treatments of Basidiomycota in Zhao et al. (2017), He et al. (2019) and Wijayawardene et al. (2022).

Agaricomycotina Doweld.

Agaricomycetes Doweld.

Agaricales Underw.

Agaricaceae Chevall.

Notes: Agaricaceae was erected by Chevallier (1826) based on the type genus *Agaricus* L. Previously, this family contained only gilled fungi. However, research-based on molecular data transferred many non-gilled fungal families such as Lycoperdaceae, Nidulariaceae and Tulostomataceae to Agaricaceae. Now, it is represented by more than 1300 species belonging to 85 genera (Kirk et al. 2008; He et al. 2019; Wijayawardene et al. 2022). Some gasteroid pufball genera included in the Agaricaceae are *Arachnion* Schwein., *Bovista* Pers., *Calvatia* Fr. and *Lycoperdon* Pers.

Chlorophyllum Massee, Bull. Misc. Inf., Kew (no. 138): 135 (1898).

Chlorophyllum (Agaricaceae, Agaricales) was introduced by Massee (1898) with *C. molybdites* (G. Mey.) Massee as the type species. *Chlorophyllum* species are widely distributed in tropical, subtropical, and temperate areas throughout the world as saprobes (Ge and Yang 2006; Kirk et al. 2008; Crous et al. 2015a, b, c; Ge et al. 2018; Dutta et al. 2020). This genus is characterized by agaricoid, secotioid or sequestrate habits, a hymenidermal pileus covering and smooth stipe, white, green or brown basidiospores either lacking a germ pore or with a germ pore that is caused by a depression in the episporium (Ge and Yang 2006; Vellinga 2002, 2003a, 2004; Crous et al. 2015a, b, c; Loizides et al. 2020). Most *Chlorophyllum* species are known to be poisonous (Vellinga and de Kok 2002; Leudang et al. 2017). There are 28 accepted species of *Chlorophyllum* in Index Fungorum (2022a, b). *Chlorophyllum* is divided into six infrageneric sections: *Chlorophyllum* Massee, *Ellipsoidospororum* Z.W. Ge, *Endoptychorum* (Czern.) Z.W. Ge, *Parvispororum* Z.W. Ge, *Rhacodium* Z.W. Ge and *Sphaerospororum* Z.W. Ge based on morphological and phylogenetic analyses (Ge et al. 2018). Only four *Chlorophyllum* species, *C. globosum* (Mossebo) Vellinga, *C. hortense* (Murrill) Vellinga, *C. molybdites* (G. Mey.) Massee and *C. rhacodes* (Vittad.) Vellinga, have been reported from Thailand (Chandrasrikul et al. 2011; Leudang et al. 2017; Ge et al. 2018; Sysouphanthong et al. 2021; Suwannarach et al. 2022).

Chlorophyllum squamulosum A.K. Dutta, Soumili Bera & K. Acharya, Phytotaxa 451: 121 (2020).

Index Fungorum number: *IF835117*; *Facesoffungi number: FoF10684. Fig. 132*

Basidiomata agaricoid, medium to large. *Pileus* 50–75 mm in diam., convex to broadly convex, often with a shallow central depression, sometimes with an upturned margin with age; surface white to cream, covered with squamules, entire at the disc, elsewhere disrupting in some specimens, mostly small plate-like, arranged in a concentric manner from center towards the margin, flat or curved upwards, greyish brown (8E3) to reddish-brown (8E4) or dark brown (8F5) at the center, elsewhere greyish brown (8D3) to brownish grey (7C2) or dull red (9C3). *Lamellae* 4–6 mm broad, adnexed, crowded with two series of lamellulae, white to cream, concolorous; edge even to slightly wavy, yellowish with KOH. *Stipe* 60–90 × 9–12 mm, central, cylindrical, gradually broader towards the base, at base 15–27 mm wide and bulbous to subbulbous, hollow, white (6A1), turning brown (6D6–6E7) on bruising or with KOH. *Annulus* double; upper portion concolorous with the stipe surface; lower portion white to cream, sometimes with greyish brown (8D3) to reddish-brown (8E4) at the margin, rarely with a brownish border; edge sometimes floccose.

Basidiospores 7.5–12 × 5–7.5 µm ($n = 50$), $Q = 1.25–1.85$, $Q_m = 1.5 \pm 0.13$, ellipsoid, smooth, hyaline, dextrinoid, with a prominent wide germ-pore, truncated, thick-walled; apiculus short, 0.5–1 µm long. *Basidia* 25–50 × 8–10 µm, cylindrical to clavate or subclavate, thin-walled, 4-spored,

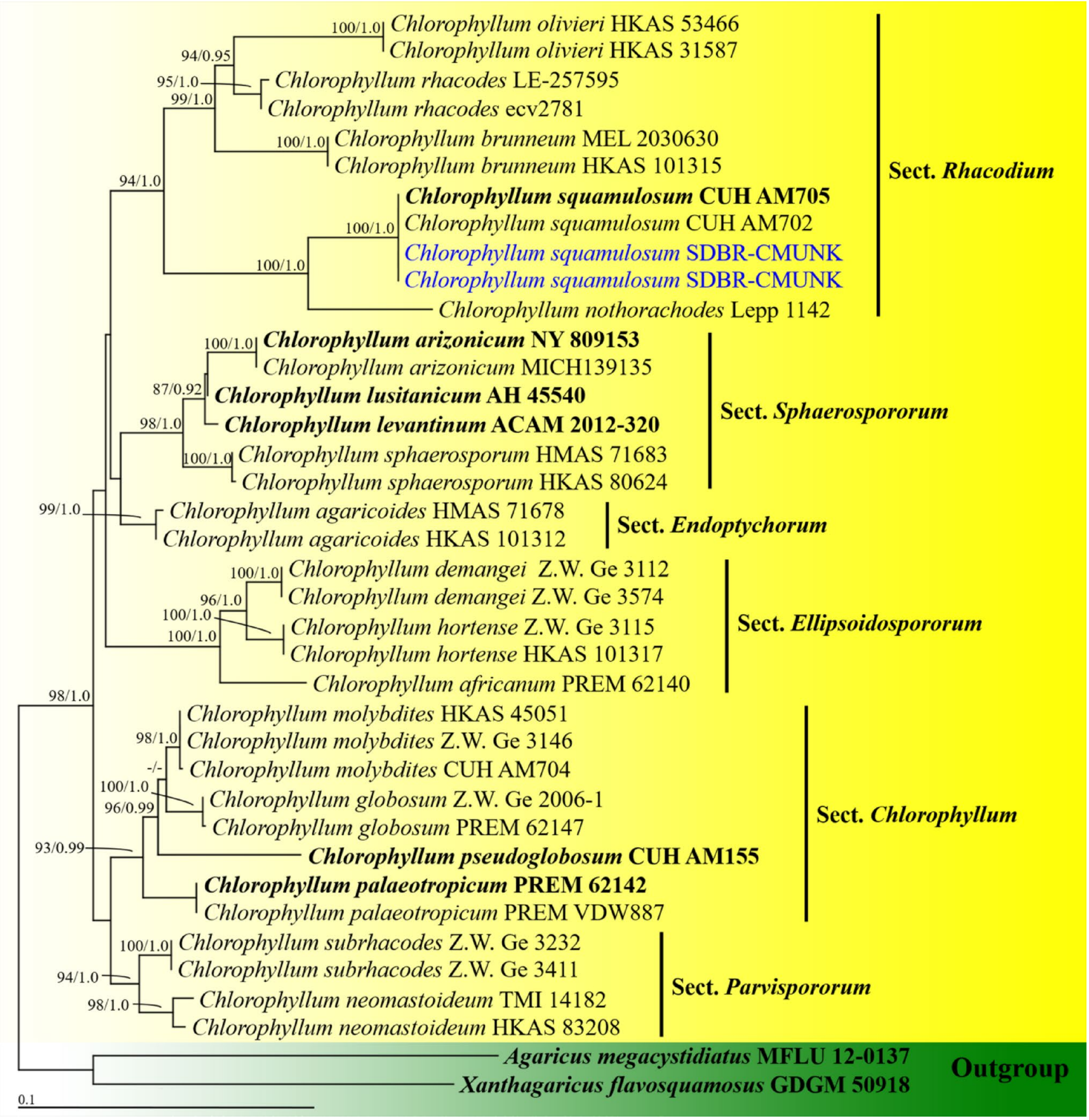


Fig. 133 Phylogenetic tree derived from maximum likelihood analysis of a combined ITS and LSU genes of 38 sequences and the aligned dataset was comprised of 1613 characters including gap. The average standard deviation of the split frequencies of the BI analysis was 0.00481. *Agaricus megacystidiatus* (MFLU 12–0137) and *Xanthagaricus flavosquamosus* (GDGM50918) were used as outgroup taxa. The numbers above branches are the bootstrap statistics percentages (left) and Bayesian posterior probabilities (right). Branches with bootstrap values ≥ 70% are shown at each branch and the bar represents 0.1 substitutions per nucleotide position. Hyphen (-) represents support values ≤ 70%/0.90. Ex-type strains are in black *bold*. The newly generated sequences are indicated in blue

sterigmata upto 10 µm long, cylindrical. *Pleurocystidia* absent. *Cheilocystidia* 17–25 × 7.5–12 µm, clavate or spheropedunculate, hyaline, thin-walled. *Annulus* hyphae 3–7 µm broad, tightly arranged, hyaline, often branched, hyphal end obtuse to clavate, thin-walled. *Pileipellis* (pileal squamules) a tightly packed hymeniderm, with cylindrical and flexuous, or narrowly clavate terminal elements, measuring 5–12.5 µm broad, with pale brown intracellular pigments, often incrusted, sometimes branched, thin-walled. *Pileus* trama hyphae 7–14 µm broad, incrusted, thin-walled.

Fig. 134 ***Lepiota metulispora*** in habitat. **a-c** HNL503136 **d-e** HNL503151

Stipitipellis hyphae 5–10 µm broad, parallel to subparallel, light yellowish with KOH, sometimes branched, non-incrusted, thin-walled. *Stipe trama* hyphae 5–12 µm broad, incrustations present, parallel to subparallel, thin-walled. *Caulocystidia* absent. *Clamp connections* absent in all the tissues.

Material examined: Thailand, Chiang Mai Province, Muang District, Chiang Mai University, 18°48′2″N 98°57′18″E, elevation 335 m, solitary on soil in grassland, 3 August 2019, J. Kumla, SDBR-CMUNK0585, 18°48′14″N 98°57′15″E, elevation 333 m, solitary on sandy humus mixed soil, 26 July 2020, J. Kumla, SDBR-CMUNK0731.

Habitat: Solitary, on sandy humus mixed soil in the dry deciduous forests and grassland.

Distribution: Known from India and Thailand (Dutta et al. 2020; this study).

GenBank numbers: SDBR-CMUNK0585- MZ4502085 (ITS), MZ452086 (LSU)

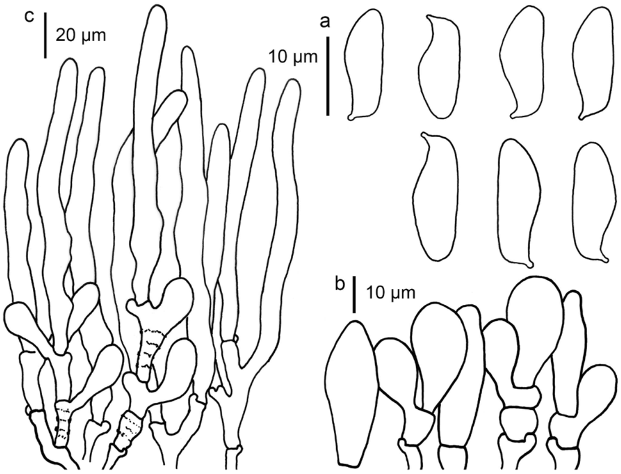


Fig. 135 ***Lepiota metulispora*** (HNL503151, **new record**). **a** Basidiospores **b** Cheilocystidia **c** Pileus covering

SDBR-CMUNK0731- MZ4502084 (ITS), MZ452070 (LSU)

Notes: *Chlorophyllum squamulosum* belongs to the *Chlorophyllum* section *Rhacodium* based on a combination of morphological and molecular data (Fig. 133). Morphologically, *C. squamulosum* is similar to *C. nothorhacodes, C. rhacodes*, *C. olivieri* and *C. brunneum* by its brownish to reddish colouration of the stipe upon bruising, truncated basidiospores and clavate cheilocystidia. The phylogenetic tree indicated that *C. squamulosum* formed a sister taxon to *C. nothorhacodes*. However, *C. nothorhacodes* differs from *C. squamulosum* by its much larger basidiocarp (pileus of up to 280 mm in diam. and stipe up to 250 mm × 25–60 mm) (Vellinga 2003a). Furthermore, *C. rhacodes* differs from *C. squamulosum* by its broader basidiospores (9.8–11.1 × 6.3–7.7 µm), comparatively larger cheilocystidia (16–43 × 8.5–25 µm) and the presence of clamp connections in the basidia, cystidia and tramal hyphae (Vellinga 2001, 2003b). *Chlorophyllum olivieri* has clamped basidia and broader cheilocystidia (35–45 µm) when compared with *C. squamulosum* (Vellinga 2001). *Chlorophyllum brunneum* differs from *C. squamulosum* by the presence of clamp connections at the base of the basidia and cystidia (Bougher and Syme 1998; Vellinga 2002, 2003a).

Lepiota (Pers.) Gray, Nat. Arr. Brit. Pl. (London) 1: 601 (1821).

Lepiota belongs to Agaricaceae, and is consisted of 450 species (He et al. 2019). Vellinga (2001) accepted *Lepiota* for six sections based on the morphology, which are Sect. *Echinatae* Fay.*,* Sect. *Fuscovinaceae* Bon & Candusso, Sect. *Lepiota* (Pers.) Gray*,* Sect. *Lilaceae* M. Bon, Sect. *Ovisporae* (J.E. Lange) Kühner and Section *Stenosporae* (J.E. Lange) Kühner. However, the genus is not monophyletic according to many molecular studies (Vellinga 2003a, b; Liang et al. 2011; Hou and Ge 2020). In this study, three species of *Lepiota* are recorded for the first time in Laos, and a new species is described from Thailand.

Lepiota metulispora (Berk. & Broome) Sacc., Syll. fung. (Abellini) 5: 38 (1887).

Index Fungorum number: IF461315; Facesoffungi number: FoF09887; Figs. 134*,* 135

Pileus 30–65 mm, sub umbonate to umbonate, expanding to plano-concave, with inflexed margin; greyish orange to brownish orange (6B5-8, 6C7-8) glabrous at umbo, with concolorous squamules toward margin on white fibrillose background; margin sulcate, with partial veil remnants, with concolorous squamules on surface. *Lamellae* free, broadly ventricose, 3–5 mm wide, white, moderately crowded, with 3 length lamellulae, with eroded edge. *Stipe* 60–80 × 5–4 mm, cylindrical or slightly tapering to apex, completely fibrillose or cortinate at annular zone, white, with white to greyish orange to brownish orange (6B5-8, 6C7-8) squamules under annular zone downward base, on white to orange-white (5A2) background. *Annulus* an annular zone, cortinate with white fibrils. *Context* in pileus white, up to 4 mm wide; in stipe hollow, concolorous with surface. *Smell and taste* unknown. *Spore print* white.

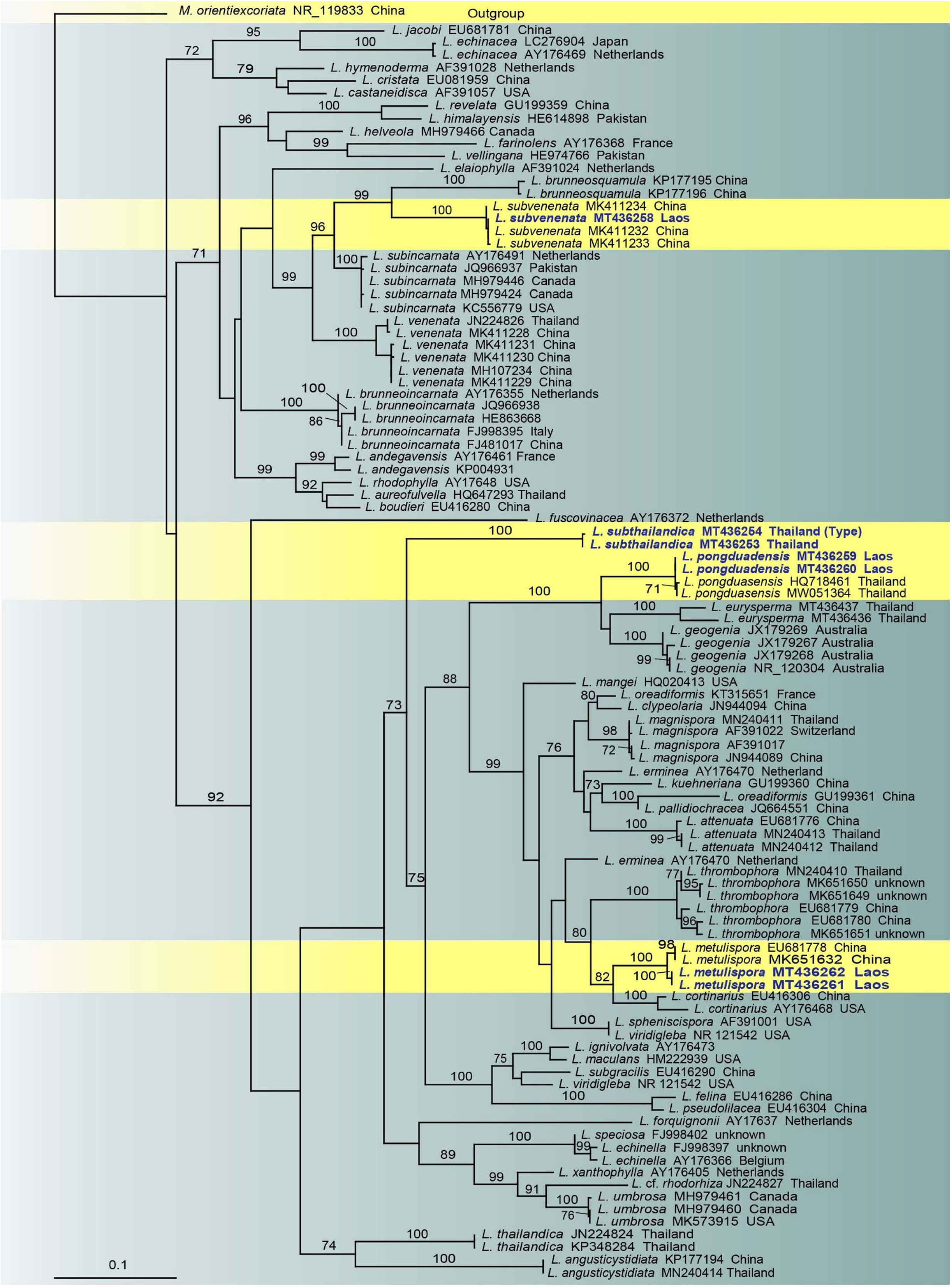
Basidiospores [50,2,2] 13–16.5 × 4–5 µm, avl × avw = 17.7 × 4.7 µm, Q = 2.91–3.30, Qav = 3.20, in side-view cylindrical, with attenuate or rounded apex, with straight abaxial side, with an inflexed hilar appendage, with suprahilar depression, fusiform to cylindrical in frontal view, slightly thick-walled, hyaline, dextrinoid, congophilous. *Basidia* 22–33 × 7–9 µm, clavate, slightly thick-walled, hyaline, 4-spored. *Cheilocystidia* 15–35 × 5–20 µm, clavate to broadly clavate, sometimes utriform, branched or with septate under element cell, thick-walled, hyaline. *Pileus covering* a trichoderm made up of two layers of element; upper layers made up of cylindrical elements with rounded or attenuate apex, 70–190 × 5–13 µm, hyaline to pale brown, slightly thick-walled, smooth-walled, with parietal pigment; under layers made up of shortly clavate to clavate elements, 35–50 × 8–14 µm, smooth or rough-walled, with hyaline to parietal pale brown pigment. *Stipe covering* of squamules similar to pileus covering. *Clamp connections* present.

Material examined: Laos, Oudomxay Province, Xay District, Houay Houm Village, N 20° 32′ 00.67″, E 101° 53′ 48. 17.16″. 917 m., 15 June 2014, P. Sysouphanthong, PS2014-1465 (HNL503136); *ibidem*, 20 July 2014, P. Sysouphanthong, PS2014-1480 (HNL503151).

Habitat and distribution: solitary or grow in a small cluster with few basidiomes, on dead leaves and humus soil, saprotrophic. The species was only reported from tropical regions viz. Sri Lanka (Pegler 1972), India (Kumar and Manimohan 2009), China and Hong Kong (Liang et al. 2011), Tanzania (Pegler 1977), Thailand (Sysouphanthong et al. 2012). This is the first report of *L. metulispora* in northern Laos.

GenBank numbers: HNL503136–MT436261 (ITS).
HNL503151–MT436262 (ITS).

Notes: Lepiota metulispora has a trichodermal pileus covering and penguin-shaped basidiospores, and it is placed in the section *Lepiota* (Vellinga 2001). The species is widespread in tropical countries. Lao specimens were found in the mature stage, colour of squamules on pileus is paler than Thai specimens, but the morphology is identical (Sysouphanthong et al. 2012). The type specimen of the species from Sri Lanka is closer to Lao and Thai specimens in morphology, but basidiospores are slightly larger and cheilocystidia are undetermined (Pegler 1972). Liang et al. (2011) studied the type material from Sri Lanka and compared it with the Chinese specimen, and the type specimen has a


M. orientiexcoriata NR_119833 China
Outgroup
95
L. jacobi EU681781 China
72
100
L. echinacea LC276904 Japan
L. echinacea AY176469 Netherlands
79
L. hymenoderma AF391028 Netherlands
L. cristata EU081959 China
L. castaneidisca AF391057 USA
100
L. revelata GU199359 China
96
L. himalayensis HE614898 Pakistan
L. helveola MH979466 Canada
99
L. farinolens AY176368 France
L. vellingana HE974766 Pakistan
L. elaiophylla AF391024 Netherlands
100
L. brunneosquamula KP177195 China
99
L. brunneosquamula KP177196 China
L. subvenenata MK411234 China
100
L. subvenenata MT436258 Laos
96
L. subvenenata MK411232 China
L. subvenenata MK411233 China
71
100
L. subincarnata AY176491 Netherlands
L. subincarnata JQ966937 Pakistan
99
L. subincarnata MH979446 Canada
L. subincarnata MH979424 Canada
L. subincarnata KC556779 USA
L. venenata JN224826 Thailand
100
L. venenata MK411228 China
L. venenata MK411231 China
L. venenata MK411230 China
L. venenata MH107234 China
L. venenata MK411229 China
100
L. brunneoincarnata AY176355 Netherlands
100
L. brunneoincarnata JQ966938
86
L. brunneoincarnata HE863668
L. brunneoincarnata FJ998395 Italy
L. brunneoincarnata FJ481017 China
99
L. andegavensis AY176461 France
99
L. andegavensis KP004931
92
L. rhodophylla AY17648 USA
L. aureofulvella HQ647293 Thailand
L. boudieri EU416280 China
L. fuscovinacea AY176372 Netherlands
100
L. subthailandica MT436254 Thailand (Type)
L. subthailandica MT436253 Thailand
L. pongduadensis MT436259 Laos
100
L. pongduadensis MT436260 Laos
L. pongduasensis HQ718461 Thailand
100
71
L. pongduasensis MW051364 Thailand
100
L. eurysperma MT436437 Thailand
L. eurysperma MT436436 Thailand
L. geogenia JX179269 Australia
100
L. geogenia JX179267 Australia
99
L. geogenia JX179268 Australia
L. geogenia NR_120304 Australia
88
L. mangei HQ020413 USA
80
L. oreadiformis KT315651 France
L. clypeolaria JN944094 China
73
L. magnispora MN240411 Thailand
98
L. magnispora AF391022 Switzerland
72
L. magnispora AF391017
76
L. magnispora JN944089 China
99
L. erminea AY176470 Netherland
73
L. kuehneriana GU199360 China
100
L. oreadiformis GU199361 China
92
L. pallidiochracea JQ664551 China
100
L. attenuata EU681776 China
99
L. attenuata MN240413 Thailand
L. attenuata MN240412 Thailand
L. erminea AY176470 Netherland
75
77
L. thrombophora MN240410 Thailand
95
L. thrombophora MK651650 unknown
100
L. thrombophora MK651649 unknown
L. thrombophora EU681779 China
96
L. thrombophora EU681780 China
80
L. thrombophora MK651651 unknown
98
L. metulispora EU681778 China
100
L. metulispora MK651632 China
82
100
L. metulispora MT436262 Laos
L. metulispora MT436261 Laos
100
L. cortinarius EU416306 China
L. cortinarius AY176468 USA
100
L. spheniscispora AF391001 USA
L. viridigleba NR 121542 USA
100
L. ignivolvata AY176473
75
L. maculans HM222939 USA
L. subgracilis EU416290 China
100
L. viridigleba NR 121542 USA
100
L. felina EU416286 China
L. pseudolilacea EU416304 China
L. forquignonii AY17637 Netherlands
100
L. speciosa FJ998402 unknown
99
L. echinella FJ998397 unknown
89
L. echinella AY176366 Belgium
99
L. xanthophylla AY176405 Netherlands
91
L. cf. rhodorhiza JN224827 Thailand
100
L. umbrosa MH979461 Canada
76
L. umbrosa MH979460 Canada
L. umbrosa MK573915 USA
100
L. thailandica JN224824 Thailand
74
L. thailandica KP348284 Thailand
100
L. angusticystidiata KP177194 China
L. angusticystidiata MN240414 Thailand
0.1

◂ **Fig. 136** Maximum likelihood phylogenetic tree based on nrITS sequences of *Lepiota* species. Bootstrap support ≥ 70% is indicated at the nodes. New sequences from this study are in blue. The GenBank accession numbers are indicated after the species name. Abbreviation *L* = *Lepiota*, *M* = *Macrolepiota*. The tree is rooted in *Macrolepiota orientiexcoriata*

smaller basidiospore size. However, it seems that the size of basidiospores is not much different in all specimens found in China, Laos, Sri Lanka and Thailand; and the morphology and size can be minorly different in different specimens. According to the analysis of nrITS sequence data (Fig. 136), Lao specimens are identical to specimens from China with high (100%) bootstrap support.

Lepiota thrombophora from Thailand is most similar to *L. metulispora* in morphology, but differ in smaller basidiospores size (10–14 × 3–5 µm) (Hyde et al. 2021); and the type specimen of *L. thrombophora* from Sri Lanka is different in dark brown squamules on pileus and shorter elements of pileus covering (25–100 × 5–15 µm). Liang et al. (2011) described *L. thrombophora* from China, based on its longer elements (up to 330 µm long). The analysis of nrITS sequence data showed that Chinese and Thai specimens of *L. thrombophora* are identical, and related to *L. metulispora* (Fig. 136). The type specimen of *L. attenuata* from China is closer to *L. metulispora* in morphology but differs in much longer elements on pileus covering (231 µm long), and basidiospores are more attenuated at the apex (Liang et al. 2011). Thai specimens of *L. attenuata* from Thailand have longer and typically attenuate elements (300 µm long) (Hyde et al. 2021). Other similar species to *L. metulispora* were discussed in Sysouphanthong et al. (2012).

Lepiota pongduadensis Sysou., Hyde & Vellinga in Sysouphanthong et al., Cryptog. Mycol. 33(1): 37 (2012).

Index Fungorum number: IF519961; Facesoffungi number: FoF09886 Figs. 137, 138

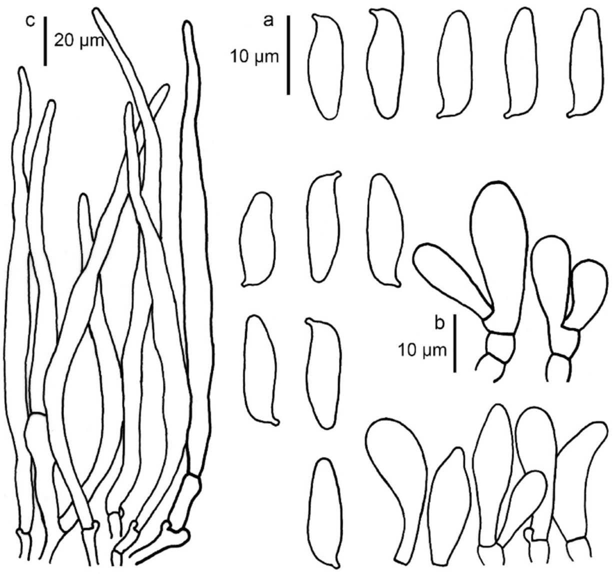
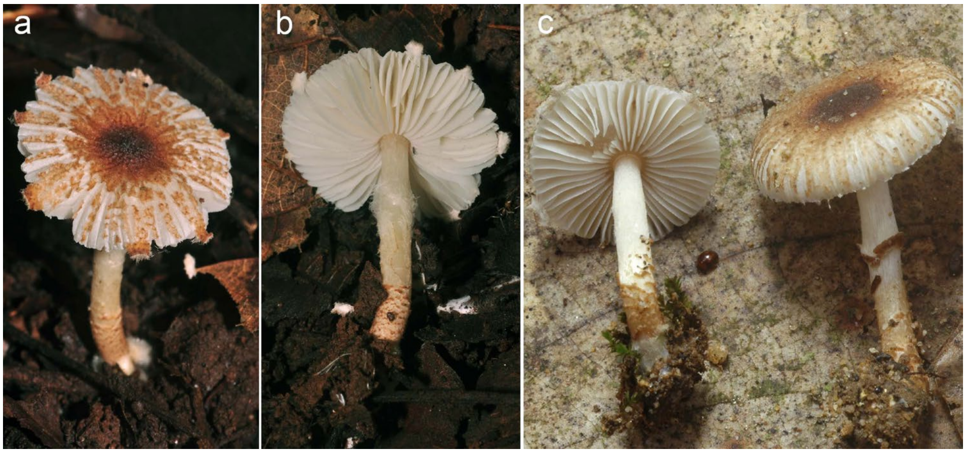


Fig. 138 ***Lepiota pongduadensis*** (HNL503131, **new record**). **a** Basidiospores **b** Cheilocystidia **c** Pileus covering

Pileus 30–45 mm, campanulate, expanding to convex or umbonate with small umbo, applanate with low umbo, straight margin; glabrous to rough at umbo, brown to dark brown (6E5-8, 7F7-8), with light brown to brown (7D6-8, 7E7-8) glabrous around umbo, later surface broken in radial streaks from around umbo towards the margin, with concolorous tomentose to crowded squamules towards the margin, on white to yellowish-white (4A2) black ground; marginal zone broken, split, fringed, cortinate with write bibrils and light brown to brown (7D6-8, 7E7-8) partial veil remnants. *Lamellae* free, slightly crowded, ventricose to broadly, 3–5 mm wide, with 2 length lamellulae, white to yellowish-white (4A2), with concolorous eroded edge. *Stipe* 35–45 × 4–6 mm, cylindrical, fibrillose or cortinate at middle zone, then with light brown to brown (7D6-8, 7E7-8) squamules downwards base, with white to yellowish-white (4A2)

Fig. 137 ***Lepiota pongduadensis*** in habitat. **a-b** HNL503131 **c** HNL503150



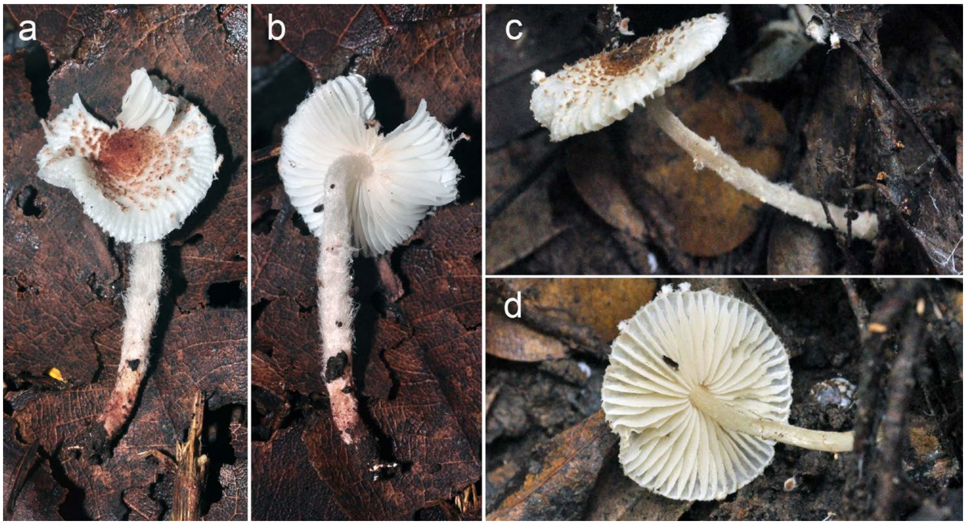


Fig. 139 ***Lepiota subthailandica*** in habitat. **a-b** MFLU 09–0166 **c-d** MFLU 10–0616 (**holotype**)

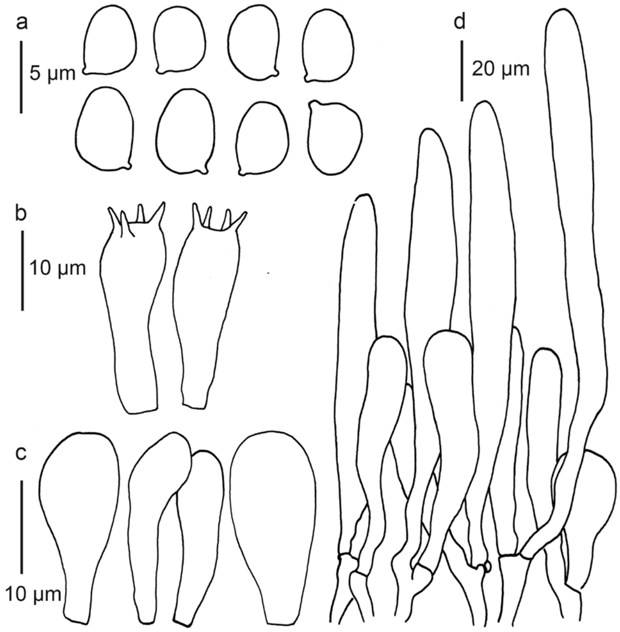


Fig. 140 ***Lepiota subthailandica*** (MFLU 10-0616, holotype). **a** Basidiospores **b** Basidia **c** Cheilocystidia **d** Pileus covering

black ground from middle to apex, with reddish-white (7A2) below middle zone downwards base. *Annulus* an annular zone, cortinate with white fibrils. *Context* white and up to 3 mm wide in pileus; hollow and concolorous with surface. *Smell and taste* unknown. *Spore print* white.

Basidiospores [50,2,2] 11.5–16.5 × 4–5.5 µm, avl × avw = 13.4 × 4.6 µm, Q = 2.8–3, Qav = 2.91, in side-view cylindrical amygdaliform, with attenuate apex, with straight abaxial side, with hilar appendage, with superhilar depression, in frontal view fusiform, hyaline, slightly thick-walled, dextrinoid, congophilous. *Basidia* 16–26 × 7–9 µm, clavate, hyaline, thick-walled, 4-spored. *Cheilocystidia* abundant, 27–35 × 6.5–15 µm, mostly fusiform or clavate, sometimes utriform, thick-walled, hyaline. *Pileus covering* a trichoderm made up of narrowly cylindrical elements, normally wider at middle and narrow to apex, with attenuate apex 70–400 × 6–13.5 µm, thick-walled, with brown parietal and intracellular pigment, smooth, sometimes incrusted at base of element and hyphae. *Stipe covering* of squamules a trichoderm similar to pileus covering. *Clamp-connections* present.

Material examined: Laos, Oudomxay Province, Xay District, Houay Houm Village, N 20° 32′ 00.67″, E 101° 53′ 48. 17.16″. 917 m., 10 July 2014, P. Sysouphanthong, PS2014-1460 (HNL503131); *ibidem*, 12 August 2014, P. Sysouphanthong, PS2014-1479 (HNL503150).

Habitat and distribution: Growing solitary to a small group; saprotrophic and terrestrial on humus soil; originally described from northern Thailand (Sysouphanthong et al. 2012). This is the first report of *L. pongduadensis* in Laos.

GenBank numbers: HNL503131–MT436259 (ITS).
HNL503150–MT436260 (ITS).

Notes: Lepiota pongduadensis is a new record from Laos; two Lao specimens were collected from Oudomxay Province of northern Laos, and they show similar morphology and nrITS sequences to the type specimen (Fig. 136). *Lepiota pongduadensis* was originally described from Chiang Mai and Chiang Rai Provinces of northern Thailand. The species is placed in the section *Lepiota* by Sysouphanthong et al. (2012) and is distinguished from other species in the section. Only a few species are similar to *L. pongduadensis* (Sysouphanthong et al. 2012). *Lepiota attenuata*, the type specimens from China, is similar to *L. pongduadensis* in morphology, but different in lacking a dark brown surface on umbo, lighter colour of squamules on pileus, and stipe covering (brownish-yellow to yellowish-brown), larger basidiospores (14.5–19 × 4–5.5 mm), shorter elements of pileus covering (80–231 × 3.8–13 mm) (Liang et al. 2011).

Lepiota subthailandica Sysouph., K.D. Hyde & Thongkl., ***sp. nov.***

MycoBank no: MB839987, Facesoffungi number: FoF09889; Figs. 139, 140

Etymology: the morphological characteristics of this species are similar to *L. thailandica*.

Holotype: MFLU 10–0616

Diagnosis: similar to *L. thailandica* in morphology, but the difference in larger basidiomata, lacking of utriform or fusiform cheilocystidia and nrITS sequences.

Pileus 10–16 mm diam., convex to umbonate, expanding to plano-concave, with straight margin; rough or with crowded squamules at center, light brown to brown (7D6-8, 7E7-8) at center, with concolorous squamules around umbo towards margin, slightly distant at marginal zone on white to orange-white (5A2) background; margin broken, sulcate or striate, appendicular, with concolorous squamules on the surface and white fibrillose remnants. *Lamellae* free, broadly ventricose, 3–4 mm wide, white, moderately crowded, with 1 length lamellulae, with eroded edge. *Stipe* 25–30 × 3–4 mm, cylindrical, slightly wider at base; completely fibrillose, crowded at annular zone down toward base, white, with light brown to brown (7D6-8, 7E7-8) squamules at base zone, on white to orange-white (5A2) background. *Annulus* with an annular zone or cortinate with white fibrils. *Context* white in pileus, up to 1 mm wide; hollow in stipe, concolorous with surface. *Taste and smell* unknown. *Spore print* white.

Basidiospores [50,2,2] 5–6 × 3.2–4 µm, avl × avw = 5.54 × 3.64 µm, Q = 1.45–1.57, Qav = 1.52, in side-view ellipsoid ovoid, in frontal view ovoid to, slightly thick-walled, dextrinoid, congophilous, cyanophilous, not metachromatic. *Basidia* 15–18 × 5–7 µm, clavate, slightly thick-walled, hyaline, 4-spored. *Cheilocystidia* 18.5–29 × 5–10 µm, narrowly clavate to clavate, rarely broadly clavate, slightly thick-walled, hyaline. *Pleurocystidia* absent. *Pileus covering* a trichoderm made up of two layer of elements; upper layer made up of cylindrical to narrowly cylindrical elements with rounded apex, sometimes swollen at middle and tapering to base and apex,

Fig. 141 ***Lepiota subvenenata*** in habitat. **a-e** HNL503121

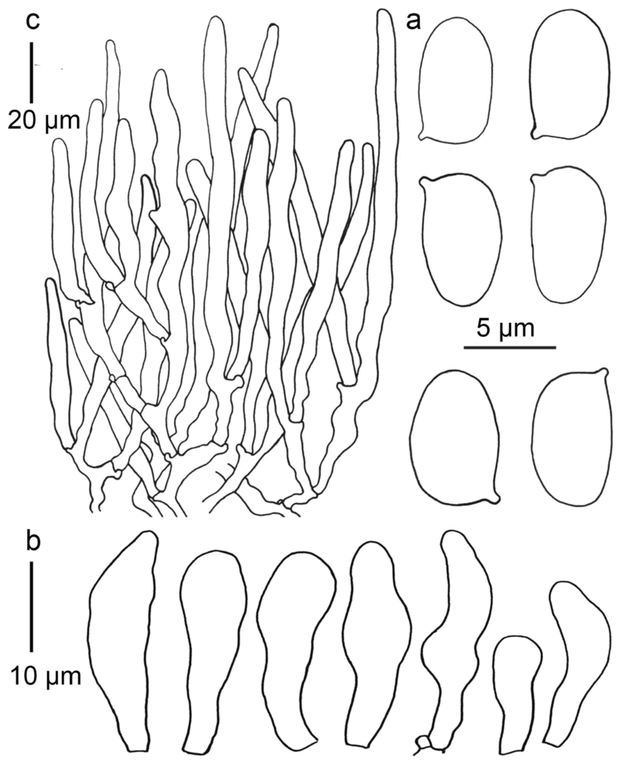


Fig. 142 ***Lepiota subvenenata*** (HNL503121, **new record**). **a** Basidiospores **b** Basidia **c** Cheilocystidia **d** Pileus covering

60–140 × 9–17.5 µm, with pale brown parietal and intracellular pigment; underpayer made up of shortly clavate elements, 30–45.0 × 10.0–20 µm, with pale brown parietal and intracellular pigment. *Stipe covering* of squamules at base zone similar to pileus covering. *Clamp connections* present in all tissues.

Material examined: Thailand, Chiang Mai Province: Mae Taeng district, Pha Deng village, N 19° 07.13′, E 98° 43.52′, 905 m, 04 July 2010, P. Sysouphanthong P98 (MFLU 09–0616, **holotype**); *ibidem*, 25 July 2008, P. Sysouphanthong PS093 (MFLU 09–0166, **paratype**).

Habitat and distribution: solitary, saprotrophic, on decayed humus soil; found in high elevation deciduous forests of northern Thailand.

GenBank numbers: MFLU 09–0616–MT436254 (ITS). MFLU 09–0166–MT436253 (ITS).

Note: *Lepiota subthailandica* has a tiny basidioma, a trichodermal structure of pileus covering and ellipsoid ovoid basidiospores; and the species is located in *Lepiota* sect. *Ovidsporae* (J.E. Lange) Kühner (Vellingar 2001). In the same section, *Lepiota subthailandica* is very similar to *L. thailandica* Sysouph., K.D. Hyde, J.C. Xu & P.E. in morphology; and they are widespread in the same location of Chiang Mai, northern Thailand. However, *L. thailandica* has smaller basidiomata (3–4 mm diam. in pileus), utriform and fusiform cheilocystidia, and shorter elements of pileus covering (55–95 × 5.5–22 µm) (Sysouphanthong et al. 2016). The second species, *L. microcarpa* Sysouph., K.D. Hyde & Vellinga, is similar in micromorphology with *L. subthailandica*. However, *L. microcarpa* has penguin-shaped basidiospores, and belongs to sect. *Lepiota* (Sysouphanthong et al. 2012). Based on the nrITS sequences analysis, two samples of *L. subthailandica* are not related to *L. thailandica*, and are separated from other species in the sect. *Ovisporae* (Fig. 136).

Lepiota subvenenata Hai J. Li, Y.Z. Zhang & C.Y. Sun.

Index Fungorum number: not found; Facesoffungi number: FoF09888; Figs. 141, 142

Pileus 30–50 mm diam., first subglobose, expanding to parabolic to convex or umbonate, plano-convex when mature, with straight margin; when young glabrous to granulose, completely light brown to brown (7D7-8), when mature surface breaking and leaving concolorous glabrous or granulose umbo, with concolorous squamules around umbo towards margin, on white to orange-white (5A2) background; margin with concolorous squamules and white partial veil remnants. *Lamellae* free, broadly ventricose, with 3 length lamellulae, up to 4 mm wide, white, crowded, with white eroded edge. Stipe 40–70 × 5–7 mm, cylindrical, with white fibrillose and light brown to brown (7D7-8) squamules at annular zone, with concolorous squamules under annular zone downwards base, on white to orange-white (5A2) background. *Annulus* an annular zone, with white fibrillose and concolorous squamules. *Context* in pileus white, 3–5 mm wide; in stipe hollow, concolorous with surface. *Taste and smell* unknown. *Spore print* white.

Basidiospores [50,1,1] 4.5–6.3 × 2.5–3.5 µm, avl × avw = 5.02 × 3 µm, Q = 1.7–1.8, Qav = 1.75, in side-view oblong ovoid, in frontal view oblong, slightly thick-walled, hyaline, dextrinoid, congophilous. *Basidia* 18–23 × 7–10 µm, clavate, slightly thick-walled, hyaline, 4-spored, rarely 2-spored. *Cheilocystidia* 13–25 × 6–10 µm, cylindrical to irregular cylindrical, narrowly clavate to clavate, sometimes fusiform or utriform, slightly thick-walled, hyaline. *Pleurocystidia* absent. *Pileus covering* a trichoderm made up of cylindrical elements with rounded or attenuate apex, 60–170 × 7–13 µm, thick-walled, with parietal pale brown and intracellular pigment. *Stipe covering* of squamules similar to pileus covering. *Clamp connections* present.

Material examined: Laos, Oudomxay Province, Xay District, Houay Houm Village, N 20° 32′ 00.67″, E 101° 53′ 48. 17.16″. 917 m., 25 July 2014, P. Sysouphanthong, PS2014-1450 (HNL503121).

Habitat and distribution: Growing in a small group, on humus soil mixed with dead leaves; known from Yunnan province of Southwest China (Zhang et al. 2019). We report the first record of *L. subvenenata* from Laos in this study.

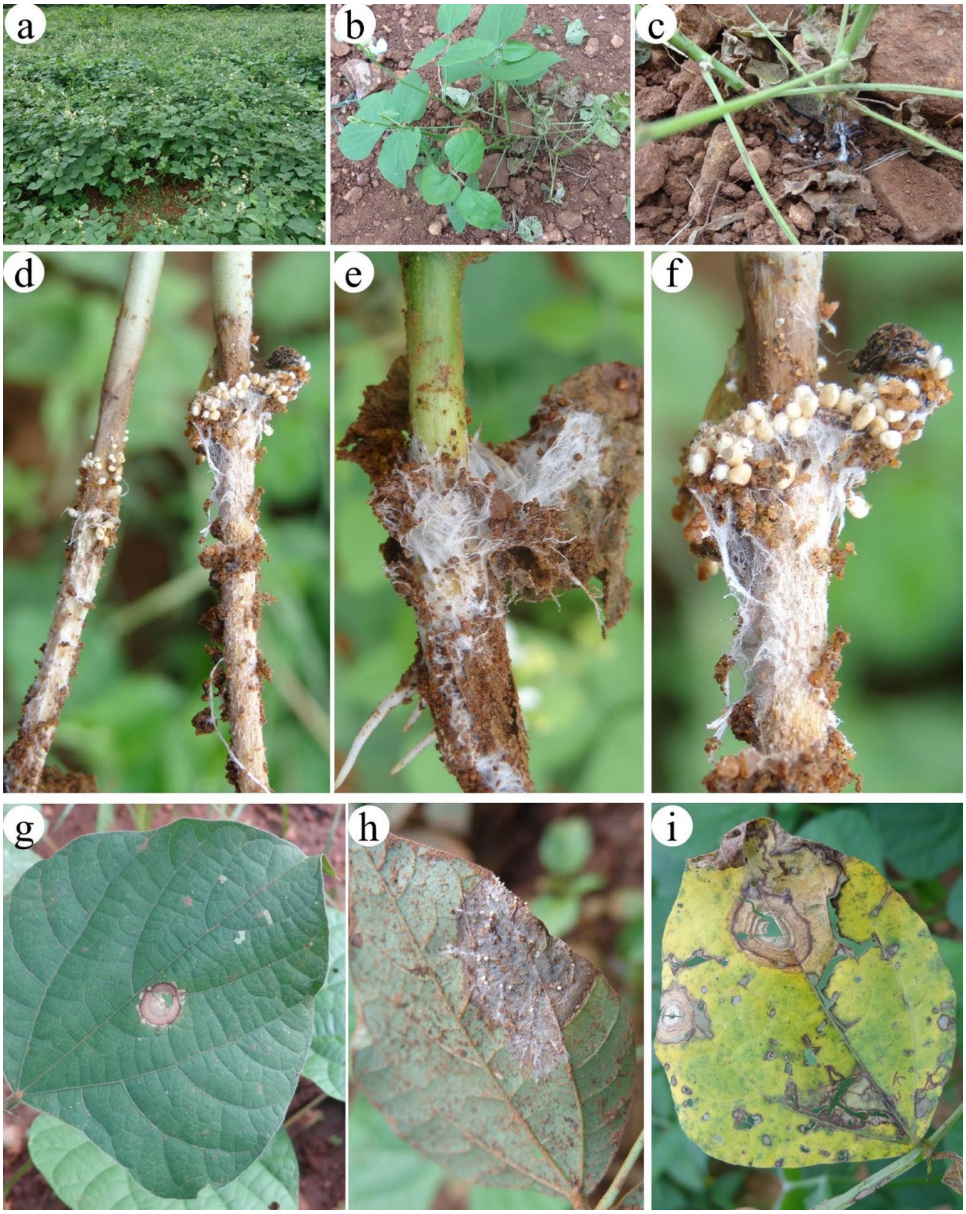


Fig. 143 **a-c** Field symptoms of sclerotial wilt under field conditions. **d-f** Collar region showing fungal pathogen colonizing the stem soil interface. **g–i** Sclerotia infecting leaves

GenBank numbers: HNL503121–MT436258 (ITS).

