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Fungal diversity notes 929–1035: taxonomic and phylogenetic contributions on genera and species of fungi

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Abstract

This article is the ninth in the series of Fungal Diversity Notes, where 107 taxa distributed in three phyla, nine classes, 31 orders and 57 families are described and illustrated. Taxa described in the present study include 12 new genera, 74 new species, three new combinations, two reference specimens, a re-circumscription of the epitype, and 15 records of sexual-asexual morph connections, new hosts and new geographical distributions. Twelve new genera comprise *Brunneofusispora*, *Brunneomurispora*, *Liua*, *Lonicericola*, *Neoeutypella*, *Paratrimmatostroma*, *Parazalerion*, *Proliferophorum*, *Pseudoastrosphaeriellopsis*, *Septomelanconiella*, *Velebitea* and *Vicosamyces*. Seventy-four new species are *Agaricus memnonius*, *A. langensis*, *Aleurodiscus patagonicus*, *Amanita flavoalba*, *A. subtropicana*, *Amphisphaeria mangrovei*, *Baorangia major*, *Bartalinia kunmingensis*, *Brunneofusispora sinensis*, *Brunneomurispora lonicerae*, *Capronia camelliae-yunnanensis*, *Clavulina thindii*, *Coniochaeta simbalensis*, *Conlarium thailandense*, *Coprinus trigonosporus*, *Liua muriformis*, *Cyphellophora filicis*, *Cytospora ulmicola*, *Dacrymyces invisibilis*, *Dictyocheirospora metroxylonis*, *Distoseptispora thysanolaenae*, *Emericellopsis koreana*, *Galiicola baoshanensis*, *Hygrocybe lucida*, *Hypoxylon teeravasati*,

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Hyweljonesia indica, *Keissleriella caraganae*, *Lactarius olivaceopallidus*, *Lactifluus midnapurensis*, *Lembosia brigadeirensis*, *Leptosphaeria urticae*, *Lonicericola hyaloseptispora*, *Lophiotrema mucilaginosis*, *Marasmiellus bicoloripes*, *Marasmius indojasminodorus*, *Micropeltis phetchaburiensis*, *Mucor orantomantidis*, *Murilentithecium lonicerae*, *Neobambusicola brunnea*, *Neoeutypella baoshanensis*, *Neoroussoella heveae*, *Neosetophoma lonicerae*, *Ophiobolus malleolus*, *Parabambusicola thysanolaenae*, *Paratrimmatostroma kunmingensis*, *Parazalerion indica*, *Penicillium dokdoense*, *Peroneutypa mangrovei*, *Phaeosphaeria cycadis*, *Phanerochaete australosanguinea*, *Plectosphaerella kunmingensis*, *Plenodomus artemisiae*, *P. lijiangensis*, *Proliferophorum thailandicum*, *Pseudoastrosphaeriellopsis kaveriana*, *Pseudohelicomyces menglunicus*, *Pseudoplagiostoma mangiferae*, *Robillarda mangiferae*, *Roussoella elaeicola*, *Russula choptae*, *R. uttarakhandia*, *Septomelanconiella thailandica*, *Spencermartinsia acericola*, *Sphaerellopsis isthmospora*, *Thozetella lithocarpi*, *Trechispora echinospora*, *Tremellochaete atlantica*, *Trichoderma koreanum*, *T. pinicola*, *T. rugulosum*, *Velebitea chrysotexta*, *Vicosamyces venturisporus*, *Wojnowiciella kunmingensis* and *Zopfiella indica*. Three new combinations are *Baorangia rufomaculata*, *Lanmaoa pallidorosea* and *Wojnowiciella rosicola*. The reference specimens of *Canalisporium kenyense* and *Tamsiniella labiosa* are designated. The epitype of *Sarcopeziza sicula* is re-circumscribed based on cyto- and histochemical analyses. The sexual-asexual morph connection of *Plenodomus sinensis* is reported from ferns and *Cirsium* for the first time. In addition, the new host records and country records are *Amanita altipes*, *A. melleialba, Amarenomyces dactylidis*, *Chaetosphaeria panamensis*, *Coniella vitis*, *Coprinopsis kubickae*, *Dothiorella sarmentorum*, *Leptobacillium leptobactrum* var. *calidus*, *Muyocopron lithocarpi*, *Neoroussoella solani*, *Periconia cortaderiae*, *Phragmocamarosporium hederae*, *Sphaerellopsis paraphysata* and *Sphaeropsis eucalypticola*.

Keywords 86 new taxa · Agaricomycetes · Ascomycota · Basidiomycota · Dacrymycetes · Dothideomycetes · Eurotiomycetes · Lecanoromycetes · Leotiomycetes · Mucoromycetes · Mucoromycota · Pezizomycetes · Sordariomycetes · Taxonomy

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Introduction

Fungi are well-known as a large and diverse group of microorganisms that play important functional roles from agricultural, ecological and economic perspectives. They are crucial to natural ecosystems as decomposers degrading dead organic materials, accelerating rock weathering and response to plant growth, nutrient cycling, as well as maintaining plant diversity (Kendrick 2000; Finlay 2008; Zechmeister-Boltenstern et al. 2015; Drinkwater et al. 2017; Horwath 2017; Hyde et al. 2018a, b; Willis 2018). They are heterotrophic and may change their lifestyles from endophytic to pathogenic to saprobic on plants or other organisms as well as other fungi depending on the environmental circumstances (Hyde et al. 2007, 2018a; Promputtha et al. 2007, 2010; Slippers and Wingfield 2007; Ghimire and Hyde 2008; Hyde and Soytong 2008; Gomes et al. 2013; Zhan et al. 2016; Ariyawansa et al. 2018; Haelewaters et al. 2018; Liyanage et al. 2018; Lofgren et al. 2018; Wang et al. 2018; Sun et al. 2019). Sixteen phyla are accepted in the Kingdom Fungi (Tedersoo et al. 2018; Wijayawardene et al. 2018b).

Hawksworth (1991, 2001) estimated 1.5 million species of fungi worldwide, with fewer than 5–10% having been described. Hawksworth and Lücking (2017) attempted to derive an updated estimate of global fungal diversity based on scientific evidence such as the extrapolations of plant/fungus ratios, including molecular and fieldwork data from the same sites. They concluded that there is an estimated 2.2–3.8 million undescribed species with taxa awaiting discovery in biodiversity hot spots, with only 120,000 species described and accepted (Hawksworth and Lücking 2017).

In our ongoing research compiling notes on new fungal taxa, reference specimens, new data, and other taxonomic contributions, more than 900 species have been introduced, re-circumscribed and illustrated worldwide based up on morphological characteristics and phylogenetic analyses. This is the ninth paper in the fungal diversity series with more than 100 species contributions which were mainly collected from China, some other Asian countries, as well as other parts of the world.

Materials and methods

Materials and methods follow the previous fungal diversity notes (Hyde et al. 2016; Tibpromma et al. 2017). Fresh and dried specimens in this study were collected from Australia, Brazil, Chile, China, Croatia, Equatorial Guinea, India, Italy, Korea, New Zealand, Russia, Saudi Arabia, Taiwan, Thailand, UK and the USA. Media agar used to cultivated fungi is shown in Table 1. The genes and primers used in this study are shown in the Table 2. Phylogenetic analyses were performed based on Bayesian inference (BI), maximum likelihood (ML) and maximum parsimony (MP) (see Table 2).

Phylum Ascomycota R.H. Whittaker
We follow the latest treatments and updated accounts of Ascomycota in Wijayawardene et al. (2017a, 2018a).