Notes: Lepiota subvenenata was described from Yunnan province of Southwest China. It is closely related to *L. venenata* Z. H. Chen & Zhu L. Yang in morphology. Lao specimens clustered with the type specimens in the nrITS phylogenetic analyses and share similar morphology (Fig. 136).

Atheliales Jülich.

Atheliales is an order mostly composed of corticioid fungi (Sulistyo et al. 2021). Based on phylogenetic analyses Sulistyo et al. (2021) accepted five families: Atheliaceae, Byssocorticiaceae, Lobuliciaceae, Pilodermataceae, and Tylosporaceae in this order. However, Wijayawardene et al. (2022) accepted only Atheliaceae and Lobuliciaceae in this order.

Atheliaceae Jülich, Biblthca Mycol. 85: 355 (1982) [1981].

This is the type family of Atheliales. Jülich (1982) included the genera *Athelopsis*, *Caerulicium*, *Confertobasidium*, *Leptosporomyces*, and *Luellia* in Atheliaceae. Wijayawardene et al. (2022) accepted 20 genera in this family. Atheliaceae mainly consists with saprotrophic taxa, with one lichenicolous species (*Athelia arachnoidea*) (Sulistyo et al. 2021).

Athelia Pers., Traité champ. Comest. (Paris): 57 (1818).

Athelia is a genus of corticioid fungi. Some species are facultative parasites of plants and of lichens (Sulistyo et al. 2021). A species of *Athelia* also engaged in a symbiotic relationship with termites (*Reticulitermes*), in which the fungus forms sclerotia that mimic termite eggs and worker termites

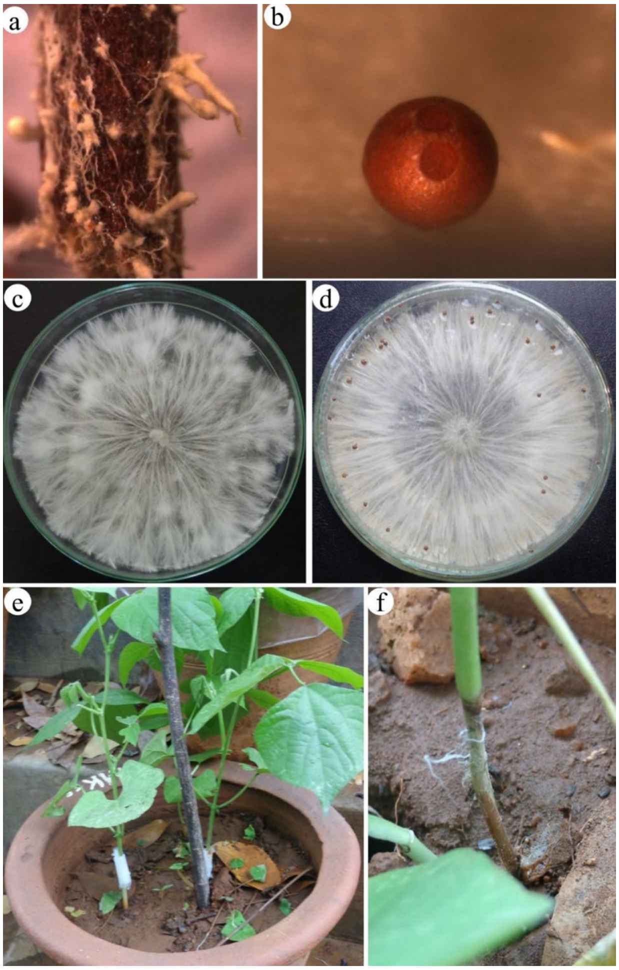


Fig. 144 **a** Stem part showing the mycelial cords colonized on the surface. **b** Sclerotia observed under stereo zoom microscope. **c-d** Pure cultures of *Athelia rolfsii* on PDA medium. **e–f** Pathogenicity test performed under greenhouse showing the color rot symptoms

handling the sclerotia as if they were eggs (Matsuura et al. 2005). Wijayawardene et al. (2022) accepted 32 species in this genus.

Athelia rolfsii (Curzi) C.C. Tu & Kimbr., Botanical Gazette Crawfordsville 139: 460 (1978).

Index Fungorum number: IF309351; *Faceoffungi number FoF13394; Figs.* 143, 144

Pathogenic on roots and stem of *Lablab purpureus*. **Sexual morph**: not observed. **Asexual morph**: numerous globoid sclerotial bodies were developed on the collar region of infected *Lablab purpureus* plants at the stem soil interface. Sclerotia measured 1–3 mm in diam. ($n = 50$), initially whitish and later turned to brownish upon maturity.

Cultural characteristics: On PDA, reaching 90 mm at 28 °C after 7 d in 12/12 h light/dark, dense white fluffy colonies developed rapidly over the culture plates and produced characteristic sclerotia near the edges of plates and on the upper lid surface. After, 12–15 days of incubation sclerotia were recorded per plate ranging to 180 – 490 (mean 358 ± 24, $n = 20$). Colonies on PDA reaching 90 mm at 28 °C after 14 d in 12/12 dark, colonies appeared white to pink with abundant aerial mycelium.

Material examined: India, Karnataka, Mysore, Doddamaragowdanahally, on infected plants of *Lablab purpureus* (L.) Sweet (Fabaceae), 17 April 2013, S. Mahadevakumar (UOM-Sr-13–4), living culture Sr-LP3.

Habitat: Wide range of hosts (Farr and Rossman 2022), *Lablab purpureus* (This study).

Distribution: Brazil, China, Cuba, Fiji, New Zealand, Panama, Papua New Guinea, Phillippines, South Africa, Spain, Sri Lanka, West Indies and USA (Farr and Rossman 2022), India (This study).

GenBank number: KJ002765 (ITS).

Notes: The characteristic foot-rot and leaf blight disease of *Lablab purpureus* are reported in the present study and the diagnostic features are presented. The disease was observed at all stages of plant growth. In the early infection stage, the collar rot affected seedlings collapsed. Initial symptoms appeared as tan water-soaked lesions usually near the stem-soil interface, with lesions that enlarged and expanded towards the shoot apex, causing rotting. Similarly, lesions expanded towards the roots causing root decay and death of the host plant. The pathogen produced numerous globoid sclerotial bodies over the surface of the host plants. The cabbage heads' rotting was recorded with sclerotia development over the head surface. The disease was most prevalent during the rainy season. In dry weather, infected tissues showed the presence of mycelial threads with very few hard, melanized sclerotial bodies. In USDA host fungal database, the record 51387 specifies a geographical record for India, which shows the sequences submitted by our group to GenBank in 2013 and referred by Paul et al. (2017), a new geographical record for *Athelia rolfsii* on *Ipomoea batatas* from Korea. Based on the morphological, and cultural characteristics and ITS-rDNA analysis, the fungal pathogen was identified as *Athelia rolfsii* (Fig. 145). This is the first report on the association of *A. rolfsii* causing root rot and leaf blight disease in *L. purpureus* from India and worldwide.

Hymenochaetales Oberw.

The concept of hymenochaetaceous fungi was initiated by Patouillard (1900) in *Série des Igniaires*, which includes xanthochoroid polypores with simple, clampless hyphae and setal elements. Later, Oberwinkler (1977) raised the order Hymenochaetales, based on the characteristics of the Hymenochaetoidae, Hymenochaetaceae (proposed earlier by Donk (1948)). Hymenochaetales comprises with homobasidiomycetes with diverse basidiomatal characters, annual to perennial, resupinate to pileate, stipitate to spathulate with smooth, poroid or hydnoid hymenophore. Microscopically, simple, clampless, mono to di or trimitic hyphal system with

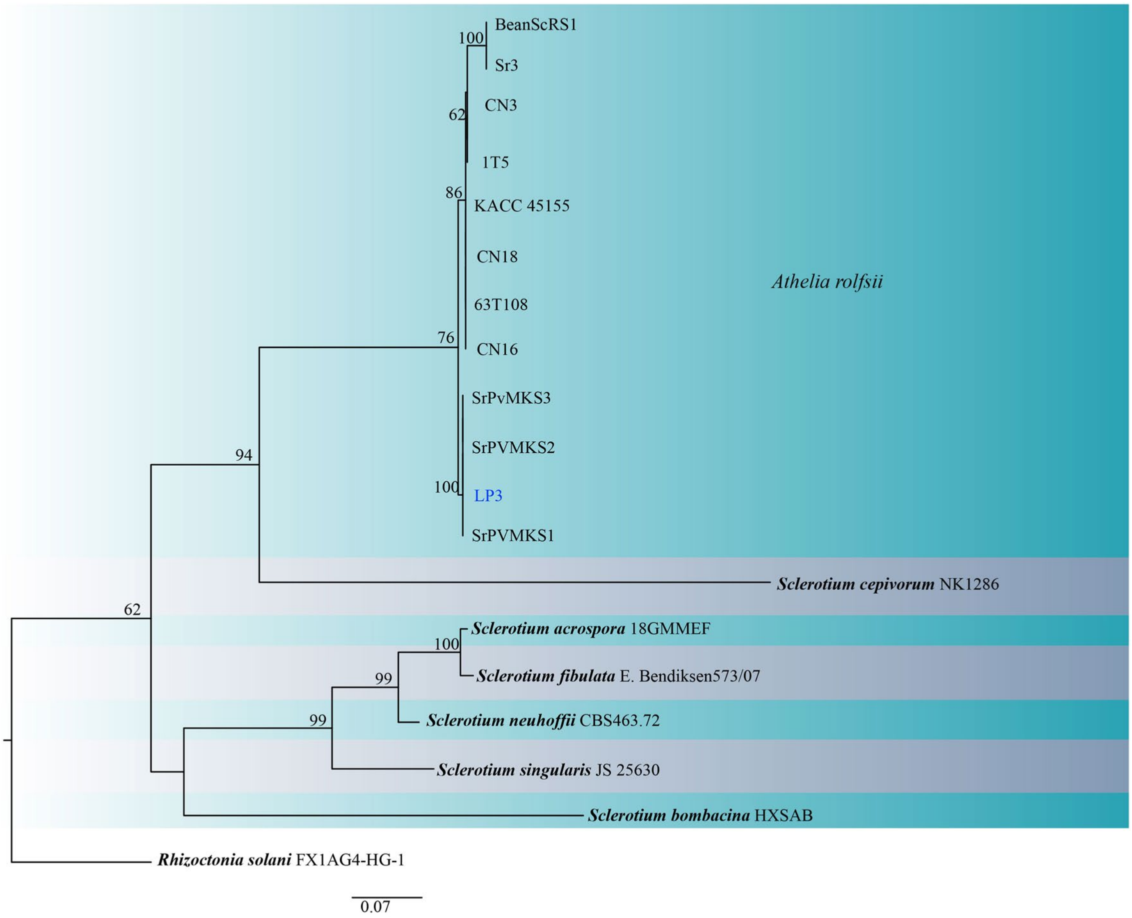


Fig. 145 Phylogenetic tree for species of *Athelia* generated from maximum likelihood (RAxML) based on ITS gene regions. The Maximum likelihood bootstrap value ≥ 50% are given at the nodes. The newly generated sequences are in blue. The tree is rooted to *Rhizoctonia solani* (FX1 AG4.HG.1)

smooth to ornamented, thin to thick-walled, hyaline to coloured, globose to cylindrical basidiospores are characteristic features. The presence or absence of sterile elements such as cystidia, cystidioles or seate also plays a vital role in identification (Fiasson and Niemela 1984).

MycoBank recorded 19 associated families (http://www.mycobank.org) whereas 1530 taxa were submitted in GenBank (https://www.ncbi.nlm.nih.gov) (as of 17 January 2022). Wijayawardene et al. (2022) accepted six families in this order.

Hymenochaetaceae Donk, Bull. Bot. Gdns Buitenz. 17(4): 474 (1948).

Donk (1948) classified the xanthochroid Aphyllophorales under Hymenochaetaceae which comprises wood-decaying white-rot fungi and medicinal fungi with styrylpyrone pigments (which are responsible for a positive xanthochoric reaction) (Dai et al. 2007, 2009). Hymenochaetaceae are described by yellow to deep brown, resupinate to pileate or stipitate basidiomata with smooth to hydnoid hymenial surface, simple mono to dimitic hyphal system, presence or absence of setae, thin to thick-walled, hyaline or coloured basidiospores (Ryvarden 1991; Dai 2010). Sharma (1995) reported 16 genera and 91 species of Hymenochaetaceae under Indian Aphyllophorales. Hymenochaetaceae is one of the largest families in Basidiomycota (Kirk et al. 2008). Dai (2010) mentioned *Phellinus* sensu lato, *Inonotus* sensu lato and *Hymenochaete* as the three largest genera of Hymenochaetaceae. There are 71 associated genera documented in MycoBank (http://www.mycobank.org) and 1,103 taxa submitted in GenBank (https://www.ncbi.nlm.nih.gov) (as of 1 January 2022). Wijayawardene et al. (2022) accepted 42 genera in this family.

Coltricia Gray, Nat. Arr. Brit. Pl. (London) 1: 644 (1821).

The genus is typified by *C. perennis* (L.) Murrill. Species of this genus are cosmopolitan and have few species that have been found to be associated with plant roots (Tedersoo et al. 2007). *Coltricia* is characterized by poroid and stipitate basidiocarps, a monomitic hyphal system lacking clamp connections and coloured, ellipsoid

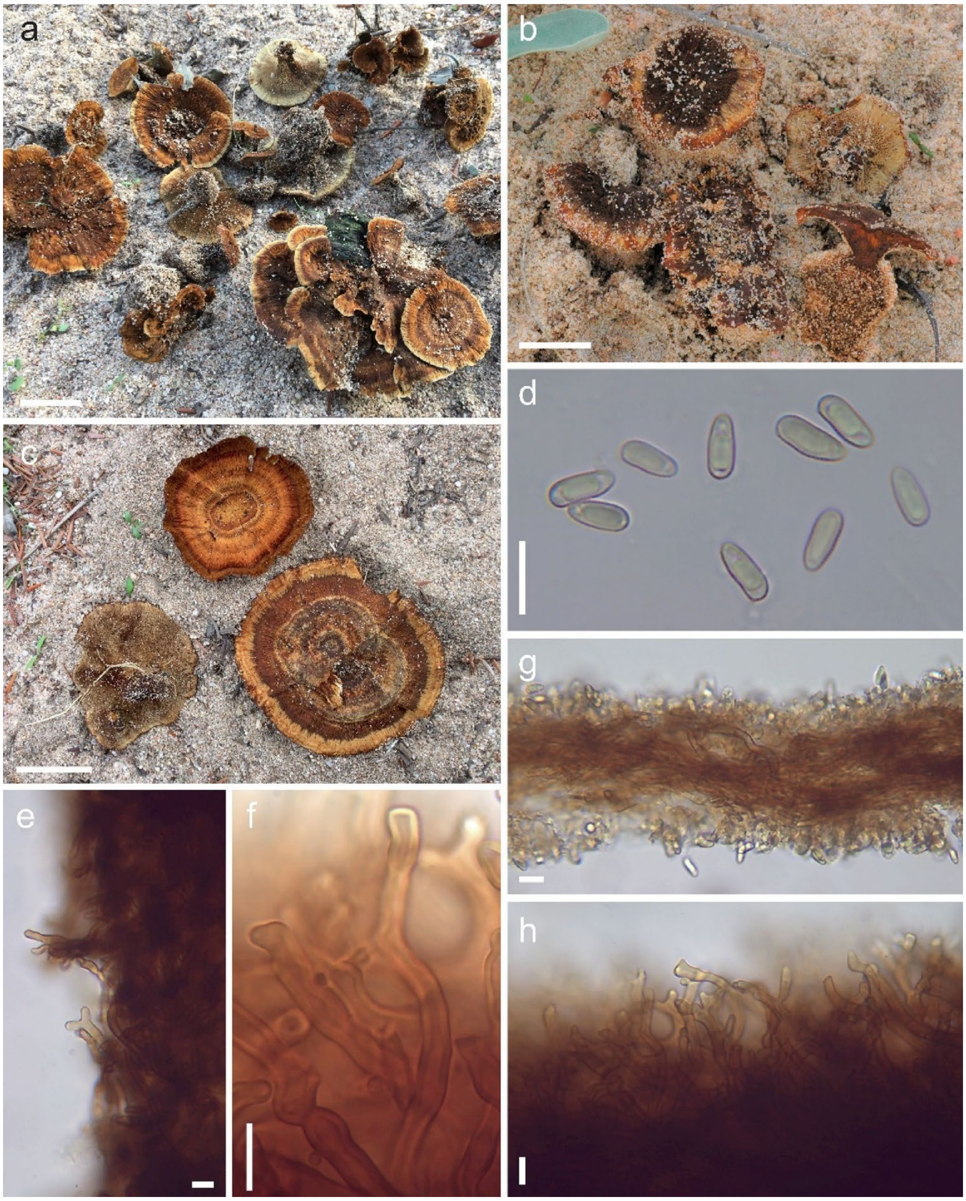


Fig. 146 ***Coltricia insularis*****. a-c** Basidiocarps. **d** Basidiospores. **e, f** Pileipellis. **g** Hymenial trama, longitudinal section. **h** Stipitipellis. All from LIP 0,401,817 (**holotype**, pictures by D. Borgarino (b) and P.-A. Moreau) except a (Hal-BP-72, sequence MT594499, picture by A. Rinaldi) and c (Hal-BP-19, sequence MT594498, picture by A. Rinaldi). Scale bars = 5 mm (a-c), 10 µm (d-g)

to subglobose, smooth basidiospores (Dai 2010). Wijayawardene et al. (2022) accepted 40 species in this genus.

Coltricia insularis P.-A. Moreau, Bellanger, Loizides & A. Rinaldi, ***sp. nov.***

Index Fungorum number IF900072; *Faceoffungi number FoF13395; Fig. 146*

Etymology. *Insularis* = of islands, a Latin adjective referring to Corsica, Cyprus and Sardinia, three Mediterranean islands in which the species was discovered.

Holotype: LIP 0401817

Pileus 15–60 mm, irregularly infundibuliform, rough, sometimes weakly lobed, subtomentose or more distinctly tomentose to subhirsute towards the centre, radially corrugated or furrowed and usually with well-defined concentric chromatic zones; colours ranging from brown, red-brown, grey-brown, purple, umber or ochraceous; margin often paler and somewhat undulating. *Hymenial surface* poroid, comprised of adnexed to irregularly decurrent, shallow, angular, or somewhat elongated pores, mostly 2–3 per mm, becoming poorly defined towards the margin and sometimes fusing to form sterile tomentose patches or a sterile marginal zone; warm grey to buff or ochraceous. *Stipe* 20–40 × 3–8 mm, usually irregularly furrowed, densely tomentose, buff or pale brown at the apex but quickly staining ochraceous or brown, darker chestnut to red-brown or orange-brown lower, deeply submerged into the substrate and often with sand and litter tightly adhered to it. *Context* corky, thick and indistinctly zonate in the pileus, darker in the stipe, chestnut to red-brown or umber.

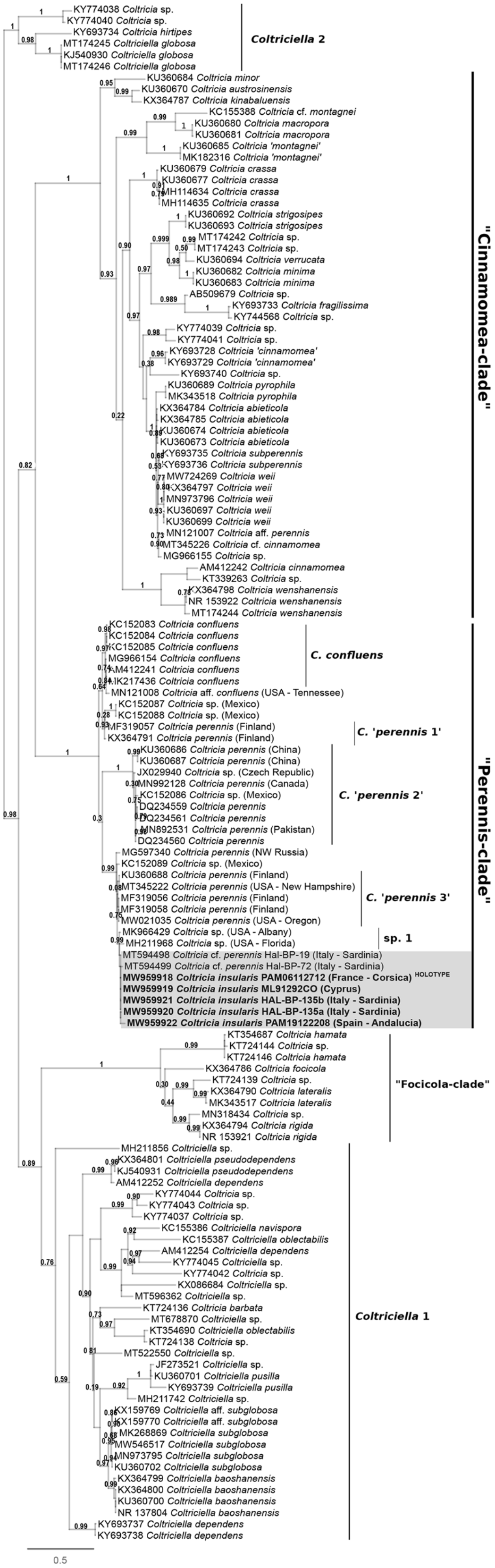


Fig. 147 Phylogenetic analyses were conducted online at www.phylogeny.fr (Dereeper et al. 2008). Multiple sequence alignments were performed with MUSCLE v. 3.7 (Edgar 2004). Maximum likelihood (ML) phylogenetic analysis was achieved with PhyML v. 3.0 (Guindon et al. 2010), using the GTR + I + Γ model of evolution and the Shimodaira Hasegawa version of the approximate likelihood-ratio test (SH-aLRT) of branch support (Anisimova et al. 2011). Phylogram was built using TreeDyn 198.3 (Chevenet et al. 2006) and edited with Inkscape 0.91 (https://inkscape.org/fr). Newly generated sequences for this study are in bold. The tree is rooted by mid-point rooting method under PhyML (Guindon et al. 2010) ▶

Spores (6.8) 7.5–9 (10.2) × 3.2–3.9 (4.1) µm, ellipsoid to broadly ellipsoid or ovoid when immature, cylindrical to fusiform when projected, with a light supra-apicular depression, pale yellow in KOH and in Melzer's, wall < 0.3 µm thick, smooth. *Basidia* 12–19 × 7–7.5 µm, 4-spored (partly 2-spored on immature specimens) with spindle-shaped straight sterigmata, shortly cylindrical, hyaline. *Hymenophoral setae* absent. *Edges* sterile, made of bunches of slender thin-walled hairs 2.3–3 µm wide, encrusted with yellowish granular deposits. *Pileipellis* 60–80 µm-thick, convoluted trichocutis, made of generative hyphae 3.5–6(7) µm wide, terminal elements 45–80 µm long, branching often with right-angled furcations, rounded to mucronate at the apex. *Stipitipellis* a trichocutis made of flexuose, mostly unbranched skeletoid hairs, 70–180 × 3.5–5.5 µm, with occasional secondary septa; wall smooth or with few hyaline mucoid deposits towards the apex, 0.8–1.2 µm thick, yellow in 5% KOH; apex rounded. *Clamps* absent from all observed septa. Smell weak, faintly acidic.

Habitat and Distribution: Associated with *Cistaceae* (*Cistus* spp., *Halimium halimifolium*) shrubs in dry, sandy places. So far collected from Cyprus, France (Corsica), Italy (Sardinia) and Spain (Andalucia), but probably widespread in xerothermic localities throughout the Mediterranean basin.

Material examined: France: Corsica (Haute-Corse), Monaccia d'Aullène, Réserve naturelle du Mucchiu Biancu, 25 Nov. 2006, D. Borgarino, L. Hugot, C. Lavoise, P.-A. Moreau & F. Richard, PAM06112616 (LIP 0401817, **holotype**).

Other material examined: Cyprus: Trimiklini, M. Loizides, 28 Feb. 2019, ML91292CO (LIP 0401819). Italy: Sardinia, Gonnesa, A. Rinaldi, 5 Dec. 2019, Hal-BP-135, LIP 0401740. Spain: Andalucia, Huelva, Almonaster-la-Real, under *Pinus halepensis* and *Cistus monspeliensis* in a semi-open heathland, A. Gasch Illescas & P.-A. Moreau, 28 Dec. 2019, PAM1912814 (LIP 0401740).

Notes: *Coltricia insularis* is a xerophilic Mediterranean species characteristic of *Cistaceae* shrublands, found especially among sands, where it may grow in dense clusters adhered to the bases of rockroses. Also known from the thermo-mediterranean zone in Cyprus and the supramediterranean zone in Andalucia, where a slenderer form of this species was collected on sandy ground, at the edge of a pine forest. In Sardinia, it occurs in pure *Halimium* stands in coastal areas. However, in places where more potential hosts are present, it might be part of the extensive ectomycorrhizal networks that are common in several Mediterranean ecological settings (Taudiere et al. 2015; Leonardi et al. 2020). From what is known about *Coltricia* mycorrhizal biology, members of the genus appear to establish ectomycorrhizal associations with a range of hosts (Rinaldi et al. 2008). *Coltricia insularis* phylogenetically belongs to the group of *Coltricia perennis*, which has not been the object of monographic revision since the advent of DNA studies. The phylogenetic analysis (Fig. 147) shows the unexpected diversity unravelled in this lineage, in which at least three main subclades can be identified among the available sequences in GenBank and UNITE. Most of these are devoid of Linnaean names and the need of typification of *C. perennis* itself (type of the genus) is obvious, considering this name has been arbitrarily applied to nearly all sequences available in the'Perennis-clade'. *Coltricia montagnei* Fr. (in Montagne 1836, p. 341), originally described from Northern France (Ardennes, near Sedan), has been variously interpreted and was only recently described in detail (Rivoire

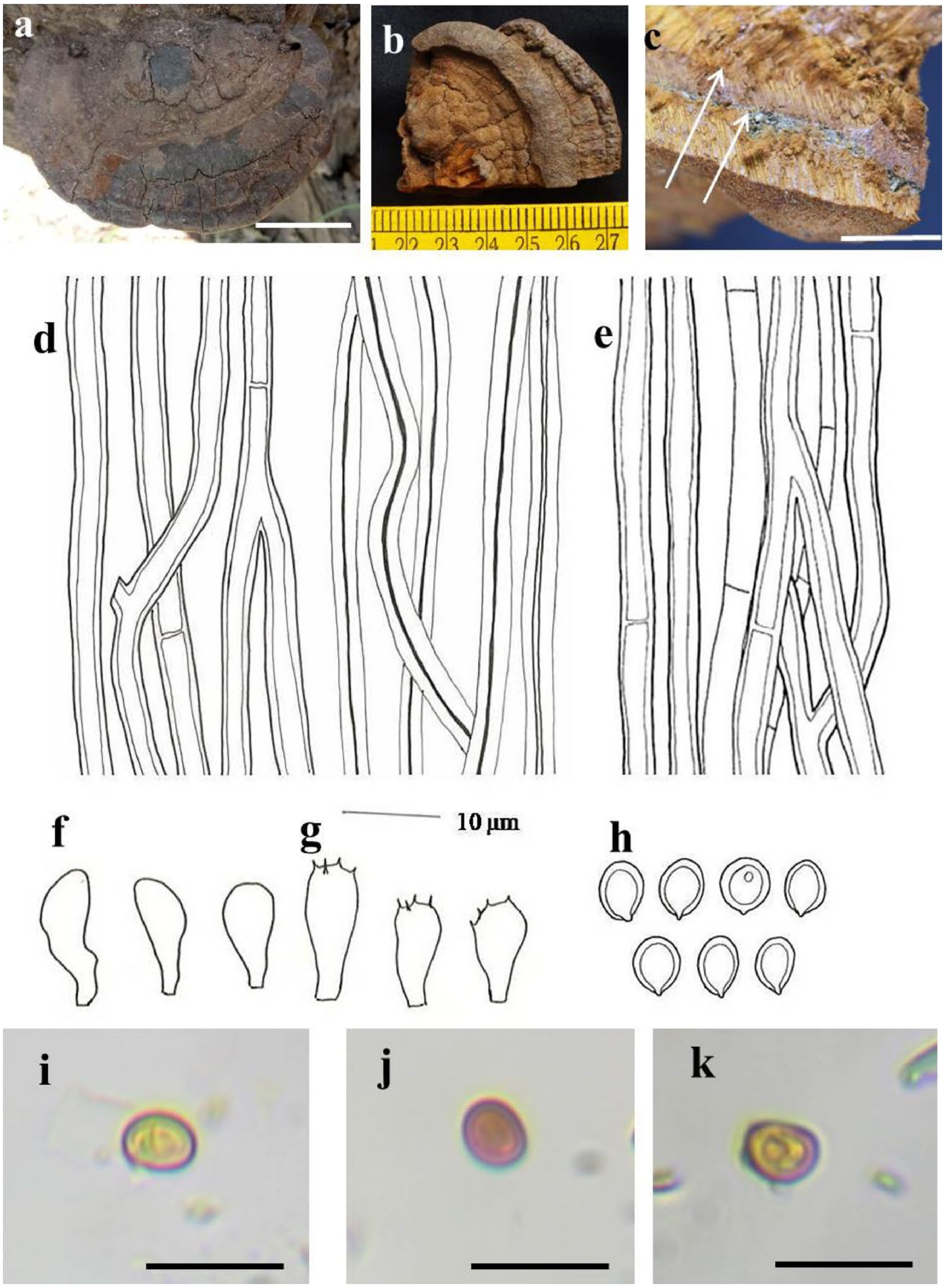


Fig. 148 ***Fulvifomes jawadhuvensis*** (MUBL4011, **holotype**). **a**-**b** Basidiocarp. **c** Stratified tube layer. **d** Tramal hyphae. **e** Context hyphae. **f** Basidioles. **g** Basidia. **h** Basidiospore **i** Basidiospore in H_2O. **j** Basidiospore in KOH. **k** Basidiospore in cotton blue. Scale: a = 3 cm. c = 1 cm. d–k = 10 µm

2020). *Coltricia confluens* Keizer (1997, p. 389), from which the isotype collection Keizer 93060 was kindly provided by the author, but unfortunately, could not be sequenced. *Coltricia insularis* differs from all currently recognized European species by spore dimensions and shape: mature specimens display spores with an average Q of around 2.3 and a typical fusiform profile. Like *C. perennis* and *C. confluens* (but not *C. montagnei*), the hyphae of pileipellis are frequently T-branched, but the taxonomic importance of this feature requires further observations. *Coltricia'confluens'* and a sister Mexican species (Fig. 147), represent an independent well-supported clade. Amongst the subclade 3 (Fig. 147), *C. insularis* has an American sister species (sequences ITS MH211968 and MK966429 from pine forests in Oregon); both sequences form a well-supported subclade, distinct from the two other subclades of Clade 3 representing apparently circumboreal North European, North American and Asian species. None of the collections available in these clades suggests a thermophilic or xerophilic Mediterranean origin. A detailed revision of collections representing each clade is required before a thorough comparison of this cluster of species with *C. insularis* and within the whole "Perennis-clade" can be made.

Fulvifomes Murrill, Northern Polypores (5): 49 (1914).

Fulvifomes (typified as *Fulvifomes robiniae* Murrill) was described by Murrill (1914) to include perennial, sessile, ungulate, woody xanthochoroid fungus with dimitic hyphal system, colored basidiospores and lacks setae. Earlier *Fulvifomes* was treated as a synonym of *Phellinus* Quél. (Ryvarden and Johansen 1980; Dai 1999) later, many validated the generic rank of *Fulvifomes*, by studying the macro-microscopical description, nuclear behaviour and molecular data (Fiasson and Niemelä 1984; Wagner and Fischer 2002). *Fulvifomes* was revaluated and extensive ranges of characteristics were added to the classical description which includes annual to perennial, resupinate to pileate, applanate to ungulate, smooth to rimose basidiomata, homogenous to duplex context and poroid hymenial layer with mono-dimitic to dimitic hyphal system, presence or absence of setae, cystidioles, smooth, thick-walled, colored, globose to ellipsoid, cyanophilic to acyanophilic and inamyloid basidiospores (Murrill 1914; Wagner and Fischer 2002; Dai 2010; Salvador-Montoya et al. 2018; Tchoumi et al. 2020). Salvador-Montoya et al. (2018) and Zheng et al. (2021) proposed keys to American and Chinese *Fulvifomes* spp., respectively, since few samplings were done in other parts of the world.

Approximately 331 sequences belonging to 50 taxa were submitted in NCBI (https://www.ncbi.nlm.nih.gov) and 65 associated taxa are available in MycoBank (http://www.mycobank.org) (as of 1 January 2022). Wijayawardene et al. (2022) accepted 33 species in this genus.

Fulvifomes jawadhuvensis Kezo, K., Gunaseelan, S., & Kaliyaperumal, M., ***sp. nov.***

Index Fungorum: *IF558179*; *Facesoffungi Number: FoF10745; Fig. 148*

Etymology: The species epithet *jawadhuvensis* refers to the type locality of basidiomata collection.

Holotype: MUBL4011

Basidiocarps perennial, solitary, pileate, sessile, light in weight, hard when dry. *Pileus* dimidiate, convex to meagrely ungulate, with no distinct crust, projecting up to 5.7 cm, 9.5 cm wide and 3.4 cm thick near the base. *Pilear surface* velvety, light brown (6D6) to rust-brown (6E8) and meagerly warted when young, on maturity pilei becoming rough, weakly rimose, concentrically, narrowly sulcate, weakly zonate. *Margin* entire, round to obtuse, brown (6E4) to dark brown (6F5), velutinate when young, developing into brownish grey (6F2) to greyish brown (6E3), glabrous on maturity. *Pore surface* raw umber brown (5F8) to brown (6E7). *Pores* round to angular, regular, 4–8 per mm. *Dissepiments* entire, thick. *Context* up to 2.7 cm, homogeneous, yellowish-brown (5E8) to dark brown (6F7). *Tubes* yellowish-brown (5D8) to light brown (6D6), up to 0.7 cm thick, tube layers stratified, each stratum 0.2 to 0.4 cm with a thin layer of context in between.

Hyphal system strictly dimitic, Generative hyphae dominant; both skeletal and generative hyphae acyanophilous; tissue darkening with KOH without swelling. *Context* Generative hyphae, thin to thick-walled, hyaline to yellow, simple septate, branched, 2–6.5 µm diam.; skeletal hyphae, thick-walled with narrow lumen, unbranched, yellowish-brown, aseptate, 2–5.7 µm diam. *Trama* Generative hyphae, thin to thick-walled, yellow to brown, septate, rarely branched, 2–5.2 µm dia.; skeletal hyphae, thick-walled with narrow to wide lumen, yellowish-brown, aseptate, unbranched, 2–5.2 µm dia. Setae, cystidioles absent. *Basidioles* dominant, clavate, 7.7–14 × 3.8–7.2 µm. *Basidia* clavate to broadly clavate, with four sterigmata, 8.5–15 × 5–8.5 µm. *Basidiospores* broadly ellipsoid to subglobose, thick-walled, smooth, yellow in water, turning rust-brown in KOH, (4.8–) 5.1–6.4 (–6.9) × (4.1–) 4.4–4.9 (–5.2) µm (*n* = 50/2), Q = 1.1–1.3, CB$^-$, IKI$^-$. *Chlamydospores* globose to subglobose, thick-walled rust brown to reddish-brown, 5.2 – 8.5 × 4.1–7 µm, CB$^-$, IKI$^-$.

Specimen examined: India, Tamil Nadu, Thiruvannamalai district, Jawadhu hills, Jamunamarathur, 12.64° 54′ 19.1″ N 79° 18′ 33″ E, on living angiosperm tree (*Albizia amara* (Roxb.) Boiv., Fabaceae), 09 February 2018, Kezhocuyi Kezo (MUBL4011, **holotype**).

GenBank numbers: MW040079 (ITS), MW048886 (LSU), MW690924 (*tef1*).

Notes: *Fulvifomes jawadhuvensis* shares similarities with *F. grenadensis* by having dimidiate to ungulate pileus, round to obtuse margin, absences of cystidioles, but

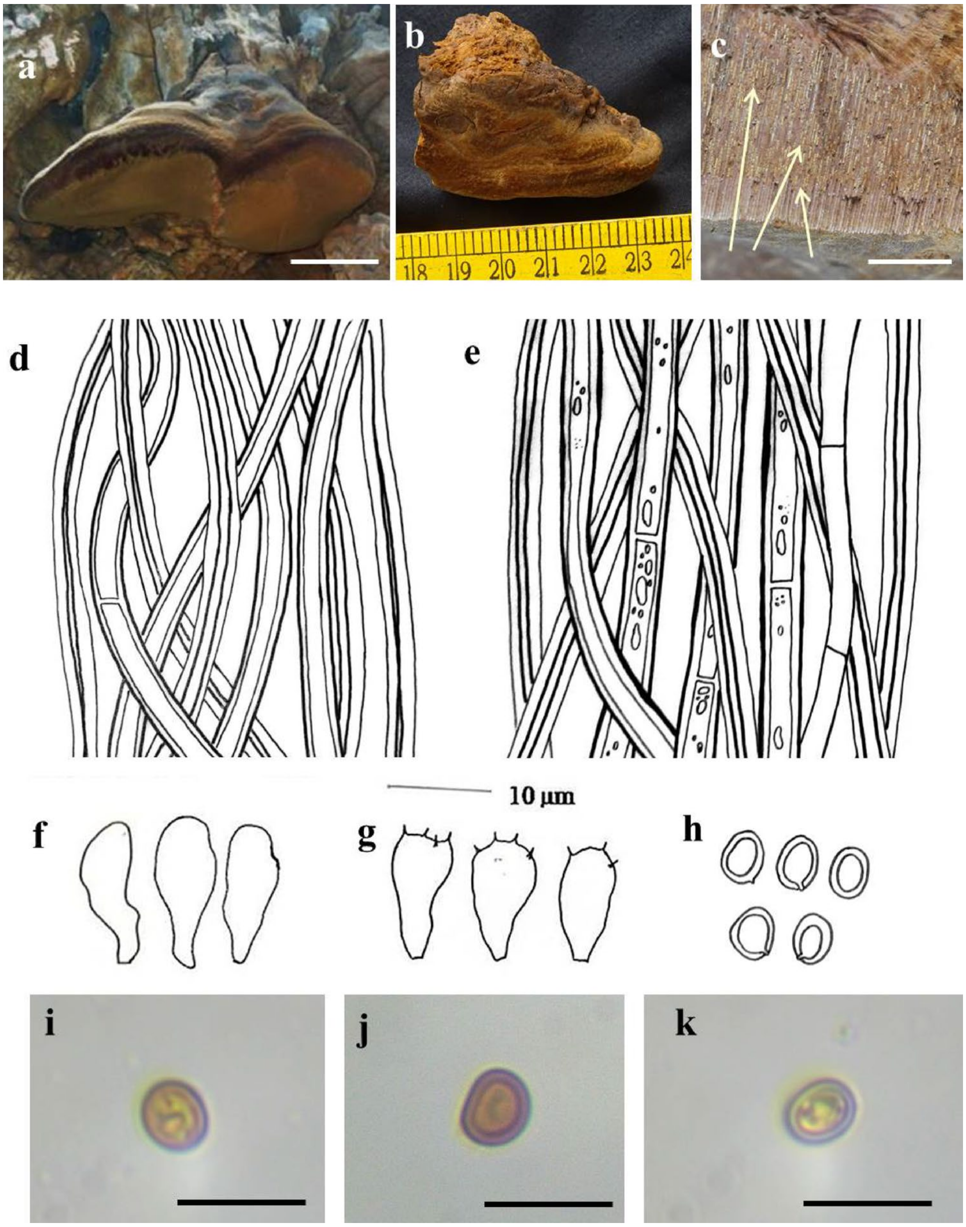


Fig. 149 ***Fulvifomes malaiyanurensis*** (MLCASB020, **holotype**). **a**–**b** Basidiocarp. **c** Stratified tube layer. **d** Tramal hyphae. **e** Context hyphae. **f** Basidioles. **g** Basidia. **h** Basidiospore. **i** Basidiospore in H_2O. **j** Basidiospore in KOH. **k** Basidiospore in cotton blue. Scale: a = 3 cm, c = 1 cm, d–k = 10 µm

the former lacks distinct crust after velvety pileus wears off and no. of pores per mm. Larger broadly ellipsoid to subglobose spores in *F. jawadhuvensis* differ from smaller spores in *F. grenadensis* (4–6 × 3–4 µm) (Ryvarden 2004). The new Indian species share other common characteristics with *F. elaeodendri*, *F. hainanensis, F. thailandicus,* in having dimidiate to ungulate basidiomata, zonate pileus with rimose patten (except *F. hainanensis*), pores per mm, distinctly thick-walled, colored basidiospores, absence of setae, but significantly varies basidiospores size and absences of cystidioles (Zhou 2014; Tchoumi et al. 2020). *Fulvifomes jawadhuvensis* and *F. centroamericanus* share only dimidiate pilei and absences of cystidioles and differ in other features; the former varies entirely from *F. krugiodendrii* (Ji et al. 2017). *Fulvifomes jawadhuvensis* shows variations with *F. nonggangensis* and *F. tubogeneratus* in basidiomata characters and microscopic illustrations (Zheng et al. 2021).

Fulvifomes malaiyanurensis Gunaseelan, S., Kezo, K. & Kaliyaperumal, M., ***sp. nov.***

MycoBank: MB821517; Facesoffungi number: FoF10744; Fig. 149

Etymology: The species epithet *"malaiyanurensis"* refers to the type locality of the collection site.

Holotype: CAL 1618

Basidiocarps perennial, solitary, sessile, broadly attached to substrate, hard, light when dry. *Pilei* dimidiate, ungulate

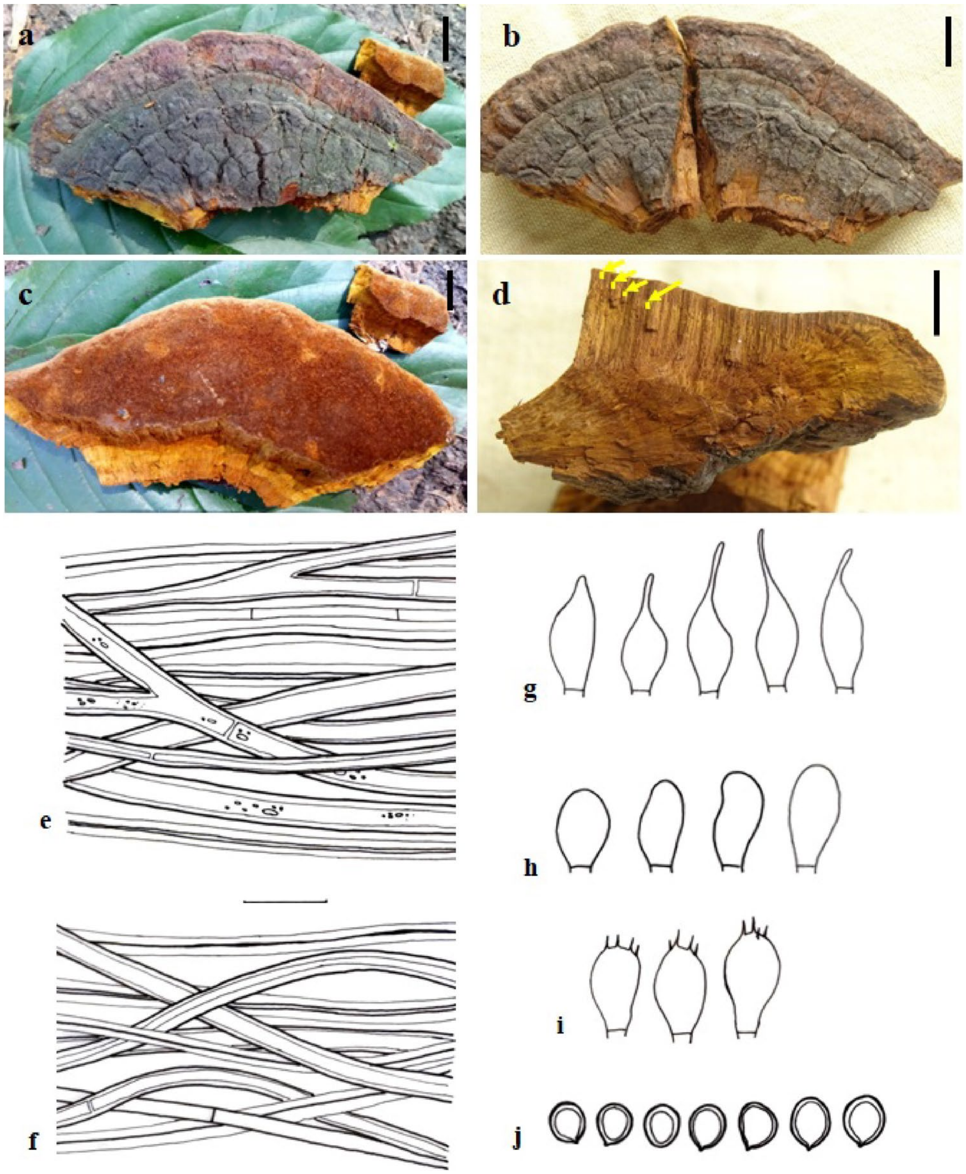


Fig. 150 ***Fulvifomes thiruvannamalaiensis*** (MUBL4013, **holotype**). **a** Habitat. **b** Pilear surface. **c** Pore surface. **d** Stratified layer (yellow arrows and lines indicates each stratum). **e** Contextual hyphae. **f** Tramal hyphae. **g** Cystidioles. **h** Basidioles. **i** Basidia. **j.** Basidiospores. Scale bars: **a–d** = 1 cm, **e–j** = 10 µm

to triquetrous, projecting up to 5 cm, 12 cm wide and 4 cm thickness near the attachment. *Pilear surface* velutinate towards the margin, partially, concentrically zonate, brown (6E6) to greyish brown (6F3), cracked during collection. *Margin* obtuse often round, velvety shining, brown (5E8) to yellowish brown (5E4). *Pore surface* umber-brown (5E8). *Pores* regular, circular to angular, 5–7 per mm. *Dissepiments* thick, entire. *Context* yellowish-brown (5C7) to dark golden brown (5C7), woody corky, up to 2 cm thick. *Tube layer* brown (6D7), up to 2 cm long in distinctly stratified, individual layer up to 0.5 cm in length.

Hyphal system strictly dimitic, skeletal and generative hyphae acyanophilous, tissue darkening with KOH without swelling. *Context*: Hyphal system subparallel, generative hyphae dominant hyaline to yellow, simple septate, thin to thick-walled, 2.2–6.4 µm in diam, rarely septate and branched, skeletal hyphae rare, yellow to brown, thick-walled, with a narrow to wide lumen, infrequently septate, unbranched, 1.8–5.2 µm in dia. *Trama* Hyphae interwoven, color not distinct from context; generative hyphae thin to thick-walled, frequently septate 2–5.2 µm wide, skeletal hyphae thick-walled, unbranched, aseptate with narrow to wide lumen 2.7–5.2 µm. Hymenial setae, cystidia and cystidioles absent. *Basidioles* clavate, 5–16 × 3–7 µm. *Basidia* broadly clavate, with four sterigmata, 7–16 × 5–8 µm. *Basidispores* broadly ellipsoid to subglobose, smooth, yellow to golden yellow in water, turning golden brown to rust-brown in KOH, thick-walled, (4.2–) 4.6–5.4 (–5.7) × (3.9–) 4.2 – 4.9 (–5.2) µm, Q = 1.09, (*n* = 50/2), Q = 1.05–1.25, CB^{-}, IKI^{-}. *Chlamydospores* globose to subglobose, thick-walled, rust-brown to reddish-brown, 5.7– 12.8 × 5.2–11.6 µm, CB^{-}, IKI^{-}.

Material examined: India, Tamil Nadu, Vizhupuram district, Malaiyanur, 37° 25′ 19.1″ N 23° 36′ 33″ W, on living angiosperm tree (*Tamarindus indica* L., Fabaceae), 25 October 2016, Sugantha Gunaseelan, MLCASB020, **holotype**.

Additional specimen examined: India, Tamil Nadu, Vizhupuram district, Malaiyanur, 37° 25′19.1″ N 23° 36′33″ W, on living angiosperm tree (*Tamarindus indica*, Fabaceae), 25 October 2016, Sugantha Gunaseelan, (MLCASB021, Isotype).

GenBank numbers: MLCASB020-MF155651 (ITS), MF155652 (LSU).

MLCASB021- MW048883 (LSU), MW690925 (*tef1*).

Notes: *Fulvifomes malaiyanurensis* is similar to *F. thailandicus* (Zhou 2015) in sharing yellowish-brown, broadly attached basidiomata, pore, dimitic hyphal and absence of cystidioles. However, *F. malaiyanurensis* is distinct by having ungulate to triquetrous, yellowish-brown, velutinate basidiocarp, acyanophilic subglobose basidiospores, lacking cystidioles. *Fulvifomes malaiyanurensis* differs from *F. grenadensis* (Ryvarden 2004), *F. hainanensis* (Zhou 2014) and *F. imbricatus* (Zhou 2015) in pileus character, pore per mm, shape and size of basidiospore. *F. malaiyanurensis* share a similar pileial character with *F. robinae* (Salvador-Montoya et al. 2018) but differs in hyphal system and basidiospore but shares pores/mm. *Fulvifomes malaiyanurensis* shares similarities with *F. elaeodendri* and *F. yoroui* in triquetrous up to ungulate basidiomata and pores per mm (Tchoumi et al. 2020; Olou et al. 2019) and differs in other characters. Macroscopically, *F. malaiyanurensis* may resemble African (Tchoumi et al. 2020), Asian *(*Zhou 2014, 2015; Liu et al. 2020; Du et al. 2021) and American (Ji et al. 2017) known species but shows variation in other taxonomic characters.

Fulvifomes thiruvannamalaiensis Gunaseelan, S., Kezo, K. and Kaliyaperumal, M., ***sp. nov.***

Index Fungorum number: IF558486; Facesoffungi number: FoF10726; Fig. 150

Etymology: The species epithet ″thiruvannamalaiensis″ refers to the type locality of collection site.

Holotype: MUBL4013

Basidiocarp perennial, solitary, sessile, applanate, broadly attached to the substrate by the narrow side, hard, woody when dry. *Pileus* dimidiate, convex to meagrely ungulate, lacks crust, projecting up to 4.8 cm in length, 10.4 cm in width and 3.4 cm thick near the attachment. *Pilear surface* partly covered with microalgae, glabrous, light brown (6D8, 6E7), rust-brown (6E8) to dark brown (6F7), finely cracked with small brownish grey scales (6E3, 6F2) concentric and radially sulcate, but coarse and deep sulci, scrupose zones near the attachment/older region, meagrely wavy near the margin. *Margin* entire, round to obtuse, velutinate to smooth, dark brown (6F7), brownish grey (6F2), often wavy. *Pore surface* yellowish raw umber brown (5F8), yellowish-brown (5E8) to brown (6E7, 6F8). *Pores* round, regular, 4–7 per mm. *Dissepiments* entire, thick. *Context* up to 1.6 cm, homogeneous, fibrous to corky, brown (6E7, 6F8) to dark brown (6F7). *Tubes* yellowish-brown (5E8), light brown (6D6) to brown (6E7, 6F8), up to 1.3 cm thick, tube layers stratified with thin-walled bright yellowish generative hyphae usually running between the old tubes, each stratum up to 0.4 cm.

Hyphal system strictly dimitic, skeletal and generative hyphae acyanophilous; tissue darkening with KOH without swelling. *Context* Generative hyphae dominant, thin to thick-walled, simple septate, branched, hyaline to brown, 1.2–4.8 µm diam.; skeletal hyphae, thick-walled with narrow to wide lumen, unbranched, aseptate, yellow to brown, 2.4–4.3 µm diam. *Trama* Generative hyphae, thin to thick-walled, septate, rarely branched, hyaline to brown, 1.2–4.8 µm diam.; skeletal hyphae, thick-walled with narrow to wide lumen, aseptate, unbranched, brown, 2.4–4.8 µm diam. *Setae* absent. *Cystidioles* thin-walled, hyaline, varies in shape, fusoid to ventricose with elongated apical portion, 12.9–27 × 2.8–7.2 µm. *Basidioles* clavate to broadly clavate, 8.5–15.5 × 3.5–6.5 µm. *Basidia* clavate to broadly clavate, with four sterigmata, 9.4–15.7 × 5.2–8 µm. *Basidiospores* broadly ellipsoid to subglobose, thick-walled, smooth, yellow in water, turning brown in KOH, (5.3–) 5.5–6.7 (–6.9) × (4.6–) 4.8–5.1(–5.5) µm (*n* = 30/2), Q = 1.05–1.3, CB$^-$, IKI$^-$.

Material examined: India, Tamil Nadu, Thiruvannamalai district, Jawadhu hills, Jamunamarathur, 12.64° 54′ 19.1″ N 79° 18′33″ E, on living angiosperm tree (*Albizia amara*, Fabaceae), 09 February 2018, Sugantha Gunaseelan, MUBL4013, **holotype**.

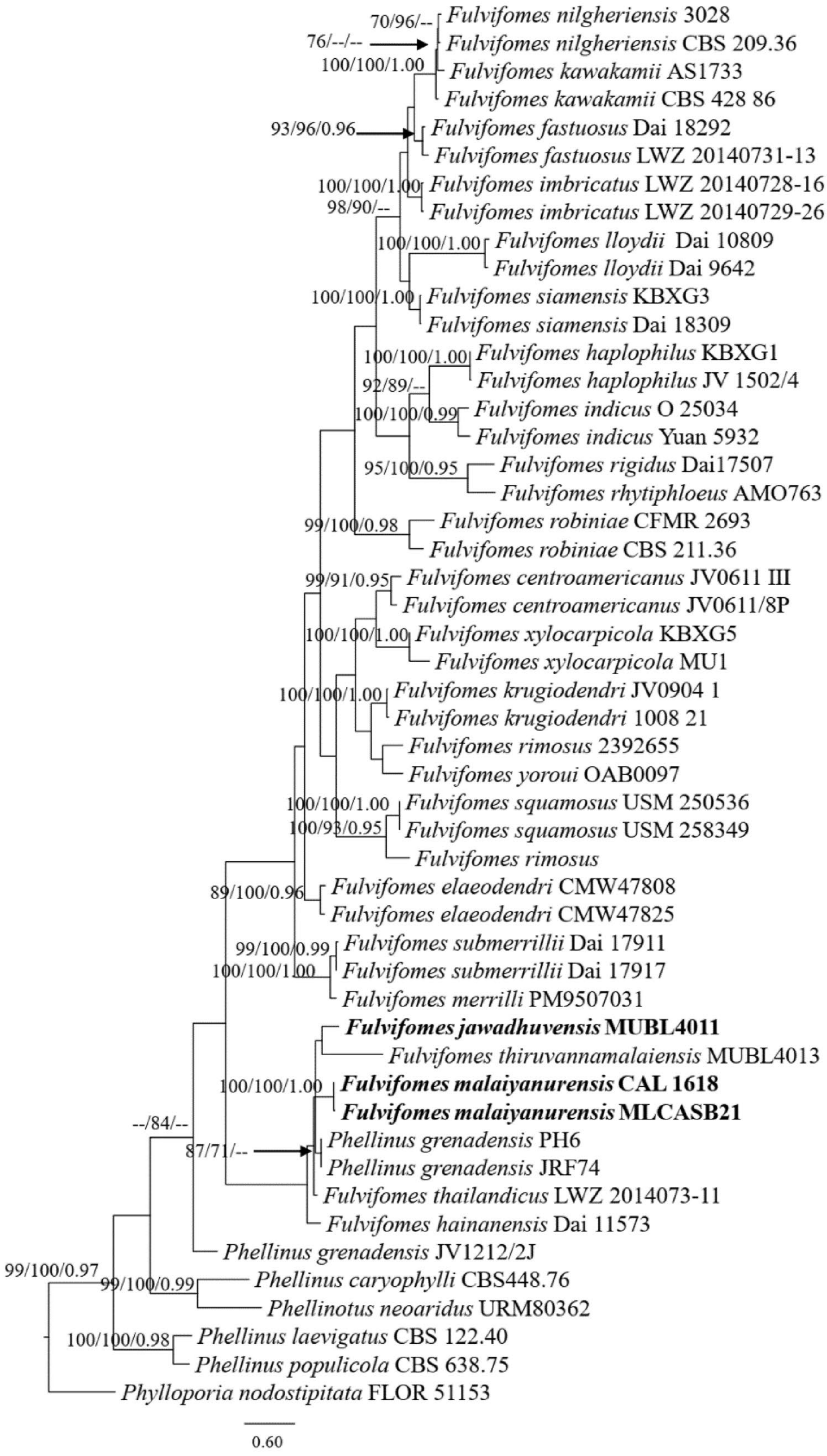
GenBank numbers: MZ221598 (ITS), MZ221600 (LSU).

Notes: *Fulvifomes thiruvannamalaiensis*, characterized by perennial, solitary, dimidiate, applanate to ungulate basidiomes, significantly cracked pilear surface with brownish-grey scales, stratified tube layer with dimitc hyphal system and thick-walled yellow to brown, acyanophilic subglobose to ellipsoid basidiospores.

African species, *F. yoroui* (Olou et al. 2019) shows close resemblance with *F. thiruvannamalaiensis*, in sharing perennial, pileate, ungulate basidiomata, dimitic hyphal system and presence of fusoid cystidioles, but the size and shape of the basidiospores (subglobose to globose basidiospores 5.5–6.5 × 4.7–5.6 µm), differ from *F. thirvannamalaiensis*. *Fulvifomes krugiodendri* (Ji et al. 2017), *F. rimosus* (Hattori et al. 2014) and *F. thailandicus* (Zhou 2015) are closely similar to *F. thirvannamalaiensis* morphologically by sharing dimidiate, concentrically sulcate, cracked basidiocarp, dimitic hyphal system and presence of fusoid cystidioles, yet differs in the number of pores and the size of basidiospores.

Despite few morphological resemblances between *F. elaeodendri* (Tchoumi et al. 2020) such as sulcate, glabrous pileus becoming cracked with age, stratified tube layer the

Fig. 151 Phylogram of *Fulvifomes* species, obtained from maximum likelihood (RAxML) of combined ITS, LSU, and *tef1* datasets. Bootstrap values (BS) from maximum likelihood (ML, left) and Maximum parsimony (MP, middle) greater than 70% and Bayesian posterior probabilities (PP), greater than 0.95, are indicated above the nodes as ML/MP/BYPP. The tree is rooted with *Phylloporia nodostipitata* FLOR 51153. New species and new records are indicated in black **bold**



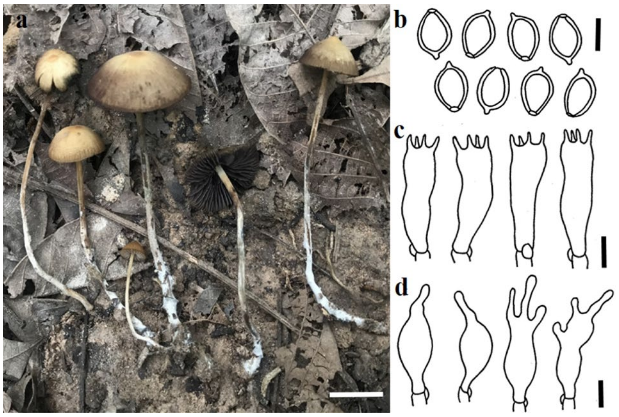


Fig. 152 ***Psilocybe keralensis*** (SDBR-CMUNK0448, **new record**). **a**. Basidiomata. **b**. Basidiospores. **c**. Basidia. **d**. Cheilocystidia. Scale bars: a = 10 mm; b–d = 5 µm

distinct microscopical traits viz., absence of cystidioles and the size of the basidiospores are distinguishing *F. thiruvannamalaiensis* from *F. elaeodendri*. *Fulvifomes centroamericanus* (Ji et al. 2017), *F. hainanensis* (Zhou 2014) and *F. imbricatus* (Zhou 2015) besides having dimitic hyphal systems are significantly distinct from *F. thiruvannamalaiensis* in morphology and microscopic features, by having uncracked pilear surface, shape and size of basidiospores.

Fulvifomes thiruvannamalaiensis shares a few similar morphological traits with the American species, *F. cedrelae, F. robinae* and *F. squamosus* (Salvador-Montoya et al. 2018) by having perennial, applanate, ungulate, sessile basidiomata with sulcate, cracked pilei, homogenous context and stratified tubes, however, the former differs from the later in hyphal system, number of pores and size of the basidiospore. The Chinese species *F. submerrillii* (Liu et al. 2020), shows high variations both morphologically and microscopically from the newly described Indian *F. thiruvannamalaiensis* (Fig. 151).

Hymenogastraceae Vittad, [as 'Hymenogastereae'], Monogr. Tuberac. (Milano): 11 (1831)

Note: Hymenogastraceae was erected by Vittadini (1893) with contained gilled and false-truffle fungi. According to the recent study by He et al. (2019), Hymenogastraceae is one of the larger families in the *Agaricales* and comprises 10 genera, namely *Anamika* K.A. Thomas, Peintner, M.M. Moser & Manim., *Flammula* (Fr.) P. Kumm., *Galerina* Earle, *Gymnopilus* P. Karst., *Hebeloma* (Fr.) P. Kumm., *Hymenogaster* Vittad., *Naucoria* (Fr.) P. Kumm., *Phaeocollybia* R. Heim, *Psathyloma* Soop, J.A. Cooper & Dima and *Psilocybe* (Fr.) P. Kumm. Now, it is represented by more than 1500 species in Hymenogastraceae (Matheny et al. 2006; Redhead et al. 2007; Kirk et al. 2008; He et al. 2019).

Psilocybe (Fr.) P. Kumm., Führ. Pilzk. (Zerbst): 21 (1871)

Psilocybe was first introduced by Kummer (1871) with *P. semilanceata* (Fr.) P. Kumm. as the type species. This genus is saprotrophic and widely distributed in both tropical and temperate areas (Singer and Smith 1958; Guzmán 1978, 1983; Redhead et al. 2007; Kirk et al. 2008), while *Psilocybe* sensu lato is known to include *Deconica*. Both *Psilocybe* and *Deconica* have been characterized by typically hygrophanous basidiomata, brown to yellow–brown pileus, lilac-brown to dark brown to dark purple-brown spore prints, ellipsoid to rhomboid to subhexagonal basidiospores with a distinct apical germ pore (Singer and Smith 1958; Guzmán 1978, 1983; Redhead et al. 2007). Most *Psilocybe* contains psychedelic compounds, e.g. baeocystin, psilocin and psilocybin (Stamets 1996), whereas *Deconica* possesses none of these compounds (Marcano et al. 1994). Traditionally, *Psilocybe* and *Deconica* belong to Strophariaceae, order Agaricales (Guzmán 1978, 1983). However, multi-phylogenetic analyses have revealed that *Psilocybe* formed a monophyletic genus in Hymenogastraceae, order Agaricales, which clearly separates it from *Deconica* (Ramírez-Cruz et al. 2013). There are more than 300 accepted species of *Psilocybe* in the Index Fungorum (2022a, b), however, only eight *Psilocybe* species have been reported in Thailand (*P. cubensis* (Earle) Singer, *P. magnispora* E. Horak, Guzmán & Desjardin, *P. samuiensis* Guzmán, Bandala & J.W. Allen, *P. subaeruginascens* Höhn, *P. thaiaerugineomaculans* Guzmán, Karun. & Ram.-Guill., *P thaicordispora* Guzmán, Ram.-Guill. & Karun., *P. thaiduplicatocystidiata* Guzmán, Karun. & Ram.-Guill., and *P. thailandensis* E. Horak, Guzmán & Desjardin and *P. thaizapoteca* Guzmán, Karun. & Ram.-Guill.) (Guzmán et al. 1993, 2012; Horak et al. 2009; Chandrasrikul et al. 2011).

Psilocybe keralensis K.A. Thomas, Manim. & Guzmán, Mycotaxon 83: 196, 2002.

Index Fungorum number: IF380972; Facesoffungi number: *FoF10681;Fig.* 152

Pileus 13–25 mm diameter, hemisphearic, subconic or campanulate, hygrophanous, brownish-orange (6C4) to greyish orange (5B6), fading to light orange (5A4) to orange-white (5A2), surface glabrous, lucidus when dry and often somewhat bluish when touched or on drying, especially at the edge, not viscid and the margin finely translucent striate when moist; context pale yellow (2A3) or yellowish-white (2A2), bruising ink blue. *Lamellae* adnate to slightly sinuate, close, light orange (5A4) to orange (5A6) to brownish grey (9C2) or reddish-brown (9E5), often with ink blue tinge, edges serrulate and remaining whitish. *Stipe* 45–80 × 1.5–3 mm, equal, sometimes flattened and becoming tapered toward the base, nearly concolorous with the pileus, darker below, often with ink blue to blackish tinge when touched or when dry, and shiny when dry; surface

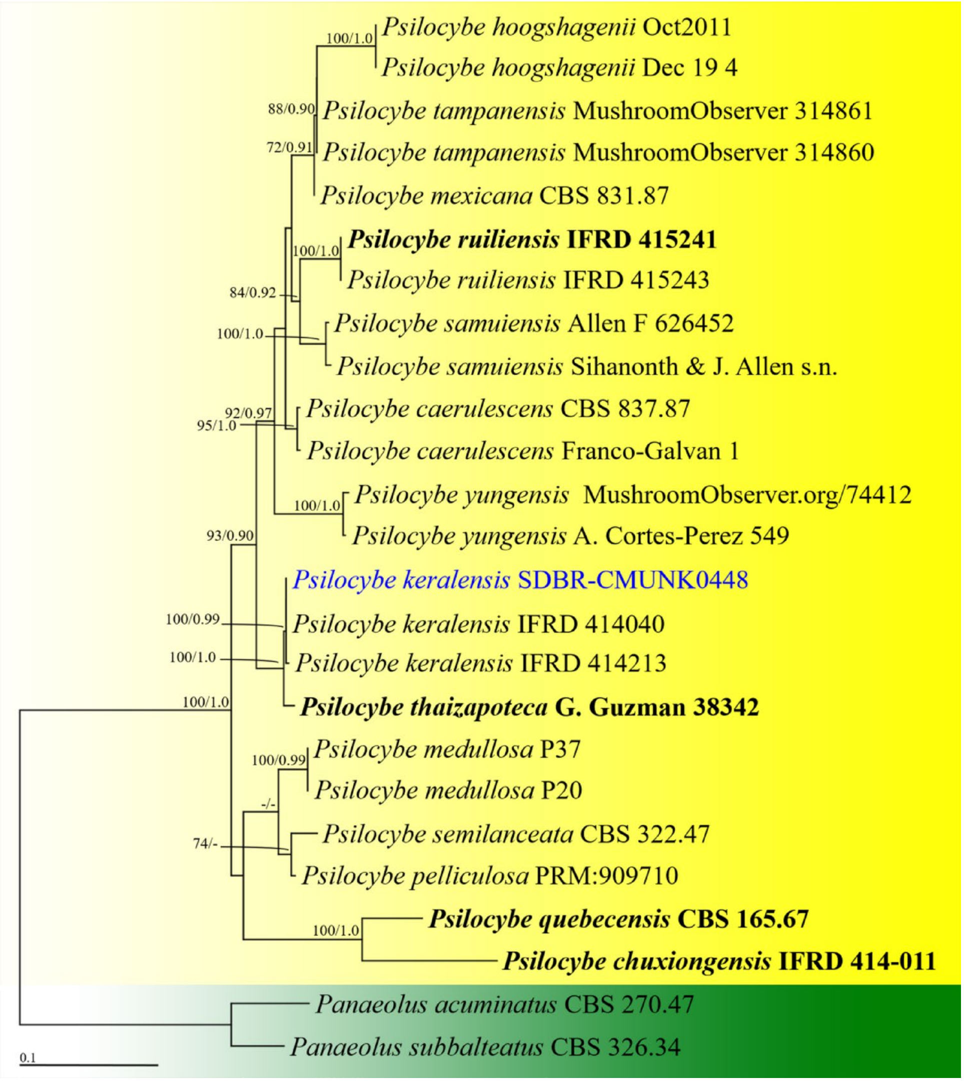


Fig. 153 Phylogenetic tree derived from maximum likelihood analysis of a combined ITS and LSU genes of 25 sequences and the aligned dataset was comprised of 1640 characters including gap. The average standard deviation of the split frequencies of the BI analysis was 0.00962. *Panaeolus acuminatus* (CBS 270.47) and *Pa. subbalteatus* (CBS 326.34) were used as outgroup taxa. The numbers above branches are the bootstrap statistics percentages (left) and Bayesian posterior probabilities (right). Branches with bootstrap values ≥ 70% are shown at each branch and the bar represents 0.1 substitutions per nucleotide position. Hyphen (-) represents support values ≤ 70/0.90. Ex-type strains are in black bold. The newly generated sequences are indicated in blue

longitudinally striate and covered with appressed whitish fibrils or flocculose, sometimes uneven and with scrobicula and grooves; base with white mycelium and often radicating; annulus absent; context fragile, yellowish and yellowish-brown towards the surface and base, staining somewhat ink blue when bruised. *Spore print* dark brown.

Basidiospores 6–10 × 5–7 × 4–6 µm, often subrhomboid or ovoid, sometimes ellipsoid, occasionally inconspicuous subhexagonal in face view, Q = 1.1–1.7, Q_m = 1.35 ± 0.13, ellipsoid or subovoid, sometimes nearly oblong inside view, Q = 1.2–1.8, Q_m = 1.55 ± 0.15; yellowish-brown with a purple tinge in water, dark yellow to yellowish-brown in KOH, dark purplish-brown in deposit; wall smooth, slightly thick (0.5–1 µm), complex, with 0.8–1.5 µm wide apical germ pore. *Basidia* 18–28 × 5–8 µm, hyaline, long subcylindric to clavate, often constricted in middle and narrowed in the lower half, 4-spored and 2-spored, rarely 1-spored; sterigmata up to 6 µm. *Pleurocystidia* are relatively rare and scattered, 13–22 × 4–6.5 µm, hyaline, ventricose to sublageniform, sometime fusoid or clavate, occasionally nearly cylindric-clavate or obclavate, often with a 1–7.5 × 1–2 µm neck or rostrum, not branched, the top or apex often seems wall thickened or contain some matter. *Cheilocystidia* abundant, 14–35.5 × 4–8 µm, hyaline, similar to pleurocystidia, mostly with a 1.5–13 × 1–3 µm rostrum or neck, sometimes with an acuminate apex, the top or apex often seems wall thickened or contain some matter. *Pileipellis* an ixocutis, 15–80 µm thick, made up of creeping, interwoven, 2–6 µm wide filiform to slender tubular hyphae, hyaline and colourless, wall-smoothed and thin; subpileipellis more pigmented to dark yellow in KOH. *Subhymenium* subcellular, hyaline, composed of irregular vesiculose to polygonal or subglobose cells. *Caulocystidia* abundant, 14–49 × 3.5–12 µm, scattered, gregarious to clustered at the upper part of the stipe, hyaline, similar to cheilocystidia, hyaline, thick-walled. *Clamp connections* present in all tissues.

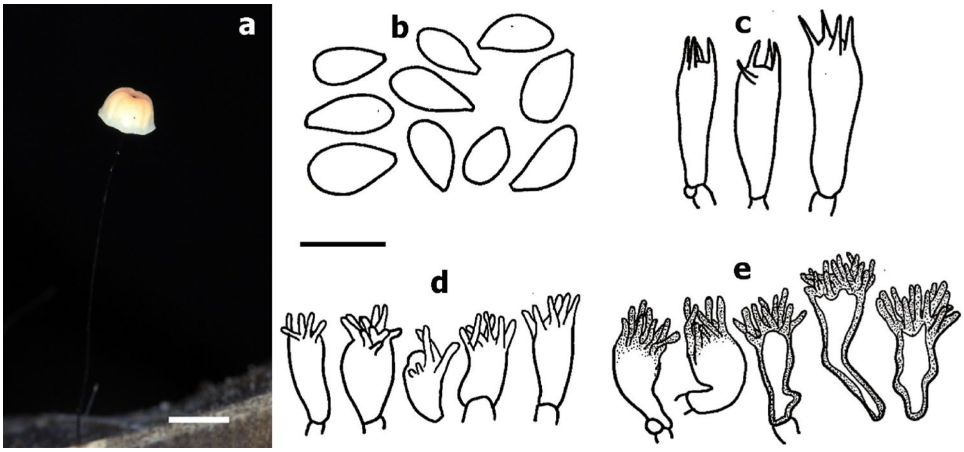


Fig. 154 ***Marasmius pallidoaurantiacus*** BKF10248 (**holotype**). **a** Basidiomata, **b** Basidiospores, **c** Basidium, **d** Checlocystidia, **e** Pileipellis cell. Scale bars: a = 2 mm, b–e = 10 µm. Photographs and drawing by N. Wannathes

Material examined: Thailand, Ubon Ratchathani Province, Phibun Mangsahan, District, 15° 3′ 25″ N 105° 26′ 50″ E, elevation 164 m, on soil, 4 May 2019, N. Suwannarach & J. Kumla, SDBR-CMUNK0448.

Habitat: Growing solitary to scattered on dung or soil of meadows, or grassland in an open area.

Distribution: India (Thomas et al. 2002), Southwestern China (Ma et al. 2016) and Thailand (This study).

GenBank numbers: MZ452082 (ITS), MZ452083 (LSU).

Notes: Morphologically, *P. keralensis* is similar to *P. columbiana* Guzmán; however, *P. columbiana* differs significantly in the absence of pleurocystidia. It has been known to only be from Colombia (Guzmán 1978, 1983; Guzmán et al. 2005). Phylogenetically, *P. keralensis* formed a sister taxon to *P. thaizapoteca* (Fig. 153). However, the large pileus (20–50 mm in diameter) and small basidiospores (6–7 × 3–4.5 × 3–3.5 µm) of *P. thaizapoteca* clearly differ from *P. keralensis* (Guzmán et al. 2012).

Marasmiaceae Roze ex Kühner.

Note: Marasmiaceae was erected by Kühner (1980) with a combination of Marasmieae, Collybieae and Myceneae of Tricholomataceae R. Heim in Singer (1986) classification. Molecular phylogeny has revealed that Marasmiaceae is monophyletic, containing ten genera (*Amyloflagellula* Singer, *Brunneocorticium* Sheng H. Wu, *Campanella* Henn., *Chaetocalathus* Singer, *Crinipellis* Pat., *Hymenogloea* Pat., *Marasmius* Fr., *Moniliophthora* H.C. Evans, Stalpers, Samson & Benny, *Neocampanella* Nakasone, Hibbett & Goranova and *Tetrapyrgos* E. Horak) with more than 1590 species, *Marasmius* being the generic type (Matheny et al. 2006; Kirk et al. 2008; He et al. 2019) of this family.

Marasmius Fr., Fl. Scan.: 339 (1836).

Marasmius is a large genus of plant debris decomposers (Singer 1976a, b, 1986; Antonín and Noordeloos 2010) that is represented by approximately 600 species worldwide (He et al. 2019). The genus was first introduced by Fries (1835) and *Marasmius rotula* (Scop.). Fr. was later designated as the type species by Singer and Smith (1946). *Marasmius* is characterized by small or possibly large to robust basidiomata, convex or campanulate, striate to sulcate, white to strongly pigmented pilei, well-developed lamellar, thin and typically tough, cylindrical, often brown or darkly fuscous stipe, white spore print, hyaline, smooth and inamyloid spores and hymeniform pileipellis of smooth or diverticulate cells (Singer 1976a, b, 1986; Antonín 2007). Generic circumscription of *Marasmius* sensu stricto was restricted (Wilson and Desjardin 2005) and the infrageneric classification has been revised based on the results of a phylogenetic analysis of combined sequences of LSU and ITS incorporated with other notable morphological features (Oliveira et al. 2020b).

Marasmius pallidoaurantiacus Wannathes, N. Suwannarach, J. Kumla & S. Lumyong, ***sp. nov***.

MycoBank number: MB 840,379; *Facesoffungi number*: *FoF 10682;Fig.* 154

Etymology: 'pallio' = pale, 'aurantiacus' = orange colour, refers to the pileus colour

Holotype: BKF10248

Pileus 1–2 mm diam., hemispherical, umbilicate, with a tiny dark brown papilla at center; dull, dry, glabrous, slightly striate; orange white (5A2) to pale orange (5A3) with darker disc. *Context* thin, white. *Lamellae* adnate to a small collarium, distant (10–11), broad (1 mm), orange white (5A2), non-marginate. *Stipe* 8–13 × 0.2 mm, cylindrical, central; glabrous, dull, dry; insititious; dark brown overall, sometime stipe arising directly from dark brown rhizomorph.

Basidiospores 7–10(–11) × 4–5(–6) µm [x = 8.20 ± 1.35 × 4.18 ± 0.58, Q = 1.75–2.57, q = 1.97 ± 0.30, *n* = 25] ellipsoid, fusoid, smooth, hyaline, inamyloid, thin-walled. *Basidia* 14–16 × 4–6 µm, clavate, with 4 sterigmata, thin-walled, inamyloid. *Cheilocystidia* abundant, of *Siccus*- type broom cells; main body 5–7 × 4–6 µm, cylindrical to clavate, hyaline, inamyloid, thin-walled; apical setulae

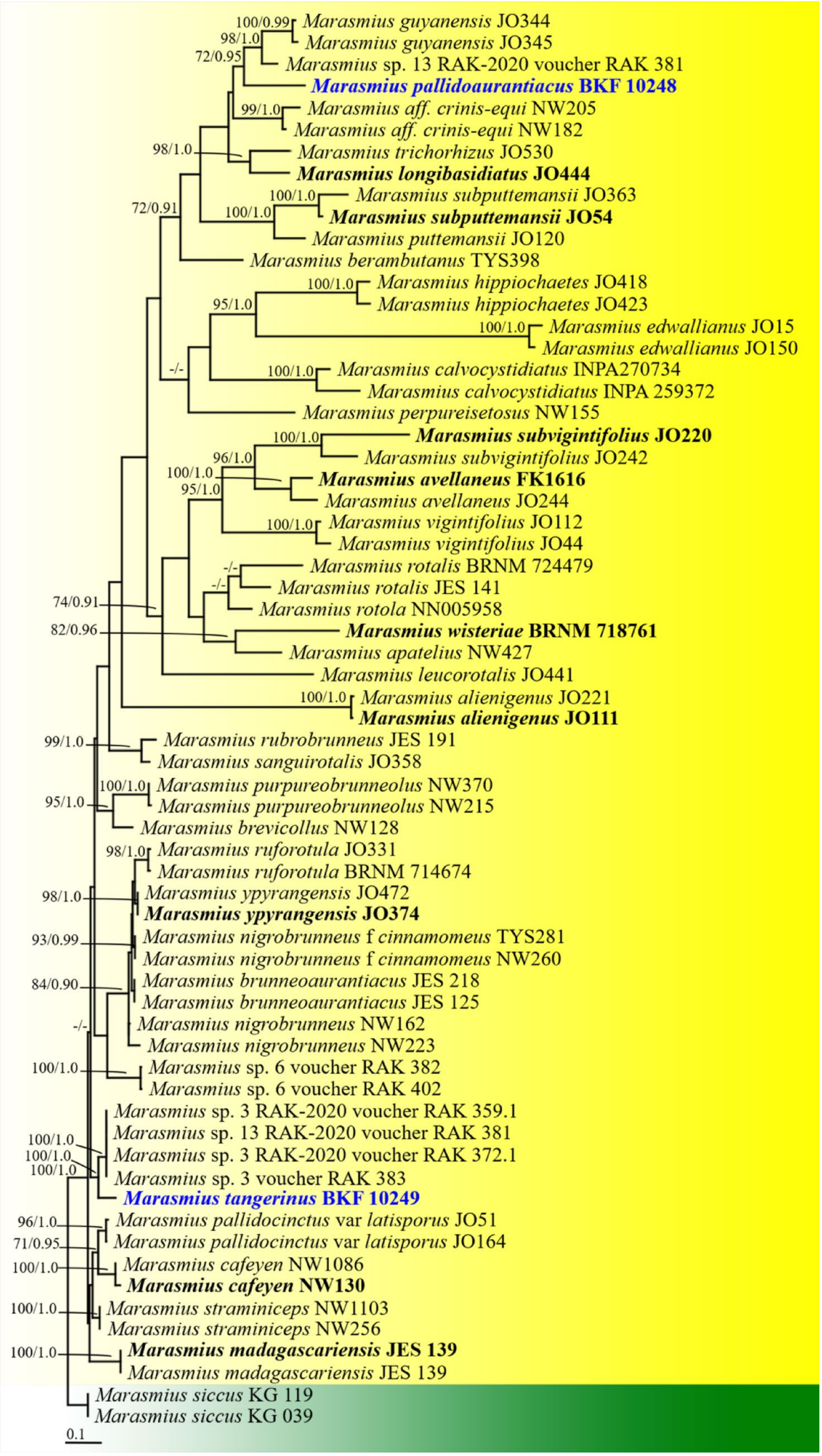


Fig. 155 Phylogenetic tree derived from maximum likelihood analysis of a combined ITS gene of 65 sequences and the aligned dataset was comprised of 1116 characters including gap. The average standard deviation of the split frequencies of the BI analysis was 0.00825. *Marasmius siccus* KG 039 and KG 119 were used as outgroup. Numbers above branches are the bootstrap statistics percentages (left) and Bayesian posterior probabilities (right). Branches with bootstrap values ≥ 70% are shown at each branch and the bar represents 0.1 substitutions per nucleotide position. Hyphen (-) represents support values ≤ 70%/0.95. Ex-type strains are in black bold. The newly generated sequences are indicated in blue and bold type species

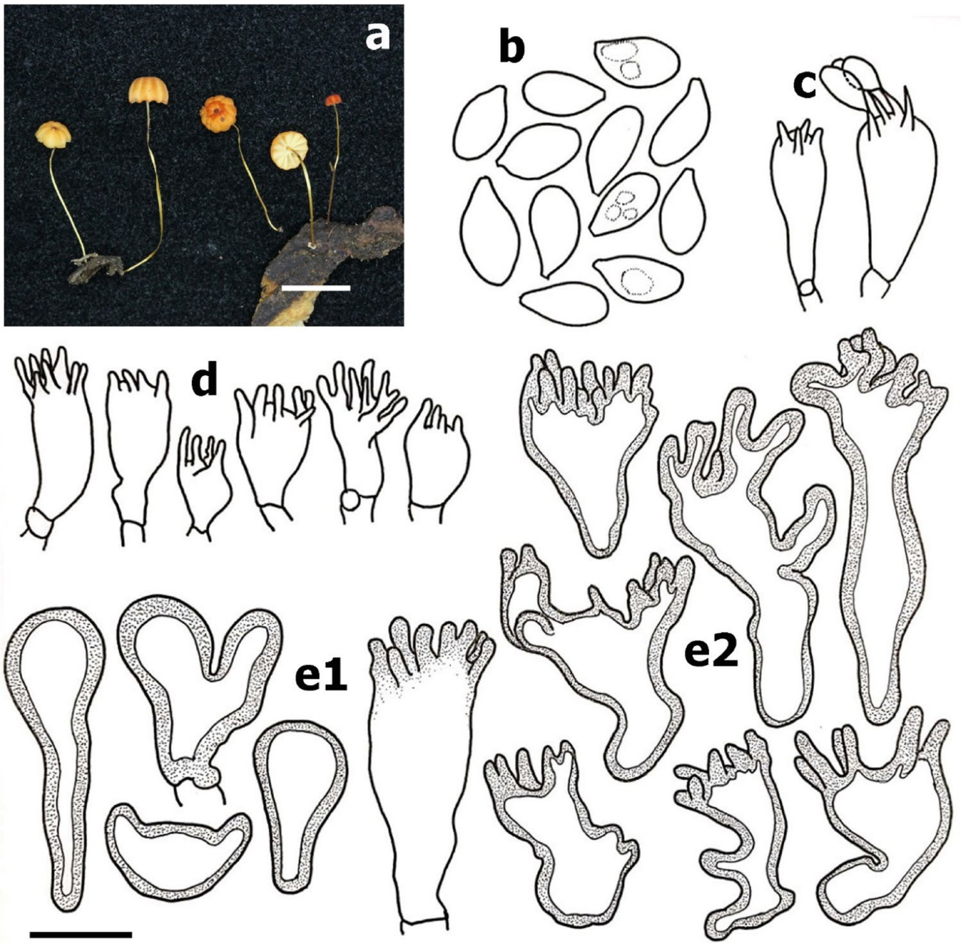


Fig. 156 ***Marasmius tangerinus*** BKF10249 (**holotype**). **a** Basidiomata, **b** Basidiospores, **c** Basidium, **d** Checlocystidia, **e** Pileipellis cell. Scale bars: a = 5 mm, b–e = 10 µm. Photographs and drawing by N. Wannathes

1–4 × 1 µm, cylindrical to conical, obtuse, hyaline to pale yellow, thin- to thick-walled. *Pleurocystidia* absent. *Pileipellis* hymeniform, mottled, composed of *Siccus*-type broom cells; main body 10–14 × 4–6 µm, clavate to broadly clavate, flexuose, pale yellow, inamyloid, thin- to thick-walled; apical setulae (1–) 2–6 × 1 µm, cylindrical, regular in outline, obtuse, brown, thick-walled. *Pileus trama* interwoven, inamyloid. *Lamellar trama* interwoven, hyphae 2–5 µm diam., cylindrical, inflated, smooth, hyaline, inamyloid, thin-walled, non-gelatinous. *Stipitipellis* subparallel, hyphae 2–4 µm diam., cylindrical, dark brown, smooth, inamyloid, thick-walled (up to 1 µm), non-gelatinous. *Stipe trama* subparallel, hyphae 2–5 µm diam., cylindrical, hyaline to pale yellow, smooth, dextrinoid, thin-walled, non-gelatinous. *Caulocystidia* absent. *Clamp connections* present in almost all tissues.

Material examined: Thailand, Nakhon Ratchasima Provinve, Khao Yai National Park, 33 km marker on Hyw 2090, 22 Sep 2018, collectors N Wannathes, N Suwannarach J Kumla, S Lumyong, BKF10248 (**holotype**), NW1108 (**isotype**).

Habit, habitat and known distribution: Gregarious on dicotyledonous leave, known only from Thailand.

GenBank numbers: MZ452673 (ITS).

Notes: *Marasmius pallidoaurantiacus* is characterized by a tiny, hemispherical with dark brown conical papilla at the center, slightly striate, plae orange pileus, collariate, distant lamellae, thin stipe, sometimes arising directly from the rhizomorph, ellipsoid to fusoid basidiospores with mean 8.2 × 4.2 µm, and the presence of *Siccus*-type broom cell cheilocytidia. This new species is morphologically similar to *Marasmius pallenticeps* Singer, which was originally described from Argentina. The latter differs by forming a pure white pileus, stipe usually arising directly from rhizomorphs and the presence of nodes (Desjardin and Ovrebo 2006). *Marasmius pallidoaurantiacus* pilei appear pigmented like those of *M. longibasidiatus* J.S. Oliveira, a species recently described from Brazil. This species differs by forming bigger (1.3–4 mm diam.), sulcate pileus, longer basidia (33–42 × 7.8–10 µm) and pileipellis composed of mixed *Siccus* type broom cell and non-setulost cells (Oliveira 2020). Phylogenetic analyses inferred from ITS sequence data (Fig. 155) confirmed that *M. pallidoaurantiacus* is a distinct species from other related morphological species and other taxa within this genus.

Fig. 157 **Basidiomata of *Rhizomarasmius cunninghamietorum*** **a**. HGASMF01-10,709 (**holotype**), **b.** HGASMF01-10,708 (**paratype**). Scale bars: = 1 cm

Marasmius tangerinus Wannathes, N. Suwannarach, J. Kumla & Lumyong, ***sp. nov***.

MycoBank number: MB840380; *Facesoffungi number*: *FoF10683; Fig. 156*

Etymology: 'tangerinus' = tangerine colour, refers to the pileus colour

Holotype: BKF10249

Pileus 2–3 mm diam., hemispherical to convex, umbilicate, with a tiny dark brown papilla at center; dull, dry, glabrous, striate; orange red (8A8) overall when young, orange red (8A8) at disc, orange (6B7) to tangerine (6B8) at margin in age. *Context* thin, white. *Lamellae* adnate to a small collarium, distant (10–11), narrow (0.5 mm), pale orange (5A3), marginate with orange. *Stipe* 13–20 × 0.3 mm, cylindrical, central, glabrous, dull, dry, insititious, golden brown (5D7) overall, sometimes stipe arising directly from golden brown rhizomorph.

Basidiospores 8–10 × (4–)4.5–5 µm [x = 8.56 ± 0.71 × 4.92 ± 0.28, Q = 1.6–2.0, q = 1.74 ± 0.16, *n* = 25] ellipsoid, fusoid, smooth, hyaline, inamyloid, thin-walled. *Basidia* 16–18 × 6–8 µm, clavate, with 4 sterigmata, thin-walled, inamyloid. *Cheilocystidia* abundant, of *Siccus*- type broom cells; main body 10–14 × 5–7 µm, cylindrical to clavate, sometime branched, hyaline, inamyloid, thin-walled; apical setulae 1–4 × 1(–2) µm, cylindrical to conical, obtuse, pale yellow, thin- to thick-walled. *Pleurocystidia* absent. *Pileipellis* hymeniform, not mottled, composed of 2 type of cells: (a) *Siccus*-type broom cells; main body 18–38 × 10–16 µm, clavate to broadly clavate or turbinate, irregular in outline, hyaline to pale yellow, inamyloid, thin- to thick-walled; apical setulae 2–10 × 1–4 µm, cylindrical to conical, regular in outline, obtuse, yellow to pale brown, inamyloid, thick-walled; (b) non-setulose cell, 8–32 × 10–15 µm, clavate to broadly clavate, sometime branched, yellow to pale brown, inamyloid, thick-walled. *Pileus trama* interwoven, inamyloid. *Lamellar trama* interwoven, hyphae 4–8 µm diam., cylindrical, inflated, smooth, hyaline, inamyloid, thin-walled, non-gelatinous. *Stipitipellis* subparallel, hyphae 4–6 µm diam., cylindrical, pale brown, smooth, dextrinoid, thick-walled (up to 1 µm), non-gelatinous. *Stipe trama* subparallel, hyphae 2–4 µm diam., cylindrical, hyaline, smooth, dextrinoid, thin-walled, non-gelatinous. *Caulocystidia* absent. *Clamp connections* present in almost all tissues.

Material examined: Thailand, Nakhon Ratchasima Provinve, Khao Yai National Park, 33 km marker on Hyw 2090, 22 Sep 2018, collectors N Wannathes, N Suwannarach J Kumla, S Lumyong, BKF10249 (**holotype**), NW1224 (**isotype**).

Habit, habitat and known distribution: Gregarious on dicotyledonous wood, known only from Thailand.

GenBank numbers: MZ452087 (ITS).

Notes: *Marasmius tangerinus* is characterized by a tiny, hemispherical, bright orange pileus, with dark brown papilla at the center, collariate, distant lamellae, thin stipe, sometimes arising directly from the rhizomorph, ellipsoid to fusoid basidiospores with mean 8.6 × 4.9 µm, pileipellis composed of mixed *Siccus* type broom cell and non-setulost cells, with the presence of cheilocytidia, and ligicolous habit. *Marasmius tangerinus* is morphologically similar to *M. trichorhizus* Speg. which has been characterized from a neotropic realm. The latter species differ by forming more lamellae (12–15), longer stipe (4–71 mm long), and smaller basidiospores with mean 6.9 × 3.4 µm (Oliveira 2020). The phylogenetic analyses of the ITS sequence data (Fig. 155) indicate that *M. tangerinus* is a distinct species from other related morphological species and other taxa within this genus.

Physalacriaceae Corner, Beih. Nova Hedwigia 33: 10 (1970).

Notes: The family was typified by *Physalacria* Peck (Peck 1883), which contained a number of marasmoid fungi, including the important tree pathogen *Armillaria* (Fr.)

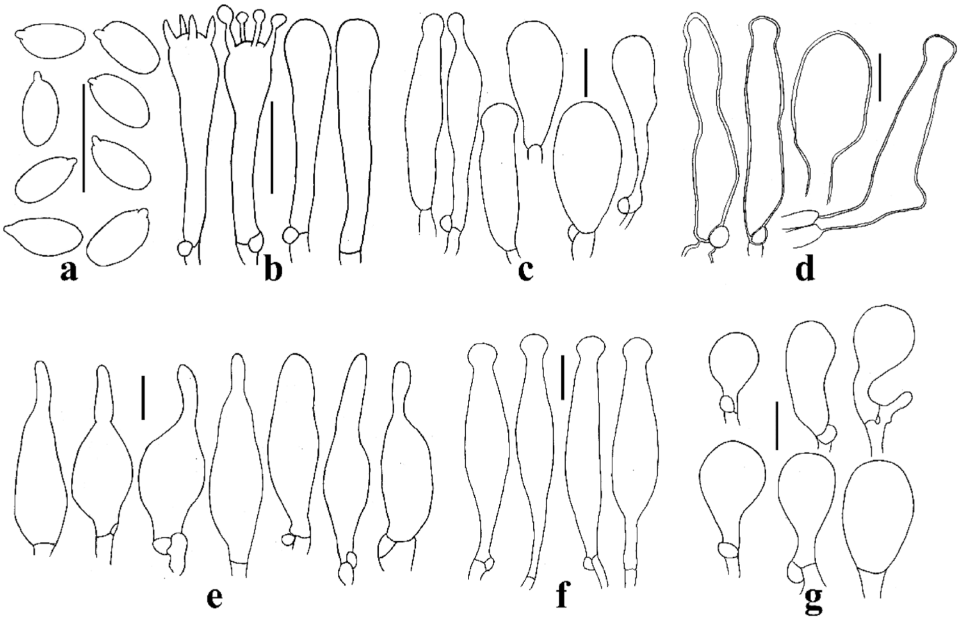


Fig. 158 Microscopic structures of *Rhizomarasmius cunninghamietorum* (holotype). **a**. Basidiospores, **b**. Basidia and Basidioles, **c**. Cheilocystidia, **d**. Caulocystidia, **e**. Pileiocystidia, **f**. Pleurocystidia, **g**. Terminal cells of pileipellis, Scale bars = 10 µm

Staude and edible fungi *Flammulina* P. Karst., this group usually have pilocystdia and non-dextrinoid tissue (Petersen and Hughes 2010). More than 28 genera included in this family by Index Fungorum (2022a, b) and are accepted by Wijayawardene et al. (2022).

Rhizomarasmius R.H. Petersen, Mycotaxon 75: 333 (2000).

Notes: Petersen (2000) accommodated two *Marasmius* species, *M. pyrrhocephalus* Berk. and *M. undatus* (Berk.) Fr. to form a new genus, *Rhizomarasmius* R.H. Petersen. This genus is characterized by convex to hemispherical pileus, distant, thick, ascending, white lamellae and central stipe apically pale and darkening downward to brown-black, smooth basidiospores, pileipellis forming a hymeniderm layer of clavate, globose to sphaeropedunculate, smooth elements and scattered, elongate pileocystidia, as well as the presence of cheilo-, pleuro- and caulocystidia (Petersen 2000; Antonín and Noordeloos 2010). Most members of marasmoid are saprotrophic or parasitic fungi (Pacioni and Lalli 1989; Filippi 1991; Ronikier and Ronikier 2011; Moreau et al. 2015). *Rhizomarasmius epidryas* (Kühner ex A. Ronikier) A. Ronikier and M. Ronikier is a common arctic-alpine saprotrophic fungus (Ronikier 2009, 2011), and this species was originally described by Kühner as *Marasmius epidryas* Kühner in 1935 (Kühner 1936). Wilson and Desjardin (2005) and Noordeloos and Antonín (2008) transferred this species into *Mycetinis* Earle. However, later established that the species belongs to the new genus *Rhizomarasmius* by Anna & Macheł Ronikier and changed the current name accordingly (Ronikier 2009, 2011). Recently Moreau et al. (2015) added two members, *Rhizomarasmius oreinus* (Pacioni & Lalli) Vizzini, Antonín & A. Urb. and *R. setosus* (Sowerby) Antonín & A. Urb. To date, there are five species described within this genus. Petersen (2000), Petersen and Hughes (2010) and Ronikier and Ronikier (2011), showed *Rhizomarasmius* to form a well-supported clade in phylogenetic analyses.