Class Dothideomycetes O.E. Erikss. & Winka
The Classification of families in Dothideomycetes follow Hyde et al. (2013), Liu et al. (2017a) and Wijayawardene et al. (2018a). The subclasses, orders and families of Dothideomycetes are listed in alphabetical order.

Subclass Dothideomycetidae P.M. Kirk

Capnodiales Woron.

Teratosphaeriaceae Crous & U. Braun
Teratosphaeriaceae was introduced by Crous et al. (2007a) and is typified by *Teratosphaeria* Syd. & P. Syd. The family was introduced to accommodate several important leaf spot and extremotolerant species initially included in the genera *Teratosphaeria*, *Mycosphaerella* and related asexual morph genera. Recently, 59 genera were listed in this family (Wijayawardene et al. 2018a). The latest treatments of genera in *Teratosphaeriaceae* were outlined in Quaedvlieg et al. (2014), Wäli et al. (2014) and Hyde et al. (2017).

Hyweljonesia R.G. Shivas et al.
A monotypic genus, *Hyweljonesia* was introduced in *Teratosphaeriaceae* by Shivas et al. (2016) to accommodate *H. queenslandica* R.G. Shivas et al. (as the type

Table 1 Abbreviations of media agar used for fungal cultivation in this study

Name	Abbreviation
Cornmeal dextrose agar	CMD
Creatine sucrose agar	CREA
Czapek yeast autolysate agar	CYA
Malt extract agar	MEA
Oat agar	OA
Potato carrot agar	PCA
Potato dextrose agar	PDA
Sea water agar	SWA
Spezieller nährstoffarmer agar	SNA
Synthetic mucor agar	SMA
Water agar	WA
Yeast extract sucrose agar	YES

Table 2 Genes sequenced, primers used and phylogenetic analyses performed in this study

Family	Genes/loci	Primers	Phylogenetic analysis	References
Agaricaceae	LSU, TEF1-α and ITS (*Agaricus*); ITS (*Coprinus*)	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), EF1-983F/EF1-1567R (TEF1-α) (*Agaricus*); ITS1/ITS4 (ITS, *Coprinus*)	BI and ML (*Agaricus*); ML (*Coprinus*)	Vilgalys and Hester (1990), White et al. (1990), O'Donnell (1993), Glass and Donaldson (1995), Carbone and Kohn (1999), Liu et al. (1999), Rehner (2001), Samuels et al. (2002), Matheny (2005), Hong et al. (2006), Cai et al. (2014), Raspé et al. (2016)
Amanitaceae	LSU and RPB2	LR0R/LR5(LSU), rpb2-Am-6F/Am-7R (RPB2)	ML	
Amphisphaeriaceae	LSU, SSU and ITS	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU)	BI, ML and MP	
Asterinaceae	LSU	LR0R/LR5 (LSU)	BI	
Auriculariaceae	ITS and LSU	ITS5/ITS4 (ITS), LR0R/LR5 (LSU)	BI and ML	
Boletaceae	ATP6, RPB2 and TEF1-α	ATP6-1M40F/ATP6-2 M (ATP6), bRPB2-6F/bRPB2-7.1R (RPB2), EF1-983F/EF1-2218R (TEF1-α)	ML	
Botryosphaeriaceae	ITS and TEF1-α (*Dothiorella*); ITS, TEF1-α and TUB2 (*Sphaeropsis*)	ITS5/ITS4 (ITS), EF1-728F/EF1-986R (TEF1-α), BT2a/BT2b (TUB2)	BI and ML (*Dothiorella*); BI, ML and MP (*Sphaeropsis*)	
Chaetosphaeriaceae	LSU, ITS and TUB2	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), BT2a/BT2b (TUB2)	BI and ML	
Clavulinaceae	ITS	ITS1/ITS4 (ITS)	ML	
Coniochaetaceae	LSU and ITS	ITS5/ITS4 (ITS), LR0R/LR7 (LSU)	ML	
Conlariaceae	LSU, SSU and ITS	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU)	BI and ML	
Cordycipitaceae	ITS and LSU	ITS5/ITS4 (ITS), LR0R/LR7 (LSU)	ML and MP	
Cyphellophoraceae	ITS, LSU and SSU	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU)	BI and ML	
Cytosporaceae	ITS, LSU, and ACT	ITS1/ITS4 (ITS), NL1/NL4 (LSU), ACT512F/ACT783R (ACT)	ML	
Dacrymycetaceae	ITS	ITS5/ITS4 (ITS)	BI, ML and MP	
Diaporthomycetidae, genera *incertae sedis* *(Proliferophorum)*	LSU, SSU and ITS	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU)	BI and ML	
Diatrypaceae	ITS and TUB2	ITS1/ITS4 (ITS), BT2a/BT2b (TUB2)	BI, ML and MP	
Dictyosporiaceae	ITS, LSU and TEF1-α	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), EF1-983F/EF1-2218R (TEF1-α)	BI, ML and MP	
Didymosphaeriaceae	ITS and LSU	ITS1/ITS4 (ITS), LR0R/LR5 (LSU)	BI	
Distoseptisporaceae	ITS, LSU and TEF1-α	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), EF1-983F/EF1-2218R (TEF1-α)	BI, ML and MP	
Herpotrichiellaceae	ITS, LSU and SSU	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU)	BI and ML	
Hydnodontaceae	ITS	ITS5/ITS4 (ITS)	BI, ML and MP	
Hygrophoraceae	ITS	ITS1/ITS4 (ITS)	ML	