Rhizomarasmius cunninghamietorum Chun Y. Deng, J.P. Li & Gafforov, ***sp. nov.***

Index Fungorum number: IF558751; Facesoffungi number: FoF10408; Figs. 157, 158

Etymology: the species epithet refers to the host genus *Cunninghamia.*

Holotype: HGASMF01-10709

Basidiomata gregarious, marasmioid, marasmielloid or collybioid. *Pileus* 9–36 mm in diameter, convex to plano-convex when young, expanding to applanate with age, obtuse or slightly depressed at the centre, often wrinkled, slightly sticky, sometimes hygrophanous, translucent when mosit, radially striate or sulcate from the margin up to 3/4 of the radius nearly to the centre, with transversely sulcate between each radial striate when old, involute then inflexed to reflexed at margin, with marginal zone often undulating with age, almost white overall when young, with somewhat milk white (1A2) pigment, then change to generally orange white (6A2), pale orange (6A3) or cinnamon (6D6) overall, paler towards margin, henna (7E8) to dark brown (8E8) at disc when old, darker in the groove, paler at margin. *Lamellae* adnate, sometimes with slightly decurrently tooth, furcate, intervenose, or anastomosing, often split, linear to ventricose, subdistant, L = 10–14, l = 1–2, white overall, often with light brown (6D4) to reddish brown (8E8) tint, up to 3 mm broad. *Stipe* 6–23 × 1–3 mm, central, insititious,

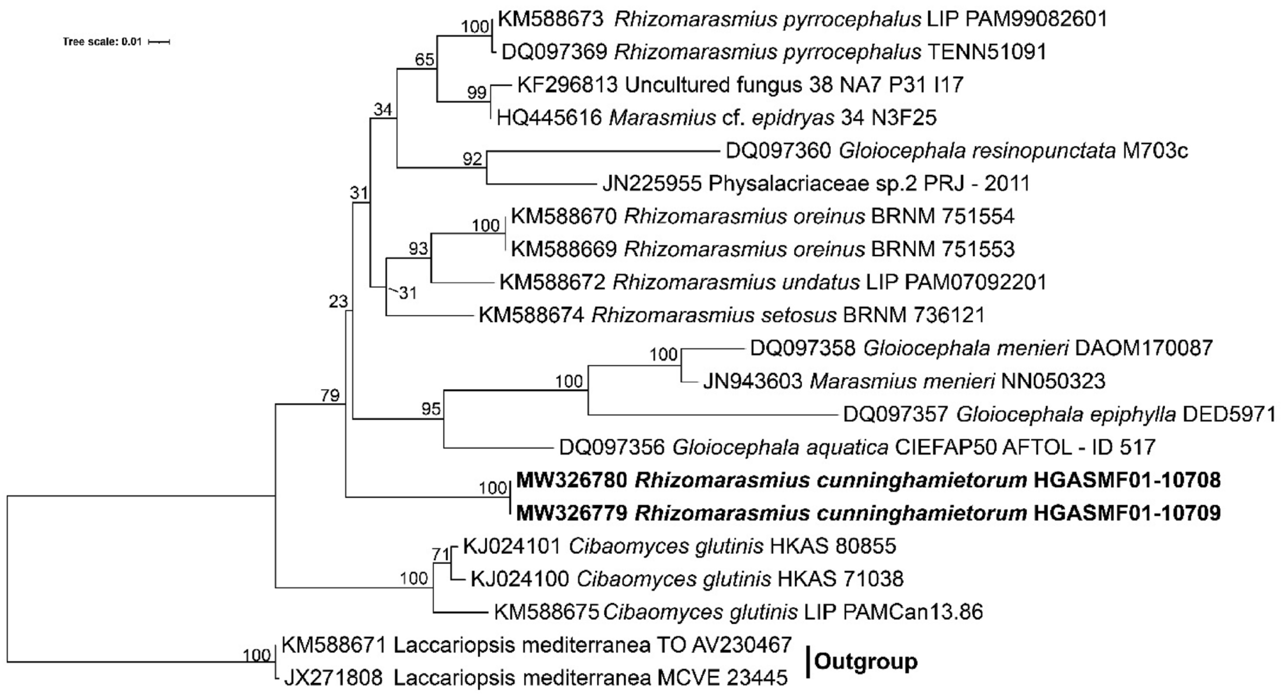


Fig. 159 Phylogenetic tree derived from maximum likelihood analysis of a combined ITS and LSU sequence data. The tree is rooted with *Laccariopsis mediterranea* and *Hydropus mediterraneus*. Branches with bootstrap values ≥ 70% are shown at each branch and the bar represents 0.1 substitutions per nucleotide position. Ex-type strains are in black **bold**. The newly generated sequences are indicated in blue and **bold** type species

hollow, pruinose, more or less cylindrical above, sometimes broadened in somewhere, often tapering towards base, pallid at the apex, orange white (6A2) or pale orange (6A3) to dark brown (8E8) below, black at base. *Basidiospores* (3.5)5–6.5 (7) × 3–4 µm (average = 5.77 × 3.42 µm, E = 1.43–2(–2.16), Q = 1.69), ellipsoid, amygdaliform, thin-walled, non-dextrinoid, hyaline, smooth. *Basidia* 21–35 × 4.5–6 µm, 4-spored, clavate, hyaline. *Basidioles* 21–35.5 × 4–6 µm, clavate, cylindrical, hyaline. *Cheilocystidia* sparse to abundant, 11–50 × 7–17 µm, ellipsoid, cylindrical, irregular clavate, narrowly utriform to narrowly fusiform with capitate apex, thin-walled. *Pleurocystidia* scattered, sparse, narrowly utriform to narrowly fusiform with capitate apex, 39–64.5 × 7–12.5 µm. *Pileipellis* a hymeniform layer of clavate to sphaeropedunculate smooth cells measuring 12.5–29.5 × 9–15.5 µm, possibly gelatinized. *Pileiocystidia* 35.5–51 × 8–16.5 µm, fusiform, narrowly lageniform to lageniform with capitate apex, thin-walled. *Stipitipellis* a cutis, of cylindrical, parallel, slightly thick-walled, non-dextrinoid, up to 19.5 µm wide hyphae. *Caulocystidia* 35–59 × 6–12 µm, cylindrical to broadly cylindrical with or without capitate apex, sometimes lobed, thick-walled. *Clamp connections* present in all tissue.

Material examined: China, Guizhou Province, Qiandongnan Miao Autonomous Prefecture, Liping County, Dongfeng tree farm, on the dead trunk of *Cunninghamia lanceolata* (Lamb.) Hook., (Cupressaceae), 17 October 2020, Ji-Peng Li (LJP563), HGASMF01-10,709 (**holotype**), *ibid*., 17 October 2020, Ji-Peng Li (LJP564), HGASMF01-10,708 (**paratype**).

GenBank numbers: HGASMF01-10709- MW326779 (ITS), MW332104 (LSU).

HGASMF01-10708- MW326780 (ITS), MW332105 (LSU)

Notes: *Rhizomarasmius cunninghamietorum* has an insititious stipe, a pileipellis as a hymeniform layer of clavate to sphaeropedunculate smooth cells, with narrowly lageniform to lageniform with capitate apex pileocystidia. These morphological characteristics of *R. cunninghamietorum* are consistent with the circumscription of *Rhizomarasmius* (Moreau et al. 2015). The phylogenetic evidence showed that *R. cunninghamietorum* formed a single branch and was clearly separate from the known species of *Rhizomarasmius* and closer to its related genera *Cibaomyces* and *Gloiocephala* (Fig. 159). However, *Cibaomyces* was accepted as a monotypic genus based on the subglobose to broadly ellipsoid basidiospores with conspicuous spines and *Gloiocephala* sensu Singer with smooth spores, subcapitate to capitate cystidia, a gelatinized trama (Singer 1976a, b, 1986) is probably polyphyletic (Moncalvo et al. 2002; Binder et al. 2006; Vizzini et al. 2012; Hao et al. 2014). Thus, *Rhizomarasmius* is probably polyphyletic based on the phylogenetic analysis generated here. Morphologically, among the

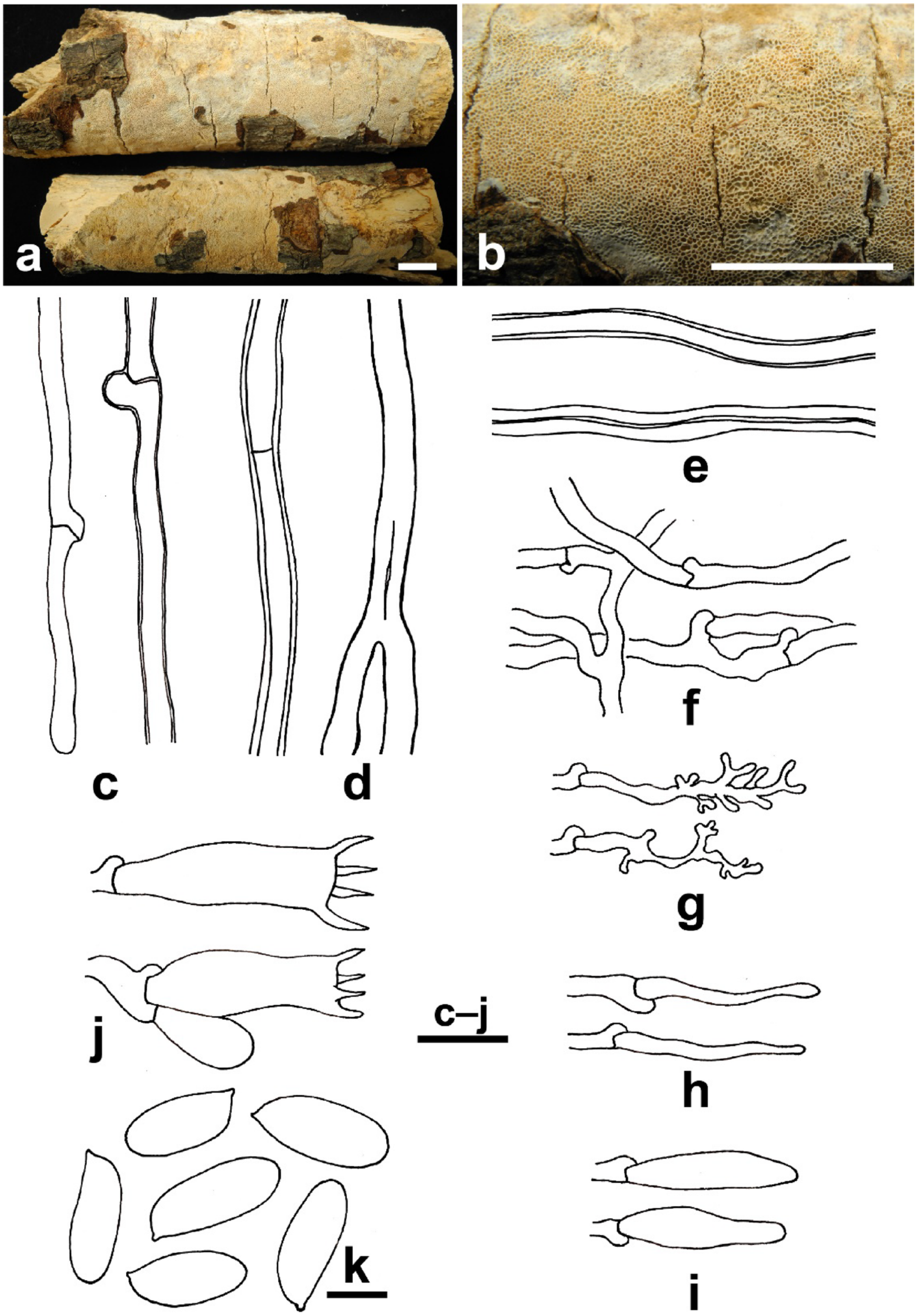


Fig. 160 ***Grammothele taiwanensis*** (GC 1704–17, **holotype**). **a, b** Basidiomata. **c** Generative hyphae from trama. **d** Skeletal hyphae from trama. **e** Generative hyphae from context. **f** Skeletal hyphae from context. **g** Dendrohyphidia. **h** Hyphidia. **i** Cystidioles. **j** Basidia. **k** Basidiospores. Scale bars: **a–b** = 1 cm, **b–j** = 10 µm, **k** = 5 µm

known species of *Rhizomarasmius*, *R. epidryas* has entirely brown-black and distinctly velutinose stipe, bigger basidiospores (average 8.85 × 5.7 µm) and narrowly clavate or cylindrical pleurocystidia (Ronikier 2009); *R. setosus* with different habitat on leaf petioles and its microscopic features without clamps (Antonín and Noordeloos 2010); *Rhizomarasmius oreinus* has smooth red-brown pileus, entirely tomentose pubescent stipe and bigger basidiospores (average 12.5 × 8.8 µm, Moreau et al. 2015); *R. pyrrhocephalus* has pubescent to tomentose stipe, and bigger basidiospores (average 8.2 × 3.7 µm, Desjardin 1989) and *R. undatus* has longer (5.0–6.3 cm) and strigose stipe (Smith 1836).

Polyporales Gäum.

Notes: Polyporales is a large group of Agaricomycetes, accommodating about 2500 species (He et al. 2019). The latest treatments and updated accounts of Polyporales are followed in Justo et al. (2017), He et al. (2019), and Wijayawardene et al. (2022).

Polyporaceae Fr. ex Corda [as 'Polyporei'], Icon. fung. (Prague) 3: 49 (1839).

Notes: Polyporaceae, typified by *Polyporus* P. Micheli ex Adans, currently includes 90 genera, most of which are polypores, rarely corticioid species (Justo et al. 2017; He et al. 2019; Wijayawardene et al. 2022). Microscopically, the hyphal system is usually dimitic or trimitic, rarely monomitic; the generative hyphae are usually with clamp-connections; cystidia are mostly absent; basidiospores are thin- to thick-walled, smooth to ornamented and colorless to brown. All species produce a white rot (Justo et al. 2017).

Grammothele Berk. & M.A. Curtis, Journal of the Linnean Society. Botany 10: 327 (1869).

Notes: *Grammothele*, typified by *G. lineata* Berk. & M.A. Curtis, accommodates 24 species (Zhou and Dai 2012; Ryvarden 2015; Yuan 2015; Wu et al. 2016; Hyde et al. 2019). The genus is characterized by having resupinate basidiomata with shallow poroid hymenophore consisting of angular, partly sinuous, irregular or incomplete pores, dimitic or trimitic hyphal system with clamped generative hyphae and dextrinoid skeletal hyphae, usually presence of dendrohyphidia, and ellipsoid to cylindrical basidiospores that are thin-walled, smooth, colorless and not reacting both in Melzer's reagent and Cotton Blue. Species of *Grammothele* commonly occur on hardwoods and monocotyledons in tropical to subtropical regions, causing a white rot (Ryvarden 1979, 2015). Previous phylogenetic studies have shown that *Grammothele* is polyphyletic and closely related to some other genera in the Polyporaceae, such as *Porogramme* (Pat.) Pat., *Theleporus* Fr. and *Tinctoporellus* Ryvarden (Zhou and Dai 2012; Yuan 2015; Wu et al. 2016; Hyde et al. 2019).

Grammothele taiwanensis C.C. Chen, ***sp. nov.***

Index Fungorum number: *IF900073; Facesoffungi number*: *FoF13396; Fig. 160*

Etymology: Referring to the type locality, Taiwan.

Holotype: GC 1704-17

Basidiomata annual, resupinate, effused, adnate, corky when dry, up to 15 cm long, 6 cm wide, and 1.3 mm thick in section, sparsely cracked, growing beneath the bark; margin sterile, cottony or slightly fimbriate, sometimes indistinct. *Pore surface* cream, buff-yellow or buff upon drying, not changing in KOH; pores angular, 3–5 per mm; dissepiments thin, entire, sometimes lacerate. *Tubes* concolorous with pore surface, corky, up to 1 mm deep. *Context* cream, corky, up to 0.3 mm thick, or sometimes invisible. *Hyphal system* dimitic in both context and trama; generative hyphae nodose-septate; tissues not changing in KOH. *Context* generative hyphae colorless, unbranched, 2.5–3.5 µm diam, thin-walled; skeletal hyphae, colorless, slightly flexuous, occasionally branched, 2.5–3.5 µm diam, thick-walled with a wide lumen or almost solid, weekly dextrinoid. *Tramal* generative hyphae colorless, flexuous, frequently branched, 2–3.5 µm diam, thin-walled; skeletal hyphae colorless, slightly flexuous, rarely branched, 3–4.5 µm diam, thick-walled with a wide lumen or subsolid, often agglutinated in bundles, weekly dextrinoid. *Cystidia* absent. *Cystidioles* fusoid, colorless, thin-walled, 14–20 × 4.5–5 µm. *Dendrohyphidia* colorless, thin-walled, 9–23 × 1.5–2.5 µm. *Hyphidia* colorless, thin-walled, 19–26 × 2–3 µm. *Basidia* clavate or suburniform, with four sterigmata and a basal clamp connection, colorless, thin-walled, 17–25 × 6–7 µm. *Basidiospores* cylindrical, colorless, thin-walled, smooth, inamyloid, nondextrinoid, acyanophilous, mostly 7.9–10.5 × 3.3–4.4 µm. (7.8–)8.4–10.5(–12.3) × (3.5–)3.7–4.4(–5.1) µm, L = 9.4 µm, W = 4.1 µm, Q = 2.23–2.43 (*n* = 30) (***holotype***). (7–)7.9–9.4(–10.6) × (3–)3.3–3.9(–4.3) µm, L = 8.6 µm, W = 3.6 µm, Q = 2.3–2.45 (*n* = 30) (GC 1704–16).

Material examined: China: Taiwan, Nantou County, Yuchih Township, Shuishetashan Trail, 23° 51′ N, 120° 56′ E, 980 m, on angiosperm branch, 8 April 2017, GC 1704–17 (TNM F31469, **holotype**).

GenBank number: MW440487 (ITS).

Additional specimen examined: China: Taiwan, Nantou County, Yuchih Township, Shuishetashan Trail, 23° 51′ N, 120° 56′ E, 980 m, on angiosperm branch, 8 April 2017, GC 1704–16 (TNM F31468).

GenBank number: MW440486 (ITS).

Notes: Grammothele taiwanensis is characterized by having resupinate, cream to buff basidiomata with larger pores (3–5 per mm), dimitic hyphal system with clamped generative hyphae and weekly dextrinoid skeletal hyphae, presence of fusoid cystidioles, dendrohyphidia and hyphidia, and cylindrical basidiospores (7.9–10.5 × 3.3–4.4 µm). *Grammothele taiwanensis* resembles *G. pulchella* (Bres.) Ryvarden in having similar pore and basidiospore sizes [4–5 per mm, 7–10 × 3–4 µm in Hjortstam and Ryvarden (1982), as *G. ochracea* Ryvarden] and presence of dendrohyphidia; however, *G. pulchella* differs from this species in having cork-colored to wood-colored pore surface and pale brown context, and absence of cystidioles and hyphidia (Hjortstam and Ryvarden 1982). *Grammothele taiwanensis* is also similar to *G. hainanensis* F. Wu & L.W. Zhou and *G. hondurensis* (Murrill) Ryvarden, but the latter two species have hyphal pegs and smaller basidiospores [*G. hainanensis*: 7–8.1 × 2.3–2.9 µm in Wu et al. (2016); *G. hondurensis*: 5–8 × 3–3.5 µm in Ryvarden (1985)]. Phylogenetically, two sequences of *G. taiwanensis* formed an isolated lineage with high support (Fig. 161).

Incrustoporiaceae Jülich, Biblthca Mycol. 85: 373 (1982) [1981].

Fig. 161 Phylogram generated from maximum likelihood analysis based on ITS sequence data of *Grammothele taiwanensis* (in bold) and related species. The selection of strains and species consulted Zhou and Dai (2012), Yuan (2015), Wu et al. (2016) and Hyde et al. (2019). *Funalia trogii* is used as the outgroup taxa. Forty-six strains are included in the sequence analyses, which comprise 665 characters with gaps. The tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of is presented. Bootstrap support values for ML ≥ 70%, BYPP ≥ 0.9 are given above the nodes

Notes. Incrustoporiaceae was established by Jülich (1981) and typified by *Incrustoporia* Domański. This family was treated as a synonymy of Polyporaceae according to the 10th edition of Dictionary of the Fungi (Kirk et al. 2008). Justo et al. (2017) provided a revised family-level classification of the Polyporales based on phylogenetic analyses inferred from ITS, nLSU and *rpb2* genes, and four genera were accepted in Incrustoporiaceae, viz., *Incrustoporia*, *Piloporia* Niemelä, *Skeletocutis* Kotl. & Pouzar and *Tyromyces* P. Karst.

Skeletocutis Kotlába & Pouzar, Ceská Mykologie 12 (2): 103 (1958).

Notes: Skeletocutis Kotl. & Pouzar was established in 1958 and its type species is *S. amorpha* (Fr.) Kotl. & Pouzar (Kotlába and Pouzar 1958). The genus has resupinate to pileate basidiocarps, encrusted generative hyphae covered by fine crystals and tiny basidiospores, these are the most important characteristics of the genus. In addition, species in *Skeletocutis* cause white rot disease (Niemelä 1998). Species in this genus have wide distribution in the world, but the majority of the known species so far are found in the Northern Hemisphere (Gilbertson and Ryvarden 1986; Núñez and Ryvarden 2001; Ryvarden and Melo 2014). There are more than 60 taxa recorded in *Skeletocutis* and 25 of them occur in China (Cui and Dai 2008; Dai 2012; Zhou and Qin 2012; Bian et al. 2016; Fan et al. 2017; Du and Dai 2020).

Recently, taxonomic and phylogenetic studies of polypore fungi from China have been extensively carried out, and many new genera or new species have been found (Zhao et al. 2015; Han et al. 2016; Chen and Cui 2017; Chen et al. 2017a, b; Song and Cui 2017; Zhou and Cui 2017; Xing et al. 2018; Cui et al. 2019; Shen et al. 2019; Wu et al. 2019; Zhu et al. 2019; Sun et al. 2020a, b; Liu et al. 2021a, b), however, only very few studies have been focused on *Skeletocutis* of the Incrustoporiaceae. In this study, two new species of *Skeletocutis* are described from China based on morphological characteristics and phylogenetic analyses inferred from ITS + nLSU sequences.

Skeletocutis cangshanensis B.K. Cui & Shun Liu, ***sp. nov.***

Index Fungorum number: IF559465; Facesoffungi number: FoF10674; Figs. 162a, 163

Differs from other Skeletocutis species by its white pore surface when fresh, white to buff-yellow upon drying, small and circular to angular pores (7–10 per mm), and cylindrical basidiospores (2.7–3.5 × 0.8–1.5 µm*).*

Etymology. *Cangshanensis* (Lat.): refers to the type locality (Cangshan Park) of the type specimen.

Holotype: Cui 17978.

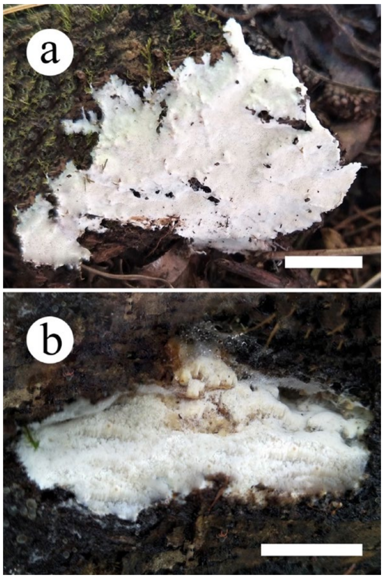


Fig. 162 Basidiocarps of *Skeletocutis* species. a. *S. cangshanensis*; **b.** *S. subchrysella* (scale bars: **a, b** = 2 cm)

Fruiting body. Basidiocarps annual, resupinate, not easily separated from substrate, soft leathery, without odour or taste when fresh, becoming corky upon drying, up to 8.5 cm long, 3.5 cm wide, and 1 mm thick at center. Pore surface white when fresh, becoming white to buff-yellow upon drying; pores circular to angular, 7–10 per mm; dissepiments thick, entire. Subiculum white, corky, up to 0.2 mm thick. Tubes darker than poroid surface, corky, up to 0.5 mm long.

Hyphal Structure. Hyphal system dimitic; generative hyphae with clamp connections, hyaline, thin- to slightly thick-walled, dominant at dissepiment edge; skeletal hyphae thick-walled with a wide to narrow lumen; IKI–, CB–, unchanged in KOH.

Subiculum. Generative hyphae frequent, hyaline, thin- to slightly thick-walled, rarely branched and bearing fine crystals, 1.5–2.8 µm in diameter; skeletal hyphae dominant, thick-walled with a narrow lumen, flexuous, unbranched, interwoven, 2–3.5 µm in diameter.

Tubes. Generative hyphae frequent, thin-walled, frequently branched, usually covered by fine crystals, sharply pointed encrustations, especially at dissepiment edge, 1.5–2.5 µm in diameter; skeletal hyphae dominant, thick-walled with a wide to narrow lumen, occasionally branched, subparallel along the tubes, not agglutinated, 2–3 µm in diameter. Dissepiment edge dimitic with smooth skeletal hyphae, and dominant winding, encrusted generative hyphae. *Cystidia* absent, cystidioles abundant, bottle-shaped, with a conical apex, 7.5–17 × 3.2–4.7 µm. *Basidia* clavate, with a basal clamp connection and four sterigmata, 9.6–13.5 × 3.2–4.7 µm; basidioles in shape similar to basidia, but slightly smaller.

Spores. Basidiospores cylindrical, hyaline, thin-walled, smooth, IKI–, CB–, (2.6–)2.7–3.5 × 0.8–1.5 µm, L = 3.02 µm, W = 1.02 µm, Q = 2.76–3.23(*n* = 90/3).

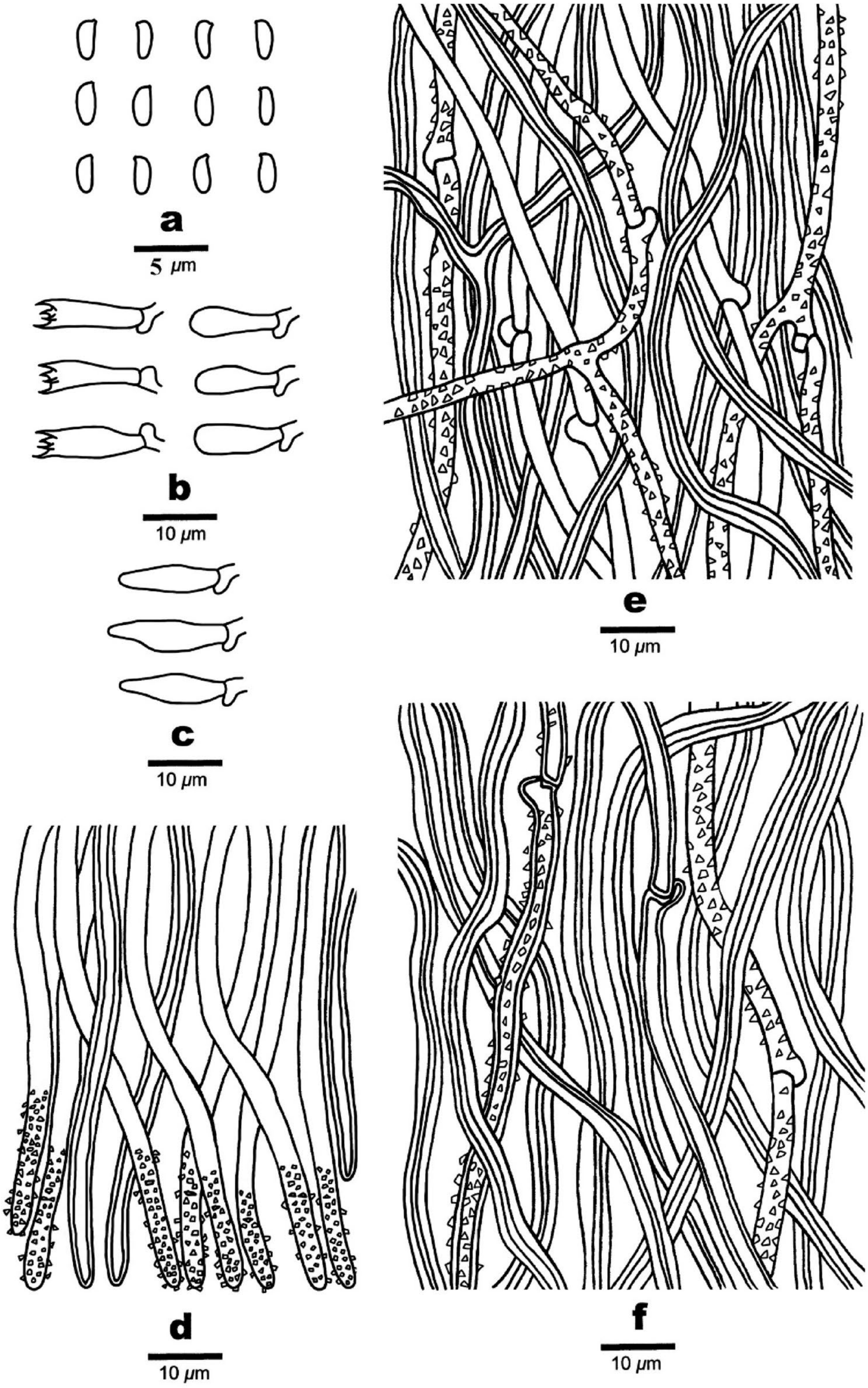


Fig. 163 Microscopic structures of *Skeletocutis cangshanensis* (drawn from the holotype). **a.** Basidiospores; **b.** Basidia and basidioles; **c.** Cystidioles; **d.** Section of dissepiment edge; **e.** Hyphae from trama; **f.** Hyphae from subiculum. Scale Bars: **a** = 5 μm; **b–f** = 10 μm

Material examined: China, Yunnan Province, Dali, Cangshan Park, on angiosperm stump, 4 November 2019, Cui 17978 (**holotype**, BJFC).

Additional specimens examined. China, Yunnan Province, Dali, Cangshan Park, on fallen angiosperm branch, 4 November 2019, Cui 17990, 17994 (Paratypes, BJFC).

GenBank numbers: Cui 17978—MZ327279 (ITS), MZ348535 (LSU), Cui 17990—MZ327280 (ITS), MZ348536 (LSU).

Cui 17994—MZ327281 (ITS), MZ348537(LSU).

Notes: In the phylogenetic tree, the three specimens of *Skeletocutis cangshanensis* formed a highly supported lineage (Fig. 164), and grouped together with *S. bambusicola* L.W. Zhou & W.M. Qin. Morphologically, both *S. cangshanensis* and *S. bambusicola* have similar pores, but *S. bambusicola* differs by having wider basidiospores (2.5–3 × 1.5–2 μm) and growth on *Bambusa* (Zhou and Qin 2012). *Skeletocutis lepida* A. Korhonen & Miettinen, *S. mopanshanensis* C.L. Zhao and *S. yunnanensis* L.S. Bian, C.L. Zhao & F. Wu were also discovered from Yunnan Province. *Skeletocutis lepida* differs from the new species by having narrower basidiospores (2.9–3 × 0.5–0.6 μm; Korhonen et al. 2018); *S. mopanshanensis* differs by having larger pores (4–5 per mm) and basidiospores (4.7–6.6 × 3.2–4.5 μm; Wu et al. 2017); *S. yunnanensis* differs by having larger pores (5–6 per mm) and basidiospores (3.4–4.5 × 1–1.2 μm; Bian et al. 2016).

Skeletocutis subchrysella B.K. Cui & Shun Liu, ***sp. nov.***

Index Fungorum number: IF559466; Facesoffungi number: FoF10675; Figs. 162b, 165

Diagnosis: Differs from other *Skeletocutis* species by its white to cream pore surface when fresh, cream to cinnamon-buff upon drying, and allantoid basidiospores (2.7–3.2 × 0.7–1 μm).

Etymology. *Subchrysella* (Lat.): refers to the new species resembling *Skeletocutis chrysella* Niemelä in morphology.

Holotype: Cui 17748.

Fruiting body. Basidiocarps annual, resupinate, not easily separated from substrate, soft leathery, without odour or taste when fresh, becoming corky upon drying, up to 6 cm long, 1.5 cm wide, and 3 mm thick at center. Pore surface white to cream when fresh, becoming cream to cinnamon-buff upon drying; pores angular, 6–8 per mm; dissepiments slightly thick, entire to lacerate. Subiculum cream, corky, up to 0.5 mm thick. Tubes darker than poroid surface, corky, up to 2 mm long.

Hyphal Structure. Hyphal system dimitic; generative hyphae with clamp connections, hyaline, thin-walled, dominant at dissepiment edge; skeletal hyphae with a wide to narrow lumen; IKI–, CB–, unchanged in KOH.

Subiculum. Generative hyphae frequent, hyaline, thin-walled, unbranched and bearing fine crystals, 1.5–2.8 μm in diameter; skeletal hyphae dominant, thick-walled with a narrow lumen, flexuous, unbranched, interwoven, 2–4 μm in diameter.

Tubes. Generative hyphae frequent, thin-walled, unbranched, usually covered by fine crystals, sharply pointed encrustations, especially at dissepiment edge, 1.5–2.5 μm in diameter; skeletal hyphae dominant, thick-walled with a wide to narrow lumen, unbranched, subparallel along the tubes, not agglutinated, 2–3.7 μm in diameter. Dissepiment edge dimitic with smooth skeletal hyphae, and dominant winding, encrusted generative hyphae. *Cystidia* absent, cystidioles abundant, bottle-shaped, with a conical apex, 8–13.8 × 2–3.6 μm. *Basidia* clavate, with a basal clamp connection and four sterigmata, 10.3–15.6 × 3.2–4.5 μm; basidioles in shape similar to basidia, but slightly smaller.

Spores. Basidiospores allantoid, hyaline, thin-walled, smooth, IKI–, CB–, (2.6–)2.7–3.2 × (0.5–)0.7–1 μm, L = 2.93 μm, W = 0.8 μm, Q = 3.33–4.5(n = 60/2).

Material examined: China, Sichuan Province, Shimian County, Liziping National Nature Reserve, on fallen angiosperm trunk, 14 September 2019, Cui 17748 (**holotype**, BJFC).

Additional specimen examined: China, Yunnan Province, Baoshan, Gaoligongshan Nature Reserve, on fallen angiosperm trunk, 8 November 2019, Cui 18141 (**paratype**, BJFC).

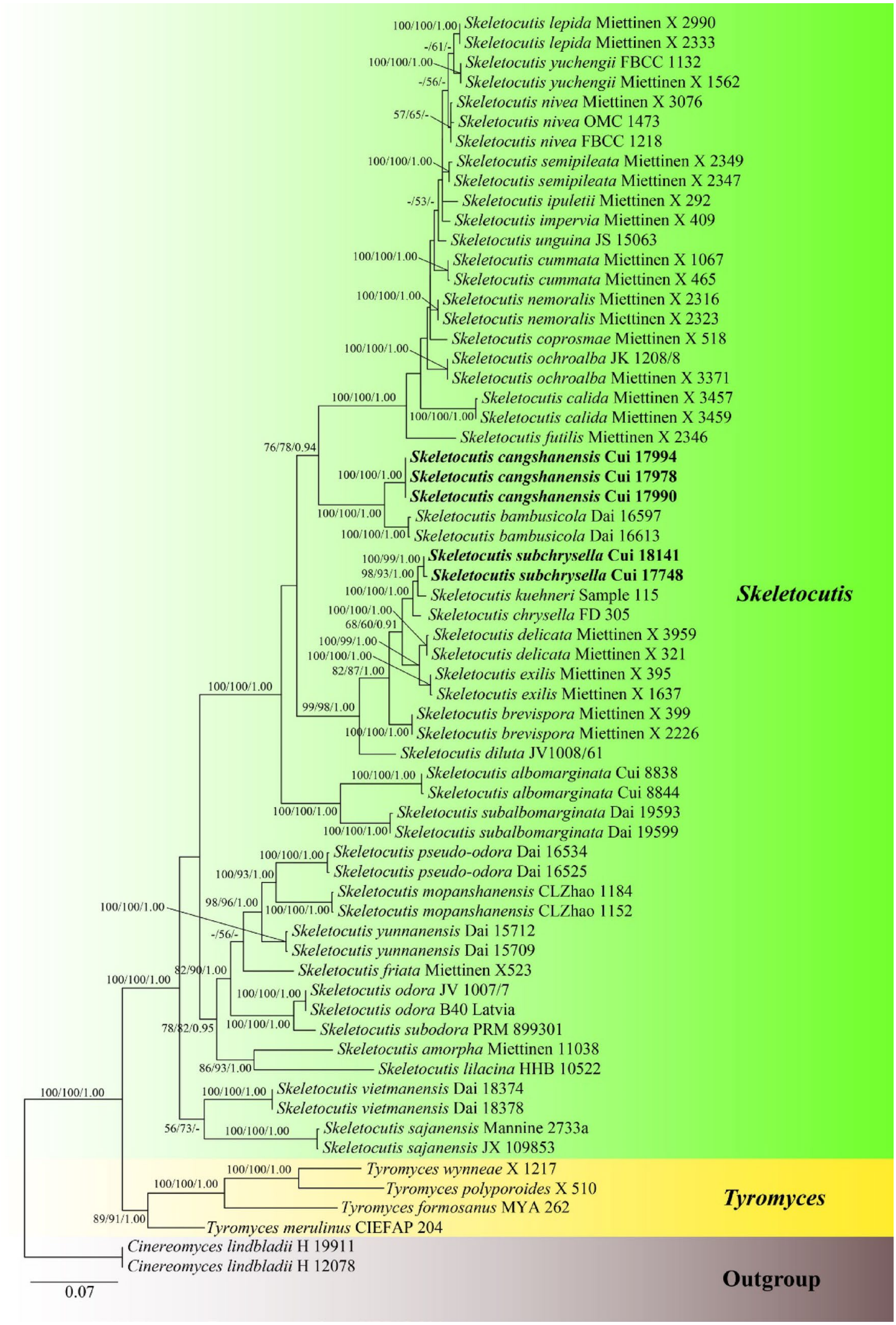
GenBank numbers: Cui 17748- MZ327278 (ITS), MZ348534 (LSU).

Cui 18141- MZ327278 (ITS), MZ348538(LSU).

Notes: In the phylogenetic tree (Fig. 164), *Skeletocutis subchrysella* grouped with *S. chrysella*, *S. delicata* Niemelä & Miettinen, *S. exilis* Miettinen & Niemelä and *S. kuehneri* A. David. Morphologically, they all have allantoid basidiospores; but *S. chrysella* differs from *S. subchrysella* in its trimitic hyphal system and longer basidiospores (2.8–4.5 × 0.7–1 μm; Niemelä 1998); *S. delicata* and *S. exilis* differ by having larger pores (3–6 per mm in *S. delicata*, 3–5 per mm in *S. exilis*) and basidiopores (3.2–4.2 × 1.1–1.4 μm in *S. delicata*, 3.2–3.9 × 0.9–1.1 μm in *S. exilis*; Miettinen and Niemelä 2018); *S. kuehneri* differs by having thin and brittle basidiocarps and growth on dead wood of *Picea* and *Pinus* (David 1982). *Skeletocutis bambusicola*, *S. lepida*, *S. mopanshanensis* and *S. yunnanensis* were also discovered from Yunnan Province. *Skeletocutis bambusicola* differs from the new species by having smaller pores (8–11 per mm) and ellipsoid basidiospores (2.7–3.1 × 1.5–1.9 μm; Zhou and Qin 2012); *S. lepida* differs by having half-resupinate basidiocarps with ochraceous upper surface when dry (Korhonen et al. 2018); *S. mopanshanensis* differs by having larger pores (4–5 per mm) and basidiospores (4.7–6.6 × 3.2–4.5 μm; Wu et al. 2017); *S. yunnanensis* differs by having larger basidiospores (3.4–4.5 × 1–1.2 μm; Bian et al. 2016).

Psathyrellaceae Vilgalys, Moncalvo & Redhead, in Redhead et al., Taxon 50(1): 226 (2001).

Wächter and Melzer (2020) based on phylogenetic and morphological characteristics, introduced six new monophyletic genera to this family. Wijayawardene et al. (2022) accepted 21 genera in *Psathyrellaceae*.


100/100/1.00 Skeletocutis lepida Miettinen X 2990
-/61/- Skeletocutis lepida Miettinen X 2333
100/100/1.00 Skeletocutis yuchengii FBCC 1132
-/56/- Skeletocutis yuchengii Miettinen X 1562
Skeletocutis nivea Miettinen X 3076
57/65/- Skeletocutis nivea OMC 1473
Skeletocutis nivea FBCC 1218
100/100/1.00 Skeletocutis semipileata Miettinen X 2349
Skeletocutis semipileata Miettinen X 2347
-/53/- Skeletocutis ipuletii Miettinen X 292
Skeletocutis impervia Miettinen X 409
Skeletocutis unguina JS 15063
100/100/1.00 Skeletocutis cummata Miettinen X 1067
Skeletocutis cummata Miettinen X 465
100/100/1.00 Skeletocutis nemoralis Miettinen X 2316
Skeletocutis nemoralis Miettinen X 2323
Skeletocutis coprosmae Miettinen X 518
100/100/1.00 Skeletocutis ochroalba JK 1208/8
Skeletocutis ochroalba Miettinen X 3371
100/100/1.00 Skeletocutis calida Miettinen X 3457
100/100/1.00 Skeletocutis calida Miettinen X 3459
Skeletocutis futilis Miettinen X 2346
76/78/0.94
Skeletocutis cangshanensis Cui 17994
100/100/1.00 Skeletocutis cangshanensis Cui 17978
Skeletocutis cangshanensis Cui 17990
100/100/1.00 Skeletocutis bambusicola Dai 16597
100/100/1.00 Skeletocutis bambusicola Dai 16613
100/99/1.00 Skeletocutis subchrysella Cui 18141
98/93/1.00 Skeletocutis subchrysella Cui 17748
100/100/1.00 Skeletocutis kuehneri Sample 115
100/100/1.00 Skeletocutis chrysella FD 305
68/60/0.91 Skeletocutis delicata Miettinen X 3959
100/99/1.00 Skeletocutis delicata Miettinen X 321
100/100/1.00 Skeletocutis exilis Miettinen X 395
82/87/1.00 Skeletocutis exilis Miettinen X 1637
99/98/1.00 Skeletocutis brevispora Miettinen X 399
100/100/1.00 Skeletocutis brevispora Miettinen X 2226
Skeletocutis diluta JV1008/61
100/100/1.00
100/100/1.00 Skeletocutis albomarginata Cui 8838
Skeletocutis albomarginata Cui 8844
100/100/1.00 Skeletocutis subalbomarginata Dai 19593
100/100/1.00 Skeletocutis subalbomarginata Dai 19599
100/100/1.00 Skeletocutis pseudo-odora Dai 16534
100/93/1.00 Skeletocutis pseudo-odora Dai 16525
98/96/1.00 Skeletocutis mopanshanensis CLZhao 1184
100/100/1.00 Skeletocutis mopanshanensis CLZhao 1152
100/100/1.00 Skeletocutis yunnanensis Dai 15712
-/56/- Skeletocutis yunnanensis Dai 15709
82/90/1.00 Skeletocutis friata Miettinen X523
100/100/1.00
100/100/1.00 Skeletocutis odora JV 1007/7
Skeletocutis odora B40 Latvia
78/82/0.95 100/100/1.00 Skeletocutis subodora PRM 899301
Skeletocutis amorpha Miettinen 11038
86/93/1.00 Skeletocutis lilacina HHB 10522
100/100/1.00 Skeletocutis vietmanensis Dai 18374
Skeletocutis vietmanensis Dai 18378
56/73/- 100/100/1.00 Skeletocutis sajanensis Mannine 2733a
Skeletocutis sajanensis JX 109853
100/100/1.00
Skeletocutis
100/100/1.00 Tyromyces wynneae X 1217
100/100/1.00 Tyromyces polyporoides X 510
Tyromyces formosanus MYA 262
89/91/1.00 Tyromyces merulinus CIEFAP 204
Tyromyces
Cinereomyces lindbladii H 19911
Cinereomyces lindbladii H 12078
Outgroup
0.07

◀ **Fig. 164** Maximum likelihood tree illustrating the phylogeny of *Skeletocutis* based on the combined sequences dataset of ITS + nLSU. Branches are labeled with maximum likelihood bootstrap higher than 50%, parsimony bootstrap proportions higher than 50% and Bayesian posterior probabilities more than 0.90 respectively. **Bold** names = New species

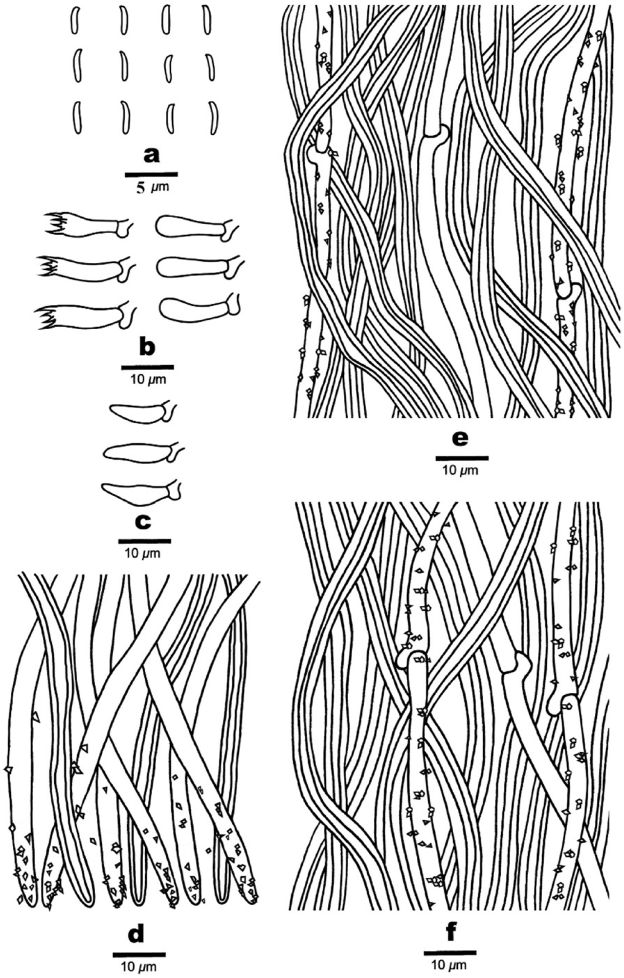


Fig. 165 Microscopic structures of *Skeletocutis subchrysella* (drawn from the holotype). **a.** Basidiospores; **b.** Basidia and basidioles; **c.** Cystidioles; **d.** Section of dissepiment edge; **e.** Hyphae from trama; **f.** Hyphae from subiculum. Scale bars: **a** = 5 µm; **b–f** = 10 µm

Coprinopsis cinerea (Schaeff.) Redhead, Vilgalys & Moncalvo, in Redhead et al., Taxon 50 (1): 227 (2001).

Index Fungorum number: IF474379; Faceoffungi number: FoF11681; Figs. 166, 167, 168

Saprobic on roots of *Vigna unguiculata*. **Sexual morph**: Basidiomycetous. *Basidiocarp* 0.3–4 cm long, formed on the roots of cowpea, mycelial strands encircled the host tissues on the root region, and basidiocarp emerged upon incubation in moist chamber. *Pileus* strongly convex, and/or parasol-shaped to flat or depressed, hymenium borne on gills, becoming deliquescent and inky, lamellae thin, basidia unmodified, basidiospores 7.5–12.2 × 5 – 10 µm diam., ballistosporic, blue-black, smooth with a distinct germ pore. **Asexual morph**: not obesrved.

Cultural characteristics: On PDA medium, colony were white and free from fruiting bodies till 5 days but later, development of basidiocarp was noticed which later enlarged and produced typical fruiting body. Upon examination of the basidiocarp from the PDA plates, microscopic examination of basidiospores revealed that they were same in morphological features.

Material examined: India, Karnataka, Mysore, Doddamaragowdanahally, on infected leaves of *Vigna unguiculata* (L.) Walp. (Fabaceae) placed on PDA as secondary saprophytes, 18 May 2017 Mahadevakumar (UOM-IOE-18/24), living culture (MD8).

Habitat: commonly found on dung or wood chips (Kamada 2002), roots and leaves of *Vigna unguiculate* (This study).

Distribution: worldwide.

GenBank number: OM812073(ITS).

Notes: Coprinopsis species are known to grow on various substrates as secondary saprophytes and are also known to occur as primary components of soil and leaf litter. However, an association of *Coprinopsis* species has not been reported on any crop plants. Cowpea plants affected with a characteristic white cottony mycelium profusely grown on roots were observed which were eventually wilted and dried off which caused the death of the host plants. Infected materials were collected and subjected to pathogen isolation. Few infected parts were incubated at room temperature and observed for mycelial development. To our surprise, a characteristic mushroom fruiting bodies were developed. Therefore, the spores were photographed and subjected for identification. Here, the mushrooms are developed in three parts. Infected roots collected from the field, root samples incubated at room temperature and leaves incubated in a moist chamber (in a Petri plate) showed the development of small basidiocarp. Upon microscopic examination, it was identified as *Coprinopsis* sp. based on fruiting bodies, basidia, basidiospores, sterigmata and other associated structures. This is the first time that *C. cinerea* is reported from Fabaceae, *Vigna unguiculata* representing a new host record (Fig. 169).

Thelephorales Corner ex Oberw.

Notes: The order was established by Oberwinkler (1976) based on the type family Thelephoraceae Chevall. Thelephorales is reported to incorporate two families: Thelephoraceae and Bankeraceae Donk, and ten major clades: *Amaurodon*, *Boletopsis*, *Hydnellum/Sarcodon*, *Lenzitopsis*, *Odontia*, *Phellodon/Bankera*, *Pseudotomentella/Polyozellus*, *Sarcodon*, *Thelephora/Tomentella* and *Tomentella* (Stalpers 1993; Vizzini et al. 2016). Twelve genera and about 800 described

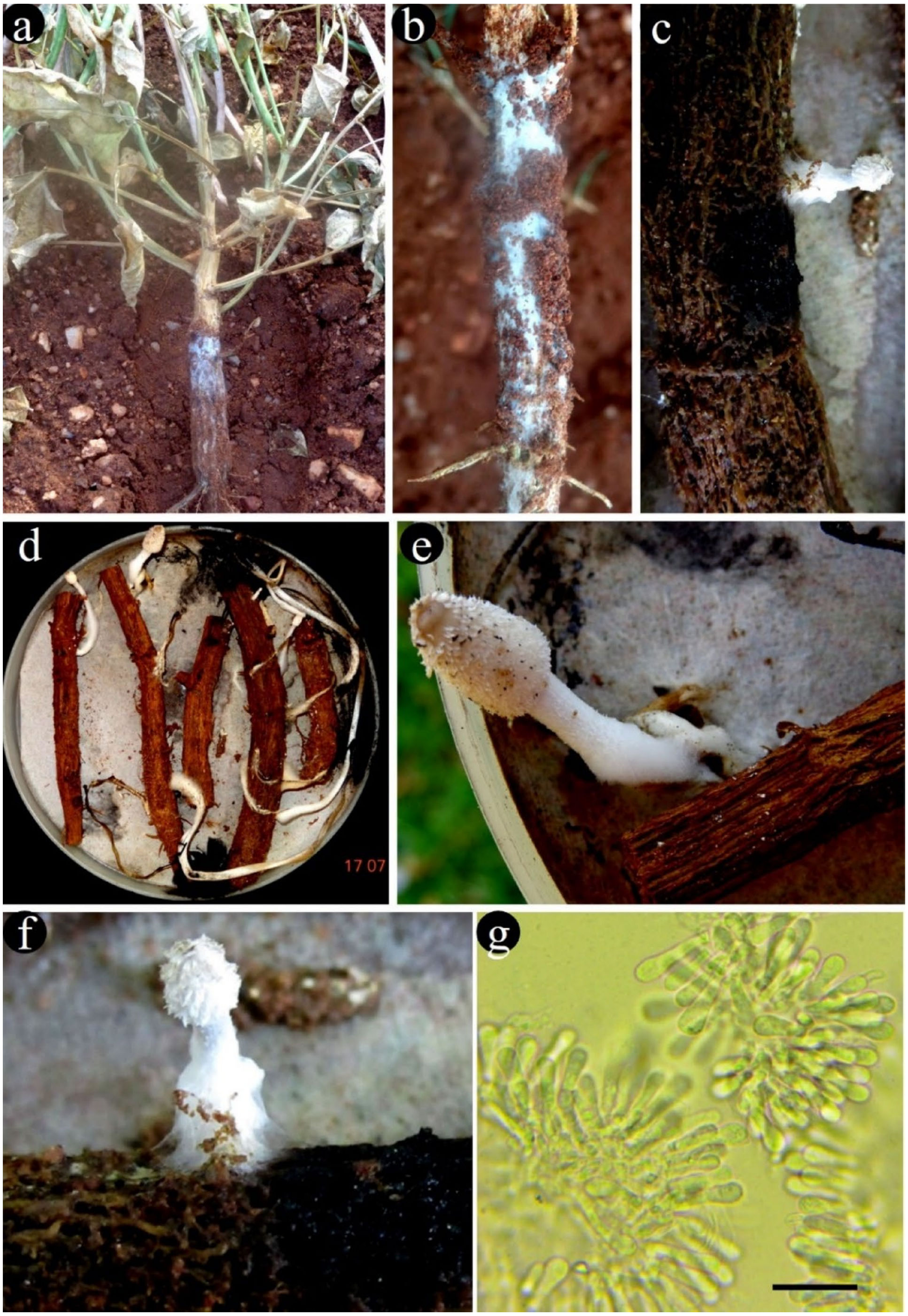


Fig. 166 ***Coprinopsis cinerea* associated with root rot of cowpea**: **a** Cowpea root showing fungal mycelium. **b** Close view of root showing white mycelium. **c** Root sample incubated at room temperature showing the formation of young basidiocarp. **d** Root samples showing emergence of basidiocarps on incubation at room temperature. **e–f** Close view of basidiocarp showing characteristic feature of *Coprinopsis cinerea*. **g** Basidium of *Coprinopsis cinerea* recorded. Scale bar: **g** = 20 µm

species are accommodated within the order according to Index Fungorum 2022a, b (http://www.indexfungorum.org). Wijayawardene et al. (2022) accepted 14 genera in this order.