Table 2 continued

Family	Genes/loci	Primers	Phylogenetic analysis	References
Hypocreaceae	TEF1-α and RPB2	EF1-728F/TEF1rev (TEF1-α), fRPB2-5F/fRPB2-7cR (RPB2)	BI and ML	
Hypocreales, genera *incertae sedis* (*Emericellopsis*)	ITS and TUB2	ITS1/ITS4 (ITS), BT2a/BT2b (TUB2)	ML	
Hypoxylaceae	ITS, LSU, RPB2 and TUB2	ITS1/ITS4 (ITS), LR0R/LR5 (LSU), fRPB2-5F/fRPB2-7cR (RPB2), BT2a/BT2b (TUB2)	BI, ML and MP	
Lachnaceae	ITS and LSU	ITS1/ITS4 (ITS), LR0R/LR7 (LSU)	BI and ML	
Lasiosphaeriaceae	LSU, TUB2, ITS and RPB2	ITS1/ITS4 (ITS), LR0R/LR5 (LSU), BT2a/BT2b (TUB2), fRPB2-5F/fRPB2-7cR (RPB2)	BI, ML and MP	
Lentitheciaceae	LSU, SSU, ITS and TEF1-α	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU), EF1-983F/EF1-2218R (TEF1-α)	BI and ML	
Leptosphaeriaceae	LSU, SSU and ITS	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU)	BI and ML	
Lophiotremataceae	ITS, LSU, SSU, TEF1-α and RPB2	ITS1/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU), EF1-983F/EF1-2218R (TEF1-α), fRPB2-5f/fRPB2-7cR (RPB2)	BI and ML	
Marasmiaceae	ITS and LSU	ITS1/ITS4 (ITS), LR0R/LR3 (LSU)	BI and ML	
Melanconiellaceae	ITS, LSU and RPB2	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), fRPB2-5f/fRPB2-7cR (RPB2)	BI, ML and MP	
Micropeltidaceae	LSU and SSU	LR0R/LR5 (LSU), NS1/NS4 (SSU)	ML and MP	
Microthyriales, genera *incertae sedis* (*Parazalerion)*	LSU	LR0R/LR5 (LSU)	ML	
Mucoraceae	ITS and LSU	ITS1/ITS4 (ITS), LR0R/LR5F (LSU)	ML	
Muyocopronaceae	LSU and SSU	LR0R/LR5 (LSU), NS1/NS4 (SSU)	BI and ML	
Occultibambusaceae	LSU, SSU, ITS, RPB2 and TEF1-α	ITS5/ITS4 (ITS), LR0R/LR7 (LSU), NS1/NS4 (SSU), EF1-983F/EF1-2218R (TEF1-α), fRPB2-5f/fRPB2-7cR (RPB2)	BI, ML and MP	
Omphalotaceae	ITS and LSU	ITS1/ITS4 (ITS), LR0R/LR7 (LSU)	BI and ML	
Parabambusicolaceae	SSU, ITS, LSU and TEF1-α	ITS1/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU), EF1-983F/EF1-2218R (TEF1-α)	BI and ML	
Periconiaceae	ITS, LSU and TEF1-α	ITS1/ITS4 (ITS), LR0R/LR5 (LSU), EF1-983F/EF1-2218R (TEF1-α)	BI and ML	
Pezizaceae	ITS and LSU	ITS1/ITS4 (ITS), LR0R/LR7 (LSU)	ML	
Phaeosphaeriaceae	LSU, SSU, TEF1-α and ITS	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU), EF1-983F/EF1-2218R (TEF1-α)	BI and ML	
Phanerochaetaceae	ITS and LSU	ITS5/ITS4 (ITS), LR0R/LR5 (LSU)	BI, ML and MP	
Phyllachoraceae	LSU, SSU, and ITS	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU)	BI and ML	
Plectosphaerellaceae	LSU, ITS and TEF1-α	ITS1/ITS4 (ITS), LR0R/LR5 (LSU), EF1-983F/EF1-2218R (TEF1-α)	BI and ML	
Psathyrellaceae	ITS	ITS1/ITS4 (ITS)	ML	
Pseudoastrosphaeriellaceae	LSU, SSU, ITS, RPB2 and TEF1-α	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU), EF1-983F/EF1-2218R (TEF1-α), fRPB2-5f/fRPB2-7cR (RPB2)	BI and ML	
Pseudoplagiostomataceae	ITS, LSU, TUB2 and TEF1-α	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), BT2a/BT2b (TUB2), EF1-983F/EF1-2218R (TEF1-α)	BI, ML and MP	
Roussoellaceae	LSU, SSU, TEF1-α, ITS and RPB2	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU), EF1-983F/EF1-2218R (TEF1-α), fRPB2-5f/fRPB2-7cR (RPB2)	BI and ML	

Table 2 continued

Family	Genes/loci	Primers	Phylogenetic analysis	References
Russulaceae	ITS and LSU	ITS1/ITS4 (ITS), LR0R/LR3 (LSU)	ML (*Lactarius*); BI and ML (*Lactifluus*), BI (*Russula*)	
Savoryellaceae	LSU and ITS	ITS5/ITS4 (ITS), LR0R/LR5 (LSU)	BI and ML	
Schizoparmaceae	ITS, LSU, HIS3 and TEF1-α	ITS4/ITS5 (ITS), LR0R/LR5 (LSU); H3-1A/H3-1B (HIS3), EF1-728F/EF1-986R (TEF1-α)	MP	
Sporocadaceae	ITS and LSU	ITS5/ITS4 (ITS), LR0R/LR5 (LSU)	BI and ML	
Stereaceae	ITS and LSU	ITS5/ITS4 (ITS), LR0R/LR5 (LSU)	BI, ML and MP	
Sulcatisporaceae	LSU and ITS	ITS5/ITS4 (ITS), LR0R/LR5 (LSU)	ML	
Teratosphaeriaceae	ITS and LSU	ITS5/ITS4 (ITS), LR0R/LR7 (LSU)	ML	
Thyridariaceae	LSU, SSU, TEF1-α, ITS and RPB2	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), NS1/NS4 (SSU), EF1-983F/EF1-2218R (TEF1-α), fRPB2-5f/fRPB2-7cR (RPB2)	BI and ML	
Trichocomaceae	TUB2 and CMD	BT2a/BT2b (TUB2), CMD5/CMD6 (CMD)	ML	
Tubeufiaceae	ITS, LSU, TEF1-α and RPB2	ITS5/ITS4 (ITS), LR0R/LR5 (LSU), EF1-983F/EF1-2218R (TEF1-α), fRPB2-5f/fRPB2-7cR (RPB2)	BI and ML	

species) isolated from a cocoon of an unidentified microlepidoptera parasitized by a chalcidoid wasp (*Hymenoptera*: *Chalcoidea*), collected from tropical forests of northern Queensland, Australia. The genus is characterized by white, septate, smooth-walled, hyaline to subhyaline mycelial hyphae often form hyphal tufts from which straight, unbranched, light brown, smooth-walled, and septate conidiophores arise laterally. Subhyaline, cuneiform, smooth-walled conidia are produced on characteristic integrated, pale brown and minutely verruculose conidiogenous cells forming apical whorls (1–5) of conidiogenous cells with inconspicuous conidial scars (Shivas et al. 2016). In this study, a new species, *H. indica* is introduced, which was collected as a saprobe associated with leaves of *Shorea robusta* Roth colonized by black moulds in India. Phylogenetic analysis from maximum likelihood based on a combined LSU and ITS sequence dataset (Fig. 1) is provided to clarify its phylogenetic affinities within *Teratosphaeriaceae*.

Hyweljonesia indica **P.N. Singh & S.K. Singh, *sp. nov.***

MycoBank number: MB821804; *Facesoffungi number*: FoF03526, Fig. 2

Etymology: The specific epithet "*indica*" refers to the country of origin.

Holotype: AMH 9889

Colour codes follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978).

Saprobic on leaves of *Shorea robusta* (*Dipterocarpaceae*) forests in terrestrial habitats. **Sexual morph** Undetermined. **Asexual morph** Vegetative hyphae smooth-walled, septate, subhyaline to light olivaceous, up to 4 µm wide. *Conidiophores* arising from loose to compact hyphal tufts, macronematous, lateral, unbranched to rarely branched at base, 0–1-septate, straight, smooth-walled, light olivaceous, 4.5–24.5 µm long ($\bar{x}$ = 9.6 µm, n = 30); base flared, 3.5–8.5 µm wide ($\bar{x}$ = 5.87 µm, n = 30); apex narrow, cylindrical, 1.5–4.5 µm wide ($\bar{x}$ = 2.74 µm, n = 30). *Conidiogenous cells* terminal, 1(–2), straight, smooth-walled, subhyaline to olivaceous, cylindrical to clavate, scars inconspicuous, 5.5–12.8 × 2–5 µm ($\bar{x}$ = 10.3 × 3.28 µm, n = 30). *Conidia* acrogenous to rarely acropleurogenous, produced in apical whorl of 1–12 conidia, simple, aseptate, obovoid to pyriform, smooth-walled, hyaline, apex rounded, base truncate, hilum refractive, 2.4–6.8 × 1.5–2.6 µm ($\bar{x}$ = 4.6 × 2 µm, n = 30).

Culture characteristics: Colonies on PDA reaching average 12.5 mm diam. in 12 days, after 2 weeks of incubation at 25 °C, colonies were circular, margin regular, smooth, and orange white (6A2). Later turning to grey (2C1), mucoid, centre raised, umbonate, periphery white (6A1), with abundant hyphal tufts, sulcate, up to 7500 × 132–220 µm. Reverse brownish orange (5C4), margin smooth-walled, wrinkled.

Material examined: INDIA, Uttar Pradesh, Gorakhpur District, on *Shorea robusta* (leaf infested with black mold), 5 May 2016, P.N. Singh, AMH 9889 (**holotype**), ex-type living culture, NFCCI 4146 (National Fungal Culture Collection of India-WDCM 932).

GenBank numbers: ITS = MF322773, LSU = MF322775.

Notes: Detail study of in vitro cultural characteristics and morphology revealed a few morphological similarities with *Hyweljonesia queenslandica*. However, *H. indica* is distinct in having obovoid to pyriform conidia which are significantly larger when compared to the cuneiform conidia of *H. queenslandica* (Fig. 2). Conidiogenous cells of *H. indica* mostly arise singly from the conidiophores, while they are produced in 1–5 whorls of *H. queenslandica* (Shivas et al. 2016).

Sequence analysis of ITS and LSU positions *Hyweljonesia indica* in the genus *Hyweljonesia* closely related to *H. queenslandica* with strong bootstrap support (100% ML; Fig. 1). The BLASTn search of ITS sequence shows 95% similarity (468/491) with *H. queenslandica* (BRIP 61322b) and same similarity was recorded for LSU sequence with 98% similarity (838/851). Thus following the guidelines of Jeewon and Hyde (2016) this is a new species. To our understanding this genus and species is isolated and reported for the first time from India as a saprobic black mold associated with leaves of *Shorea robusta*.

Subclass Pleosporomycetidae C.L. Schoch et al.

Pleosporales Luttr. ex M.E. Barr

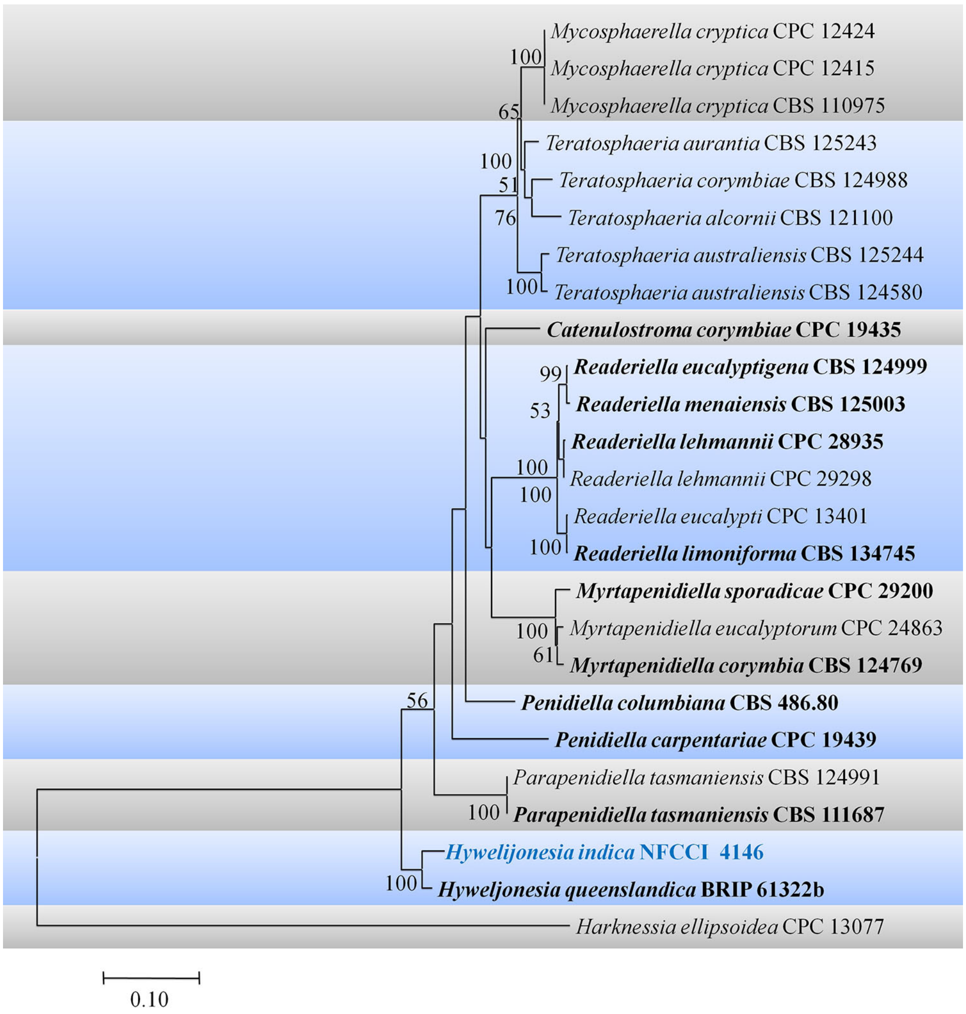
Dictyosporiaceae Boonmee & K.D. Hyde

We follow the latest treatments and updated accounts of *Dictyosporiaceae* in Boonmee et al. (2016), Wang et al. (2016), Hyde et al. (2017), Tibpromma et al. (2018) and Yang et al. (2018b). Recently, 12 genera were listed in this family (Wijayawardene et al. 2018a).

Dictyocheirospora M.J. D'souza et al.

Dictyocheirospora was introduced by Boonmee et al. (2016) with *D. rotunda* M.J. D'souza et al. as the type species. Boonmee et al. (2016) included *Dictyocheirospora* in the new family *Dictyosporiaceae* based on the fact that *Dictyocheirospora* species have dark sporodochial colonies, and produce aeroaquatic cheiroid dictyospores. Many species were subsequently accommodated in this genus (Wang et al. 2016; Hyde et al. 2017; Tibpromma et al. 2018; Yang et al. 2018b) and 17 species are listed in Index Fungorum (2019). In this study, *Dictyocheirospora metroxylonis* Konta & K.D. Hyde, sp. nov. is introduced from dead *Metroxylon sagu* (*Arecaceae*) in Thailand based on morphological and multigene phylogenetic support.

Fig. 1 Phylogram generated from maximum likelihood analysis based on the combined ITS and LSU sequences of representative species in *Teratosphaeriaceae*. Bootstrap support value for maximum likelihood equal to or greater than 50% are indicated at the nodes. The novel species is shown in blue. The ex-type strains are indicated in bold. The tree is rooted to *Harknessia ellipsoidea* (CPC 13077)