Thelephoraceae Chevall. [as'*Thelephoreae*'], Fl. Gén. Env. Paris (Paris) 1: 84 (1826).

Notes: Thelephoraceae was proposed by Chevall (1826), and *Thelephora* Ehrh. ex Willdwas regarded as its type genus. Thelephoraceae, as a relatively large one, comprises nine genera within the Thelephorales (Wijayawardene et al. 2022). Many species in the family, as ectomycorrhiza formers, are believed to be of great ecological importance in maintaining the balance of terrestrial ecosystems (Haug et al. 2005; Jakucs and Erős-Honti 2008; Kuhar et al. 2016).

Tomentella Pers. ex Pat., Hyménomyc. Eur. (Paris): 154 (1887).

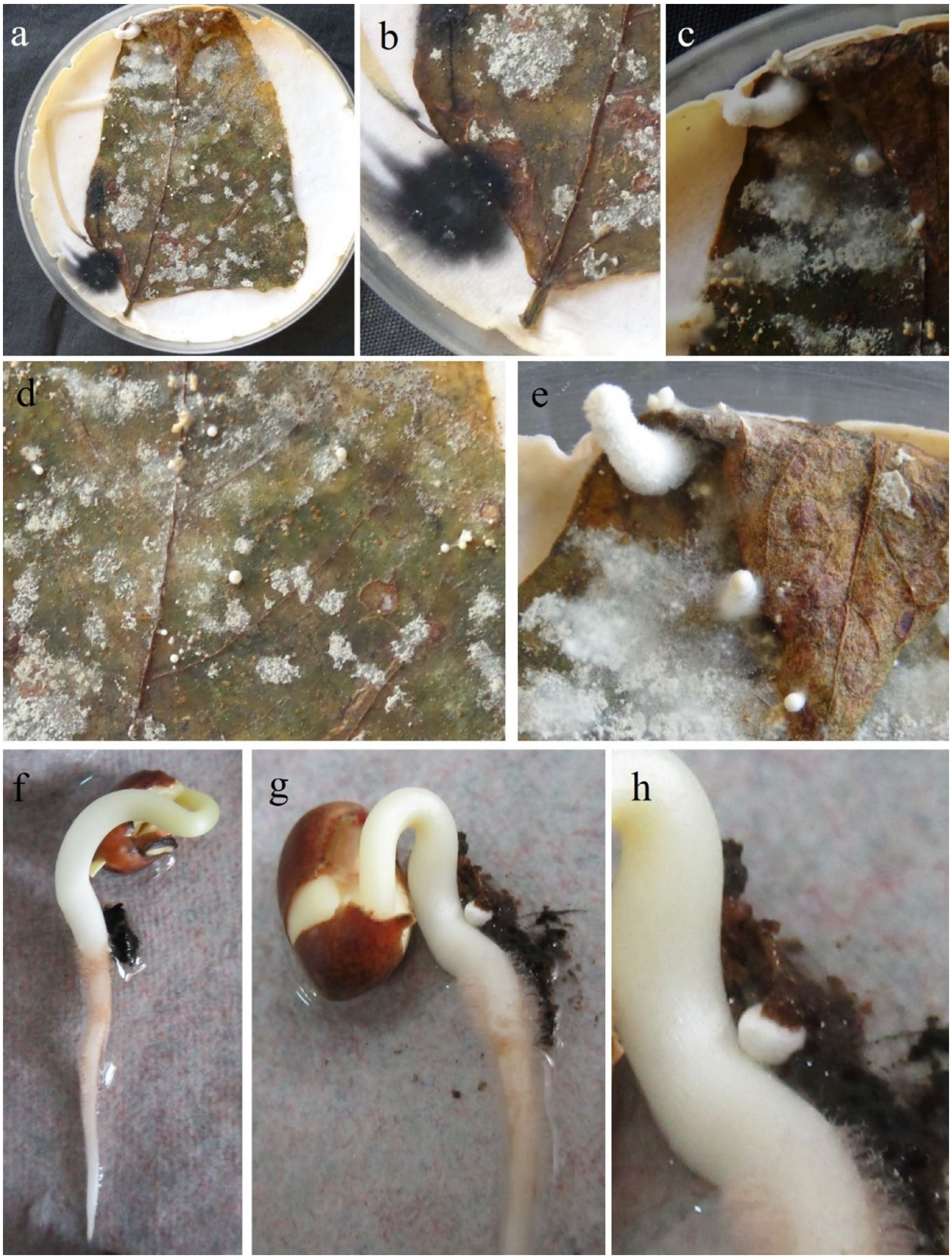


Fig. 167 ***Coprinopsis cinerea*** **developed on cowpea leaves: a – e** Cowpea leaves showing the mycelial cords and development of basidiomata upon incubation at room temperature. **f–h** Mycelium colonizing the young root system under in-vitro condition

Notes: *Tomentella* was validated by Patouillard (1887). Species of the genus usually form cottony or spider web–likereproductive structures and grow on fallen wood, leaf litter, soil and other substrates (Larsen 1974; Tedersoo et al. 2003). Around 400 names have been recorded and about 200 species were described. The species of *Tomentella* are reported to be widely distributed throughout the world and have been immensely taxonomically studied from Eurasia, North America, South America, Australia, Asia and WestAfrica (Thind and Rattan 1971; Larsen 1998; Agerer et al. 2001; Yorou and Agerer 2008; Alvarez-Manjarrez et al. 2015; Kuhar et al. 2016). During the investigation of resupinate-thelephoroid fungi from the subtropical forests in China, several *Tomentella* specimens were collected, and two undescribed species have been identified using morphological characteristics and molecular phylogenetic analyses (Fig. 173).

Tomentella exiguelata Y.H. Mu & H.S. Yuan, ***sp. nov.***

Index Fungorum number: IF900080; Facesoffungi number: FoF13398; Figs. 170, 171, 172

Etymology: Refers to the presence of slightly thick-walled basidia.

Holotype: IFP 019495

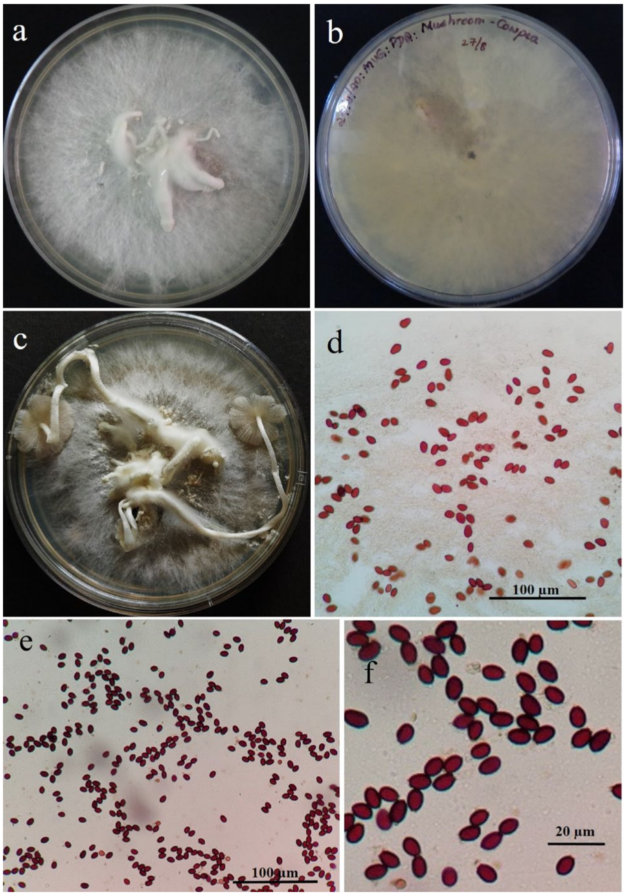


Fig. 168 Micro-morphology of basidiospores of *Coprinopsis cinerea* associated with root rot of cowpea: **a-c** Pure cultures of *Coprinopsis cinerea* established on PDA medium. **d-f** Microscopic view of basidiospores of *Coprinopsis cinerea*

Basidiocarps annual, resupinate, adherent to the substrate, mucedinoid, without odour or taste when fresh, 0.5–1 mm thick, continuous. *Hymenophoral surface* granulose, grayish brown to light brown (6D3–6D4) and concolorous withsubiculum when dry. *Sterilemargin* often determinate, farinaceous, concolorous with hymenophore. *Rhizomorphs* absent. *Subicular hyphae* monomitic; generative hyphae clamped and rarely simple septate, thin- to slightly thick-walled, moderately branched, 3–5μmdiam, without encrustation, yellow in KOH, cyanophilous in sightly thick-walled hyphae, inamyloid. *Subhymenial hyphae* clamped and rarely simple septate, thin-to slightly thick-walled, frequently branched, 3–5 μm diam; hyphal cells more or less uniform, yellow in KOH, cyanophilousin sightly thick-walled hyphae, inamyloid. *Cystidia* absent. *Basidia*10–47 μm long and 4–8 μm diam at apex, 3–5μmat base, with a clamp connection or simple septate at base, utriform, thin-walled and rarely slightly thick-walled, not stalked, sinuous, yellow in KOH, yellow in distilled water, 4-sterigmate; sterigmata 2.5–4.5μmlong and 0.5–1 μm diam at base. *Basidiospores* thick-walled, (6.2–)7.1–8.1(–8.3) × (5.4–)5.8–6.9(–7.1) μm, L = 7.33 μm, W = 6.21 μm, Q = 1.18–1.21 (*n* = 60/2), subglobose, triangular or lobed in frontal view and subglobose to ellipsoid in lateral view, echinulate to aculeolate, yellow in KOH and in distilled water, cyanophilous, inamyloid; echinuli usually isolated, sometimes grouped in 2 or more, up to 2.5 μm long.

Material examined: China, Zhejiang Province, Kaihua County, Gutianshan National Nature Reserve, on fallen angiosperm debris, 24 July 2018, Yuan 12805 (IFP 019495, **holotype**); on fallen angiosperm branch, 25 July2018, Yuan 12900 (IFP 019496, **paratype**).

GenBank numbers: IFP 019495- MZ329771(ITS), MZ329775 (LSU).

IFP 019496- MZ329772 (ITS), MZ329776 (LSU)

Notes: *Tomentella exiguelata* forms a close phylogenetic relationship with *T. galzinii* and *T. subtestacea* (Fig. 173). *Tomentella galzinii* and *T. exiguelata* share the following similar morphological and anatomical characteristics: mucedinoid basidiocarps adherent to the substrate, granulose hymenophoral surface, farinaceous sterile margin, similar-wide subhymenial hyphae, and not stalked and sinuous basidia. However, *T. galzinii* has discontinuous and dull green to olive-brown basidiocarps, indeterminate sterile margin, and the presence of cystidia (Bourdot and Galzin 1924). *Tomentella subtestacea* resembles *T. exiguelata* in mucedinoid basidiocarps adherent to the substrate, clamped and rarely simple septate subicular hyphae, thin-to slightly thick-walled subhymenial hyphae, utriform and not stalked basidia and echinulate basidiospores of similar length. However, *T. subtestacea* can be distinguished by reddish-brown to grayish buff hymenophoral surface, arachnoid sterile margin, and the presence of cystidia (Svrček 1958).

Tomentella fuscoaraneosa Y.H. Mu &H.S. Yuan, ***sp. nov.***

Index Fungorum number: IF900079; Facesoffungi number: FoF13399; Figs. 174, 175, 176

Etymology: Refers to the brown and arachnoid basidiocarps.

Holotype: IFP019493

Basidiocarps annual, resupinate, separable to the substrate, arachnoid, without odour or taste when fresh, 0.8–1.5 mm thick, continuous. *Hymenophoral surface* smooth, light brown to brown (7D8–7E8) and concolorous with subiculum when dry. *Sterile margin* often determinate, byssoid, concolorous with hymenophore. *Rhizomorphs* present in subiculum and margin, 10–35 μm diam; rhizomorphic surface more or less smooth; hyphae in rhizomorphmonomitic, undifferentiated, of type B, compactly arranged and of uniform; single hyphae with both clamps and simple septa, thick-walled, unbranched 2–3 μm diam, yellow in KOH, cyanophilous, inamyloid. *Subicular hyphae* monomitic; generative hyphaeclamped and rarely simple septate,

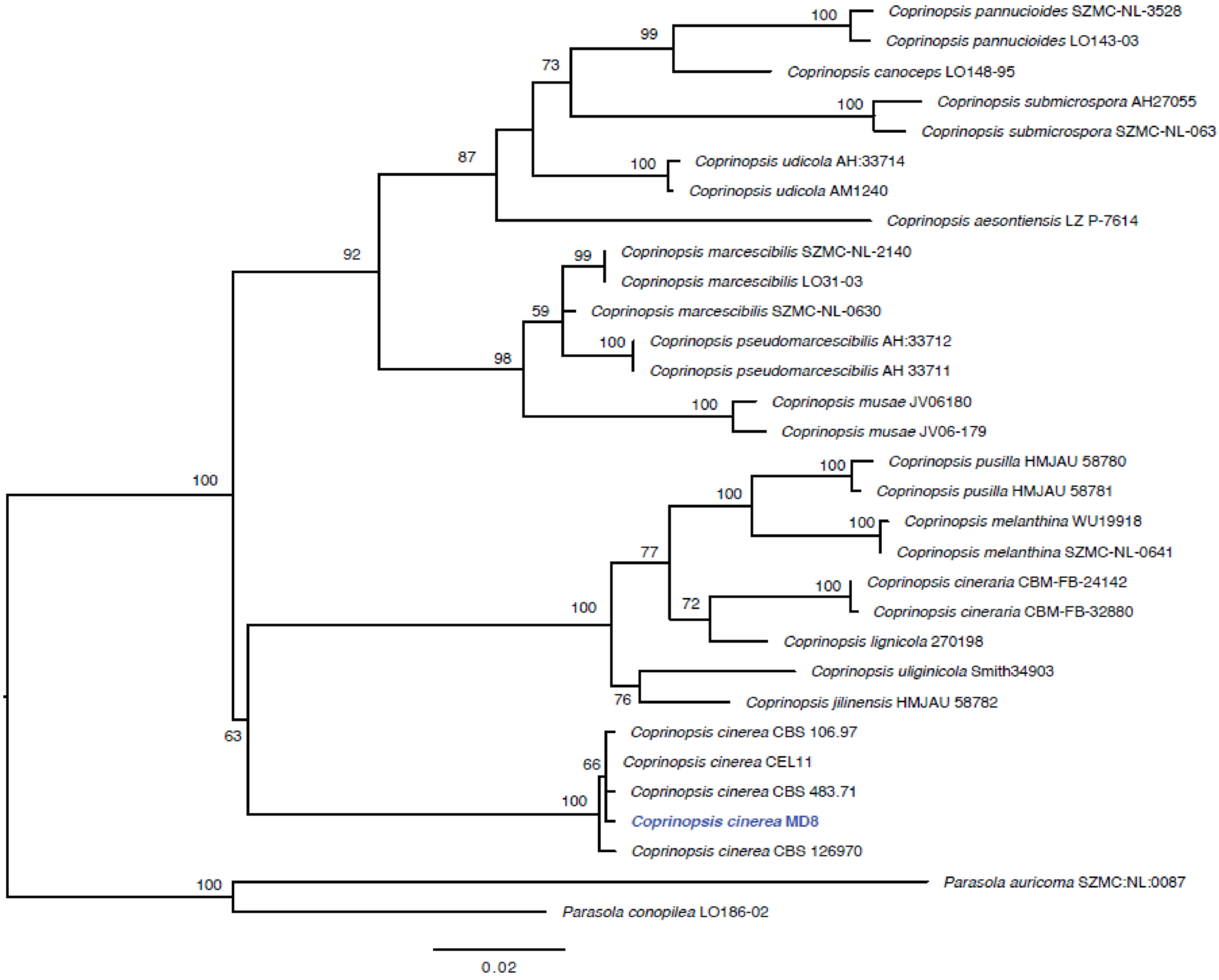


Fig. 169 Phylogenetic tree for species of *Coprinopsis* generated from maximum likelihood (RAxML) based on ITS region. The Maximum likelihood bootstrap value ≥ 50% are given at the nodes. The newly generated sequences are in blue. The tree is rooted to *Parasola auricoma* (SZMC.NL:0087) and *Parasola conopilea* (LO186.02)

thin- to slightly thick-walled, frequently branched, 2–3 µm diam, withoutencrustation, yellow in KOH, cyanophilous in sightly thick-walled hyphae, inamyloid. *Subhymenial hyphae* clamped and rarely simple septate, thin-walled, occasionally branched, 2.5–4 µm diam, without encrustation; hyphal cells short and not inflated, yellow in KOH, acyanophilous, inamyloid. *Cystidia* absent. *Basidia*10–65 µm long and 4–7 µm diam at apex, 2–4 µm at the base, with a clamp connection or simple septate at the base, utriform, thin-walled, stalked, sinuous, occasionally with transverse septa, yellow in KOH, yellow in distilled water, 4-sterigmate; sterigmata 2–5 µm long and 1–2 µm diam at the base. *Basidiospores* thick-walled, (5–)5.5–7.5(–8) × (4–)4.5–6(–7) µm, L = 6.29 µm, W = 5.32 µm, Q = 1.12–1.18 (*n* = 60/2), subglobose to ellipsoid in frontal view and subglobose to ellipsoid in lateral view, echinulateto aculeolate, yellow in KOH, yellow in distilled water, cyanophilous, inamyloid; echinuli usually isolated, sometimes grouped in 2 or more, up to 1.5 µm long.

Material examined: China, Zhejiang Province, Kaihua-County, Gutianshan National Nature Reserve, on fallen angiosperm branch, 25 July 2018, Yuan 12875(IFP 019493, **holotype**); on fallen angiosperm branch, 25 July2018, Yuan 12910 (IFP 019494, **paratype**).

GenBank numbers: IFP 019493-MZ329769 (ITS), MZ329773 (LSU).

IFP 019493-MZ329770 (ITS), MZ329774 (LSU)

Notes: *Tomentella fuscoaraneosa* is closely related to *T. aureomarginata* in the phylogeny (Fig. 173). In morphology, *T. fuscoaraneosa* is similar to *T. aureomarginata* in having a determinate and byssoid sterile margin, the presence of type B rhizomorphs, monomitic generative hyphae with clamps and simple septa, and the absence of cystidia. However, *T. aureomarginata* differs from *T. fuscoaraneosa* by having

Fig. 170 A basidiocarp of ***Tomentella exiguelata*** (IFP 019495, **holotype**). Scale bars = 0.25 cm

pelliculose basidiocarps adherent to the substrate, golden brown to yellowish-brown hymenophoral surface turning darker when dry, not stalked basidia and wider basidiospores (6–6.5 µm *vs*. 4.5–6 µm in *T. fuscoaraneosa*) with shorter echinuli (up to 1 µm *vs*. up to 1.5 µm in *T. fuscoaraneosa*) (Yuan et al. 2020). *Tomentella fuscoaraneosa* shares common features with *T. brunneoflava* in arachnoid and continuous basidiocarps, the presenceof rhizomorphs and clamped and rarely simple septate subicular hyphae and short and not inflated subhymenial hyphae. However, *T. brunneoflava* differs from *T. fuscoaraneosa* by having brownish-yellow basidiocarps adherent to the substrate and clavate and not stalked basidia (Yuan et al. 2020).

Agaricales genera incertae sedis

Gerronema Singer, Mycologia 43(5): 599 (1951).

Gerronema is a minor genus of lignicolous agaric and is distributed worldwide (Singer 1986). There are 66 epithets (excluding synonyms) listed in the Index Fungorum (2021). *Gerronema. melanomphax* Singer is the specific type species. Historically, different circumscriptions of *Gerronema* based on pigmentations established by Singer (1964) and Bigelow (1970) have been problematic. Subsequently, Redhead (1986) and Norvell et al. (1994) restricted the delimitation of *Gerromena* and characterized its descriptive features as elastic to fleshy, omphalinoid to clitocyboid basidiomata, white spore print, smooth, thin-walled, inamyloid basidiospores, cutis pileipellis often with intracellular pigment, sarcodimitics trama tissue and lignicolous habit. This circumscription correlates with the molecular phylogenetic analysis of the combined nrITS

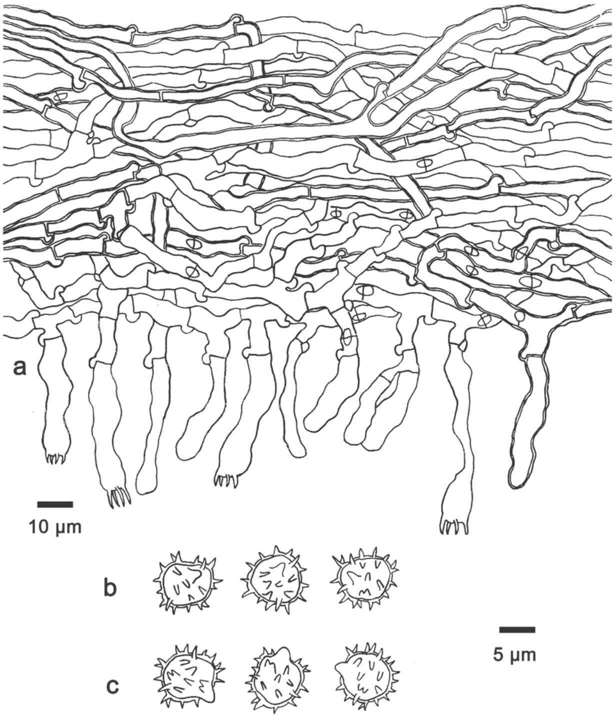


Fig. 172 Microscopic structures of ***Tomentella exiguelata*** (IFP 019495, **holotype**). **a** Section through a basidiocarp. **b** Basidiospores in frontal view. **c** Basidiospores in lateral view

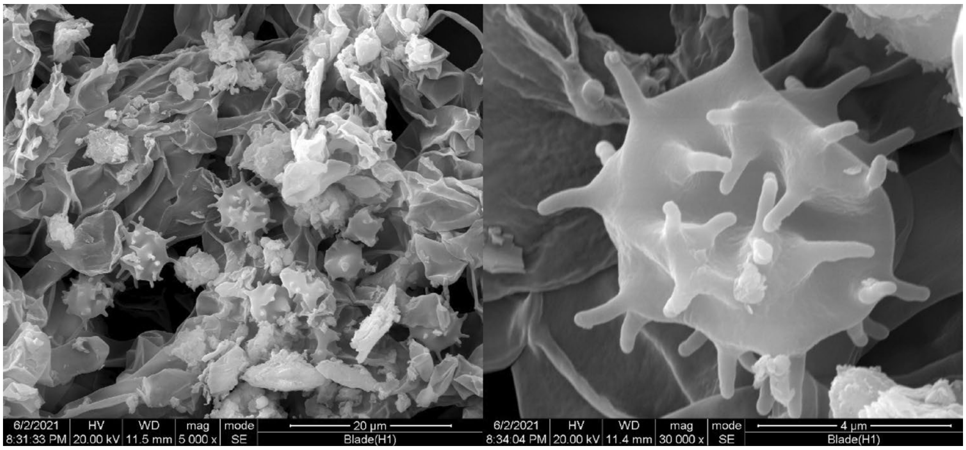


Fig. 171 SEM of basidiospores of ***Tomentella exiguelata*** (IFP 019495, **holotype**)

Fig. 173 Phylogram generated from maximum likelihood analysisbased on combined ITS and LSU sequence data. Related sequences were obtained from GenBank and Unite. One hundred and ten strains are included in the combined sequence analyses, which comprise 1451 characters withgaps. Single gene analyses were also performed and topology andclade stability compared from combinbed gene analyses. *Odontia ferruginea* (TU110988) is used as the outgroup taxon. Bootstrap support values for ML ≥ 50% are given. The newly generated sequences are in bold

and nrLSU dataset and revealed that *Gerronema* is monophyletic and forms a clade with *Megacollybia* and *Trogia* in Hydropoid calde (Antonín et al. 2019).

Gerronema atrovirens Wannathes, N. Suwannarach, J. Kumla, Phonrob & S. Lumyong, ***sp.nov***.

MycoBank number: MB840183; Facesoffungi number: FoF10685, Figs. 177a, 178

Etymology: ‘*atro*’ = dark; ‘*virens*’ = green, refers to the dark green colour of basidiomata.

Holotype: BKF10264

Pileus 21–51 mm diam., convex with depress center when young and deeply infundibuliform in age, elastic, glabrous, translucent-striate to striate at margin, dull green (27E3) at center, dark green (27F3) at margin, grey (5E1) to brownish grey (5E2) in old specimen; *Lamellar* decurrent,

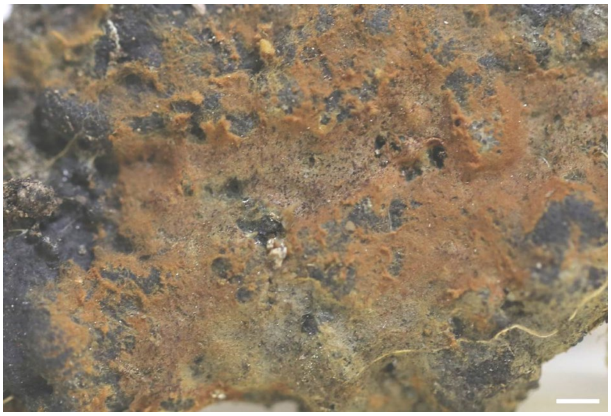


Fig. 174 A basidiocarp of ***Tomentellafuscoaraneosa*** (IFP 019493, **holotype**). Scale bars = 0.25 cm

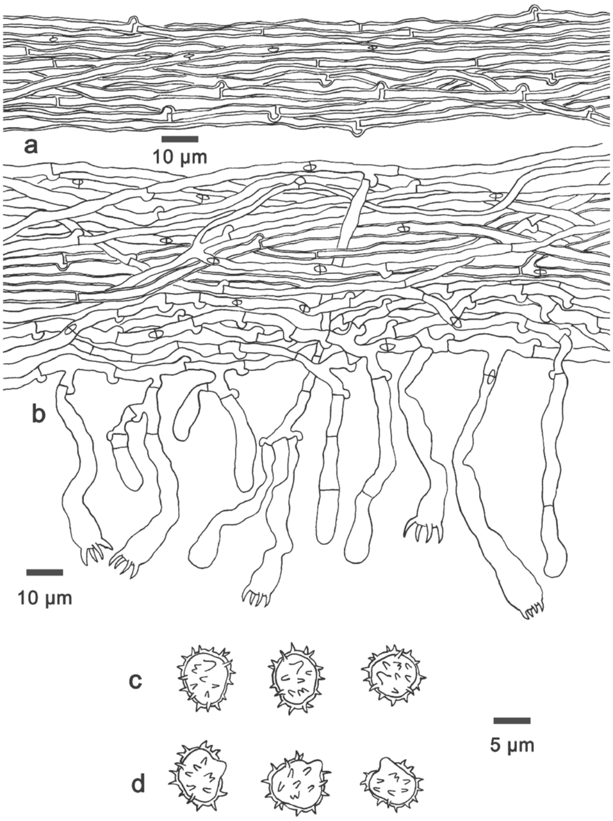
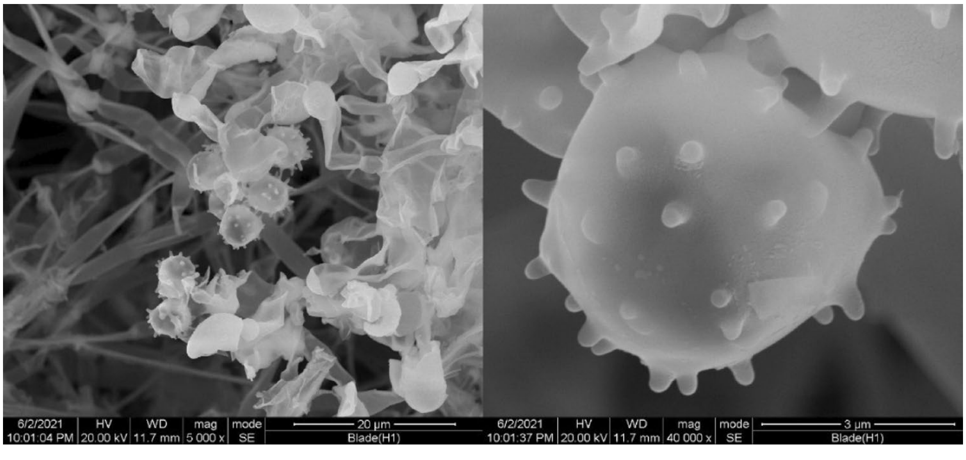


Fig. 176 Microscopic structures of *Tomentella fuscoaraneosa* (IFP 019493, **holotype**). **a** Hyphae from a rhizomorph. **b** Section through a basidiocarp. **c** Basidiospores in frontal view. **d** Basidiospores in lateral view

subdistant to close (24–28) with 1–2 series of lamellulae, narrow (up to 1.5 mm), withe (27A1), non-marginate; *Stipe* 14–36 × 2.5–4.0 mm, cylindrical, slightly broadened at base, usually flatten, flexuose, hollow, elastic, central, pubescent, greenish grey (27F2) at apex fading paler to brownish grey (5C2) at base, basal mycelium. *Context* thin, elastic. Odor and taste not distinctive.

Basidiospore 7–8 × 4–5 µm [x = 7.56 ± 0.51 × 4.36 ± 0.49, Q = 1.4–2.0, q = 1.75 ± 0.21, *n* = 25, s = 3] ellipsoid, smooth, hyaline, inamyloid, thin-walled. *Basidia* 21–27 × 6–7 µm, clavate, with 4 sterigmata, sometime with 2 sterigmata, thin-walled, inamyloid. *Cheilocystidia* abundant, 21–51 × 5–11 µm, cylindrical with 1–2 slight constrictions, flexuose, irregular in shape, sometimes 2-celled, hyaline, inamyloid, thin-walled. *Pleurocystidia* absent. *Lamellar trama* subregular to interwoven, arranged in two directions, hyphae 4–8 µm diam., cylindrical, smooth, hyaline, inamyloid, thin-walled, gelatinous. *Pileipellis* composed with cutis of repent hyphae, radially arrangement, 3–10 µm, cylindrical, incrusted, greyish green in KOH, inamyloid, thin-walled, true pileocystidia absent. *Pileus trama* sarcodimitic, subregular, composed of 2 type of hyphae: a) sarco-hyphae, elongate fusoid cell 162–195 × 5–15 µm, hyaline, smooth, inamyloid, thick-walled (up to 1 µm); b) generative hyphae 2–6 µm wide, cylindrical, branched, hyaline, smooth, inamyloid, thin-walled. *Stipitipellis* cutis, hyphae 3–8 µm diam., parallel, cylindrical, greenish brown in KOH, smooth, inamyloid, thin-walled. *Stipe trama* sarcodimitic, subparallel,

Fig. 175 SEM of basidiospores of ***Tomentella fuscoaraneosa*** (IFP 019493, **holotype**)



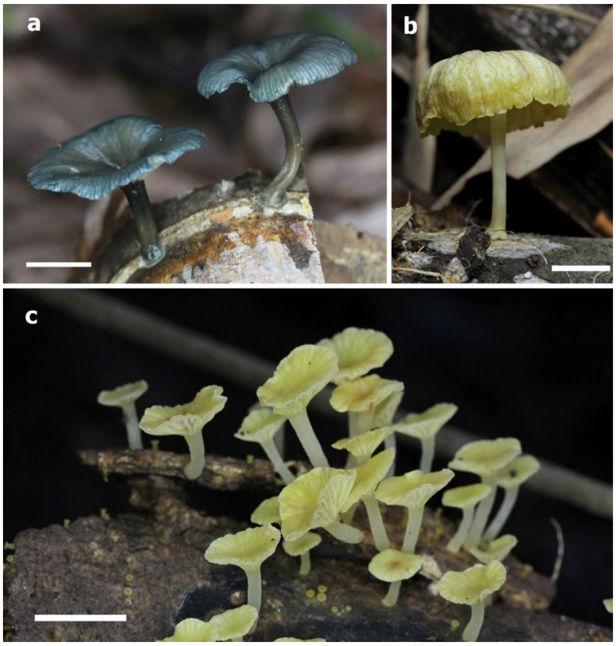


Fig. 177 **Basidiomata and habit**. **a** *Gerronema atrovirens* (**holotype**: BKF10264), **b** *G. kuruvense (*BKF10266), **c** *G. flavum* (**holotype**: BKF10253), Scale bars = 10 mm. Photographs by N. Wannathes

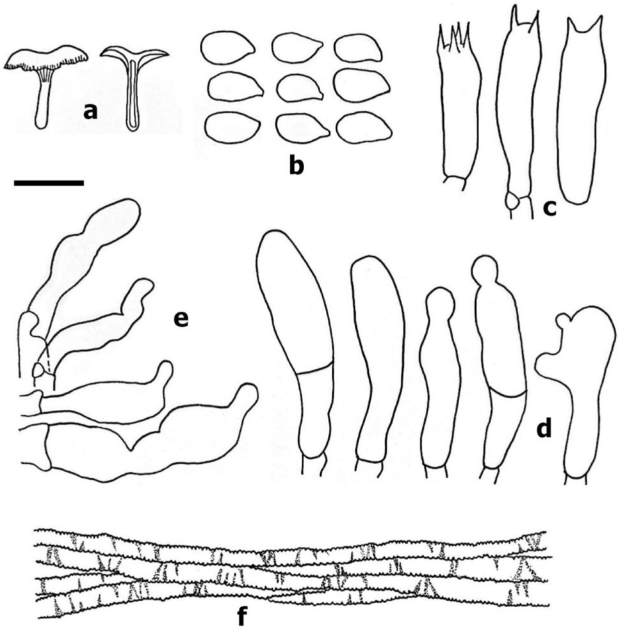


Fig. 178 ***Gerronema atrovirens*** (BKF10264, **holotype**). **a** Basidiomata, **b** Basidiospores, **c** basidium, **d** Cheilocystidia, **e** Caulocystidia **f** Pileipellis cell. Scale bars: **a** = 20 mm, **b–e** = 10 µm, **f** = 20 µm. Drawing by W. Phonrob

composed 2 type of hyphae: a) sarco-hyphae, elongate fusoid cell 125–200 × 3–25 µm, hyaline, smooth, inamyloid, thick-walled (up to 1 µm); b) generative hyphae 2–13 µm wide, cylindrical, branched, hyaline, smooth, inamyloid, thin-walled. *Caulocystidia* abundant, 19–34 × 5–9 µm, cylindrical with 1–2 constrictions, flexuose, irregular in shape, hyaline to pale green in KOH, inamyloid, thin-walled. *Clamp connections* present in all tissues.

Habit, habitat and known distribution: Gregarious on decayed bamboo wood, known only from Thailand.

Material examined: Thailand, Sukhothai Provinve, Si Satchanalai National Park, Natural trail, 22 Aug 2020, collector N Wannathes N Suwannarach and J Kumla, BKF10264 (**holotype**).

Additional material examined: Thailand, Sukhothai Province, Si Satchanalai National Park, Natural trail, 23 Aug 2020, collector N Wannathes N Suwannarach and J Kumla, BKF10265, NW1372 (**isotype**).

GenBank numbers: BKF10264- MZ452088(ITS), MZ452671(LSU).

BKF10265- MZ452668(ITS), MZ452672 (LSU)

Notes: *Gerronema atrovirens* is characterized by a medium size of omphaliod, elastic basidiomata, convex with depress center to deeply infundibuliform, translucent striate at margin, dull green pileus, decurrent, subdistant lamellae, cylindrical, central, greenish grey stipe, ellipsoid basidiospores with mean 7.6 × 4.4 µm, pileipellis composed of incrusted hyphae with greyish green colour, present of irregular cylindrical cheilocystidia and cualocystidia, sarcodimitic trama tissue, and grow on decayed bamboo wood. A new species is morphologically similar to *G. cyathiforme* (Berk. & M.A. Curtis) Singer, species originally described from a Neotropic, differs in forming a distinct radial stripes pileus, absent of cystidia, and mahogany red (in KOH) lamellar trama (Singer 1970). *Gerronema atrovirens* is also closely related *G. indigoticum* T. Bau & L.N. Liu, a green–blue species from subtropical China. The latter species differs in forming smaller pilei (9–16 mm wide) with green–blue, shorter (20–27 × 8–12 µm), simple clavate cheilocystidia, and simple clavate cualocystidia (Lui et al. 2019), and the phylogenetic analyses inferred from combined sequences (Fig. 179) confirmed that *G. atrovirens* is closely allied with *G. indigoticum* and it distinct species from related morphological species and other taxa in this genus.

Gerronema flavum Wannathes, N. Suwannarach, J. Kumla, Phonrob & S. Lumyong, ***sp.nov.***

MycoBank number: MB 840184; Facesoffungi number: FoF10686; Figs. 177c, 180

Etymology: *'flavum'* = yellow, refers to the colour of basidiomata.

Holotype: BKF10253

Pileus 4–11 mm diam., convex, umbonate when young and plano-convex with depress in center to infundibuliform in age, glabrous, radially fibrillose when young, translucent

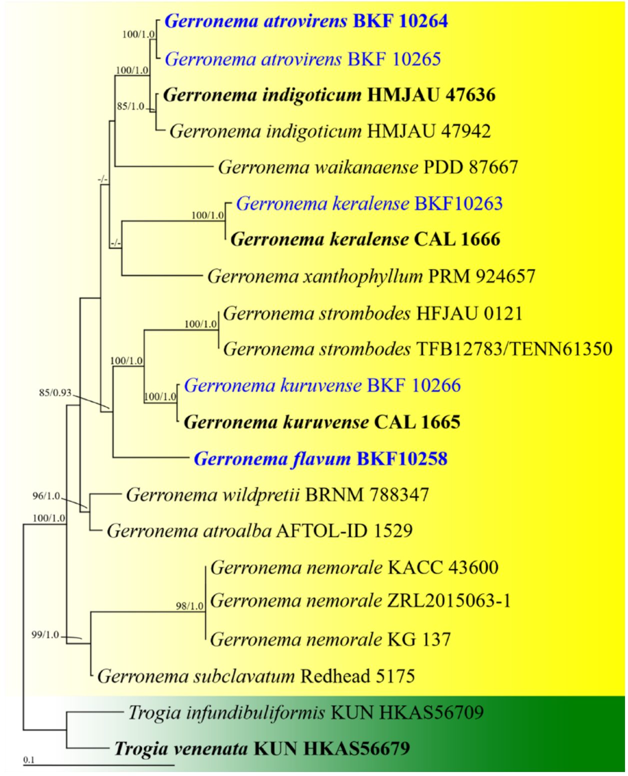


Fig. 179 Phylogenetic tree derived from maximum likelihood analysis of a combined ITS and LSU genes of 21 sequences and the aligned dataset was comprised of 1700 characters including gap. The average standard deviation of the split frequencies of the BI analysis was 0.00612. *Togia infundibuliformis* KUN HKAS56709 and *T. venenata* KUN HKAS56679 were used as outgroup. Numbers above branches are the bootstrap statistics percentages (left) and Bayesian posterior probabilities (right). Branches with support values ≥ 70%/0.90 are shown at each branch and the bar represents 0.1 substitutions per nucleotide position. Hyphen (-) represents support values ≤ 70%/0.95. Ex-type strains are in black bold. The newly generated sequences are indicated in blue and **bold** type species

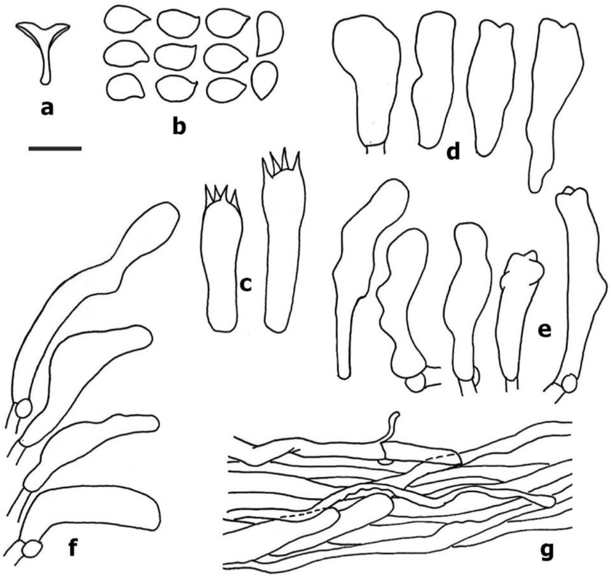


Fig. 180 ***Gerronema flavum*** (BKF10253, **holotype**). **a** Basidiomata, **b** Basidiospores, **c** Basidium, **d** Pleurocystidia, **e** Cheilocystidia, **f** Caulocystidia, **g** Pileipellis cell. Scale bars: **a** = 20 mm, **b–f** = 10 µm, **g** = 20 µm. Drawing by W. Phonrob

striate to striate at marging in age, dull, light yellow (4A5) overall when young, sunflower yellow (4A7) overall in age, hygrophanous, become yellowish white. *Lamellar* decurrent, subdistant (14–16) with 2–3 series of lamellulae, narrow, yellowish withe (4A2), non-marginate; *Stipe* 4–19 × 1–2 mm, tapering upward when young, cylindrical in age, elastic, hollow, central, flexuose, pubescent, yellowish withe (4A2) overall. *Context* thin, Odor and taste not distinctive.

Basidiospore 7–8(–9) × 4–5(–6) µm [x = 7.68 ± 0.63 × 4.68 ± 0.56, Q = 1.3–2.25, q = 1.66 ± 0.23, *n* = 25, s = 1] broadly ellipsoid, smooth, hyaline, inamyloid, thin-walled. *Basidia* 25–32 × 6–9 µm, clavate, with 4 sterigmata, thin-walled, inamyloid. *Cheilocystidia* abundant, 25–40 × 5–8 µm, knobby cylindrical to clavate, irregular in shape, hyaline, inamyloid, thin-walled. *Pleurocystidia* abundant, 24–33 × 9–11 µm, clavate to cylindrical, sometime knobbed, hyaline, inamyloid, thin-walled. *Lamellar trama* interwoven, hyphae 3–6 µm diam., cylindrical, smooth, hyaline, inamyloid, thin-walled. *Pileipellis* composed with cutis of repent hyphae, radially arrangement, 4–15 µm, cylindrical, non-incrustation, hyaline in KOH, inamyloid, thin-walled, true pileocystidia absent. *Pileus trama* sarcodimitic, interwoven, composed of 2 type of hyphae: a) sarco-hyphae, elongate fusoid cell 50–60 × 10–14 µm, hyaline, smooth, inamyloid, thin-walled; b) generative hyphae 3–11 µm wide, cylindrical, branched, hyaline, smooth, inamyloid, thin-walled. *Stipitipellis* cutis, hyphae 3–10 µm diam., parallel, cylindrical, hyaline to pale yellow in KOH, smooth, inamyloid, thin-walled. *Stipe trama* sarcodimitic, parallel, composed 2 type of hyphae: a) sarco-hyphae, elongate fusoid cell 87–165 × 4–15 µm, hyaline, smooth, inamyloid, thick-walled (1–4 µm); b) generative hyphae 3–12 µm wide, cylindrical, branched, hyaline, smooth, inamyloid, thin-walled. *Caulocystidia* abundant, 28–47 × 7–9 µm, cylindrical to clavate, irregular in shape, flexuose, hyaline KOH, inamyloid, thin-walled. *Clamp connections* present in all tissues.

Habit, habitat and known distribution: Gregarious on decayed wood, known only from Thailand.

Material examined: Thailand, Nakhon Ratchasima Provinve, Khao Yai National Park, trial to Pha Kluai Mai waterfall, 21 Sep 2018, collector N Wannathes, N Suwannarach J Kumla, S Lumyong, BKF10253 (**holotype**).

GenBank numbers: BKF10253- MZ1452142 (ITS), MZ452170 (LSU).

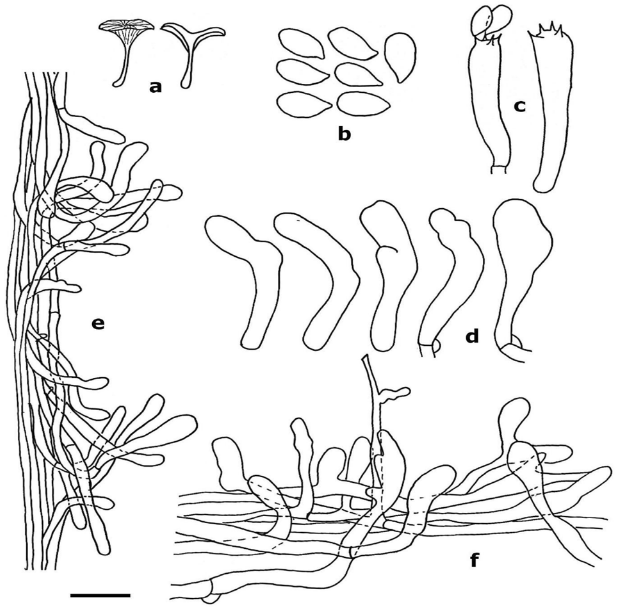


Fig. 181 ***Gerronema keralense*** (BKF10263) **a** Basidiomata, **b** Basidiospores, **c** Basidium, **d** Cheilocystidia, **e** Caulocystidia **f** Pileipellis cell. Scale bars: **a** = 20 mm, **b–e** = 10 µm, **f** = 20 µm. Drawing by W. Phonrob

Notes: *Gerronema flavum* is characterized by a small omphaliod basidiomata that appears convex with depressed center infundibuliform, radially fibrillose, glabrous, yellow pileus, decurrent, subdistant lamellae, cylindrical, central, yellowish white stipe, broadly ellipsoid basidiospores with mean dimensions of 7.7 × 4.7 µm. The pileipellis is composed of hyaline with non-incrusted hyphae, the presence of irregular cylindrical cheilo-, pleuro- and cualocystidia, and sarcodimitic trama tissue. *Gerronema kuruvense* K.P.D. Latha & Manim and *G. subchrysophyllum* (Murrill) Singer are morphologically similar to a new species, namely *Gerronema kuruvense*, which was originally described from tropical India. It is distinguished by forming orange yellow pileus, bigger basidiospores with mean dimensions of 9.5 × 5.9 µm., an absence of cheilo- and pleurocystidia and the presence of diverticulate caulocystidia (Latha et al. 2018). *Gerronema subchrysophyllum*, a North American species, differs by having a larger basidiomata of nearly double the size (pilei 4–21 mm wide and stipe 4–32 mm long), simple clavate cheilocystidia and a lack a pleurocystidia (Singer 1970). The phylogenetic analyses inferred from combined sequences (Fig. 179) confirmed that *G. flavum* is a distinct species. This was further confirmed via an examination of other related morphological species and other taxa within this genus.

Gerronema keralense K. P. D. Latha & Manim Phytotaxa 364 (1): 85–88 (2018).

Index Fungorum number: IF824928; Facesoffungi number: FoF10687; Fig. 181

Pileus 20 mm diam., infundibuliform, appressed-fibrillose, brownish orange to light brown (5C5-5D5); *Lamellar* decurrent to deeply decurrent, distant (12) with 2–3 series of lamellulae, greyish yellow (4B6) up to 1.5 mm.; *Stipe* 21 × 0.75 mm, central, cylindrical, pruinose, slightly broadened at base, solid, greyish yellow (4B6) overall. *Context* thin, Odor and taste not distinctive.

Basidiospore 7–9 × (3–)4–5 µm [x = 7.76 ± 0.78 × 4.4 ± 0.65, Q = 1.4–2.3, q = 1.79 ± 0.25, *n* = 25, s = 1] ellipsoid, smooth, hyaline, inamyloid, thin-walled. *Basidia* 25–34 × 5–7 µm, clavate, with 4 sterigmata, thin-walled, inamyloid. *Cheilocystidia* scattered, 27–31 × 5–8 µm, clavate, flexuose, irregular in shape, hyaline, inamyloid, thin-walled. *Pleurocystidia* absent. *Lamellar trama* subregular, hyphae 4–15 µm diam., smooth, hyaline, inamyloid, thin-walled. *Pileipellis* cutis with pileocystidia, 3–12 µm, cylindrical, hyaline in KOH, inamyloid, inclusion cytoplasm turns to brown to light brown in Melzer's reagent, thin-walled. *Pileus trama* sarcodimitic, subregular, composed of 2 type of hyphae a) sarco-hyphae, elongate fusoid cell 98–196 × 10–14 µm, hyaline, smooth, inamyloid, thin-walled; b) generative hyphae 2–5 µm wide, cylindrical, branched, hyaline, smooth, inamyloid, thin-walled. *Stipitipellis* cutis, hyphae 3–6 µm diam., parallel, cylindrical, pale yellow in KOH, smooth, inamyloid, slightly thick-walled. *Stipe trama* sarcodimitic, parallel, composed 2 type of hyphae: a) sarco-hyphae, elongate fusoid cell 74–230 × 7–10 µm, hyaline, smooth, inamyloid, slightly thick-walled; b) generative hyphae 3–7 µm wide, cylindrical, branched, hyaline, smooth, inamyloid, slightly thick-walled. *Caulocystidia* 28–47 × 7–9 µm, agglutinated, cylindrical to clavate, hyaline in KOH, inamyloid, slightly thick-walled. *Clamp connections* present in all tissues.