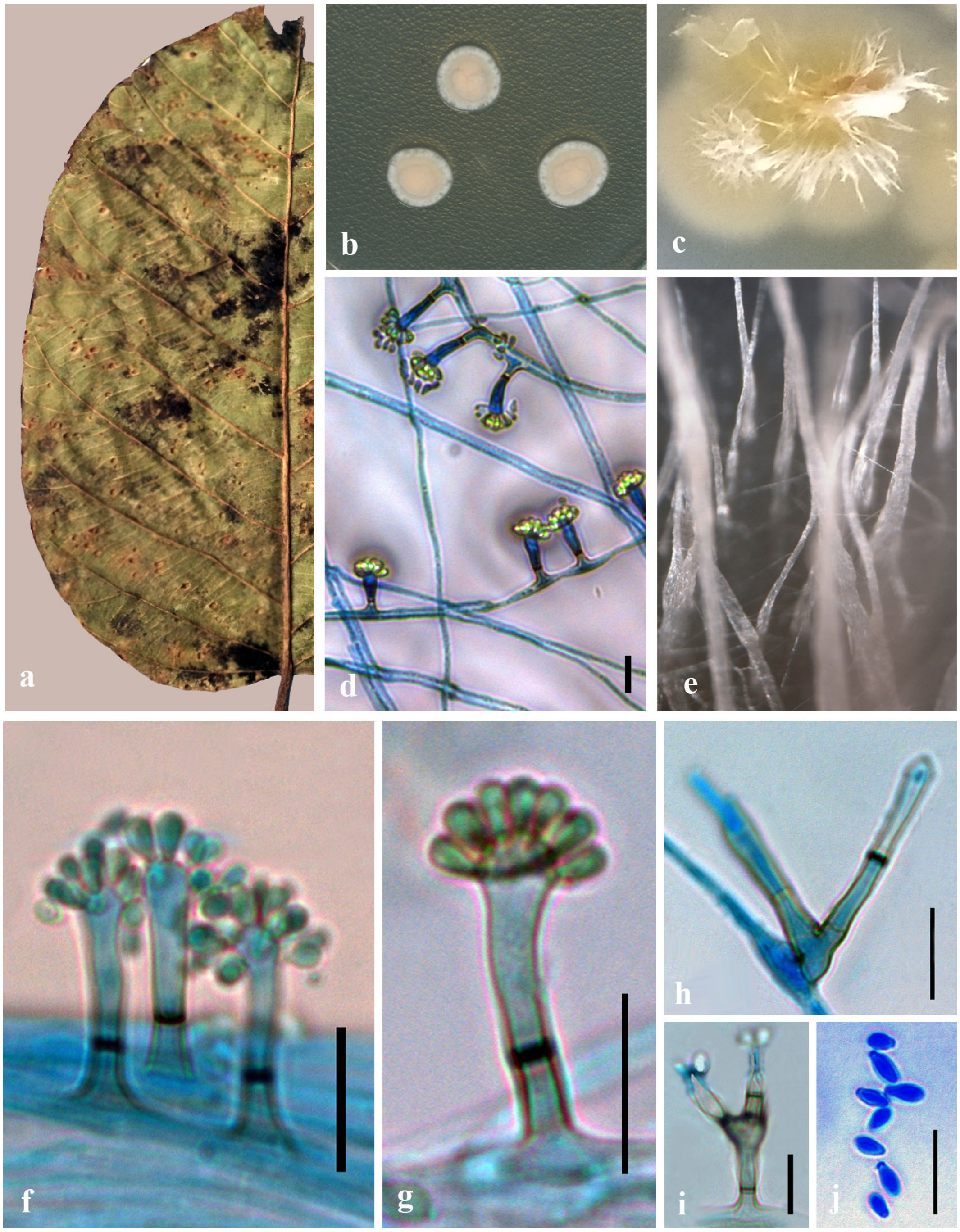


Fig. 2 ***Hyweljonesia indica*** (AMH 9889, **holotype**). **a** Lower surface of *Shorea robusta* leaf showing patches of black moulds. **b** Colony characteristics on PDA (front view). **c** Enlarged view of single colony on PDA showing mycelial tufts. **d** Conidiophores bearing conidiogenous cells and whorls of conidia arising from tuft of mycelial hyphae. **e** Tufts of white vegetative mycelial hyphae in stereoscopic view. **f** Numerous conidiophores arising laterally from loose and tufted mycelial hyphae. **g** Enlarged view of single conidiophore bearing whorl of conidia. **h** Conidiophore branched at base. **i** Conidiophore bearing two conidiogenous cells and attached conidia. **j** Obovoid to pyriform hyaline conidia with refractive conidial scars. *Scale bars* **d**, **f–j** = 10 µm

Dictyocheirospora metroxylonis Konta & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555290; *Facesoffungi number*: FoF04833, Fig. 4

Etymology: Name reflects the host genus *Metroxylon*.

Holotype: MFLU 15-0028

Saprobic on dead *Metroxylon sagu*. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Sporodochia* on natural substrate in small groups, punctiform, 100–200 µm diam. ($\bar{x}$ = 130 µm, n = 10), velvety, greyish to dark brown. *Mycelium* immersed, composed of brown, smooth, thin-walled, septate, branched hyphae. *Conidiophores* micronematous, pale brown, smooth, thin-walled. *Conidiogenous cells* 3–8 × 3–5 µm ($\bar{x}$ = 5.2 × 4.6 µm, n = 10), holoblastic, integrated, terminal, determinate, pale brown, smooth-walled. *Conidia* 45–69 × 15–29 µm ($\bar{x}$ = 61 × 20 µm, n = 20), solitary, monoblastic, acrogenous, cheiroid, pale brown, consisting of 4–6 rows of cells, rows digitate, cylindrical, inwardly curved at the tip, arising from a basal cell, each arm composed of 9–14 cells, distoseptate, constricted at thr septa, large guttule in each central cell. *Conidial arm* 29–58 × 5–7 µm ($\bar{x}$ = 47 × 6 µm, n = 10) (Fig. 3).

Culture characteristics: Conidia germinated on MEA within 24 h and germ tubes produced from the basal cells of the conidium. Colonies on MEA reaching 7–7.5 cm diam. after 2 weeks, at 25–28 °C, initially white, becoming grey-light brown, not sporulating on media.

Material examined: THAILAND, Krabi Province, on dead *Metroxylon sagu* Rottb. (*Arecaceae*), 8 December 2014, S. Konta, KBR04d (MFLU 15-0028, **holotype**), ex-type living culture, MFLUCC 15-0282.

GenBank numbers: ITS = MH742321, LSU = MH742313, SSU = MH742317, (MFLUCC 15-0282a); ITS = MH742322, LSU = MH742314, SSU = MH742318, TEF1-α = MH764301 (MFLUCC 15-0282b); ITS = MH742323, LSU = MH742315, SSU = MH742319, TEF1-α = MH764302 (MFLUCC 15-0282c); ITS = MH742324, LSU = MH742316, SSU = MH742320, TEF1-α = MH764303 (MFLUCC 15-0282d).

Notes: *Dictyocheirospora metroxylonis* differs from other *Dictyocheirospora* species by its conidial size, and number of rows and cell numbers in each row. Phylogenetic analyses of a combined ITS, LSU, SSU and TEF1-α sequence dataset (Fig. 3) show that *D. metroxylonis* forms a distinct lineage, clustered with other *Dictyocheirospora* species with moderate support in ML analysis (84% ML) and high support in BI analysis (0.99 BYPP). Since *Dictyocheirospora* has been introduced in *Dictyosporiaceae* (Dothideomycetes), many species were subsequently introduced to this genus with morphological and phylogenetic evidence. Interestingly, *D. metroxylonis* strain MFLUCC 150282d formed a clear zone against contaminated fungi on MEA during our experiment (Fig. 4, r).

Didymosphaeriaceae Munk

We follow the latest treatment and updated accounts of *Didymosphaeriaceae* in Ariyawansa et al. (2014), Wanasinghe et al. (2018) and Tibpromma et al. (2018). There are 26 genera accepted in *Didymosphaeriaceae* (Wijayawardene et al. 2018a). Here we introduce a monotypic genus *Vicosamyces*.

Vicosamyces Firmino, A.R. Machado & O.L. Pereira, ***gen. nov.***

MycoBank number: MB822577; *Facesoffungi number*: FoF03786

Etymology: The generic epithet "*Vicosamyces*" refers to the city "Viçosa", where the type was collected.

Biotrophic or *necrotrophic* associated with plant disease on living leaves, forming a large, irregular, slightly raised, rough, orange brown wound, with orange margin. **Sexual morph** *Ascomata* immersed in orange brown wound tissue, solitary, brown, globose to pyriform, ostiolate. *Peridium* thin-walled, composed of dark brown, pseudoparenchymatous cells, of *textura angularis* to *textura prismatica*. *Hamathecium* comprising numerous, cylindrical, filiform, septate, unbranched, hyaline pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical, subsessile to short pedicellate, with furcate pedicel, apically rounded with well-developed ocular chamber. *Ascospores* overlapping 1–2-seriate, brown, 2-celled, apiosporous, smaller at the lower cell, subfusoid to clavate, or obovoid, narrower towards the lower cell. **Asexual morph** Undetermined.