Habit, habitat and known distribution: Solitary on decayed wood, known from topical India and Thailand.

Material examined: Thailand, Sukhothai Province, Si Satchanalai National Park, Natural trial, 15 June 2019, collector N Wannathes, N Suwannarach J Kumla, S Khuna, BKF10263.

GenBank numbers: BKF10263- MZ452107 (ITS), MZ452144 (LSU).

Notes: *Gerronema keralense* is characterized by a medium-sized omphaliod basidiomata, infundibuliform, brownish orange to light brown pileus, decurrent to deeply decurrent, distant, greyish yellow lamella, cylindrical, central, greyish yellow stipe, ellipsoid basidiospores with mean dimensions of 7.8 × 4.4 µm, pileipellis with pileocystidia, non-incrusted hyphae, cytoplasmic inclusion that turned from brown to light brown in Melzer's reagent, the presence of irregular cylindrical cheilo-, cualocystidia and sarcodimitic trama tissue. Our Thai

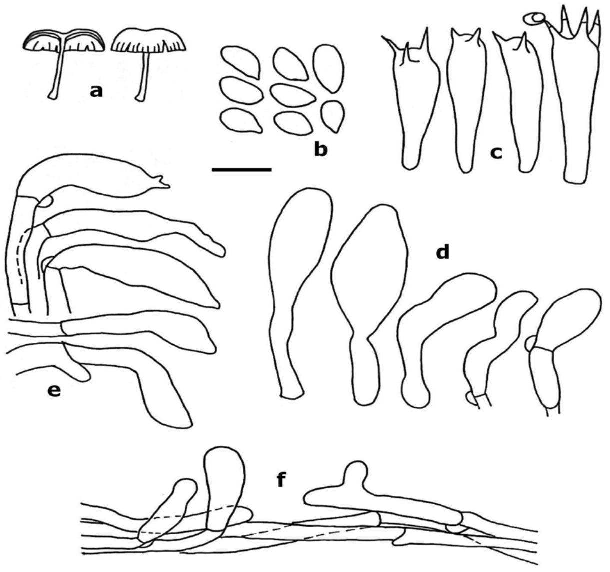


Fig. 182 ***Gerronema kuruvense*** (BKF10266), **a** Basidiomata, **b** Basidiospores, **c** Basidium, **d** Cheilocystidia, **e** Caulocystidia **f** Pileipellis cell. Scale bars: **a** = 20 mm, **b–e** = 10 µm, **f** = 20 µm. Drawing by W. Phonrob

description is consistent with *Gerronema keralense* that was originally described from India, except for the type specimen that formed an applanate with a slight central depression pileus (Latha et al. 2018). Notably, these variations may be caused by a mutuality of basidiomata. *Gerronema keralense* is morphologically similar to *G. kuruvense* K.P.D. Latha & Manim, but the latter differs by having bigger basidiospores with mean dimensions of 9.1 × 4.9 µm, a cytoplasmic inclusion of pileocystidia that never changes colour with Melzer's reagent and caulocystidia that are not agglutinated (Latha et al. 2018).

Gerronema kuruvense K. P. D. Latha & Manim. Phytotaxa 364 (1): 82–85 (2018).

Index Fungorum number: IF824927; Facesoffungi number: FoF10688; Figs. 177b, 182

Pileus 27 mm diam., convex with depress center, appressed-fibrillose, pale yellow (3A3); *Lamellar* subdecurrent, distant (16) with 2–3 series of lamellulae, narrow, light yellow (3A5) up to 2 mm.; *Stipe* 25 × 1 mm, central, cylindrical, pubescent, slightly broadened at base, hollow, yellowish white (3A2) overall. *Context* thin, Odor and taste not distinctive.

Basidiospore 8–10(–11) × 4–5(–6) µm [x = 9.08 ± 0.81 × 4.88 ± 0.43, Q = 1.6–2.25, q = 1.89 ± 0.25, *n* = 25, s = 1] ellipsoid, smooth, hyaline, inamyloid, thin-walled. *Basidia* 22–36 × 7–8 µm, clavate, with 2 sterigmata, sometime with 3–4 sterigmata, thin-walled, inamyloid. *Cheilocystidia* scattered, 21–51 × 5–11 µm, clavate, flexuose, irregular in shape, sometimes 2-celled, hyaline, inamyloid, thin-walled. *Pleurocystidia* absent. *Lamellar trama* interwoven, arranged in two directions, hyphae 3–14 µm diam., cylindrical, smooth, hyaline, inamyloid, thin-walled. *Pileipellis* cutis with scattered ascending pileocystidia, 4–14 µm, cylindrical, hyaline in KOH, inamyloid, thin-walled. *Pileus trama* sarcodimitic, subregular to interwoven, composed of 2 type of hyphae: (a) sarco-hyphae, elongate fusoid cell 94–212 × 10–14 µm, hyaline, smooth, inamyloid, thin-walled; (b) generative hyphae 3–7 µm wide, cylindrical, branched, hyaline, smooth, inamyloid, thin-walled. *Stipitipellis* cutis, hyphae 3–8 µm diam., parallel, cylindrical, hyaline in KOH, smooth, inamyloid, slightly thick-walled (up to 0.5 µm). *Stipe trama* sarcodimitic, parallel, composed 2 type of hyphae: a) sarco-hyphae, elongate fusoid cell 80–230(– over 250) × 8–15 µm, hyaline, smooth, inamyloid, thick-walled (1–2 µm); b) generative hyphae 3–6 µm wide, cylindrical, branched, hyaline, smooth, inamyloid, thin-walled. *Caulocystidia* abundant, 28–47 × 7–9 µm, cylindrical to clavate, irregular in shape, flexuose, hyaline in KOH, inamyloid, slightly thick-walled (up to 0.5 µm). *Clamp connections* present in all tissues.

Habit, habitat and known distribution: Solitary on decayed wood, known from topical India and Thailand.

Material examined: Thailand, Sukhothai Province, Si Satchanalai National Park, trial to Tad Duan waterfall, 30 Aug 2020, collector N Wannathes, N Suwannarach J Kumla, S Khuna, W Phonrob, S Tabtan, BKF10266.

GenBank numbers: BKF10266-MZ452090 (ITS), MZ452669(LSU).

Notes: *Gerronema kuruvense* is characterized by a medium-sized omphaliod basidiomata that is convex with a depressed center. It has a pale-yellow pileus that is subdecurrent, distant, with light yellow lamella, cylindrical, central, yellowish white stipe, ellipsoid basidiospores with mean dimensions of 9.1 × 4.9 µm. The pileipellis is composed of hyaline with pileocystidia, non-incrusted hyphae, the presence of irregular cylindrical cualocystidia and seldomly present cheilocystidia and sarcodimitic trama tissue. The Thai specimen is almost indistinguishable from *Gerronema kuruvense*, which was originally described from topical India. The holotype forms a smaller size basidiomata (pilei 4–11 mm wide and stipe 3–18 mm long) and lacks cheilocystidia (Latha et al. 2018). *Gerronema kuruvense* is morphologically similar to *G. strombodes* (Berk. & Mont.) Singer, but differs by forming larger basidiomata (pilei 25–80 mm wide and stipe of 30–60 × 2–6.8 mm) greyish white pileus, pileipellis lacking pileocystidia and a complete lack of caulocystidia (Singer 1970).

Tricholomopsis Singer, Schweiz. Z. Pilzk. 17: 56 (1939).

Tricholomopsis was established to accommodate a group of saprophytic tricholomatoid fungi which have a fibrillose or squamulose pileus, inamyloid smooth basidiospores, and

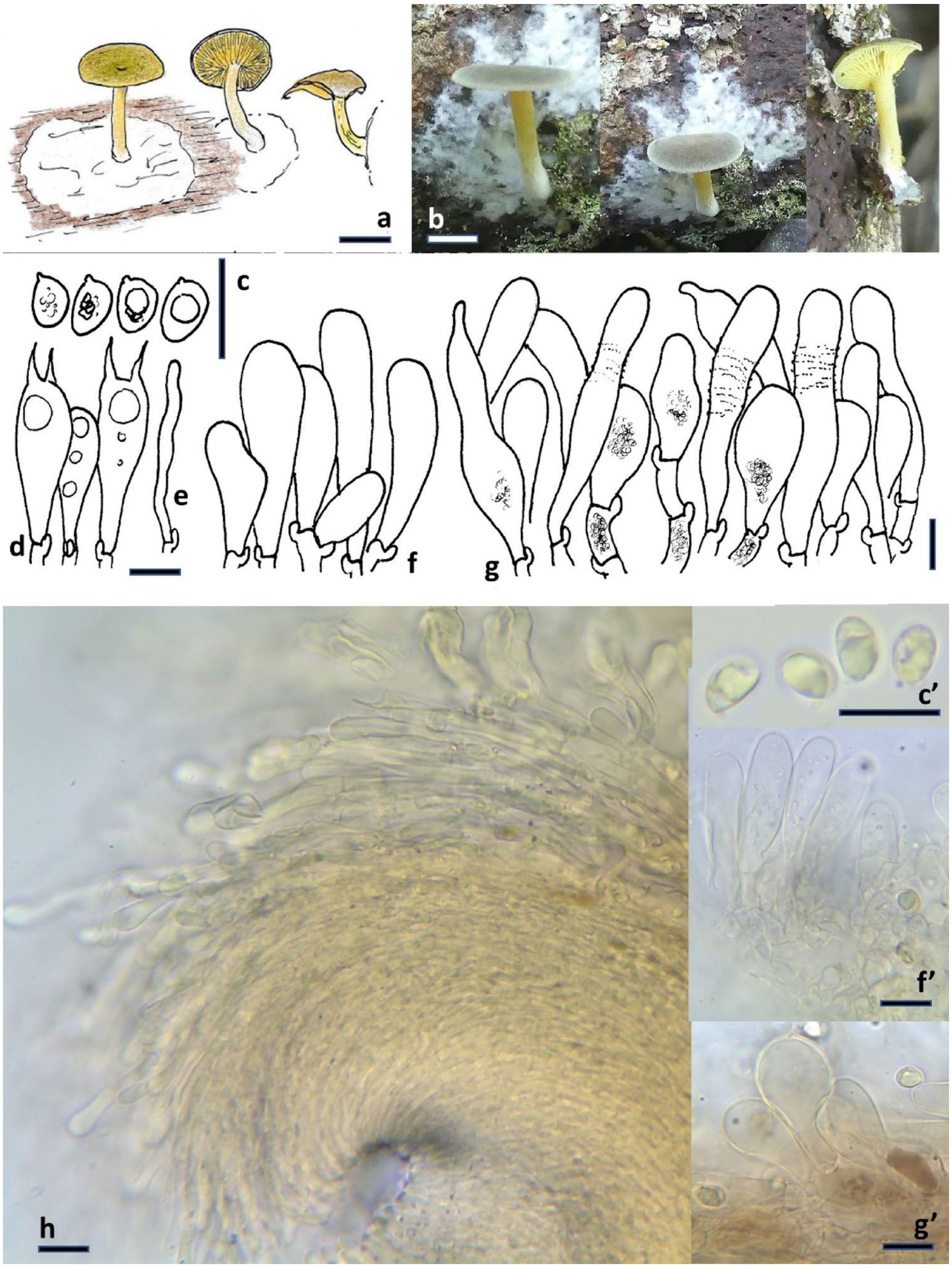


Fig. 183 ***Tricholomopsis lechatii*** (LIP0202264, **holotype**). **a, b** Basidiocarp **c** Basidiospores **d** Basidia **e** One hymenophoral hyphid. **f** Cheilocystidia. **g** Pileus covering. **h** Pileus margin, radial section. Drawings and macrophotos by R. Courtecuisse, microphotos by P.-A. Moreau

a sterile lamella edge covered with large prominent cheilocystidia (Mao et al. 2021). There are 76 species epithets in the index fungorum for this genus.

Tricholomopsis lechatii Courtec., S. Dumez, S. Welti & P.-A. Moreau, ***sp. nov.***

MycoBank number: MB843163, Facesoffungi number: FoF13397; Fig. 183

Etymology: The species is warmly dedicated to our friend Christian Lechat (1952–2022), who recently and suddenly died. He was an eminent specialist of the Hypocreales worldwide and a very enthusiastic and faithful member of the numerous field trips organized in the Tropics by one of us (RC). He was present when this species was collected.

Holotypus: 0202264 (LIP).

Pileus 10–14 mm diam, slightly convex or almost flat, showing a little umbilic (not deep) in the centre or slightly eccentric; shape regular, circular or almost so, sometimes slightly elliptical when seen from above. Surface remarkably dull, finely tomentose or even velvety under lens. Color very special, dirty olivaceous with ochraceous hue at center but more yellow at the margin, which is slightly enrolled or at least very obtuse and scarcely pectinate at the extreme edge. *Lamellae* adnate, rather crowded, with two rather regular rows of smaller gills, thin. Color rather bright and deep,

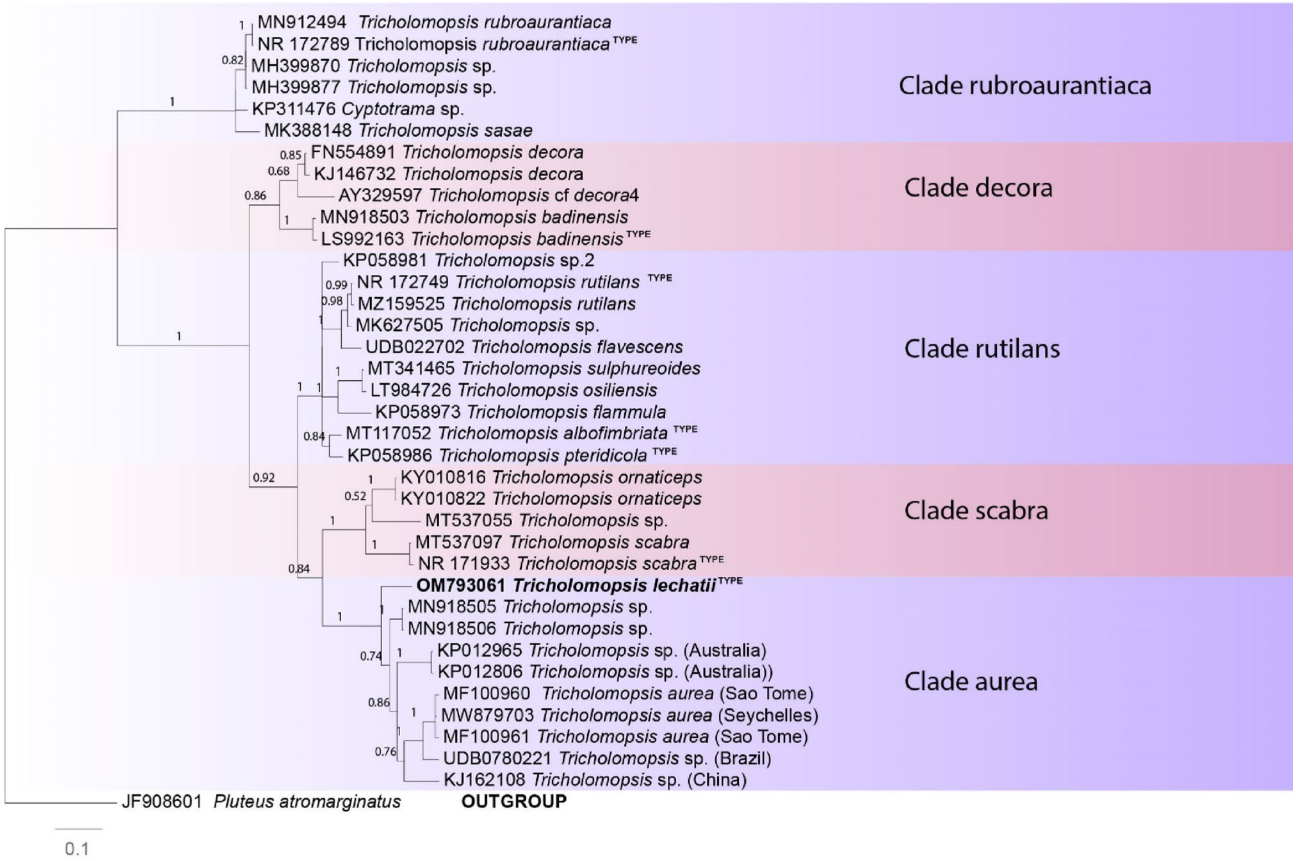


Fig. 184 Phylogenetic analyses were conducted online at www.phylogeny.fr (Dereeper et al. 2008). Multiple sequence alignments were performed with MUSCLE v. 3.7 (Edgar 2004). Maximum likelihood (ML) phylogenetic analysis was achieved with PhyML v. 3.0 (Guindon et al. 2010), using the GTR + I + Γ model of evolution and the Shimodaira Hasegawa version of the approximate likelihood-ratio test (SH-aLRT) of branch support (Anisimova et al. 2011). Phylogram was built using TreeDyn 198.3 (Chevenet et al. 2006) and edited with Inkscape 0.91 (https://inkscape.org/fr). Newly generated sequences for this study are in bold. The tree is rooted by a sequence of *Pluteus atromarginatus* (Pluteaceae)

mustard yellow. Edge rather thick, clearly bearing a row of small, densely crowded, aggregates of crystals. *Stipe* up to 15 × 2 mm, slightly excentrical, cylindraceous, more or less narrowly fistulose, dull yellow, paler than the gills but sometimes pale brownish toward mid-length, arising from a thin greyish mycelial patch of subiculum (up to 35 mm diam.), which sometimes climbs up to the stipe up to a few millimeters, thus greyish at the basis. *Context* yellowish in the stipe, deeper yellow in the cap. *Smell* none. *Taste* not recorded.

Basidiospores 6.2–7.5 × 4.8–5 µm, rather broad, elliptical to slightly tear-shaped, apex broader and generally clearly rounded (not elongate nor conical). Apiculus small, faintly distinct. Content with many droplets (sometimes a large one) and confuse, cloudy or punctate around them. Wall smooth, inamyloid, not cyanophilic. *Basidia* 20–28 × 5–8 µm, 2-spored (very few 1-spored and only one 3-spored seen) with very long and sharp sterigmata (up to 10 µm), containing large droplets, the bigger ones at the top. Clamp present at the base of all basidia. *Subhymenium* ramose, rather thick with short, clamped hyphae up to 1.5–2.5 µm wide, somewhat wavy with some longer hyphae parallel to the hymenium. *Hymenophoral trama* parallel in a wavy arrangement, weakly interwoven, made of clamped hyphae 4–8 µm wide. *Edge* sterile; *cheilocystidia* very numerous and prominent, cylindrical to slightly clavate, often regularly thickened toward apex, 35–45 × 8–12 µm, thin-walled, hyaline; base clamped, originated from simple or rarely forked hyphae. *Pleurocystidia* absent; facial sterile cells present as sparse slender "hyphids" cylindrical or slightly thickened at apex, up to 4 µm wide. *Pileipellis* a trichoderm of more or less straightly erected, unicellular or sometimes articulate elements, rather densely arranged, 30–70 × 7–15 µm, the apex mostly rounded or sometimes irregular, rarely mucronate to appendiculate or exceptionally forked; pigmentation epiparietal and vacuolar: wall yellowish, very finely incrusting (minutely punctate or finely marked with transverse zebra depending on the focus made on the cell wall) in all parts

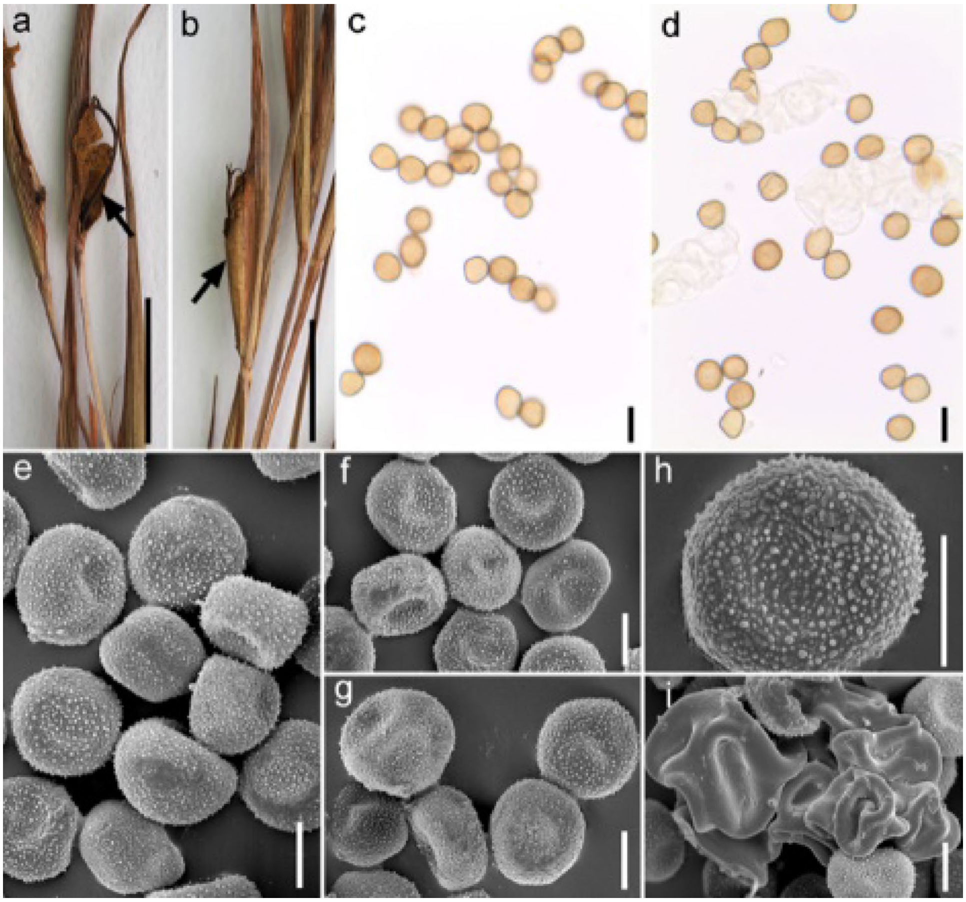


Fig. 185 ***Sporisorium anadelphiae-leptocomae*** (SOMF 30250, **holotype**). **a, b** Habit (black arrows in **a** and **b** show sori). **c** Spores in LM. **d** Spores and sterile cells in LM. **e–h** Spores in SEM. **i** Spores and sterile cells in SEM. Scale bars: **a, b** = 0.5 cm, **c, d** = 10 µm, **e–i** = 5 µm

of the basidiome; vacuolar pigment abundant in subpellis, also present in broad elements of suprapellis, brown-yellow.

Habitat: Saprobic on rotten wood of unidentified Angiosperm, wet tropical forest, along a wet depression. So far only known from the type locality, French Guiana.

Material examined: French Guiana: Saül, Roche Bateau trail, 23 Aug. 2018, R. Courtecuisse & C. Lechat, RC/Guy18.018 (LIP 0202264, **holotype**).

GenBank numbers: LIP 0202264-OM793061 (ITS), OM793062 (LSU).

Notes: *Tricholomopsis lechatii* phylogenetically belongs to the *T. aurea*-complex, a pantropical group of collybioid species so far rather poorly documented in molecular databases (Fig. 184). *Tricholomopsis aurea* was originally described from DR Congo (as *Marasmius aureus*; Beeli, 1928), and recently transferred in the genus *Tricholomopsis* by Desjardin and Perry (2017) based on recent collections from São Tomé. Although the species is reported as common in many tropical regions (GBIF data: https://www.gbif.org/en/species/332554), only few sequences from the neotropics are available, and the ITS marker indicates only faint differences between African and American collections (Desjardin and Perry 2017, consider them as conspecific at this time). The new species described here differs significantly from *T. aurea*, by a pileipellis of trichodermioid structure, with a well-differentiated subpellis and a distinct vacuolar pigment (responsible of the grey-brown tomentum on pileus), whilst *T. aurea* has a thin cutis-like structure, resulting in a glabrous, golden yellow surface with ± inflate terminal elements with granular intracellular pigmentation (Pegler 1983).

Only few neotropical species of *Tricholomopsis* were recorded in the Neotropics, and none can be attributed to *T. lechatii. Tricholomopsis tropica* Dennis from Trinidad is devoid of yellow tinge in context and displays abundant hymenial gloeocystidia (Pegler 1983), what makes its classification in this genus somewhat doubtful; *T. atrogrisea* Pegler from Martinique, possibly more related to *T. lechatii*, has a gelatinized pileipellis made of adpressed hyphae; *T. elegans* Dennis (Dennis 1961) could be the closest relative of *T. lechatii* but differs at least by smaller, subglobose spores (4.5–5 µm long) and 4-spored basidia. No species described so far display either the spectacular pale grey mycelial patch observed in *T. lechatii*, nor its conspicuous 2-spored basidia (Fig. 183).

Ustilaginomycotina Doweld.

We follow the latest treatment and updated account of Ustilaginomycotina in Begerow and McTaggart (2018).

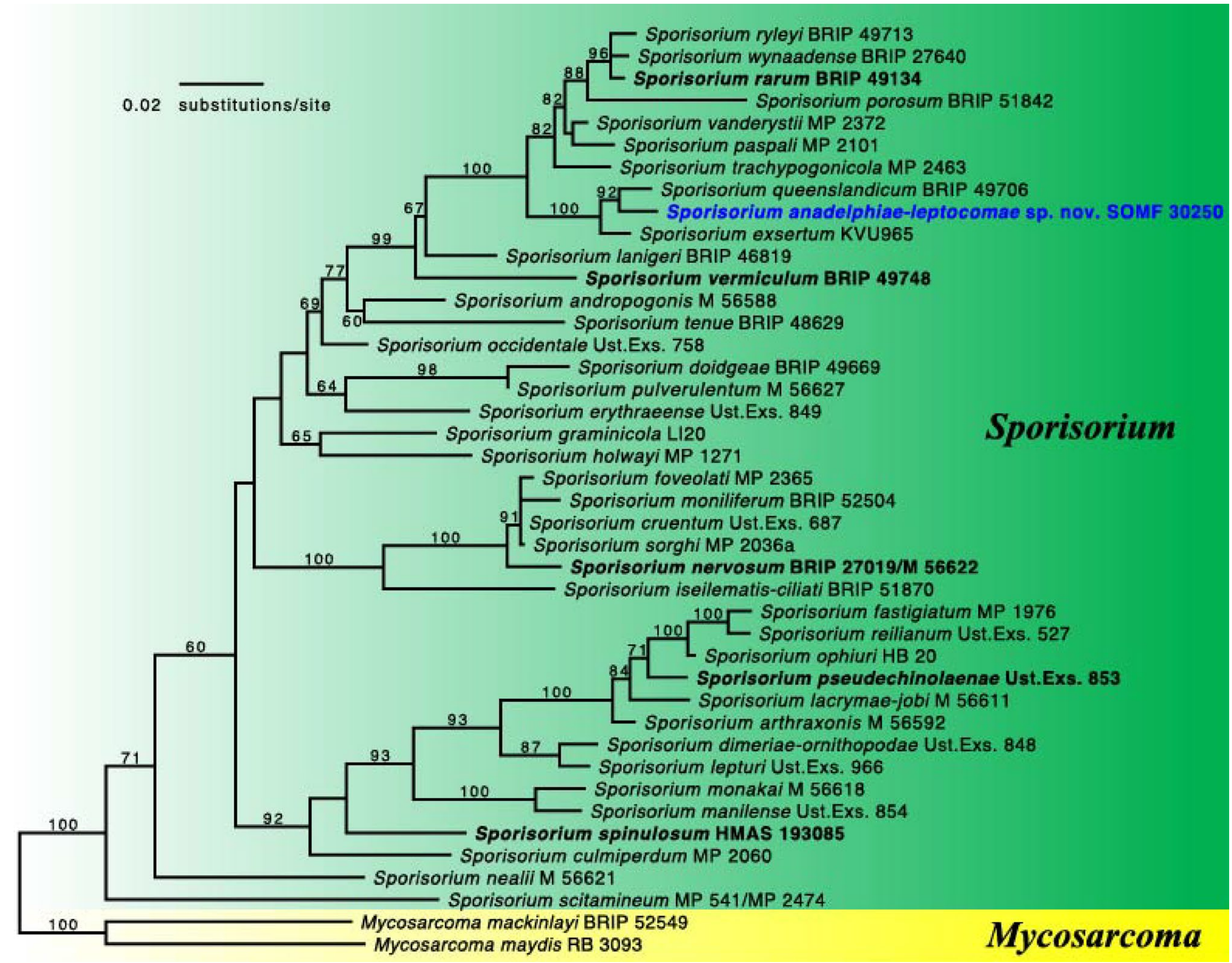


Fig. 186 Most likely tree generated using maximum likelihood analysis (RAxML 8.2.11, Stamatakis 2014) based on concatenated MAFFT v7.450 (Katoh and Standley 2013) alignments of ITS and LSU dataset. The tree is rooted with *Mycosarcoma maydis* Bref. and *M. mackinlayi* (McTaggart & R.G. Shivas) McTaggart et al. Values at nodes indicate bootstrap values inferred by 1000 replicates; only values ≥ 60% are shown

Ustilaginomycetes R. Bauer et al.

The classification of the orders in Ustilaginomycetes follows Begerow and McTaggart (2018).

Ustilaginales G. Winter.

There are seven families in this order: Anthracoideaceae Denchev, Clintamraceae Vánky, Geminaginaceae Vánky, Melanotaeniaceae Begerow et al., Pericladiaceae Vánky, Ustilaginaceae Tul & C. Tul., and Websdaneaceae Vánky (He et al. 2019; but excluding Cintractiellaceae Vánky, see McTaggart et al. 2020).

Ustilaginaceae Tul & C. Tul. [as 'Ustilagineae'], Annls Sci. Nat., Bot., sér. 3 7: 14 (1847).

Ustilaginaceae was introduced by Tulasne and Tulasne (1847). Twenty-eight genera are currently recognized in this family (He et al. 2019).

Sporisorium Ehrenb. ex Link, in Willdenow, Sp. pl., Edn 4 6(2): 86 (1825).

Sporisorium is a grass-infecting genus of smut fungi. It is characterized by sori formed in different parts of the inflorescence or destroying the entire inflorescence, sometimes also comprising the upper part of the stem. The sori are initially enclosed by a thick, brownish peridium that later ruptures irregularly exposing a single, stout columella surrounded by a mass of spores and sterile cells.

Until ten years ago, with 326 species *Sporisorium* was perceived by far the most species-rich genus of smut fungi. A new concept for *Ustilago*, *Sporisorium*, and *Macalpinomyces* was proposed by McTaggart et al. (2012a, b). In its modern circumscription, *Sporisorium* comprises 198 species (Vánky 2011, 2013; Denchev et al. 2012, 2016; McTaggart et al. 2012b; Denchev and Denchev 2013, 2016; Wang et al. 2015).

During an examination of specimens of grasses in the herbarium MA of the Real Jardín Botánico (Madrid, Spain), a smut fungus belonging to *Sporisorium* was found on a specimen of *Anadelphia leptocoma* (MA 690545) from Burkina Faso. Based on distinct morphology and phylogenetic evidence (Fig. 186), this fungus is introduced here as a novel species.

Sporisorium anadelphiae-leptocomae T. Denchev, Denchev, Kemler, M.P. Martín & Begerow, ***sp. nov.***

Index Fungorum number: *IF558175*; *Facesoffungi number*: *FoF09652;* Fig. 185.

Etymology: The specific epithet refers to the host species.

Holotype: SOMF 30250

Parasitic on *Anadelphia leptocoma*. *Infection* systemic. *Sori* destroying the racemes, 5–10 mm long, fusiform, all racemes of an infected plant affected; initially covered by a thick, yellow–brown peridium which later ruptures irregularly, exposing a single columella, surrounded by a powdery, dark reddish-brown mass of spores and sterile cells. Columella shorter than the sorus, flagelliform, apically slightly branched, sometimes slightly flattened or with shallow longitudinal furrows. Sori at first completely enclosed by the spatheoles, later more or less visible. *Sterile cells* firmly packed in irregular groups, collapsed, 9–14(–17) μm long, usually larger than the spores, hyaline to pale yellow; wall 0.6–1.0 μm thick. In SEM, smooth, sometimes partially rugulose. *Spores* subglobose, slightly irregular, broadly ellipsoidal, ellipsoidal or ovoid, (6.5–)7.5–9.5(–10.5) × (6–)7–8.5(–9.5) (8.6 ± 0.6 × 7.8 ± 0.6) μm (*n* = 300), medium reddish brown; wall evenly thickened, 0.5–0.7 μm thick, smooth. In SEM, minutely echinulate-verruculose, ornaments up to 0.2 μm high, densely punctate between the main ornaments.

Material examined: Burkina Faso, Cascades Region, Léraba Province, Sindou Department, Tourni, dam, riverbed with seeping water, fallow fields, 10°46′ N, 05°09′ W, alt. 200–500 m, on *Anadelphia leptocoma (*Trin.*)* Pilg. *(*Poaceae*)*, 28 October 1997, S. Lægaard, H. Mipro & T. Soberé, no. 18421 (SOMF 30250, **holotype**; MA 690545, **isotype**).

GenBank numbers: MW599285(ITS), MW599284 (LSU).

Notes: *Anadelphia* Hack. is a small genus of Poaceae Barnhart, tribe Andropogoneae Dumort., subtribe Andropogoninae J. Presl (including 514 species in 25 genera) (Soreng et al. 2017). *Anadelphia* comprises 14 species (Clayton et al. 2015) characterized by compound inflorescence composed of racemes. *Anadelphia leptocoma* is distributed in Tropical Africa (from Senegal to Zambia), mainly in West Tropical Africa (Clayton et al. 2015; Poilecot et al. 2015; Ibrahim et al. 2018). It is a characteristic grass of the savannahs (Poilecot et al. 2015).

Seven smut fungi have been previously reported on hosts in *Anadelphia* and its closely related genera, *Elymandra* Stapf and *Monocymbium* Stapf: *Anthracocystis anadelphiae* (Vienn.-Bourg.*)* McTaggart & R.G. Shivas, *Jamesdicksonia anadelphiae* (Vienn.-Bourg.*)* Piątek, *J. anadelphiae-trichaetae* T. Denchev & Denchev, *Macalpinomyces elymandrae* (Vienn.-Bourg.*)* Vánky, *Sporisorium anadelphiae-trichaetae* T. Denchev & Denchev, *S. monocymbii (*Syd.*)* Vánky, and *Tilletia elymandrae* Vienn.-Bourg. *(*Denchev and Denchev 2016*)*. *Sporisorium anadelphiae-leptocomae* can be easily distinguished from *S. anadelphiae-trichaetae* by having (i) sori that destroy the racemes entirely, while the sori of *S. anadelphiae-trichaetae* affect only the spikelets, and (ii) minutely echinulate-verruculose spores with ornaments up to 0.2 μm in height, while *S. anadelphiae-trichaetae* possesses moderately echinulate spores, with spinules up to 0.7 μm in height. The sori of *Sporisorium monocymbii*, destroying spikelets or groups of spikelets and forming a very characteristic, strongly branched body *(*see Figs. 45, 47, 48 in Denchev and Denchev 2016*)*, also differ from those of *S. anadelphiae-leptocomae*. Additionally, *Sporisorium monocymbii* has minutely echinulate spores, with spinules up to 0.3(–0.4) μm in height and larger sterile cells, 9–19(–24) μm long *vs* 9–14(–17) μm long for *S. anadelphiae-leptocomae***.**

The phylogenetic analysis of *Sporisorium*, based on combined ITS and LSU sequences resulted in a similar topology to previous analyses (McTaggart et al. 2012a). *Sporisorium anadelphiae-leptocomae* formed a statistically very well supported clade (100% bootstrap) together with *S. queenslandicum* Vánky et al., infecting *Sehima nervosa* (Roem. & Schult.) Stapf, and *S. exsertum* (McAlpine) L. Guo, infecting *Themeda* spp. Sister to this clade is a group containing *S. rarum* R.G. Shivas et al., *S. ryleyi* Vánky & R.G. Shivas, *S. paspali* (Speg.) Vánky, *S. porosum* (Langdon) McTaggart & R.G. Shivas, *S. trachypogonicola* Vánky & C. Vánky, *S. vanderystii* (Henn.) Langdon & Full., and *S. wynaadense* (Sundaram) Vánky & R.G. Shivas. All of the species from these two clades are parasitizing grasses from the tribe Andropogoneae, with the exception of *S. paspali*, infecting *Paspalum* spp., belonging to the tribe Paspaleae (Fig.*).

The smut fungi of Burkina Faso are very poorly known with only six species reported from this country: *Anthracocystis ehrenbergii* (J.G. Kühn) McTaggart & R.G. Shivas, *A. livingstoneana (*Vánky*)* McTaggart & R.G. Shivas, *Moesziomyces penicillariae (*Bref.*)* Vánky, *Sporisorium reilianum* (J.G. Kühn) Langdon & Full., *S. scitamineum* (Syd) M. Piepenbr. et al., and *S. sorghi* Ehrenb. ex Link (Vánky et al. 2011; Piepenbring et al. 2020).

Table 5 Updated list of fungal taxa published in the previous fungal diversity notes

FDN number	Species name	Status	Country/Region	Comment
Fungal diversity notes 1–110 (Liu et al. 2015)				
1	*Amphibambusa*	New genus	Thailand	Placed in Caniaceae by Wijayawardene et al. (2020)
2	*Amphibambusa bambusicola*	New species		
3	*Amphisphaeria sorbi*	New species	Italy	N/C
4	*Atrotorquata spartii*	New species	Italy	N/C
5	*Oxydothis atypica*	New species	Thailand	was introduced without molecular data, was not included in Konta et al. 2016
6	*Pestalotiopsis digitalis*	New species	New zealand	N/C
7	*Pestalotiopsis dracontomelon*	New species	Thailand	N/C
8	*Pestalotiopsis italiana*	New species	Italy	N/C
9	*Conicomyces pseudotransvaalensis*	New species	Japan	N/C
10	*Dinemasporium nelloi*	New species	Italy	N/C
11	*Diaporthe thunbergiicola*	New species	Thailand	N/C
12	*Diatrype palmicola*	New species	Thailand	N/C
13	*Phaeoisaria pseudoclematidis*	New species	Thailand	N/C
14	*Colletotrichum sedi*	New species	Russia	N/C
15	*Natantispora unipolaris*	New species	Taiwan	N/C
16	*Saagaromyces mangrovei*	New species	Saudi arabia	N/C
17	*Myrothecium macrosporum*	New species	Thailand	Nom. illegit., Art. 53.1
18	*Neogaeumannomyces*	New genus	Thailand	N/C
19	*Neogaeumannomyces bambusicola*	New species		
20	*Meliola tamarindi*	Reference specimen	Thailand	N/C
21	*Hapalocystis berkeleyi*	Reference specimen	Italy	N/C
22	*Cytospora berberidis*	New species	China	N/C
23	*Cytospora sibiraeae*	New species	China	N/C
24.*	*Annulohypoxylon leptascum*	New record	Brazil	N/C
25.*	*Annulohypoxylon nitens*	New sequence data	Thailand	N/C
26.*	*Annulohypoxylon stygium*	New sequence data	Sri Lanka	N/C
27.*	*Annulohypoxylon thailandicum*	New species	Thailand	N/C
28.*	*Biscogniauxia marginata*	New sequence data	France	N/C
29.*	*Fasciatispora nypae*	Reference specimen	Thailand	N/C
30.*	*Hypoxylon fendleri*	New sequence data	Venezuela	N/C
31.*	*Hypoxylon lenormandii*	New sequence data	Cuba	N/C
32.*	*Hypoxylon monticulosum*	New sequence data	Thailand	N/C
33.*	*Flammeascoma*	New genus	Thailand	N/C
34.*	*Flammeascoma bambusae*	New species		
35.*	*Palmiascoma*	New genus	Thailand	N/C
36.*	*Palmiascoma gregariascomum*	New species		
37.*	*Chaetocapnodium*	New genus	Thailand	*Chaetocapnodium siamense* Hongsanan & K.D. Hyde [as 'siamensis']
38.*	*Chaetocapnodium siamensis*	New species		
39.*	*Phragmocapnias philippinensis*	New species	Philippines	*Chaetocapnodium philippinense* (Abdollahzadeh et al. 2020)
40.*	*Brunneomycosphaerella*	New genus	Italy	Placed in Mycosphaerellales genera incertae sedis by (Wijayawardene et al. 2022)
41.*	*Brunneomycosphaerella laburni*	New species		
42.*	*Dictyosporium aquaticum*	New species	Egypt	N/C
43.*	*Dictyosporium meiosporum*	New species	Thailand	N/ C
44.*	*Dictyosporium thailandicum*	New species	Thailand	N/C
45.*	*Didymella cirsii*	New species	Italy	N/C
46.*	*Microsphaeropsis olivacea*	first report of the sexual morph	Germany	N/C
47.*	*Phoma medicaginis*	Additional collection	Italy	*Ascochyta medicaginicola* (Chen et al. 2015)
48.*	*Kalmusia italica*	New species	Italy	N/C
49.*	*Kalmusia spartii*	New species	Italy	N/C
50.*	*Montagnula graminicola*	New species	Italy	N/C
51.*	*Paraconiothyrium nelloi*	New species	Italy	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
52	*Paraconiothyrium thysanolaenae*	New species	Thailand	N/C
53	*Paraphaeosphaeria spartii*	New species	Italy	N/C
54	*Pseudocamarosporium cotinae*	New species	Russia	*Pseudocamarosporium cotini* Norph., Bulgakov & K.D. Hyde [as 'cotinae']
55	*Psiloglonium colihuae*	Reference specimen	Thailand	N/C
56	*Psiloglonium multiseptatum*	New species	Thailand	N/C
57	*Psiloglonium sasicola*	Reference specimen	Thailand	N/C
58	*Aliquandostipite manochii*	New species	Thailand	*Aliquandostipite manochiae* Sri-indr., Boonyuen, Suetrong, K.L. Pang & E.B.G. Jones [as 'manochii']
59	*Keissleriella sparticola*	New species	Italy	*Keissleriella spartiicola* Singtr. & K.D. Hyde [as 'sparticola']
60	*Leptosphaeria doliolum*	Additional collection	Italy	N/C
61	*Leptosphaeria ebuli*	New species	Italy	N/C
62	*Paraleptosphaeria nitschkei*	Reference specimen	Italy	N/C
63	*Plenodomus agnitus*	Reference specimen	Germany	N/C
64	*Lophiostoma pseudodictyosporium*	New species	Italy	N/C
65	*Lophiostoma ravennicum*	New species	Italy	N/C
66	*Lophiotrema eburnoides*	New species	Japan	*Lophiotrema eburneoides* Kaz. Tanaka, A. Hashim. & K. Hiray. [as 'eburnoides']
67	*Byssosphaeria musae*	New species	Thailand	N/C
68	*Pseudotrichia rubriostiolata*	New species	Thailand	N/C
69	*Pseudotrichia thailandica*	New species	Thailand	N/C
70	*Sarimanas*	New genus	Japan	N/C
71	*Sarimanas pseudofluviatile*	New species		
72	*Sarimanas shirakamiense*	New species	Japan	N/C
73	*Neomicrothyrium*	Valid publication of the genus		*Zeloasperisporium* (Hongsanan et al. 2015)
74	*Pallidocercospora acaciigena*	New record	Thailand	N/C
75	*Pseudocercospora tamarindi*	New species	Thailand	N/C
76	*Zasmidium musae*	First report of the sexual morph	Thailand	N/C
77	*Paradictyoarthriniaceae*	New family	Thailand	N/C
78	*Paradictyoarthrinium tectonicola*	New species		
79	*Allophaeosphaeria*	New genus	Italy	*Septoriella neodactylidis* (Marin-Felix et al. 2019)
80	*Allophaeosphaeria dactylidis*	New species		
81	*Allophaeosphaeria muriformia*	New species	Italy	*Allophaeosphaeria muriformis* (Marin-Felix et al. 2019)
82	*Neosetophoma clematidis*	New species	Italy	N/C
83	*Neosetophoma italica*	New species	Italy	N/C
84	*Phaeosphaeria musae*	New species	Thailand	Nom. inval., Art. 39.1 (Melbourne)
85	*Wojnowicia dactylidicola*	New species	Italy	*Galiicola dactylidicola* (Thambugala et al. 2017)
86	*Wojnowicia dactylidis*	New species	Italy	*Wojnowiciella dactylidis* (Hernandez-Restrepo et al. 2016)
87	*Wojnowicia lonicerae*	New species	Italy	*Wojnowiciella lonicerae* (Hernandez-Restrepo et al. 2016)
88	*Splanchnonema pupula*	Reference specimen	Italy	N/C
89	*Alternaria cesenica*	New species	Italy	N/C
90	*Camarosporium aborescentis*	New species	Russia	*Camarosporium arborescentis* (Wanasinghe et al. 2017)
91	*Camarosporium aureum*	New species	Russia	N/C
92	*Camarosporium caraganicola*	New species	Russia	*Camarosporidiella caraganicola* (Wanasinghe et al. 2017)
93	*Multiseptospora*	New genus	Thailand	Placed in Parabambusicolaceae by Wijayawardene et al. (2022)
94	*Multiseptospora thailandica*	New species		
95	*Saccotheciaceae*	New family		N/C
96	*Tothia spartii*	New species	Italy	N/C
97	*Chaetothyrium agathis*	New species	Philippines	*Chaetothyrium agathidis* Hongsanan & K.D. Hyde [as 'agathis']
98	*Trichomerium siamensis*	New species	Thailand	*Trichomerium siamense* Hongsanan & K.D. Hyde [as 'siamensis']
99	*Paralecia*	New genus	Italy	Placed in Cladoniaceae by Wijayawardene et al. (2022)
100	*Paralecia pratorum*	New species		
101	*Lauriomyces synnematicus*	New species	Thailand	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
102	*Agaricus flavicentrus*	New species	Thailand	N/C
103	*Agaricus hanthanaensis*	New species	Sri Lanka	N/C
104	*Agaricus parvibicolor*	New species	Thailand	N/C
105	*Agaricus sodalis*	New species	Thailand	N/C
106	*Cantharellus luteostipitatus*	New species	Madagascar	N/C
107	*Lactarius atrobrunneus*	New species	Thailand	N/C
108	*Lactarius politus*	New species	Thailand	N/C
109	*Phylloporia dependens*	New species	China	N/C
110	*Russula cortinarioides*	New species	US	N/C
Fungal diversity notes 111–252 (Ariyawansa et al. 2015)				
111	*Pseudomassariosphaeria*	New genus	Italy	Lophiostomataceae (Magaña-Dueñas et al. 2020)
112	*Pseudomassariosphaeria bromicola*	New species		
113	*Pseudomassariosphaeria grandispora*	New combination	Italy	*Massariosphaeria grandispora* (Magaña-Dueñas et al. 2020)
114	*Flammeascoma lignicola*	New species	Thailand	N/C
115	*Ascocylindricaceae*	New family	Saudi arabia	N/C
116	*Ascocylindrica*	New genus		
117	*Ascocylindrica marina*	New species		
118	*Lembosia xyliae*	New species	Thailand	N/C
119	*Diplodia crataegicola*	New species	Italy	N/C
120	*Diplodia galiicola*	New species	Italy	N/C
121	*Caryosporaceae*	New family	Thailand	N/C
122	*Caryospora aquatica*	New species		
123	*Cucurbitaria ephedricola*	Reference specimen	Italy	N/C
124	*Heracleicola*	New genus	Italy	*Ascochyta* (Chen et al. 2017a, b)
125	*Heracleicola premilcurensis*	New species		*Ascochyta premilcurensis* (Chen et al. 2017a, b)
126	*Neodidymella*	New genus	Thailand	N/C
127	*Neodidymella thailandicum*	New species		Neodidymella thailandica Phook., R.H. Perera & K.D. Hyde [as 'thailandicum']
128	*Austropleospora osteospermi*	Type species description	Australia	N/C
129	*Austropleospora archidendri*	New combination		N/C
130	*Pseudopithomyces*	New genus		Reference specimens or changes in classification
131	*Pseudopithomyces chartarum*	New combination		N/C
132	*Pseudopithomyces palmicola*	New species	Thailand	N/C
133	*Pseudopithomyces maydicus*	New combination	Thailand	N/C
134	*Pseudopithomyces sacchari*	New combination		N/C
135	*Floricola viticola*	New species	Italy	*Teichospora viticola* (Jaklitsch et al. 2016)
136	*Brunneoclavispora*	New genus	Thailand	N/C
137	*Brunneoclavispora bambusae*	New species		
138	*Neolophiostoma*	New genus	Thailand	N/C
139	*Neolophiostoma pigmentatum*	New species		
140	*Sulcosporium*	New genus	Thailand	N/C
141	*Sulcosporium thailandica*	New species		*Sulcosporium thailandicum* Phook. & K.D. Hyde [as 'thailandica']
142	*Pseudoasteromassaria*	New genus	Japan	N/C
143	*Pseudoasteromassaria fagi*	New species		N/C
144	*Keissleriella dactylidicola*	New species	Italy	N/C
145	*Neomassariosphaeria*	Changes in classification		Amniculicolaceae (Jones et al. 2015)
146	*Lophiostoma caulium*	Reference specimen	Italy	*Sigarispora caulium* (Thambugala et al. 2015)
147	*Lophiohelichrysum*	New genus	Italy	N/C
148	*Lophiohelichrysum helichrysi*	New species		
149	*Aquasubmersa japonica*	New species	Japan	N/C
150	*Pseudomonodictys*	New genus	Thailand	Parabambusicolaceae (Wijayawardene et al. 2022)
151	*Pseudomonodictys tectonae*	New species		
152	*Byssosphaeria rhodomphala*	Reference specimen	Thailand	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
153	*Microthyrium buxicola*	New species	Italy	N/C
154	*Tumidispora*	New genus	Thailand	N/C
155	*Tumidispora shoreae*	New species		
156	*Alloleptosphaeria clematidis*	New species	Italy	N/C
157	*Allophaeosphaeria cytisi*	New species	Italy	*Arezzomyces cytisi* (Marin-Felix et al. 2019)
158	*Allophaeosphaeria subcylindrospora*	New species	Italy	*Septoriella subcylindrospora* (Marin-Felix et al. 2019)
159	*Dematiopleospora luzulae*	New species	Italy	N/C
160	*Entodesmium artemisiae*	New species	Russia	*Ophiobolus artemisiae* (Phookamsak et al. 2017)
161	*Galiicola*	New genus	Italy	N/C
162	*Galiicola pseudophaeosphaeria*	New species		
163	*Loratospora luzulae*	New species	Italy	N/C
164	*Nodulosphaeria senecionis*	New species	Italy	N/C
165	*Ophiosphaerella aquaticus*	New species	Thailand	*Ophiosphaerella aquatica* Z.L. Luo, Hong Y. Su & K.D. Hyde [as 'aquaticus']
166	*Populocrescentia*	New genus	Italy	N/C
167	*Populocrescentia forlicesenensis*	New species		
168	*Vagicola*	New genus		N/C
169	*Vagicola vagans*	New combination		*Septoriella vagans* (Marin-Felix et al. 2019)
170	*Alternaria ethzedia*	Illustration of the sexual morph	Italy	N/C
171	*Elongatopedicellata*	New genus	Thailand	N/C
172	*Elongatopedicellata lignicola*	New species		
173	*Roussoella magnatum*	New species	Thailand	*Roussoella magnata* D.Q. Dai & K.D. Hyde [as 'magnatum']
174	*Roussoella angustior*	New species	Thailand	*Roussoella angusta* D.Q. Dai & K.D. Hyde [as 'angustior']
175	*Shrungabeeja longiappendiculata*	New species	Thailand	N/C
176	*Massariosphaeria*	Family placement		Cyclothyriellaceae (Wijayawardene et al. 2022)
177	*Wicklowiaceae*	New family		N/C
178	*Mycocalicium hyaloparvicellulum*	New species	Italy	N/C
179	*Acarospora septentrionalis*	New species	Iceland	N/C
180	*Acarospora castaneocarpa*	New species	Finland	N/C
181	*Chapsa multicarpa*	New species	Thailand	N/C
182	*Fissurina carassensis*	New species	Brazil	N/C
183	*Sticta fuscotomentosa*	New species	Colombia	N/C
184	*Sticta subfilicinella*	New species	Colombia	N/C
185	*Helvella pseudolacunosa*	New species	China	N/C
186	*Helvella rugosa*	New species	China	N/C
187	*Dictyosporella*	New genus	Egypt	N/C
188	*Dictyosporella aquatica*	New species		
189	*Chaetosphaeria rivularia*	New species	France	*Chaetosphaeria rivularis* Réblová & J. Fourn. [as 'rivularia']
190	*Beauveria gryllotalpidicola*	New species	Thailand	N/C
191	*Beauveria loeiensis*	New species	Thailand	N/C
192	*Seimatosporium sorbi*	New species	Italy	*Sporocadus sorbi* (Liu et al. 2018)
193	*Seimatosporium pseudorosarum*	New species	Italy	N/C
194	*Colletotrichum aciculare*	New species	Thailand	*Colletotrichum truncatum* (Jayawardena et al. 2016)
195	*Colletotrichum fusiforme*	New species	Thailand	N/C
196	*Colletotrichum hymenocallidicola*	New species	Thailand	*Colletotrichum orchidearum* Damm et al. (2019)
197	*Tinhaudeus*	New genus	Taiwan	N/C
198	*Tinhaudeus formosanus*	New species		N/C
199	*Pestalotiopsis subshorea*	New species	China	N/C
200	*Pestalotiopsis dracaenea*	New species	China	*Pestalotiopsis dracaenae* Yong Wang bis, Yu Song, K. Geng & K.D. Hyde [as 'dracaenea']
201	*Pestalotiopsis montellica*	Changes in classification	China	N/C
202	*Phaeoacremonium tectonae*	New species	Thailand	N/C
203	*Cytospora parasitica*	New species	Russia	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
204	*Cytospora tanaitica*	New species	Russia	N/C
205	*Annulohypoxylon palmicola*	New species	Thailand	N/C
206	*Biscogniauxia effusa*	New species	China	N/C
207	*Nemania fusoidispora*	New species	China	N/C
208	*Agaricus pseudolangei*	New species	Thailand	N/C
209	*Agaricus haematinus*	New species	Thailand	N/C
210	*Agaricus atrodiscus*	New species	Thailand	N/C
211	*Agaricus exilissimus*	New species	Thailand	N/C
212	*Amanita melleialba*	New species	China	N/C
213	*Amanita pseudosychnopyramis*	New species	China	N/C
214	*Amanita subparvipantherina*	New species	China	N/C
215	*Entoloma calabrum*	New species	Italy	N/C
216	*Cora barbulata*	New species	Costa rica	N/C
217	*Dictyonema gomezianum*	New species	Costa rica	N/C
218	*Inocybe granulosa*	New species	Sweden	*Mallocybe granulosa* (Matheny and Kudzma 2019)
219	*Xerocomellus sarnarii*	New species	Italy	N/C
220	*Cantharellus eucalyptorum*	New species	Madagascar	N/C
221	*Cantharellus nigrescens*	New species	Madagascar	N/C
222	*Cantharellus tricolor*	New species	Madagascar	N/C
223	*Cantharellus variabilicolor*	New species	Madagascar	N/C
224	*Cortinarius alboamarescens*	New species	Denmark	N/C
225	*Cortinarius brunneoalbus*	New species	USA	N/C
226	*Cortinarius ochroamarus*	New species	Finland	N/C
227	*Cortinarius putorius*	New species	USA	N/C
228	*Cortinarius seidlii*	New species	USA	*Cortinarius seidliae* Ammirati, Niskanen & Liimat. [as 'seidlii']
229	*Dendrominiaceae*	New family		N/C
230	*Punctulariopsis cremeoalbida*	New combination		N/C
231	*Punctulariopsis efibulata*	New combination	US	N/C
232	*Hymenochaete micropora*	New species	China	N/C
233	*Hymenochaete subporioides*	New species	China	N/C
234	*Neoantrodiellaceae*	New family		N/C
235	*Neoantrodiella*	New genus		N/C
236	*Neoantrodiella gypsea*	New combination		N/C
237	*Neoantrodiella thujae*	New combination		N/C
238	*Xylodon ramicida*	New species	Finland	N/C
239	*Colospora*	New genus	Indonesia	N/C
240	*Colospora andalasii*	New species		
241	*Russula guangxiensis*	New species	China	N/C
242	*Russula hakkae*	New species	China	N/C
243	*Tremella dirinariae*	New species	US	N/C
244	*Tremella graphidis*	New species	US	N/C
245	*Tremella pyrenulae*	New species	US	N/C
246	*Absidia caatinguensis*	New species	Brazil	N/C
247	*Absidia koreana*	New species	Korea	N/C
248	*Gongronella koreana*	New species	Korea	N/C
249	*Mortierella pisiformis*	New species	Taiwan	N/C
250	*Mortierella formosana*	New species	Taiwan	N/C
251	*Neocallimastix cameroonii*	New species	UK	N/C
252	*Piromyces irregularis*	New species	Czech Republic	N/C
Fungal diversity notes 253–366 (Li et al. 2016)				
253	*Dothiorella rhamni*	New species	Russia	N/C
254	*Dothiorella vidmadera*	Reference specimen	Italy	*Dothiorella sarmentorum* (Zhang et al. 2021)
255	*Eutiarosporella dactylidis*	New combination	Italy	N/C
256	*Mucoharknessia anthoxanthi*	New species	Italy	N/C
257	*Neophaeocryptopus*	New genus		*Dothiora* (Crous et al. 2018)