Type species: *Vicosamyces venturisporus* Firmino, A.R. Machado & O.L. Pereira

Notes: *Vicosamyces* is introduced as a new genus based on morphology and phylogenetic support (LSU and ITS sequence dataset). Phylogenetic analysis of a combined LSU and ITS sequence dataset (Fig. 5) shows the fungus belongs to *Didymosphaeriaceae*, clustering with the genus *Austropleospora* R.G. Shivas & L. Morin. *Vicosamyces* has 2-celled, apiospores, while, *Austropleospora* has muriform ascospores (Morin et al. 2010; Thambugala et al. 2014; Ariyawansa et al. 2015a). Both genera have been found as biotrophic or necrotrophic pathogens associated with plant disease on living leaves, or stems. However, these two genera are associated with different symptoms on the host tissue. *Austropleospora* forms subglobose ascomata, solitary or in groups, immersed in small, brown, raised necrotic spots on *Chrysanthemoides monilifera* ssp. *rotundata* (*Asteraceae*) (Morin et al. 2010; Thambugala et al. 2014). *Vicosamyces* forms globose to pyriform ascomata, solitary, immersed in large, orange-brown wound, with orange margin on leaves of *Eugenia* sp. (*Myrtaceae*). In this study, the phylogenetic relationship of *Austropleospora* and *Vicosamyces* was not well-resolved. Phylogenetic analysis obtained from more informative genes will provide a better phylogenetic relationship of these genera.

Vicosamyces venturisporus Firmino, A.R. Machado & O.L. Pereira, ***sp. nov.***

MycoBank number: MB822578; *Facesoffungi number*: FoF03787, Fig. 6

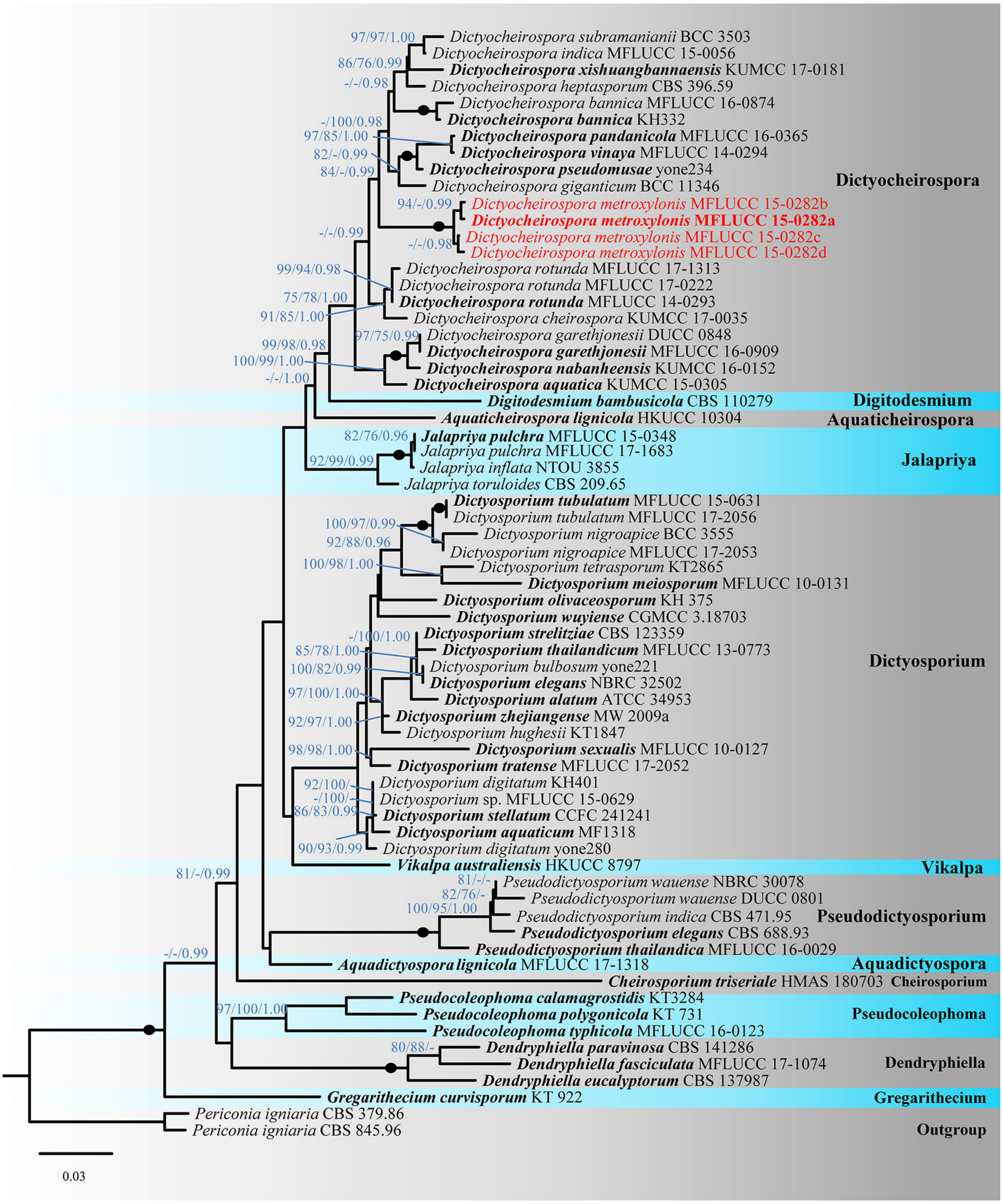


Fig. 3 Maximum likelihood majority rule consensus tree for the analysed *Dictyosporiaceae* isolates based on a dataset of combined ITS, LSU and TEF1-α sequence data. Bootstrap support values for maximum likelihood (ML) and maximum parsimony (MP) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above the nodes as ML/MP/PP. Branches with 100% ML, 100% MP and 1.00 BYPP are shown as black circle at the nodes. The tree is rooted with *Periconia igniaria* (CBS 379.86, CBS 845.96). The new taxon is in red and ex-type strains are in black bold

Etymology: The specific epithet "*venturisporus*" refers to the ascospores which are similar in shape to the ascospores of the genus *Venturia*.

Holotype: VIC 44320

Biotrophic or *necrotrophic* associated with plant disease on living leaves, forming a large, irregular, slightly raised, rough, orange brown wound, with orange margin. **Sexual morph** *Ascomata* 240–340 × 250–310 µm, immersed in orange brown wound, solitary, brown, globose to pyriform, ostiolate. *Peridium* thin-walled, composed of dark brown, pseudoparenchymatous cells, of *textura angularis* to *textura prismatica*. *Hamathecium* comprising 2–2.5 µm wide,

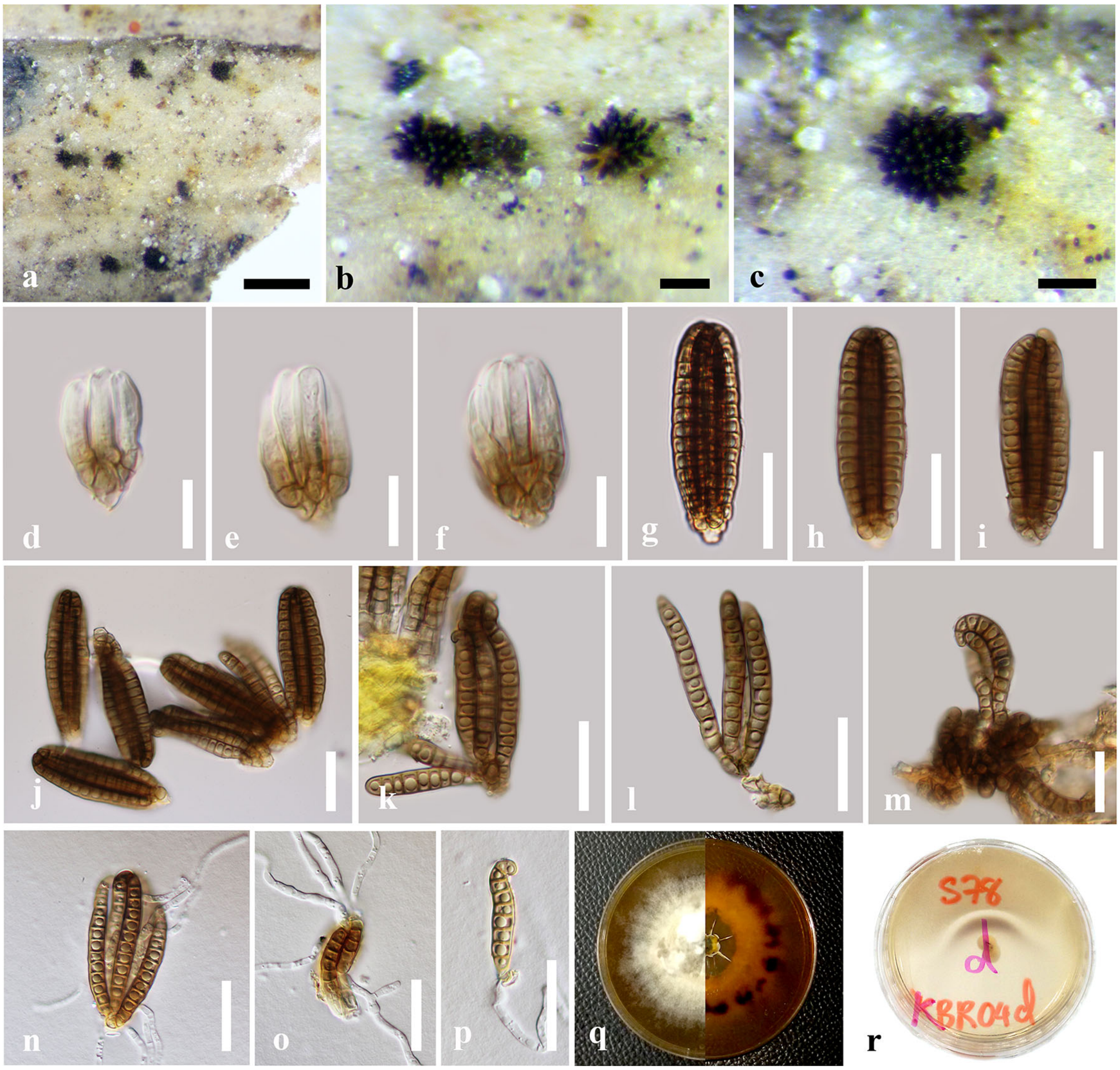


Fig. 4 ***Dictyocheirospora metroxylonis*** (MFLU 15-0028, **holotype**). **a** Sporodochia on the substrate. **b–c** Close up sporodochia on the substrate. **d–f** Immature conidia. **g–m** Mature conidia. **n–p** Germinating conidium. **q** Colony on MEA. **r** Colony on MEA with clear zone against contaminated fungi. *Scale bars* **a** = 500 µm, **b**, **c** = 100 µm, **g–p** = 20 µm, **d–f** = 10 µm

numerous, cylindrical, filiform, septate, unbranched, hyaline pseudoparaphyses. *Asci* 125–152.5 × 14–15 µm, 8-spored, bitunicate, fissitunicate, cylindrical, subsessile to short pedicellate, with furcate pedicel, apically rounded with well-developed ocular chamber. *Ascospores* 22.5–30 × 6–8 µm, overlapping 1–2-seriate, upper cell brown with reddish tint, lower cell pale brown with a reddish tint, 2-celled, apiosporous, smaller at the lower cell, subfusoid to clavate, or obovoid, narrower towards the lower cell, with rounded to acute ends, slightly constricted at the septum, guttulate, smooth-walled. **Asexual morph** Undetermined.

Material examined: BRAZIL, Minas Gerais, Viçosa, Recanto das Cigarras, on leaves of *Eugenia* sp. (*Myrtaceae*), 10 September 2015, A.R. Machado (VIC 44320, **holotype**).

GenBank numbers: ITS = MF802825, LSU = MF802828 (CDA1494); ITS = MF802826, LSU = MF802829 (CDA1495); ITS = MF802827, LSU = MF802830 (CDA495).

Lentitheciaceae Y. Zhang ter et al.

The family *Lentitheciaceae* was introduced by Zhang et al. (2009a) with *L. fluviatile* (Aptroot & Van Ryck.) K.D. Hyde as the type species. Thirteen genera are included in this family (Wanasinghe et al. 2014a, 2018; Knapp et al. 2015; Phookamsak et al. 2015a; Tanaka et al. 2015; Wijayawardene et al. 2015, 2018a; Dayarathne et al. 2018). We follow the latest treatment and updated accounts of *Lentitheciaceae* in Wanasinghe et al. (2014a), Wijayawardene et al. (2015), Tibpromma et al. (2017) and Dayarathne et al. (2018). Based on phylogenetic analysis of a combined LSU, SSU, ITS and