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
258	*Neophaeocryptopus cytisi*	New species	Italy	*Dothiora cytisi* (Crous et al. 2018)
259	*Saccothecium rubi*	New species	Italy	N/C
260	*Psiloglonium macrosporum*	New species	Thailand	N/C
261	*Pseudocamarosporium pini*	New combination	Italy	N/C
262	*Towyspora*	New genus	UK	N/C
263	*Towyspora aestuari*	New species		
264	*Lindgomyces okinawaensis*	New species	Japan	N/C
265	*Lophiostoma pseudoarmatisporum*	New species	Japan	N/C
266	*Sigarispora ononidis*	New species	Italy	N/C
267	*Aposphaeria corallinolutea*	New record	Thailand	N/C
268	*Multilocularia*	New genus	Thailand	N/C
269	*Multilocularia bambusae*	New species		
270	*Multiseptospora thysanolaenae*	New species	Thailand	N/C
271	*Parastagonospora cumpignensis*	New species	Italy	*Parastagonospora campignensis* Tibpromma, Camporesi & K.D. Hyde [as 'cumpignensis']
272	*Comoclathris pimpinellae*	New species	Russia	N/C
273	*Angustospora*	New genus	Egypt	N/C
274	*Angustospora nilensis*	New species		
275	*Polyplosphaeria thailandica*	New species	Thailand	N/C
276	*Longiostiolum*	New genus	Thailand	Longiostiolaceae (Wijayawardene et al. 2022)
277	*Longiostiolum tectonae*	New species		
278	*Pseudodidymosphaeria phlei*	New species	Italy	N/C
279	*Clematidis*	New genus	Italy	Pseudolophiotremataceae (Wijayawardene et al. 2022)
280	*Clematidis italica*	New species		N/C
281	*Crassiparies*	New genus	Japan	Neohendersoniaceae (Wijayawardene et al. 2022)
282	*Crassiparies quadrisporus*	New species		
283	*Farasanispora*	New genus	Saudi arabia	N/C
284	*Farasanispora avicenniae*	New species		
285	*Parameliola*	New genus	Thailand	N/C
286	*Parameliola dimocarpi*	New species		
287	*Parameliola acaciae*	New species	Thailand	N/C
288	*Kirschsteiniothelia tectonae*	New species	Thailand	N/C
289	*Ocellularia arachchigei*	New species	Sri Lanka	N/C
290	*Ocellularia ratnapurensis*	New species	Sri Lanka	N/C
291	*Rhabdodiscus albodenticulatus*	New species	Sri Lanka	N/C
292	*Pseudolachnella brevifusiformis*	New species	Japan	N/C
293	*Phragmoporthe conformis*	reference species	Italy	N/C
294	*Cytospora salicicola*	New species	Russia	N/C
295	*Colletotrichum menispermi*	New species	Russia	N/C
296	*Colletotrichum quinquefoliae*	New species	Russia	N/C
297	*Ochronectria thailandica*	New species	Thailand	N/C
298	*Moelleriella phukhiaoensis*	New species	Thailand	N/C
299	*Moelleriella pongdueatensis*	New species	Thailand	N/C
300	*Ophiocordyceps formosana*	New record	China	Nom. inval., Arts 41.5, F.5.1 (Shenzhen)
301	*Ophiocordyceps karstii*	New species	China	N/C
302	*Aniptodera aquibella*	New species	Thailand	N/C
303	*Humicola koreana*	New species	Korea	N/C
304	*Seimatosporium pseudocornii*	New species	Italy	*Seimatosporium pseudocorni* Wijayaw., Camporesi & K.D. Hyde [as 'pseudocornii']
305	*Seimatosporium pseudorosae*	New species	Italy	N/C
306	*Cryptovalsa ampelina*	reference specimen	Italy	N/C
307	*Diatrype thailandica*	New species	Thailand	*Allodiatrype thailandica* (Konta et al. 2020)
308	*Annulohypoxylon albidiscum*	New species	Thailand	N/C
309	*Astrocystis thailandica*	New species	Thailand	N/C
310	*Camporesia*	New genus		N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
311	*Camporesia sambuci*	New species	Italy	N/C
312	*Durotheca macrostroma*	New species	Thailand	N/C
313	*Halorosellinia rhizophorae*	New species	Thailand	N/C
314	*Hypoxylon lilloi*	New species	Argentina	N/C
315	*Rosellinia chiangmaiensis*	New species	Thailand	N/C
316	*Petrakia echinata*	Reference specimen	Italy	N/C
317	*Agaricus coccyginus*	New species	China	N/C
318	*Agaricus luteofibrillosus*	New species	China	N/C
319	*Clarkeinda trachodes*	Reference specimen	Sri Lanka	N/C
320	*Amanita atrobrunnea*	New species	Thailand	N/C
321	*Amanita digitosa*	New species	Thailand	N/C
322	*Amanita gleocystidiosa*	New species	Thailand	N/C
323	*Amanita pyriformis*	New species	Thailand	N/C
324	*Amanita strobilipes*	New species	Thailand	N/C
325	*Cortinarius albosericeus*	New species	Canada	N/C
326	*Cortinarius badioflavidus*	New species	US	N/C
327	*Cortinarius denigratus*	New species	Canada	N/C
328	*Cortinarius duboisensis*	New species	US	N/C
329	*Cortinarius fragrantissimus*	New species	Canada	N/C
330	*Cortinarius roseobasilis*	New species	US	N/C
331	*Cortinarius vinaceobrunneus*	New species	Canada	N/C
332	*Cortinarius vinaceogrisescens*	New species	US	N/C
333	*Cortinarius wahkiacus*	New species	US	N/C
334	*Musumecia alpina*	New species	China	N/C
335	*Musumecia sardoa*	New species	Italy	N/C
336	*Cyanoboletus hymenoglutinosus*	New species	India	Nom. inval., Art. 40.7 (Shenzhen)
337	*Leccinellum indoaurantiacum*	New species	India	Nom. inval., Art. 40.7 (Shenzhen)
338	*Galzinia longibasidia*	New sequence data	Iran	N/C
339	*Leptocorticium tenellum*	New sequence data	Chile	N/C
340	*Fomitiporia atlantica*	New species	Brazil	N/C
341	*Fomitiporia subtilissima*	New species	Brazil	N/C
342	*Inonotus shoreicola*	New species	Thailand	N/C
343	*Ganoderma wuzhishanensis*	New species	China	*Ganoderma wuzhishanense* T.C. Wen, Hapuar. & K.D. Hyde [as 'wuzhishanensis']
344	*Dentocorticium ussuricum*	New sequence data	Russia	N/C
345	*Lentinus stuppeus*	Reference specimen	Thailand	N/C
346	*Bondarzewia tibetica*	New species	China	N/C
347	*Lactifluus armeniacus*	New species	Thailand	N/C
348	*Lactifluus ramipilosus*	New species	Thailand	N/C
349	*Russula amethystina*	New species	China	N/C
350	*Russula wangii*	New species	China	N/C
351	*Anaeromyces robustus*	New species		N/C
352	*Neocallimastix californiae*	New species		N/C
353	*Piromyces finnis*	New species		N/C
354	*Phytophthora estuarina*	New species	Brazil	N/C
355	*Phytophthora rhizophorae*	New species	Brazil	N/C
356	*Salispina*	New genus	Brazil	Salispinaceae (Wijayawardene et al. 2022)
357	*Salispina intermedia*	New species		
358	*Salispina lobata*	New combination		
359	*Salispina spinosa*	New combination		
360	*Mortierella calciphila*	New species	Poland	N/C
361	*Absidia stercoraria*	New species	Korea	N/C
362	*Gongronella orasabula*	New species	Korea	N/C
363	*Mucor caatinguensis*	New species	Brazil	N/C
364	*Mucor koreanus*	New species	Korea	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
365	*Mucor merdicola*	New species	Brazil	N/C
366	*Rhizopus koreanus*	New species	Korea	N/C
Fungal diversity notes 367–490 (Hyde et al. 2016)				
367	*Asterina cynometrae*	New species	Philippines	N/C
368	*Dothiorella iranica*	New host	Italy	N/C
369	*Dothiorella sarmentorum*	New host	Russia	N/C
370	*Dothiorella vidmadera*	New host	Russia	*Dothiorella sarmentorum* (Zhang et al. 2021)
371	*Pallidocercospora thailandica*	New combination	Thailand	N/C
372	*Dothiora buxi*	New species	Italy	N/C
373	*Gloniopsis calami*	New species	Thailand	N/C
374	*Pseudocoleophoma typhicola*	New species	UK	N/C
375	*Pseudodictyosporium thailandica*	New species	Thailand	N/C
376	*Neomicrosphaeropsis cytisi*	New species	Italy	N/C
377	*Neomicrosphaeropsis cytisinus*	New species	Italy	*Neomicrosphaeropsis cytisina* Tennakoon, Camporesi & K.D. Hyde [as 'cytisinus']
378	*Neomicrosphaeropsis minima*	New species	Italy	N/C
379	*Neodidymelliopsis ranunculi*	New species	Italy	N/C
380	*Platychora ulmi*		Italy	N/C
381	*Stagonosporopsis centaureae*	New species	Italy	N/C
382	*Montagnula cirsii*	New species	Italy	N/C
383	*Tremateia arundicola*	New species	Italy	*Tremateia arunicola* Wanas., E.B.G. Jones & K.D. Hyde [as 'arundicola']
384	*Tremateia guiyangensis*	New species	UK	N/C
385	*Lentithecium unicellulare*	New species	China	N/C
386	*Lentithecium voraginesporum*	New species	Egypt	N/C
387	*Leptosphaeria cirsii*	New species	Saudi arabia	N/C
388	*Leptosphaeria irregularis*	New species	Italy	N/C
389	*Lindgomycetaceae*	New family		N/C
390	*Arundellina typhae*	New species	UK	N/C
391	*Lindgomyces pseudomadisonensis*	New species	UK	N/C
392	*Vaginatispora fuckelii*	New record	Japan	*Neovaginatispora fuckelii* (Hashimoto et al. 2018)
393	*Hermatomyces mirum*	New combination	China	*Hermatomyces mirus* (Starbäck) C.G. Lin, Bhat & K.D. Hyde [as 'mirum']
394	*Hermatomyces subiculosa*	New species	Thailand	N/C
395	*Lophiotrema bambusae*	New species	Thailand	*Atrocalyx bambusae* (De Silva et al. 2018)
396	*Lophiotrema fallopiae*	New species	Japan	N/C
397	*Neomassaria*	New genus	Italy	N/C
398	*Neomassaria fabacearum*	New species		
399	*Stagonospora forlicesenensis*	New species	Italy	N/C
400	*Bertiella ellipsoidea*	New species	Thailand	N/C
401	*Occultibambusa aquatica*	New species	Thailand	N/C
402	*Occultibambusa chiangraiensis*	New species	Thailand	N/C
403	*Camarosporioides*	New genus	Germany	N/C
404	*Camarosporioides phragmitis*	New species		
405	*Chaetosphaeronema achilleae*	New species	Russia	N/C
406	*Dematiopleospora alliariae*	New species	Italy	*Hawksworthiana alliariae* (Wanasinghe et al. 2018)
407	*Dematiopleospora cirsii*	New species	Italy	N/C
408	*Juncaceicola italica*	New species	Italy	N/C
409	*Leptospora rubella*	Reference specimen	UK	N/C
410	*Leptospora galii*	New species	Italy	N/C
411	*Leptospora thailandica*	New species	Thailand	N/C
412	*Muriphaeosphaeria ambrosiae*	New species	Russia	N/C
413	*Nodulosphaeria italica*	New species	Italy	N/C
414	*Poaceicola arundinis*	New species	Italy	*Septoriella arundinis* (Marin-Felix et al. 2019)
415	*Pseudophaeosphaeria*	New genus	Italy	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
416	*Pseudophaeosphaeria rubi*	New species		
417	*Wojnowicia italica*	New species	Italy	N/C
418	*Comoclathris italica*	New species	Italy	N/C
419	*Neoroussoella lenispora*	New species	China	N/C
420	*Neotorula submersa*	New species	China	N/C
421	*Aquaphila albicans*	Reference specimen	Thailand	N/C
422	*Chlamydotubeufia helicospora*	New species	Thailand	*Dematiohelicomyces helicosporus* (Lu et al. 2018)
423	*Helicoma guttulatum*	New species	Thailand	N/C
424	*Neoacanthostigma septoconstrictum*	Reference specimen	Thailand	N/C
425	*Tubeufia hyalospora*	New species	Thailand	N/C
426	*Tubeufia roseohelicospora*	New species	Thailand	N/C
427	*Pleurotrema thailandica*	New species	Thailand	N/C
428	*Alloarthopyrenia*	New genus	Italy	N/C
429	*Alloarthopyrenia italica*	New species		
430	*Neomassarina*	New genus	Thailand	Neomassarinaceae (Wijayawardene et al. 2022)
431	*Neomassarina thailandica*	New species		
432	*Aspergillus koreanus*	New species	Korea	N/C
433	*Ceramothyrium menglunense*	New species	China	N/C
434	*Minimelanolocus submersus*	New species	China	N/C
435	*Trichomerium bambusae*	New species	Thailand	N/C
436	*Terriera thailandica*	New species	Thailand	N/C
437	*Helvella tinta*	New species	China	N/C
438	*Helvella floriforma*	New species	China	N/C
439	*Helvella oblongispora*	New distribution record	China	N/C
440	*Peziza fruticosa*	New species	Italy	N/C
441	*Coronophora myricoides*	New species	China	N/C
442	*Diaporthe aseana*	New species	Thailand	N/C
443	*Diaporthe eres*	New host	Italy	N/C
444	*Diaporthe foeniculina*	New record	Italy	N/C
445	*Diaporthe garethjonesii*	New species	Thailand	N/C
446	*Diaporthe siamensis*	New host	Thailand	N/C
447	*Cytospora cotini*	New species	Russia	N/C
448	*Colletotrichum insertae*	New species	Russia	N/C
449	*Blastophorum aquaticum*	New species	China	*Cylindrotrichum aquaticum* (Luo et al. 2019)
450	*Ophiocordyceps hemisphaerica*	New species	Brazil	N/C
451	*Ophiocordyceps lacrimoidis*	New species	Brazil	N/C
452	*Purpureocillium sodanum*	New species	Iran	N/C
453	*Alfaria spartii*	New species	Italy	N/C
454	*Emericellopsis persica*	New species	Iran	N/C
455	*Meliola citri-maximae*	New species	Thailand	N/C
456	*Meliola pseudosasae*	Reference specimens	China	N/C
457	*Arthrinium paraphaeospermum*	New species	Thailand	N/C
458	*Bartaliniaceae*	New family		Published with the identifier 'Index Fungorum number: IF511183', but this identifier was not issued for the name published Index Fungorum (2022a, b)
459	*Neotruncatella endophytica*	New species	Korea	*Hymenopleella endophytica* (Liu et al. 2019a, b, c, d)
460	*Cainia globosa*	New species	Italy	N/C
461	*Ciliochorella phanericola*	New species	Thailand	N/C
462	*Neopestalotiopsis cocoës*	New species	Thailand	N/C
463	*Neopestalotiopsis musae*	New species	Thailand	
464	*Pestalotiopsis sequoiae*	New species	Italy	N/C
465	*Anthostomella ravennica*	New species	Italy	N/C
466	*Anthostomella thailandica*	New species	Thailand	N/C
467	*Sporidesmium pyriformatum*	New species	Thailand	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
468	*Sporidesmium aquaticivaginatum*	New species	Thailand	N/C
469	*Sporidesmium olivaceoconidium*	New species	Thailand	N/C
470	*Distoseptispora multiseptata*	New species	Thailand	N/C
471	*Distoseptispora tectonae*	New species	Thailand	N/C
472	*Distoseptispora tectonigena*	New species	Thailand	N/C
473	*Paracapsulospora*	New genus	Thailand	N/C
474	*Paracapsulospora metroxyli*	New species		
475	*Clavulinopsis aurantiaca*	New species	Brazil	N/C
476	*Ramariopsis atlantica*	New species	Brazil	N/C
477	*Cortinarius fulvescens*	neo-type	Canada	N/C
478	*Cortinarius fulvescentoideus*	New species	Finland	N/C
479	*Cortinarius nymphatus*	New species	Canada	N/C
480	*Cortinarius pseudobulliardioides*	New species	Finland	N/C
481	*Cortinarius tenuifulvescens*	New species	Canada	N/C
482	*Rhodocybe indica*	New species	India	N/C
483	*Rhodocybe luteobrunnea*	New species	India	N/C
484	*Rhodocybe griseoaurantia*	New species	India	N/C
485	*Cyathus pyristriatus*	New species	Thailand	N/C
486	*Polyporus mangshanensis*	New species	India	N/C
487	*Russula indoalba*	New species	India	N/C
488	*Russula pseudoamoenicolor*	New species	India	N/C
489	*Lactarius dirkii*	New species	Korea	N/C
490	*Cunninghamella gigacellularis*	New species	Brazil	N/C
Fungal diversity notes 491–602 (Tibpromma et al.** 2017**)				
491	*Morenoina calamicola*	New species	Thailand	N/C
492	*Barriopsis thailandica*	New species	Thailand	N/C
493	*Polythrincium trifolii*	reference specimens	China	N/C
494	*Dothiora buxi*	asexual morph report	Russia	N/C
495	*Hysterium centramurum*	New species	Thailand	*Ericboehmia centramura* Gardiennet et al. (2019)
496	*Hysterobrevium mori*	New host	Italy	N/C
497	*Angustimassarina alni*	New species	Germany	N/C
498	*Angustimassarina arezzoensis*	New species	Italy	N/C
499	*Angustimassarina premilcurensis*	New species	Italy	N/C
500	*Angustimassarina italica*	New species	Italy	N/C
501	*Angustimassarina lonicerae*	New species	Italy	N/C
502	*Biatriosporaceae*	New family		N/C
503	*Berkleasmium ariense*	New species	India	N/C
504	*Platystomum rosae*	New host	Italy	N/C
505	*Sigarispora muriformis*	New species	Italy	N/C
506	*Vaginatispora appendiculata*	New host	Thailand	N/C
507	*Lophiotrema guttulata*	New species	Thailand	*Atrocalyx guttulata* (De Silva et al. 2018)
508	*Lophiotrema vagabundum*	New host	Italy	N/C
509	*Hermatomyces chiangmaiensis*	New species	Thailand	N/C
510	*Hermatomyces chromolaenae*	New species	Thailand	N/C
511	*Melanommataceae*	New combination/family		N/C
512	*Aposphaeria corallinolutea*	Asexual morph report	Russia	N/C
513	*Nigrograna cangshanensis*	New species	China	N/C
514	*Roussoellaceae*	New family		N/C
515	*Parathyridaria robiniae*	New species	Italy	N/C
516	*Paraphaeosphaeria viciae*	New species	Italy	N/C
517	*Pseudoasteromassaria spadicea*	New species	Thailand	N/C
518	*Keissleriella cirsii*	New species	Russia	N/C
519	*Pleurophoma italica*	New species	Italy	N/C
520	*Pseudodidymosphaeria phlei*	New host	Italy	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
521	*Inflatispora caryotae*	New species	Thailand	N/C
522	*Ascochyta italica*	New species	Italy	N/C
523	*Ascochyta medicaginicola*	New host	Italy	N/C
524	*Ascochyta rosae*	New species	Italy	N/C
525	*Calophoma petasitis*	New species	Italy	N/C
526	*Didysimulans*	New genus	Italy	N/C
527	*Didysimulans italica*	New species		
528	*Didysimulans mezzanensis*	New species	Italy	N/C
529	*Nothophoma quercina*	New host	Italy	N/C
530	*Stagonosporopsis ailanthicola*	New species	Italy	N/C
531	*Paraleptosphaeria padi*	New species	Russia	N/C
532	*Subplenodomus galicola*	New species	Italy	N/C
533	*Entodesmium italica*	New species	Italy	*Ophiobolus italicus* (Phookamsak et al. 2017)
534	*Neosetophoma garethjonesii*	New species	UK	N/C
535	*Nodulosphaeria guttulatum*	New species	Italy	N/C
536	*Nodulosphaeria multiseptata*	New species	Italy	N/C
537	*Nodulosphaeria sambuci*	New species	Italy	N/C
538	*Phaeosphaeria calamicola*	New species	Thailand	N/C
539	*Phaeosphaeriopsis yuccae*	New species	Russia	N/C
540	*Camarosporium laburnicola*	New species	Russia	*Camarosporidiella laburnicola* (Wanasinghe et al. 2017)
541	*Camarosporium moricola*	New species	Russia	*Camarosporidiella moricola* (Wanasinghe et al. 2017)
542	*Penicillium punicae*	New species	Korea	N/C
543	*Exophiala italica*	New species	Italy	N/C
544	*Gongronella brasiliensis*	New species	Brazil	N/C
545	*Mucor stercorarius*	New species	Korea	N/C
546	*Gnomoniopsis sanguisorbae*	reference specimen	Italy	N/C
547	*Sillia italica*	New species	Italy	N/C
548	*Cytospora gelida*	New species	Russia	N/C
549	*Cytospora ceratosperma*	New record	Russia	N/C
550	*Hypocrella calendulina*	Asexual morph reported	Thailand	N/C
551	*Moelleriella thanathonensis*	New species	Thailand	N/C
552	*Myrothecium septentrionale*	New species	Thailand	N/C
553	*Colletotrichum sambucicola*	New species	Italy	N/C
554	*Myrmecridium fluviae*	New species	Korea	N/C
555	*Truncatella spartii*	New host	Italy	*Heterotruncatella spartii* (Liu et al. 2019a, b, c, d)
556	*Rosellinia mearnsii*	New species	China	N/C
557	*Evlachovaea indica*	New species	India	N/C
558	*Helvella costifera*	reference specimen	China	N/C
559	*Helvella crispoides*	New species	Thailand	N/C
560	*Cookeina tricholoma*	Reference specimen	Sri Lanka	N/C Wijayawardene et al. (2022)
561	*Amanita cornelii*	New species	India	N/C
562	*Amanita emodotrygon*	New species	India	N/C
563	*Lepiota cylindrocystidia*	New species	Thailand	N/C
564	*Lepiota flavocarpa*	New species	Thailand	Nom. Inval., Art. F.5.1 (Shenzhen)
565	*Lepiota maerimensis*	New species	Thailand	N/C
566	*Leucocoprinus cretaceus*	New record	Sri Lanka	N/C
567	*Entoloma magnum*	New species	India	N/C
568	*Inocybe brunneosquamulosa*	New species	India	*Pseudosperma brunneosquamulosum* (Matheny and Kudzma 2019)
569	*Inocybe luteobrunnea*	New species	India	*Pseudosperma luteobrunneum* (Matheny and Kudzma 2019)
570	*Inocybe rubrobrunnea*	New species	India	N/C
571	*Marasmius luculentus*	New species	India	N/C
572	*Favolaschia auriscalpium*	New record	Sri Lanka	N/C
573	*Favolaschia manipularis*	New record	Sri Lanka	N/C
574	*Cyptotrama asprata*	New record	Thailand	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
575	*Austroboletus appendiculatus*	New species	India	N/C
576	*Boletellus emodensis*	New record	Sri Lanka	N/C
577	*Rubroboletus demonensis*	New species	Italy	N/C
578	*Rubroboletus eastwoodiae*	New combination		N/C
579	*Strobilomyces longistipitatus*	New species	India	N/C
580	*Clavulina grisea*	New species	Brazil	N/C
581	*Clavulina ossea*	New species	Brazil	N/C
582	*Clavulina paraincrustata*	New species	Brazil	N/C
583	*Fomitopsis flabellata*	New species	Brazil	N/C
584	*Fomitopsis roseoalba*	New species	Brazil	N/C
585	*Favolus gracilisporus*	New species	Korea	N/C
586	*Lentinus sajor-caju*	New record	Sri Lanka	N/C
587	*Lentinus squarrosulus*	New record	Sri Lanka	N/C
588	*Lentinus velutinus*	New record	Sri Lanka	N/C
589	*Panus subfasciatus*	New species	Thailand	N/C
590	*Polyporus brevibasidiosus*	New species	Korea	N/C
591	*Polyporus koreanus*	New species	Korea	N/C
592	*Polyporus orientivarius*	New species	Korea	N/C
593	*Polyporus parvovarius*	New species	Korea	N/C
594	*Polyporus subdictyopus*	New species	Korea	N/C
595	*Polyporus ulleungus*	New species	Korea	N/C
596	*Wolfiporia pseudococos*	New species	China	N/C
597	*Coprinopsis cerkezii*	New species	Croatia	N/C
598	*Russula yanheensis*	New species	China	N/C
599	*Russula virescens*	New record	Sri Lanka	N/C
600	*Dacrymyces chiangraiensis*	New species	Thailand	N/C
601	*Femsjonia monospora*	New species	China	N/C
602	*Tremella fuciformis*	New record	Sri Lanka	N/C
Fungal diversity notes 603–708 (Hyde et al. 2017)				
603	*Jahnula guttulaspora*	New species	China	N/C
604	*Murispora rubicunda*	Description of collection of type species of genus	Germany	N/C
605	*Angustimassarina coryli*	New species	Italy	N/C
606	*Sardiniella celtidis*	New species	Italy	N/C
607	*Leptoxyphium glochidion*	New host	Thailand	N/C
608	*Dictyocheirospora cheirospora*	New species	China	N/C
609	*Epicoccum cedri*	New species	Italy	N/C
610	*Epicoccum pruni*	New species	Russia	N/C
611	*Neodidymelliopsis moricola*	New species	Russia	N/C
612	*Pseudopithomyces kunmingnensis*	New species	China	*Pseudopithomyces kunmingensis* Karun. & K.D. Hyde [as 'kunmingnensis'],
613	*Dothiora coronillae*	New species	Italy	N/C
614	*Dothiora spartii*	New species	Italy	N/C
615	*Neophaeocryptopus spartii*	New species	Italy	N/C
616	*Dyfrolomyces phetchaburiensis*	New species	Thailand	N/C
617	*Fuscostagonosporaceae*	New family		N/C
618	*Fuscostagonospora cytisi*	New species	Italy	N/C
619	*Hermatomyces nabanheensis*	New species	China	N/C
620	*Hysterium rhizophorae*	New species	Thailand	N/C
621	*Rhytidhysteron*	New record		N/C
622	*Kirschsteiniothelia rostrata*	New species	Thailand	N/C
623	*Poaceascoma halophila*	New species	Thailand	N/C
624	*Setoseptoria scirpi*	New species	UK	N/C
625	*Alternariaster trigonosporus*	New species	Russia	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
626	*Hongkongmyces thailandica*	New species	Thailand	N/C
627	*Paucispora kunmingense*	New species	China	N/C
628	*Brooksia tropicalis*	Description of type species of genus	Papua New Guinea	N/C
629	*Microthyriaceae*	New family		N/C
630	*Dictyosporina*	New genus	China	N/C
631	*Dictyosporina ferruginea*	New species		
632	*Lophium zalerioides*	New species	Brazil	N/C
633	*Nigrograna thymi*	New species	Italy	N/C
634	*Periconia aquatica*	New species	Italy	N/C
635	*Periconia minutissima*	Reference specimen	China	N/C
636	*Periconia submersa*	New species	China	N/C
637	*Acericola*	New genus	Italy	N/C
638	*Acericola italica*	New species		
639	*Amarenomyces dactylidis*	New species	Italy	N/C
640	*Ophiosimulans plantaginis*	New species	Italy	*Paraophiobolus plantaginis* (Qing Tian, Camporesi & K.D. Hyde) Phookamsak Wanas. & K.D. Hyde
641	*Phaeosphaeria acaciae*	New species	China	N/C
642	*Phaeopoacea muriformis*	New species	China	N/C
643	*Chaetothyrina artocarpi*	New species	Thailand	N/C
644	*Curvularia palmicola*	New species	Thailand	N/C
645	*Exserohilum turcicum*	Description of type species of genus	Italy	N/C
646	*Stemphylium vesicarium*	New host	Italy	N/C
647	*Carinispora nypae*	New record	Brunei	N/C
648	*Bryomyces scapaniae*	Description of type species of genus	Austria	N/C
649	*Immotthia hypoxylon*	Description of type species of genus	US	*Immotthia atrograna* (Cooke & Ellis) M.E. Barr Barr (1993)
650	*Magnibotryascoma mali*	New species	China	N/C
651	*Bryochiton monascus*	Description of type species of genus	Sweden	N/C
652	*Tetraploa yakushimensis*	New host	Thailand	N/C
653	*Torula gaodangensis*	New species	China	N/C
654	*Chlamydotubeufia huaikangplaensis*	New record	Thailand	N/C
655	*Chlamydotubeufia krabiensis*	New species	Thailand	N/C
656	*Licopolia franciscana*	Description of type species of genus	Brazil	N/C
657	*Buelliella minimula*	Description of type species of genus	US	N/C
658	*Cocciscia hammeri*	Description of type species of genus	Norway	N/C
659	*Ramgea ozimecii*	New species	Croatia	N/C
660	*Otidea pruinosa*	New species	China	N/C
661	*Otidea stipitata*	New species	China	N/C
662	*Cytospora mali-sylvestris*	New species	Russia	N/C
663	*Diaporthe rhusicola*	New combination	Italy	N/C
664	*Diaporthe subclavata*	New record	Thailand	N/C
665	*Diatrypella vulgaris*	New record	Thailand	Nom. inval., Art. 40.7 (Melbourne)
666	*Endoxylina astroidea*	Description of type species of genus	Sweden	*Eutypa astroidea* Rappaz. In: Mycol. helv. 2(3): 378. (1987)
667	*Colletotrichum fioriniae*	New host	Italy	N/C
668	*Colletotrichum lauri*	New species	Italy	N/C
669	*Meliola clerodendri-infortunati*	New species	Thailand	N/C
670	*Ophiocordyceps cossidarum*	New species	Thailand	N/C
671	*Ophiocordyceps issidarum*	New species	Thailand	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
672	*Longitudinalis*	New genus	China	N/C
673	*Longitudinalis nabanheensis*	New species		N/C
674	*Phaeoisaria microspora*	New species	Thailand	N/C
675	*Pleurothecium floriforme*	New species	Thailand	N/C
676	*Immersidiscosia eucalypti*	New host	Italy	N/C
677	*Seimatosporium italicum*	New species	Italy	N/C
678	*Grandibotrys hyalinus*	New species	Thailand	N/C
679	*Koorchalomella salmonispora*	New species	Egypt	Ascomycota Wijayawardene et al. (2022)
680	*Xepicula leucotricha*	New record	Thailand	Ascomycota Wijayawardene et al. (2022)
681	*Rizalia guianensis*	New combination	British guiana	N/C
682	*Astrocystis bambusicola*	New species	Thailand	N/C
683	*Collodiscula chiangraiensis*	New species	Thailand	N/C
684	*Fasciatispora calami*	New species	Thailand	N/C
685	*Vamsapriya breviconidiophora*	New species	Thailand	N/C
686	*Ascotrichella hawksworthii*	Description of the type species	Chile	N/C
687	*Castellaniomyces*	New genus	Italy	N/C
688	*Castellaniomyces rosae*	New species		
689	*Biciliopsis leptogiicola*	Description of the type species	Papua New Guinea	N/C
690	*Agaricus purpurlesquameus*	New species	Thailand	N/C
691	*Agaricus rufusfibrillosus*	New species	China	N/C
692	*Tephrocybella constrictospora*	New species	Italy	N/C
693	*Steccherinum amapaense*	New species	Brazil	N/C
694	*Tyromyces amazonicus*	New species	Brazil	N/C
695	*Tyromyces angulatus*	New species	Brazil	N/C
696	*Lactifluus holophyllus*	New species	Korea	N/C
697	*Lactifluus luteolamellatus*	New species	Korea	N/C
698	*Lactifluus pseudohygrophoroides*	New species	Korea	N/C
699	*Russula benwooii*	New species	US	N/C
700	*Russula hypofragilis*	New species	US	N/C
701	*Russula obscurozelleri*	New species	US	N/C
702	*Russula parapallens*	New species	US	N/C
703	*Russula phoenicea*	New species	Canada	N/C
704	*Russula pseudopelargonia*	New species	US	N/C
705	*Russula pseudotsugarum*	New species	US	N/C
706	*Russula rhodocephala*	New species	US	N/C
707	*Russula salishensis*	New species	US	N/C
708	*Mortierella formicae*	New species	Poland	N/C
Fungal diversity notes 709–839 (Wanasinghe et al. 2018)				
709	*Diplodia seriata*	New host	Italy	N/C
710	*Dothiorella iberica*	New host	Italy	N/C
711	*Lasiodiplodia theobromae*	New host	UK	N/C
712	*Neofusicoccum australe*	New host	Thailand	N/C
713	*Pseudocercospora rosae*	New species	Uzbekistan	N/C
714	*Endoconidioma rosae-hissaricae*	New species	Italy	N/C
715	*Angustimassarina quercicola*	New host	Italy	N/C
716	*Angustimassarina rosarum*	New species	Uzbekistan	N/C
717	*Astragalicola vasilyevae*	New species	Italy	N/C
718	*Epicoccum rosae*	New species	Italy	N/C
719	*Neoascochyta rosicola*	New species	Italy	N/C
720	*Paraconiothyrium rosae*	New species	Italy	N/C
721	*Paraphaeosphaeria michotii*	New host	Italy	N/C
722	*Paraphaeosphaeria rosae*	New species	Sweden	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
723	*Paraphaeosphaeria rosicola*	New species	Italy	N/C
724	*Pseudocamarosporium pteleae*	New species	Russia	N/C
725	*Pseudocamarosporium ulmi-minoris*	New species	Italy	N/C
726	*Pseudopithomyces rosae*	New species	Italy	N/C
727	*Keissleriella rosacearum*	New species	UK	N/C
728	*Keissleriella rosarum*	New species	Italy	*Keissleriella rosacearum*
729	*Keissleriella rosae*	New species	Italy	N/C
730	*Keissleriella phragmiticola*	New species	Italy	N/C
731	*Murilentithecium rosae*	New species	Italy	N/C
732	*Phragmocamarosporium rosae*	New species	UK	N/C
733	*Pleurophoma pleurospora*	New host	Uzbekistan	*Dinemasporium pleurospora* Species Fungorum (2022a, b)
734	*Setoseptoria arundelensis*	New species	UK	N/C
735	*Setoseptoria englandensis*	New species	UK	N/C
736	*Setoseptoria lulworthcovensis*	New species	UK	N/C
737	*Coelodictyosporium rosarum*	New species	UK	N/C
738	*Lophiostoma rosae*	New species	Uzbekistan	N/C
739	*Neopaucispora*	New genus	Uzbekistan	N/C
740	*Neopaucispora rosaecae*	New species		
741	*Sigarispora caryophyllacearum*	New species	Russia	N/C
742	*Sigarispora caulium*	New host	Italy	*Sigarispora caulium* (Fr.) Thambug., Wanas., Kaz. Tanaka & K.D. Hyde, Index Fungorum 267: 1 (2015)
743	*Sigarispora junci*	New species	Italy	N/C
744	*Sigarispora medicaginicola*	New species	Russia	N/C
745	*Sigarispora rosicola*	New species	Russia	N/C
746	*Sigarispora scrophulariae*	New species	Russia	N/C
747	*Sigarispora thymi*	New species	Russia	N/C
748	*Suttonomyces rosae*	New species	Italy	N/C
749	*Marjia*	New genus	Uzbekistan	N/C
750	*Marjia tianschanica*	New species		
751	*Marjia uzbekistanica*	New species	Uzbekistan	N/C
752	*Melanocucurbitaria*	New genus	Uzbekistan	N/C
753	*Melanocucurbitaria uzbekistanica*	New species		
754	*Melanodiplodia*	New genus	Uzbekistan	N/C
755	*Melanodiplodia tianschanica*	New species		
756	*Monoseptella*	New genus	Uzbekistan	N/C
757	*Monoseptella rosae*	New species		
758	*Muriformistrickeria rosae*	New species	Italy	N/C
759	*Muriformistrickeria rubi*	New host	Sweden	N/C
760	*Pseudostrickeria rosae*	New species	Italy	N/C
761	*Uzbekistanica*	New genus	Uzbekistan	N/C
762	*Uzbekistanica rosae-hissaricae*	New species		
763	*Uzbekistanica yakutkhanika*	New species	Uzbekistan	N/C
764	*Xenomassariosphaeria*	New genus	Italy	N/C
765	*Xenomassariosphaeria rosae*	New species		
766	*Bhatiellae*	New genus	Italy	N/C
767	*Bhatiellae rosae*	New species		
768	*Dactylidina*	New genus	Italy	N/C
769	*Dactylidina dactylidis*	New combination		*Septoriella neodactylidis* Marlin-Felix et al. (2019a)
770	*Dactylidina shoemakeri*	New species	Italy	N/C
771	*Dematiopleospora donetzica*	New species	Russia	N/C
772	*Dematiopleospora rosicola*	New species	Italy	N/C
773	*Dematiopleospora salsolae*	New species	Uzbekistan	N/C
774	*Embarria*	New genus	Italy	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
775	*Embarria clematidis*	New combination		
776	*Hawksworthiana*	New genus		Nom. illegit., Art. 53.1
777	*Hawksworthiana alliariae*	New combination	Russia	*Dlhawksworthia alliariae* *Dlhawksworthia alliariae* (Thambug., Camporesi & K.D. Hyde) Wanas. & K.D. Hyde, in Wanasinghe et al., Index Fungorum 357: 1 (2018)
778	*Hawksworthiana clematidicola*	New species	Italy	*Dlhawksworthia clematidicola* *Dlhawksworthia clematidicola* (Thambug., Camporesi & K.D. Hyde) Wanas. & K.D. Hyde, in Wanasinghe et al., Index Fungorum 357: 1 (2018)
779	*Hawksworthiana lonicerae*	New species	Italy	*Dlhawksworthia lonicerae* *Dlhawksworthia lonicerae* (Thambug., Camporesi & K.D. Hyde) Wanas. & K.D. Hyde, in Wanasinghe et al., Index Fungorum 357: 1 (2018)
780	*Italica*	New genus	Italy	N/C
781	*Italica achilleae*	New species		
782	*Italica luzulae*	New combination	Italy	N/C
783	*Neosetophoma rosarum*	New species	Italy	N/C
784	*Neosetophoma rosigena*	New species	UK	N/C
785	*Neosetophoma rosae*	New species	Italy	N/C
786	*Neostagonospora artemisiae*	New species	Russia	N/C
787	*Ophiobolus artemisiicola*	New species	Russia	N/C
788	*Poaceicola arundinis*	sexual record	Italy	*Septoriella arundinis* Marin-Felix et al. (2019a)
789	*Poaceicola arundinicola*	New species	Italy	*Septoriella arundinicola* Marin-Felix et al. (2019a)
790	*Poaceicola agrostina*	New species	Italy	*Septoriella agrostina* Marin-Felix et al. (2019a)
791	*Poaceicola rosae*	New species	Italy	*Septoriella rosae* Marin-Felix et al. (2019a)
792	*Populocrescentia ammophilae*	New species	Italy	N/C
793	*Populocrescentia rosae*	New species	Uzbekistan	N/C
794	*Sclerostagonospora rosicola*	New species	Italy	N/C
795	*Sclerostagonospora lathyri*	New species	China	N/C
796	*Sclerostagonospora rosae*	New species	Italy	N/C
797	*Wojnowicia rosicola*	New species	Italy	Ascomycota Wijayawardene et al. (2022)
798	*Alternaria doliconidium*	New species	Italy	N/C
799	*Alternaria hampshirensis*	New species	UK	N/C
800	*Comoclathris rosae*	New species	Italy	N/C
801	*Comoclathris rosarum*	New species	Italy	N/C
802	*Comoclathris rosigena*	New species	Italy	N/C
803	*Pleospora rosae*	New species	Italy	N/C
804	*Pleospora rosae-caninae*	New species	Italy	N/C
805	*Sporormurispora*	New genus	Russia	N/C
806	*Sporormurispora atraphaxidis*	New species		
807	*Sporormurispora pruni*	New species	Uzbekistan	N/C
808	*Teichospora rubriostiolata*	New host	UK	*Magnibotryascoma rubriostiolatum* (Phukhamsakda et al. 2020)
809	*Cycasicola*	New genus	India	N/C
810	*Cycasicola goaensis*	New species		
811	*Neoconiothyrium*	New genus	Italy	N/C
812	*Neoconiothyrium rosae*	New species		*Pseudoneoconiothyrium rosae* *Pseudoneoconiothyrium rosae* (Phukhams., Camporesi & K.D. Hyde) Phukhams., Camporesi & K.D. Hyde, Index Fungorum 357: 1 (2018)
813	*Parathyridaria rosae*	New species	UK	N/C
814	*Pararoussoella*	New genus	UK	N/C
815	*Pararoussoella rosarum*	New species		

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
816	*Penicillium aquaticum*	New species	Korea	N/C
817	*Penicillium acidum*	New species	Korea	N/C
818	*Amandinea punctata*	New host	Sweden	N/C
819	*Lecidella elaeochroma*	New host	UK	N/C
820	*Diaporthe eres*	New host	UK	N/C
821	*Diaporthe foeniculina*	New host	Italy	N/C
822	*Diaporthe rhusicola*	New host	UK	N/C
823	*Diaporthe rosae*	New species	Thailand	N/C
824	*Diaporthe rosicola*	New species	UK	*Diaporthe eres* (Chaisiri et al. 2021)
825	*Diaporthe rudis*	New host	Italy	N/C
826	*Bartalinia rosicola*	New species	Italy	N/C
827	*Broomella rosae*	New species	Italy	N/C
828	*Seiridium rosarum*	New species	Italy	N/C
829	*Seimatosporium rosicola*	New species	Italy	*Sporocadus rosigena* (Liu et al. 2019a, b, c, d)
830	*Seimatosporium rosigenum*	New species	Italy	N/C
831	*Paraxylaria*	New genus	Uzbekistan	N/C
832	*Paraxylaria rosacearum*	New species		
833	*Castanediella camelliae*	New species	Korea	N/C
834	*Coniochaeta baysunika*	New species	Uzbekistan	N/C
835	*Coniochaeta rosae*	New species	Uzbekistan	N/C
836	*Backusella locustae*	New species	Korea	N/C
837	*Absidia jindoensis*	New species	Korea	N/C
838	*Mucor fluvius*	New species	Korea	*Mucor fluvii* Hyang B. Lee, S.H. Lee & T.T.T. Nguyen [as 'fluvius']
839	*Umbelopsis sinsidoensis*	New species	Korea	N/C
Fungal diversity notes 840–928 (Tibpromma et al. 2018)				
840	*Cercospora capsici*	New host	Thailand	N/C
841	*Dictyocheirospora nabanheensis*	New species	China	N/C
842	*Dictyocheirospora pandanicola*	New species	Thailand	N/C
843	*Dictyocheirospora xishuangbannaensis*	New species	China	N/C
844	*Dictyosporium appendiculatum*	New species	Thailand	N/C
845	*Dictyosporium digitatum*	New host	Hong Kong	N/C
846	*Dictyosporium guttulatum*	New species	Thailand	N/C
847	*Dictyosporium hongkongensis*	New species	Hong kong	N/C
848	*Dictyosporium krabiense*	New species	Thailand	N/C
849	*Dictyosporium pandanicola*	New species	Thailand	N/C
850	*Deniquelata barringtoniae*	New host	Thailand	N/C
851	*Montagnula krabiensis*	New species	Thailand	N/C
852	*Pseudopithomyces pandanicola*	New species	Thailand	N/C
853	*Hermatomyces biconisporus*	New species	China	N/C
854	*Byssosphaeria siamensis*	New host	Thailand	N/C
855	*Neooccultibambusa thailandensis*	New species	Thailand	N/C
856	*Curvularia chonburiensis*	New species	Thailand	N/C
857	*Curvularia pandanicola*	New species	Thailand	N/C
858	*Curvularia thailandicum*	New species	Thailand	*Curvularia thailandica* Tibpromma & K.D. Hyde [as 'thailandicum']
859	*Curvularia xishuangbannaensis*	New species	China	N/C
860	*Roussoella solani*	New host	China	*Neoroussoella solani* (Jayasiri et al. 2019)
861	*Polyplosphaeria nabanheensis*	New species	China	N/C
862	*Polyplosphaeria pandanicola*	New species	China	N/C
863	*Polyplosphaeria xishuangbannaensis*	New species	China	*Ernakulamia xishuangbannaensis* (Dong et al. 2020)
864	*Rostriconidium pandanicola*	New species	China	N/C
865	*Torula chromolaenae*	New host	China	N/C
866	*Torula ficus*	New host	Thailand	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
867	*Pseudoberkleasmium*	New genus	China	N/C
868	*Pseudoberkleasmium pandanicola*	New species		
869	*Pseudochaetosphaeronema pandanicola*	New species	Thailand	N/C
870	*Lasiodiplodia chonburiensis*	New species	Thailand	N/C
871	*Lasiodiplodia hyalina*	New host	Thailand	*Lasiodiplodia thailandica* (Zhang et al. 2021)
872	*Lasiodiplodia pandanicola*	New species	Thailand	*Lasiodiplodia mahajangana* (Zhang et al. 2021)
873	*Lasiodiplodia pseudotheobromae*	New host	Thailand	N/C
874	*Neofusicoccum pandanicola*	New species	China	*Neofusicoccum parvum* (Zhang et al. 2021)
875	*Pseudofusicoccum adansoniae*	New host	Thailand	N/C
876	*Helicoma freycinetiae*	New species	Thailand	N/C
877	*Neohelicomyces pandanicola*	New species	China	N/C
878	*Tubeufia freycinetiae*	New species	Thailand	N/C
879	*Tubeufia inaequalis*	New host	Thailand	N/C
880	*Tubeufia pandanicola*	New species	Thailand	N/C
881	*Tubeufia parvispora*	New species	Thailand	N/C
882	*Yunnanomyces*	New genus	China	N/C
883	*Yunnanomyces pandanicola*	New species		
884	*Stictis pandanicola*	New species	China	*Fitzroyomyces pandanicola* (Wei et al. 2021)
885	*Terriera pandanicola*	New species	Thailand	N/C
886	*Distoseptispora thailandica*	New species	Thailand	N/C
887	*Distoseptispora xishuangbannaensis*	New species	China	N/C
888	*Colletotrichum pandanicola*	New species	Thailand	N/C
889	*Malaysiascaceae*	New family		N/C
890	*Malaysiasca phaii*	New host	Thailand	N/C
891	*Acremoniisimulans*	New genus	Thailand	N/C
892	*Acremoniisimulans thailandensis*	New species		
893	*Musicillium pandanicola*	New species	Thailand	N/C
894	*Clonostachys krabiensis*	New species	Thailand	N/C
895	*Lasionectria krabiense*	New species	Thailand	N/C
896	*Paracylindrocarpon nabanheensis*	New species	China	N/C
897	*Paracylindrocarpon pandanicola*	New species	Hong Kong	N/C
898	*Paracylindrocarpon xishuangbannaensis*	New species	China	N/C
899	*Cylindrocladiella xishuangbannaensis*	New species	China	N/C
900	*Pandanaceomyces*	New genus	Thailand	N/C
901	*Pandanaceomyces krabiensis*	New species		
902	*Pseudoachroiostachys*	New genus	Thailand	N/C
903	*Pseudoachroiostachys krabiense*	New species		
904	*Volutella krabiense*	New species	Thailand	N/C
905	*Volutella thailandensis*	New species	Thailand	N/C
906	*Pseudohyaloseta*	New genus	Thailand	N/C
907	*Pseudohyaloseta pandanicola*	New species		
908	*Parasarcopodium hongkongensis*	New species	Hong Kong	N/C
909	*Pseudoornatispora*	New genus	Thailand	N/C
910	*Pseudoornatispora krabiense*	New species		
911	*Sirastachys phangngaensis*	New species	Thailand	N/C
912	*Parascedosporium putredinis*	New host	Thailand	N/C
913	*Canalisporium krabiense*	New species	Thailand	N/C
914	*Canalisporium thailandensis*	New species	Thailand	N/C
915	*Dictyochaeta pandanicola*	New species	China	N/C
916	*Dictyochaeta siamensis*	New host	Thailand	N/C
917	*Menisporopsis pandanicola*	New species	Hong Kong	N/C
918	*Thozetella pandanicola*	New species	Thailand	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
919	*Chaetomium globosum*	New record	Thailand	N/C
920	*Beltrania krabiensis*	New species	Thailand	N/C
921	*Beltraniella pandanicola*	New species	Thailand	N/C
922	*Beltraniella thailandicus*	New species	Thailand	N/C
923	*Neopestalotiopsis chiangmaiensis*	New species	Thailand	N/C
924	*Neopestalotiopsis pandanicola*	New species	China	N/C
925	*Neopestalotiopsis phangngaensis*	New species	Thailand	N/C
926	*Pestalotiopsis krabiensis*	New species	Thailand	N/C
927	*Pestalotiopsis pandanicola*	New species	Thailand	N/C
928	*Vermiculariopsiella hongkongensis*	New species	Hong Kong	N/C
Fungal diversity notes 929–1035 (Phookamsak et al. 2019)				
929	*Hyweljonesia indica*	New species	India	N/C
930	*Dictyocheirospora metroxylonis*	New species	Thailand	N/C
931	*Vicosamyces*	New genus	Brazil	N/C
932	*Vicosamyces venturisporus*	New species		
933	*Keissleriella caraganae*	New species	China	N/C
934	*Murilentithecium lonicerae*	New species	China	N/C
935	*Phragmocamarosporium hederae*	New host	China	*Phragmocamarosporium hederae* Wijayaw., R.K. Schumach. & K.D. Hyde, Index Fungorum 370: 1 (2018)
936	*Leptosphaeria urticae*	New species	UK	N/C
937	*Plenodomus artemisiae*	New species	China	N/C
938	*Plenodomus lijiangensis*	New species	China	N/C
939	*Plenodomus sinensis*	New hosts and asexual morph records	China	N/C
940	*Sphaerellopsis isthmospora*	New species	China	N/C
941	*Sphaerellopsis paraphysata*	New host	China	N/C
942	*Lophiotrema mucilaginosis*	New species	China	N/C
943	*Brunneofusispora*	New genus	China	N/C
944	*Brunneofusispora sinensis*	New species		
945	*Lonicericola*	New genus	China	N/C
946	*Lonicericola hyaloseptispora*	New species		
947	*Parabambusicola thysanolaenae*	New species	China	N/C
948	*Paratrimmatostroma*	New genus	China	N/C
949	*Paratrimmatostroma kunmingensis*	New species		
950	*Periconia cortaderiae*	New host	China	N/C
951	*Amarenomyces dactylidis*	New host	China	N/C
952	*Brunneomurispora*	New genus	China	N/C
953	*Brunneomurispora lonicerae*	New species		
954	*Galiicola baoshanensis*	New species	China	N/C
955	*Neosetophoma lonicerae*	New species	China	N/C
956	*Ophiobolus malleolus*	New species	Russia	N/C
957	*Phaeosphaeria cycadis*	New species	China	N/C
958	*Wojnowiciella kunmingensis*	New species	China	N/C
959	*Wojnowiciella rosicola*	New combination	India	N/C
960	*Pseudoastrosphaeriellopsis*	New genus	Thailand	N/C
961	*Pseudoastrosphaeriellopsis kaveriana*	New species		
962	*Neoroussoella heveae*	New species	Thailand	N/C
963	*Neoroussoella leucaenae*	New host	Thailand	N/C
964	*Roussoella elaeicola*	New species	China	N/C
965	*Neobambusicola brunnea*	New species	China	N/C
966	*Liua*	New genus	Brazil	N/C
967	*Liua muriformis*	New species		
968	*Lembosia brigadeirensis*	New species	China	N/C
969	*Dothiorella acericola*	New species	Russia	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
970	*Dothiorella sarmentorum*	New host	Thailand	N/C
971	*Sphaeropsis eucalypticola*	New host	India	N/C
972	*Parazalerion*	New genus	China	N/C
973	*Parazalerion indica*	New species		
974	*Muyocopron lithocarpi*	New host	China	N/C
975	*Pseudohelicomyces menglunicus*	New species	Thailand	N/C
976	*Cyphellophora filicis*	New species	China	N/C
977	*Capronia camelliae-yunnanensis*	New species	China	N/C
978	*Penicillium dokdoense*	New species	Korea	N/C
979	*Micropeltis phetchaburiensis*	New species	Thailand	N/C
980	*Velebitea*	New genus	Croatia	N/C
981	*Velebitea chrysotexta*	New species		
982	*Sarcopeziza sicula*	re-circumscribed	Italy	N/C
983	*Conlarium thailandense*	New species	Thailand	N/C
984	*Cytospora ulmicola*	New species	Russia	N/C
985	*Septomelanconiella*	New genus	Thailand	N/C
986	*Septomelanconiella thailandica*	New species		
987	*Pseudoplagiostoma mangiferae*	New species	China	N/C
988	*Coniella vitis*	New host	Russia	N/C
989	*Distoseptispora thysanolaenae*	New species	China	N/C
990	*Proliferophorum*	New genus	Thailand	N/C
991	*Proliferophorum thailandicum*	New species		
992	*Plectosphaerella kunmingensis*	New species	China	N/C
993	*Leptobacillium leptobactrum*	New record	India	N/C
994	*Trichoderma koreanum*	New species	Korea	N/C
995	*Trichoderma pinicola*	New species	Korea	N/C
996	*Trichoderma rugulosum*	New species	Korea	N/C
997	*Emericellopsis koreana*	New species	Korea	N/C
998	*Canalisporium kenyense*	Reference specimen	Thailand	N/C
999	*Chaetosphaeria panamensis*	New host	Taiwan	*Paragaeumannomyces panamensis* (Réblová et al. 2020)
1000	*Thozetella lithocarpi*	New species	Thailand	N/C
1001	*Coniochaeta simbalensis*	New species	India	N/C
1002	*Tamsiniella labiosa*	Reference specimen	China	N/C
1003	*Zopfiella indica*	New species	India	N/C
1004	*Amphisphaeria mangrovei*	New species	India	N/C
1005	*Bartalinia kunmingensis*	New species	China	N/C
1006	*Robillarda mangiferae*	New species	China	N/C
1007	*Neoeutypella*	New genus	China	N/C
1008	*Neoeutypella baoshanensis*	New species		
1009	*Peroneutypa mangrovei*	New species	India	N/C
1010	*Hypoxylon teeravasati*	New species	India	N/C
1011	*Agaricus memnonius*	New species	China	N/C
1012	*Agaricus langensis*	New species	China	N/C
1013	*Coprinus trigonosporus*	New species	Saudi Arabia	N/C
1014	*Amanita altipes*	New record	Thailand	N/C
1015	*Amanita flavoalba*	New species	India	N/C
1016	*Amanita melleialba*	New record	Thailand	N/C
1017	*Amanita subtropicana*	New species	India	N/C
1018	*Hygrocybe lucida*	New species	India	N/C
1019	*Marasmius indojasminodorus*	New species	India	N/C
1020	*Marasmiellus bicoloripes*	New species	India	N/C
1021	*Coprinopsis kubickae*	New record	Croatia	N/C
1022	*Baorangia major*	New species	Thailand	N/C
1023	*Baorangia rufomaculata*	New combination	US	N/C
1024	*Lanmaoa pallidorosea*	New combination	US	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
1025	*Clavulina thindii*	New species	India	N/C
1026	*Phanerochaete australosanguinea*	New species	Chile	N/C
1027	*Lactarius olivaceopallidus*	New species	India	N/C
1028	*Lactifluus midnapurensis*	New species	India	N/C
1029	*Russula choptae*	New species	India	N/C
1030	*Russula uttarakhandia*	New species	India	N/C
1031	*Aleurodiscus patagonicus*	New species	Chile	N/C
1032	*Trechispora echinospora*	New species	Equatorial Guinea	N/C
1033	*Tremellochaete atlantica*	New species	Brazil	N/C
1034	*Dacrymyces invisibilis*	New species	Chile	N/C
1035	*Mucor orantomantidis*	New species	Korea	N/C
Fungal diversity notes 1036–1150 (Hyde et al. 2019)				
1036	*Plectocarpon galapagoense*	New species	Ecuador	N/C
1037	*Caatingomyces*	New genus	Brazil	N/C
1038	*Caatingomyces brasiliensis*	New species		
1039	*Amniculicola aquatica*	New species	China	N/C
1040	*Amniculicola guttulata*	New species	China	N/C
1041	*Murispora cicognanii*	New record	China	N/C
1042	*Angustimassarina sylvatica*	New species	Italy	N/C
1043	*Camarosporidiella mori*	New species	Russia	N/C
1044	*Protofenestella ulmi*	New record	Russia	N/C
1045	*Dictyocheirospora aquadulcis*	New species	Thailand	N/C
1046	*Dictyocheirospora rotunda*	New geographical record	China	N/C
1047	*Dictyocheirospora taiwanense*	New species	Taiwan	N/C
1048	*Digitodesmium chiangmaiense*	New species	Thailand	N/C
1049	*Calophoma humuli*	New species	Russia	N/C
1050	*Neodidymelliopsis farokhinejadii*	New host	Italy	N/C
1051	*Neodidymelliopsis sambuci*	New species	Italy	N/C
1052	*Nothophoma quercina*	New host	China	N/C
1053	*Hermatomyces bauhiniae*	New species	Thailand	N/C
1054	*Vaginatispora palmae*	New species	Thailand	N/C
1055	*Vaginatispora armatispora*	New record	Thailand	N/C
1056	*Paramassaria*	New genus	Thailand	N/C
1057	*Paramassaria samaneae*	New species		
1058	*Muriphaeosphaeria angustifoliae*	New species	Uzbekistan	N/C
1059	*Neosetophoma miscanthi*	New species	Taiwan	N/C
1060	*Neosetophoma salicis*	New species	Uzbekistan	N/C
1061	*Nodulosphaeria aquilegiae*	New species	Italy	N/C
1062	*Nodulosphaeria thalictri*	New species	Italy	N/C
1063	*Phaeopoacea asparagicola*	New species	Ukraine	N/C
1064	*Phaeosphaeria penniseti*	New species	Taiwan	N/C
1065	*Pseudoberkleasmiaceae*	New family		N/C
1066	*Pseudoberkleasmium chiangmaiense*	New species	Thailand	N/C
1067	*Pyrenochaetopsis sinensis*	New species	China	N/C
1068	*Tetraploa nagasakiensis*	New geographical record	China	N/C
1069	*Torula breviconidiophora*	New species	Thailand	N/C
1070	*Torula polyseptata*	New species	Thailand	N/C
1071	*Falciformispora aquatica*	New species	Thailand	N/C
1072	*Acrogenospora sphaerocephala*	Reference specimen	Thailand	N/C
1073	*Acrogenospora thailandica*	New species	Thailand	N/C
1074	*Lembosia xyliae*	New host	Thailand	N/C
1075	*Morenoina palmicola*	New host	Thailand	N/C
1076	*Dothiorella plurivora*	New record	China	N/C
1077	*Dothiorella rhamni*	New host	Russia	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
1078	*Dothiorella styphnolobii*	New species	Russia	N/C
1079	*Dothiorella symphoricarposicola*	New host	Italy	*Dothiorella sarmentorum* (Zhang et al. 2021)
1080	*Lasiodiplodia iraniensis*	New host	Thailand	N/C
1081	*Jahnula queenslandica*	New species	Australia	N/C
1082	*Kamalomyces mangrovei*	New species	Thailand	N/C
1083	*Thysanorea uniseptata*	New species	Thailand	N/C
1084	*Penicillium circulare*	New species	Korea	N/C
1085	*Penicillium geumsanense*	New species	Korea	N/C
1086	*Penicillium mali*	New species	Netherlands	N/C
1087	*Penicillium psychrotrophicum*	New species	Korea	N/C
1088	*Penicillium wandoense*	New species	Korea	N/C
1089	*Prolixandromyces*	syn. nov		N/C
1090	*Prolixandromyces australis*	New combination		N/C
1091	*Prolixandromyces elongatus*	New combination		N/C
1092	*Prolixandromyces falcatus*	New combination		N/C
1093	*Prolixandromyces longispinae*	New combination		N/C
1094	*Prolixandromyces microveliae*	New combination		N/C
1095	*Prolixandromyces neoalardi*	New combination		N/C
1096	*Prolixandromyces polhemorum*	New combination		N/C
1097. **	*Prolixandromyces protuberans*	New combination		N/C
1098. **	*Prolixandromyces pseudoveliae*	New combination		N/C
1099. **	*Prolixandromyces tenuistipitis*	New combination		N/C
1100	*Prolixandromyces umbonatus*	New combination		N/C
1101	*Stigmatomyces chamaemyiae*	New species	Malta	N/C
1102	*Stigmatomyces cocksii*	New species	Australia	N/C
1103	*Stigmatomyces papei*	New species	Tanzania	N/C
1104	*Stigmatomyces tschirnhausii*	New species	Kenya	N/C
1105	*Stigmatomyces vikhrevii*	New species	Malaysia	N/C
1106	*Buellia viridula*	New species	Thailand	N/C
1107	*Lecidella yunnanensis*	New species	China	N/C
1108	*Micarea squamulosa*	New species	Brazil	N/C
1109	*Porina sorediata*	New species	Brazil	N/C
1110	*Cryptoschizotrema*	New genus	Brazil	N/C
1111	*Cryptoschizotrema cryptotrema*	New combination		
1112	*Pilidium concavum*	New geographical record	Thailand	N/C
1113	*Boubovia gelatinosa*	New species	China	N/C
1114	*Diaporthe italiana*	New species	Italy	N/C
1115	*Diaporthe rumicicola*	New species	Italy	N/C
1116	*Plagiostoma salicellum*	New geographical record	Italy	N/C
1117	*Distoseptispora dehongensis*	New species	China	N/C
1118	*Distoseptispora palmarum*	New species	Thailand	N/C
1119	*Acrostalagmus annulatus*	New geographical record	Thailand	N/C
1120	*Cordyceps succavus*	New species	Thailand	N/C
1121	*Blackwellomyces lateris*	New species	Thailand	N/C
1122	*Sarocladium kiliense*	New record	China	N/C
1123	*Phaeoisaria siamensis*	New species	Thailand	N/C
1124	*Canalisporium dehongense*	New species	China	N/C
1125	*Sporoschisma chiangraiense*	New species	Thailand	N/C
1126	*Ellisembia aurea*	New species	France	N/C
1127	*Neolinocarpon rachidis*	New record	Thailand	N/C
1128	*Trochilispora*	New genus	Brazil	N/C
1129	*Trochilispora schefflerae*	New species		
1130	*Pestalotiopsis aggestorum*	New geographical record	Thailand	N/C
1131	*Castanediella meliponae*	New species	Brazil	N/C
1132	*Diatrypella delonicis*	New species	Thailand	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
1133	*Peroneutypa scoparia*	New record	Thailand	N/C
1134	*Fasciatispora arengae*	New record	Thailand	N/C
1135	*Cortinarius minusculus*	New species	Finland	N/C
1136	*Cortinarius subscotoides*	New species	Finland	N/C
1137	*Coprinopsis psammophila*	New species	Libya	N/C
1138	*Coprinopsis villosa*	New geographical record	Croatia	N/C
1139	*Neoacladium*	New genus	India	N/C
1140	*Neoacladium indicum*	New species		
1141	*Cantharellus goossensiae*	New record	China	N/C
1142	*Cantharellus brunneopallidus*	New species	Madagascar	N/C
1143	*Cantharellus griseotinctus*	New species	Madagascar	N/C
1144	*Fomitiporia carpinea*	New species	China	N/C
1145	*Fomitiporia lagerstroemiae*	New species	Vietnam	N/C
1146	*Grammothele aurantiaca*	New species	Brazil	N/C
1147	*Grammothele micropora*	New species	Brazil	N/C
1148	*Grammothele brasiliensis*	New record	Brazil	N/C
1149	*Russula prasina*	New species	China	N/C
1150	*Rhizophydium koreanum*	New species	Korea	N/C
Fungal diversity notes 1151–1276 (Hyde et al. 2020a, b, c)				
1151	*Dissoconium eucalypti*	New record of the sexual morph	Italy	N/C
1152	*Pseudocercospora maetaengensis*	New species	Thailand	N/C
1153	*Hysterobrevium constrictum*	New record	China	N/C
1154	*Rhytidhysteron camporesii*	New species	China	N/C
1155	*Rhytidhysteron erioi*	New species	Thailand	N/C
1156	*Angustimassarina camporesii*	New species	Italy	N/C
1157	*Camarosporidiella camporesii*	New species	Italy	N/C
1158	*Foliophoma camporesii*	New species	Italy	N/C
1159	*Dendryphiella phitsanulokensis*	New host	Thailand	N/C
1160	*Dictyosporium muriformis*	New species	China	N/C
1161	*Ascochyta medicaginicola*	New record	Italy	N/C
1162	*Ascochyta pisi*	New host	Italy	*Didymella pisi* (Chilvers et al. 2009)
1163	*Didymella camporesii*	New species	Italy	N/C
1164	*Didymella macrostoma*	New host	Italy	N/C
1165	*Neodidymelliopsis camporesii*	New species	Italy	N/C
1166	*Neodidymelliopsis ranunculi*	New host	Italy	N/C
1167	*Nothophoma quercina*	New host	Russia	N/C
1168	*Xenodidymella camporesii*	New species	Italy	N/C
1169	*Kalmusia erioi*	New species	Thailand	N/C
1170	*Montagnula camporesii*	New species	Italy	N/C
1171	*Neokalmusia kunmingensis*	New species	China	N/C
1172	*Pseudocamarosporium camporesii*	New species	Italy	N/C
1173	*Tremateia lamiacearum*	New species	China	N/C
1174	*Tremateia camporesii*	New species	Thailand	N/C
1175	*Fuscostagonospora camporesii*	New species	Italy	N/C
1176	*Brunneoclavispora camporesii*	New species	Thailand	N/C
1177	*Keissleriella camporesiana*	New species	Italy	N/C
1178	*Keissleriella camporesii*	New species	Italy	N/C
1179	*Pseudomurilentithecium*	New genus	Italy	N/C
1180	*Pseudomurilentithecium camporesii*	New species		
1181	*Plenodomus triseptatus*	New species	Russia	N/C
1182	*Neovaginatispora fuckelii*	New host	China	N/C
1183	*Pseudochaetosphaeronema kunmingense*	New species	China	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
1184	*Camposporium appendiculatum*	New species	China	N/C
1185	*Camposporium lycopodiellae*	New combination		N/C
1186	*Camposporium multiseptatum*	New species	China	N/C
1187	*Camposporium pellucidum*	New record	China	N/C
1188	*Camposporium septatum*	New species	Thailand	N/C
1189	*Uzbekistanica pruni*	New species	Russia	N/C
1190	*Occultibambusa bambusae*	New host	Taiwan	N/C
1191	*Paramonodictys*	New genus	China	N/C
1192	*Paramonodictys solitarius*	New species		
1193	*Periconia palmicola*	New species	Thailand	N/C
1194	*Bhagirathimyces*	New genus	India	N/C
1195	*Bhagirathimyces himalayensis*	New species		
1196	*Loratospora arezzoensis*	New species	Italy	N/C
1197	*Neosetophoma camporesii*	New species	Italy	N/C
1198	*Paraloratospora*	New genus	Italy	N/C
1199	*Paraloratospora camporesii*	New species		
1200	*Paraloratospora gahniae*	New combination		N/C
1201	*Phaeosphaeria chinensis*	New host	Taiwan	N/C
1202	*Phaeosphaeriopsis pseudoagavacearum*	New record of the sexual morph	Italy	N/C
1203	*Septoriella camporesii*	New species	Italy	N/C
1204	*Wojnowiciella dactylidis*	New host	Italy	N/C
1205	*Ernakulamia tanakae*	New species	India	N/C
1206	*Pseudotetraploa rajmachiensis*	New species	India	N/C
1207	*Tetraploa dwibahubeeja*	New species	India	N/C
1208	*Tetraploa pseudoaristata*	New species	India	N/C
1209	*Tetraploa thrayabahubeeja*	New species	India	N/C
1210	*Tetraploa sasicola*	New host	Taiwan	N/C
1211	*Torula camporesii*	New species	China	N/C
1212	*Torula gaodangensis*	New host	China	N/C
1213	*Falciformispora uttaraditensis*	New species	Thailand	N/C
1214	*Diplodia mutila*	New host	Italy	N/C
1215	*Diplodia seriata*	New host	Italy	N/C
1216	*Setoapiospora*	New genus	Thailand	N/C
1217	*Setoapiospora thailandica*	New species		
1218	*Camporesiomyces*	New genus	China	N/C
1219	*Camporesiomyces mali*	New species		
1220	*Camporesiomyces patagoniensis*	New combination		N/C
1221	*Camporesiomyces vaccinii*	New combination		N/C
1222	*Verruconis mangrovei*	New species	India	N/C
1223	*Eriomycetaceae*	New family		N/C
1224	*Eriomyces*	New genus	Thailand	N/C
1225	*Eriomyces heveae*	New species		
1226	*Pyxine berteriana*	New host	China	N/C
1227	*Heterosphaeria patella*	New host	Italy	N/C
1228	*Rhexocercosporidium microsporum*	New combination		*Cadophora microspora* (Ekanayaka et al. 2019)
1229	*Rhexocercosporidium senecionis*	New species	Italy	N/C
1230	*Srinivasanomyces*	New genus	India	N/C
1231	*Srinivasanomyces kangrensis*	New species		
1232	*Helvella subtinta*	New species	China	N/C
1233	*Wilcoxina verruculosa*	New species	China	N/C
1234	*Eriocamporesia*	New genus	Thailand	N/C
1235	*Eriocamporesia aurantia*	New species		
1236	*Cytospora fusispora*	New species	India	N/C
1237	*Cytospora rosigena*	New species	Russia	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
1238	*Diaporthe camporesii*	New species	Italy	N/C
1239	*Diaporthe cynaroidis*	New record of the sexual-asexual connection	Italy	N/C
1240	*Diaporthe foeniculina*	New host	Italy	N/C
1241	*Diaporthe nigra*	New species	Italy	N/C
1242	*Neomyrmecridium guizhouense*	New species	China	N/C
1243	*Lanspora cylindrospora*	New species	India	N/C
1244	*Pseudoconlarium*	New genus	China	N/C
1245	*Pseudoconlarium punctiforme*	New species		
1246	*Colletotrichum hederiicola*	New species	Italy	N/C
1247	*Acremonium chiangraiense*	New species	Thailand	N/C
1248	*Clonostachys eriocamporesiana*	New species	Thailand	N/C
1249	*Clonostachys eriocamporesii*	New species	Thailand	N/C
1250	*Mariannaea atlantica*	New species	Brazil	N/C
1251	*Conioscypha verrucosa*	New species	China	N/C
1252	*Neomonodictys*	New genus	Thailand	N/C
1253	*Neomonodictys muriformis*	New species		
1254	*Canalisporium aquaticium*	New species	Thailand	N/C
1255	*Coniochaeta vineae*	New species	China	N/C
1256	*Pseudodactylaria camporesiana*	New species	Thailand	N/C
1257	*Neoleptosporella camporesiana*	New species	Thailand	Nom. inval., Art. 35.1 (Shenzhen)
1258	*Arthrinium marii*	New host	Italy	N/C
1259	*Pseudotruncatella camporesii*	New species	Italy	N/C
1260	*Pseudopestalotiopsis theae*	New record	China	N/C
1261	*Diatrypella yunnanensis*	New species	China	N/C
1262	*Fasciatisporaceae*	New family		N/C
1263	*Fasciatispora cocoes*	New species	Thailand	N/C
1264	*Astrocystis bambusicola*	New record	China	N/C
1265	*Melanographium phoenicis*	New species	Thailand	N/C
1266	*Xenoanthostomella*	New genus	Thailand	N/C
1267	*Xenoanthostomella chromolaenae*	New species		
1268	*Diutina bernali*	New species	Panama	N/C
1269	*Diutina sipiczkii*	New species	Panama	N/C
1270	*Cortinarius ainsworthii*	New species	Belgium	N/C
1271	*Cortinarius aurae*	New species	UK	N/C
1272	*Cortinarius britannicus*	New species	UK	N/C
1273	*Cortinarius heatherae*	New species	UK	N/C
1274	*Cortinarius scoticus*	New species	UK	N/C
1275	*Cortinarius subsaniosus*	New species	UK	N/C
1276	*Adustochaete nivea*	New species	Brazil	N/C
Fungal diversity notes 1276–1386 (Yuan et al. 2020)				
1277	*Umbelopsis heterosporus*	New species	Brazil	N/C
1278	*Aplosporella prunicola*	New host	China	N/C
1279	*Diplodia torilicola*	New species	Italy	N/C
1280	*Neodevriesia manglicola*	New species	India	N/C
1281	*Coniothyrium triseptatum*	New species	China	N/C
1282	*Neodidymelliopsis salviae*	New species	Italy	N/C
1283	*Neodidymelliopsis urticae*	New species	Italy	N/C
1284	*Magnopulchromyces*	New genus	Brazil	N/C
1285	*Magnopulchromyces scorpiophorus*	New species		
1286	*Paradictyoarthrinium diffractum*	New host	India	N/C
1287	*Ophiosphaerella chiangraiensis*	New species	Thailand	N/C
1288	*Prosthemium betulinum*	New record	Italy	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
1289	*Neoroussoella magnoliae*	New species	China	N/C
1290	*Sporormurispora paulsenii*	New species	Uzbekistan	*Sporormurispora paulsenii* D. Pem, Gafforov & K.D. Hyde, Index Fungorum 468: 1 (2021)
1291	*Helicoarctatus thailandicus*	New species	Thailand	N/C
1292	*Thaxteriellopsis obliqus*	New species	India	N/C
1293	*Scleroramularia vermispora*	New species	China	N/C
1294	*Graphis supracola*		Thailand	N/C
1295	*Podosphaera yulii*	New species	China	N/C
1296	*Golovinomyces monardae*	New record	China	N/C
1297	*Ionopezia*	New genus		Published 9 July 2020; see Ionopezia Matočec, I. Kušan & Jadan 2020 (published 31st Oct. 2020)
1298	*Ionopezia gerardii*	New combination	Croatia	N/C
1299	*Hansenopezia*	New genus		N/C
1300	*Hansenopezia retrocurvata*	New combination		
1301	*Hansenopezia decora*	New species	Croatia	N/C
1302	*Neottiella gigaspora*	New species	China	N/C
1303	*Arthrinium sorghi*	New species	Brazil	N/C
1304	*Chloridium macrocladum*	New combination	Taiwan	Nom. inval., Art. 41.5 (Shenzhen)
1305	*Diaporthe pimpinellae*	New species	Italy	N/C
1306	*Moelleriella gracilispora*	New species	China	N/C
1307	*Trichoderma ceratophylletum*	New species	China	N/C
1308	*Hirsutella hongheensis*	New species	China	N/C
1309	*Colletotrichum parthenocissicola*	New species	Russia	N/C
1310	*Dictyosporella guizhouensis*	New species	China	N/C
1311	*Xylolentia reniformis*	New species	China	N/C
1312	*Catenuliconidia*	New genus	China	N/C
1313	*Catenuliconidia uniseptata*	New species		
1314	*Lycoperdon lahorense*	New species	Pakistan	N/C
1315	*Lycoperdon pseudocurtisii*	New species	Pakistan	N/C
1316	*Cortinarius indorusseus*	New species	India	N/C
1317	*Cortinarius paurigarhwalensis*	New species	India	N/C
1318	*Cortinarius sinensis*	New species	China	N/C
1319	*Cortinarius subsanguineus*	New species	China	N/C
1320	*Cortinarius xiaojinensis*	New species	China	N/C
1321	*Humidicutis brunneovinacea*	New species	Mexico	N/C
1322	*Amyloceraceomyces*	New genus	China	N/C
1323	*Amyloceraceomyces angustisporus*	New species		
1324	*Amylocorticium ellipsosporum*	New species	China	N/C
1325	*Clavulina sphaeropedunculata*	New species	Mexico	N/C
1326	*Lentaria gossypina*	New species	Mexico	N/C
1327	*Lentaria variabilis*	New species	Mexico	N/C
1328	*Fuscoporia licnoides*	New combination	Brazil	N/C
1329	*Fuscoporia marquesiana*	New species	Brazil	N/C
1330	*Fuscoporia scruposa*	New combination	Brazil	N/C
1331	*Fuscoporia semiarida*	New species	Brazil	N/C
1332	*Rigidoporus juniperinus*	New species	Uzbekistan	N/C
1333	*Rhodofomitopsis pseudofeei*	New species	Australia	N/C
1334	*Rhodofomitopsis monomitica*	New combination		N/C
1335	*Rhodofomitopsis oleracea*	New combination		N/C
1336	*Antrodiella descendena*	New combination	Malaysia	N/C
1337	*Tyromyces minutulus*	New species	China	N/C
1338	*Russula benghalensis*	New species	India	N/C
1339	*Tomentella asiae-orientalis*	New species	China	N/C
1340	*Tomentella atrobadia*	New species	China	N/C
1341	*Tomentella atrocastanea*	New species	China	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
1342	*Tomentella aureomarginata*	New species	China	N/C
1343	*Tomentella brevis*	New species	China	N/C
1344	*Tomentella brunneoflava*	New species	China	N/C
1345	*Tomentella brunneogrisea*	New species	China	N/C
1346	*Tomentella capitatocystidiata*	New species	China	N/C
1347	*Tomentella changbaiensis*	New species	China	N/C
1348	*Tomentella citrinocystidiata*	New species	China	N/C
1349	*Tomentella coffeae*	New species	China	N/C
1350	*Tomentella conclusa*	New species	China	N/C
1351	*Tomentella cystidiata*	New species	China	N/C
1352	*Tomentella dimidiata*	New species	China	N/C
1353	*Tomentella duplexa*	New species	China	N/C
1354	*Tomentella efibulata*	New species	China	N/C
1355	*Tomentella efibulis*	New species	China	N/C
1356	*Tomentella farinosa*	New species	China	N/C
1357	*Tomentella flavidobadia*	New species	China	N/C
1358	*Tomentella fuscocrustosa*	New species	China	N/C
1359	*Tomentella fuscofarinosa*	New species	China	N/C
1360	*Tomentella fuscogranulosa*	New species	China	N/C
1361	*Tomentella fuscopelliculosa*	New species	China	N/C
1362	*Tomentella globospora*	New species	China	N/C
1363	*Tomentella gloeocystidiata*	New species	China	N/C
1364	*Tomentella griseocastanea*	New species	China	N/C
1365	*Tomentella griseofusca*	New species	China	N/C
1366	*Tomentella griseomarginata*	New species	China	N/C
1367	*Tomentella inconspicua*	New species	China	N/C
1368	*Tomentella incrustata*	New species	China	N/C
1369	*Tomentella interrupta*	New species	China	N/C
1370	*Tomentella liaoningensis*	New species	China	N/C
1371	*Tomentella longiaculeifera*	New species	China	N/C
1372	*Tomentella longiechinuli*	New species	China	N/C
1373	*Tomentella megaspora*	New species	China	N/C
1374	*Tomentella olivacea*	New species	China	N/C
1375	*Tomentella olivaceobrunnea*	New species	China	N/C
1376	*Tomentella pallidobrunnea*	New species	China	N/C
1377	*Tomentella pallidomarginata*	New species	China	N/C
1378	*Tomentella parvispora*	New species	China	N/C
1379	*Tomentella pertenuis*	New species	China	N/C
1380	*Tomentella qingyuanensis*	New species	China	N/C
1381	*Tomentella segregata*	New species	China	N/C
1382	*Tomentella separata*	New species	China	N/C
1383	*Tomentella stipitata*	New species	China	N/C
1384	*Tomentella storea*	New species	China	N/C
1385	*Scytinopogon minisporus*	New species	Mexico	N/C
1386	*Phaeotremella yunnanensis*	New species	China	N/C
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1387	*Diplodia alanphillipsii*	New species	Iran	N/C
1388	*Chaetoscutula juniperi*	New record	Spain	N/C
1389	*Dothiora coronicola*	New species	Italy	N/C
1390	*Dyfrolomyces distoseptatus*	New geographical record	Thailand	N/C
1391	*Aliquandostipite khaoyaiensis*	New record	Thailand	N/C
1392	*Minutisphaera thailandensis*	New species	Thailand	N/C
1393	*Acrocalymma fici*	New habitat and geographical record	Thailand	N/C
1394	*Dictyosporium pandanicola*	New record	Thailand	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
1395	*Camarosporidiella laburni*	New record	Uzbekistan	N/C
1396	*Cryptocoryneum rosae*	New species	China	N/C
1397	*Didymella azollae*	New species	Iran	N/C
1398	*Montagnula thailandica*	New record	Thailand	N/C
1399	*Paraconiothyrium ajrekarii*	New species	India	N/C
1400	*Spegazzinia camelliae*	New record	Thailand	N/C
1401	*Hermatomyces nabanheensis*	New record	China	N/C
1402	*Hermatomyces sphaericoides*	New record	Thailand	N/C
1403	*Poaceascoma taiwanense*	New geographical record	Thailand	N/C
1404	*Hongkongmyces kokensis*	New species	Thailand	N/C
1405	*Xenovaginatispora*	New genus	Thailand	N/C
1406	*Xenovaginatispora phichaiensis*	New species		
1407	*Longipedicellata aquatica*	New record	Thailand	N/C
1408	*Longipedicellata megafusiformis*	New species	Thailand	N/C
1409	*Submersispora variabilis*	New record	Thailand	N/C
1410	*Lophiostoma caudatum*	New host	Uzbekistan	*Sigarispora caudata* Thambugala et al. (2015)
1411	*Lophiostoma clematidis-vitalbae*	New host	Uzbekistan	N/C
1412	*Vaginatispora nypae*	New record	Thailand	N/C
1413	*Lophiotrema hydei*	New host	China	N/C
1414	*Lophiotrema lincangensis*	New species	China	N/C
1415	*Lophiotrema neoarundinariae*	New host	China	N/C
1416	*Pseudochaetosphaeronema chiangraiense*	New species	Thailand	N/C
1417	*Helminthosporium chiangraiense*	New species	Thailand	N/C
1418	*Nigrograna jinghongensis*	New species	China	N/C
1419	*Seriascoma honghense*	New species	China	N/C
1420	*Paradictyoarthrinium diffractum*	New record	Thailand	N/C
1421	*Pleopunctum thailandicum*	New species	Thailand	N/C
1422	*Phaeosphaeriopsis aloes*	New host	China	N/C
1423	*Comoclathris permunda*	Reference specimen	Uzbekistan	N/C
1424	*Lepidosphaeria strobelii*	New species	India	N/C
1425	*Ernakulamia tanakae*	New record	Thailand	N/C
1426	*Thyridaria aureobrunnea*	New species	Thailand	N/C
1427	*Cylindrotorula*	New genus		N/C
1428	*Cylindrotorula indica*	New species	India	N/C
1429	*Dendryphion hydei*	New record	China	N/C
1430	*Torula lancangjiangensis*	New species	China	N/C
1431	*Torula mackenziei*	New record	China	N/C
1432	*Wicklowia fusiformispora*	New species	Thailand	N/C
1433	*Wicklowia submersa*	New geographical record	Thailand	N/C
1434	*Helicosporium luteosporum*	New record	Thailand	N/C
1435	*Helicosporium sexuale*	New species	Thailand	N/C
1436	*Neohelicosporium irregulare*	New record	Thailand	N/C
1437	*Neohelicosporium parvisporum*	New record	Thailand	N/C
1438	*Tubeufia chiangmaiensis*	New record	Thailand	N/C
1439	*Tubeufia longihelicospora*	New species	Thailand	N/C
1440	*Tubeufia roseohelicospora*	New record	Thailand	N/C
1441	*Megacapitula villosa*	New geographical record	Thailand	N/C
1442	*Cladophialophora abundans*	New geographical record	Thailand	N/C
1443	*Cladophialophora aquatica*	New species	Thailand	N/C
1444	*Aspergillus lannaensis*	New species	Thailand	N/C
1445	*Pseudobactrodesmium stilboideum*	New combination	Thailand	N/C
1446	*Hydrophilomyces hydraenae*	New species	US	N/C
1447	*Laboulbenia divisa*	New species	Costa Rica	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
1448	*Laboulbenia triarthronis*	New species	US	N/C
1449	*Mimeomyces digitatus*	New species	Ecuador	N/C
1450	*Synandromyces makranczyi*	New species	Peru	N/C
1451	*Erysiphe salicicola*	New species	Korea	N/C
1452	*Scolecoleotia*	New genus	Italy	N/C
1453	*Scolecoleotia eriocamporesi*	New species		
1454	*Coryneum fagi*	New species	China	N/C
1455	*Diaporthe chamaeropicola*	New species	Portugal	N/C
1456	*Diaporthe foeniculina*	New record	Portugal	N/C
1457	*Diaporthe pseudophoenicicola*	New record	Portugal	N/C
1458	*Diaporthe pyracanthae*	New record	Portugal	N/C
1459	*Phaeocytostroma yomense*	New species	Thailand	N/C
1460	*Parafuscosporella nilotica*	New species	Egypt	N/C
1461	*Fusarium atrovinosum*	New record	Australia	N/C
1462	*Fusarium clavum*	New record	Australia	N/C
1463	*Fusarium queenslandicum*	New species	Australia	N/C
1464	*Mariannaea camelliae*	New species	Thailand	N/C
1465	*Thyronectria caudata*	New record	Uzbekistan	N/C
1466	*Phaeoisaria aquatica*	New record	Thailand	N/C
1467	*Phaeoisaria synnematicus*	New species	India	N/C
1468	*Pleurotheciella dimorphospora*	New species	China	N/C
1469	*Pseudodactylaria albicolonia*	New species	Thailand	N/C
1470	*Canalisporium caribense*	New record	Thailand	N/C
1471	*Rhexoacrodictys nigrospora*	New species	Thailand	N/C
1472	*Cercophora dulciaquae*	New species	Thailand	N/C
1473	*Khaleijomyces umikazeanus*	New species	Japan	N/C
1474	*Eutypa flavovirens*	New record	Italy	N/C
1475	*Eutypa lata*	New record	Italy	N/C
1476	*Xylaria apiospora*	New species	India	N/C
1477	*Xylaria haemorrhoidalis*	New record	India	N/C
1478	*Melanographium smilacis*	New species	Thailand	N/C
1479	*Chlorophyllum demangei*	New record	Laos	N/C
1480	*Chlorophyllum globosum*	New record	Laos	N/C
1481	*Chlorophyllum hortense*	New record	Laos	N/C
1482	*Micropsalliota globocystis*	New record	Laos	N/C
1483	*Micropsalliota gracilis*	New record	Laos	N/C
1484	*Xanthagaricus necopinatus*	New record	Laos	N/C
1485	*Saproamanita manicata*	New record	Thailand	*Amanita manicata*
1486	*Cortinarius alutarius*	New species	Poland	N/C
1487	*Cortinarius mammillatus*	New species	Poland	N/C
1488	*Cortinarius quercoflocculosus*	New species	Poland	N/C
1489	*Laccaria populina*	New species	Italy	N/C
1490	*Hygrocybe boertmannii*	New species	India	N/C
1491	*Marasmius benghalensis*	New species	India	N/C
1492	*Marasmius jinfoshanensis*	New species	China	N/C
1493	*Marasmius subtropicus*	New species	India	N/C
1494	*Cruentomycena uttarakhandina*	New species	India	N/C
1495	*Cyathus uniperidiolus*	New species	India	N/C
1496	*Marasmiellus palmivorus*	New record	Thailand	N/C
1497	*Coprinellus punjabensis*	New species	Pakistan	N/C
1498	*Geastrum gorgonicum*	New species	Cape	N/C
1499	*Geastrum hansagiense*	New species	Hungary	N/C
1500	*Hyphodontia yunnanensis*	New species	China	N/C
1501	*Odontia huanrenensis*	New species	China	Nom. inval., Art. 40.7 (Shenzhen)
1502	*Odontia parvispina*	New species	China	N/C
1503	*Hyphoderma australosetigerum*	New species	Chile	N/C

Table 5 (continued)

FDN number	Species name	Status	Country/Region	Comment
1504	*Efibula rodriguezarmasiae*	New species	Spain	N/C
1505	*Phanerochaete hainanensis*	New species	China	N/C
1506	*Favolus septatus*	New record	India	N/C
1507	*Lactarius pallidozonarius*	New species	China	N/C
1508	*Russula paravioleipes*	New species	China	N/C
1509	*Microbotryum polycnemoides*	New species	Turkey	N/C
1510	*Mortierella solitaria*	New species	Austria	Nom. inval., Art. 40.7 (Shenzhen)
1511	*Mucor harpali*	New species	Korea	N/C

*is FDN number that appear different in text than FDN number of itself in Table of Contents in the publication

N/C-no change

Key to the smut fungi on *Anadelphia*, *Elymandra*, and *Monocymbium* (modified after Denchev and Denchev 2016).

1 Sori in leaves and spatheoles..**2**

1*Sori in racemes, spikelets or ovaries...**3.**

2 Sori form non-erumpent streaks or patches on leaves and spatheoles. Spores (9–)9.5–15.5(–18.5) μm long, spore wall 1.2–3.0(–3.8) μm thick. [On *Anadelphia pumila*].. ***Jamesdicksonia anadelphiae.***

2*Sori form erumpent streaks on leaves and spatheoles. Spores (11.5–)13–23.5(–26.5) μm long, spore wall (2.0–)2.5–7.0(–9.0) μm thick. [On *Anadelphia trichaeta*].........***Jamesdicksonia anadelphiae-trichaetae.***

3 Sori in some ovaries of an inflorescence. [On *Elymandra androphila*]..**4.**

3*Sori in racemes or spikelets.............................**5.**

4 Spores 10.5–15 μm long; spore walls echinate, with 1–1.5 μm high spines......***Macalpinomyces elymandrae.***

4* Spores 17–27 μm long; spore walls with apically flattened or rounded, densely spaced projections, 1–2.5(–3) μm high..................................***Tilletia elymandrae.***

5 Spore balls present. Spores dimorphic. Outer spores (9.5–)10.5–15(–16) μm long. Sterile cells absent. [On *Anadelphia pumila*]..............***Anthracocystis anadelphiae.***

5* Spore balls absent. Spores not dimorphic, smaller. Sterile cells present..**6.**

6 Sori destroying all racemes. Spores minutely echinulate-verruculose, with ornaments up to 0.2 μm in height. [On *Anadelphia leptocoma*]................................***Sporisorium anadelphiae-leptocomae.***

6* Sori in spikelets or groups of spikelets. Spore ornamentation echinulate, with higher ornaments..............**7.**

7 Spore wall moderately echinulate, spinules up to 0.7 μm high. Spores (8.5–)9–11.5(–12.5) (10.5 ± 0.7) μm long. [On *Anadelphia trichaeta*]...***Sporisorium anadelphiae-trichaetae.***

7*Spore wall minutely echinulate, spinules up to 0.3(–0.4) μm high. Spores (7–)7.5–10.5(–11.5) (9.1 ± 0.6) μm long. [On *Monocymbium ceresiiforme*]...***Sporisorium monocymbii.*** (Table 5)

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Declarations

Conflict of interest Authors declare that they have no conflict of interest.

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