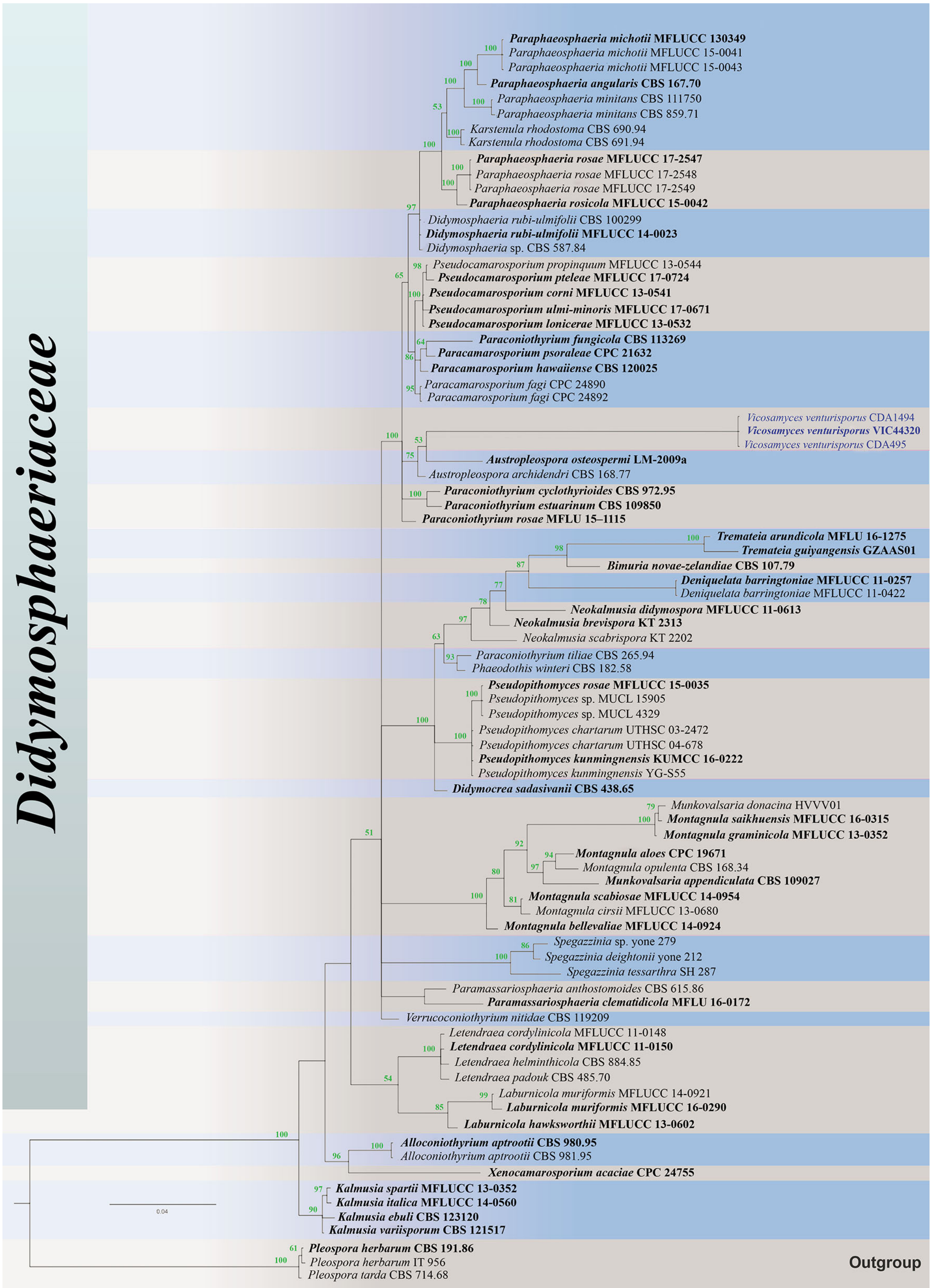


Fig. 5 Bayesian inference tree obtained from the concatenated ITS and LSU sequences including 83 taxa of representative genera in *Didymosphaeriaceae*. Taxa of *Pleosporaceae* (*Pleosporales*) were selected as the outgroup. Bayesian posterior probabilities (BYPP) represented by percentage equal or greater than 50% are shown above the nodes. The new isolates are in blue, ex-type strains are in bold

TEF1-α sequence dataset, two novel species, *Keissleriella caraganae* and *Murilentithecium lonicerae* are introduced. In addition, *Phragmocamarosporium hederae* Wijayaw. et al. associated with leaf spots on *Cycas* sp. (*Cycadaceae*) is reported in Yunnan, China for the first time.

Keissleriella Höhn

We follow the latest treatment and updated accounts of *Keissleriella* in Wanasinghe et al. (2018). Although 43 epithets of *Keissleriella* are listed in Index Fungorum (2018), only 19 species have been confirmed in *Lentitheciaceae* based on molecular data (Fig. 7).

Keissleriella caraganae Chaiwan, Phookamsak, Wanas. & K.D. Hyde, ***sp*. *nov*.**

Index Fungorum number: IF555523; *Facesoffungi number*: FoF04965, Fig. 8

Etymology: The specific epithet "*caraganae*" refers to the host genus *Caragana*, from which the holotype was collected.

Holotype: KUN-HKAS 102236

Saprobic on *Caragana arborescens* (*Fabaceae*). **Sexual morph** *Ascomata* 140–175 µm high, 170–235 µm diam., scattered, solitary or in groups, semi-immersed, visible as raised, black dots on host surface, globose to subglobose, glabrous, ostiolate at centre, with minute papilla, filled with short, brown, aseptate periphyses. *Peridium* 15–25 µm wide, thin-walled, of equal thickness, composed of several layers of small, flattened, brown to dark brown pseudoparenchymatous cells, arranged in a *textura angularis* to *textura prismatica*, intermixed with the host cells. *Hamathecium* composed of dense, 2–3 µm wide, broad filamentous, distinctly septate, anastomosed pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* 39–75 × 10–12 µm ($\bar{x}$ = 60.1 × 11.1 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded, with well-developed ocular chamber. *Ascospores* 14–20 × 3–7 µm ($\bar{x}$ = 16.9 × 5.1 µm, n = 20), overlapping 1–2-seriate, pale yellowish, fusiform to ellipsoidal, with rounded ends, (1–)3(–4)-septate, slightly constricted at the central septum, smooth-walled, with small guttules, surrunded by a distinct mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 22–29 mm diam. after 1 week at 20–25 °C, colony from above, white to cream at the margin, greenish grey in the centre; from below, white to cream at the margin, greenish grey in the centre; medium dense, circular, slightly raised,

Fig. 6 ***Vicosamyces venturisporus*** (VIC 44320, **holotype**). **a, b** Symptoms on naturally infected leaf. **c** Globose to pyriform pseudothecium immersed in the leaf tissue. **d** Immature ascus. **e** Mature ascus. **f** Immature ascospore. **g** Brown and smooth-walled ascospores. *Scale bars* **c** = 50 µm, **d–g** = 10 µm

surface smooth, with edge entire, floccose to velvety, not producing pigmentation in agar.

Material examined: CHINA, Yunnan Province, Kunming Institute of Botany, on dead hanging branch of *Caragana arborescens* Lam. (*Fabaceae*), 2 November 2017, R. Phookamsak, KIB018 (KUN-HKAS 102236, **holotype**), ex-type living culture, KUMCC 18-0163 = MFLUCC 18-0682 (KIB018A), KUMCC 18-0164 (KIB018B).

GenBank numbers: ITS = MK214368, LSU = MK214371, SSU = MK214374, TEF1-α = MK214377 (KUMCC 18-0163); ITS = MK359434, LSU = MK359439, SSU = MK359444 TEF1-α = MK359073 (KUMCC 18-0164).

Notes: *Keissleriella caraganae* is similar to other *Keissleriella* species in having ascomata with an ostiolar neck, filled with short, brown, aseptate periphyses, bitunicate, broadly cylindrical to cylindric-clavate asci and septate ascospores, surrounded by distinct mucilaginous sheath (Tanaka et al. 2015; Wanasinghe et al. 2018). Multigene phylogenetic analyses (Fig. 7) show that *K. caraganae* is sister to *K. yonaguniensis* Kaz. Tanaka & K. Hiray. (KT2604). Although it clusters with other species of *Keissleriella* and *Pleurophoma* Höhn. the clade is not well-resolved agreeing with previous studies (Tibpromma et al. 2017; Hyde et al. 2018b; Wanasinghe et al. 2018). *Keissleriella caraganae* has ellipsoidal to fusiform, pale yellowish, 3-septate ascospores, whereas *K. yonaguniensis* has cylindrical, yellowish, 5-septate ascospores, with rounded ends (Tanaka et al. 2015). Both *K. caraganae* and *K. rosacearum* Phukhams. et al. (MFLU 15-1044) have fusiform, pale yellowish, 3-septate ascospores, but *K. rosacearum* was collected from *Rosa canina* L. (*Rosaceae*) in Italy (Wanasinghe et al. 2018). Multigene phylogenetic analysis (Fig. 7) shows that these two species form distinct lineages in different clades.

Murilentithecium Wanas. et al.

We follow the latest treatment and updated accounts of *Murilentithecium* in Wanasinghe et al. (2018). Generic notes were also provided by Wanasinghe et al. (2014a). Three species (including our new species) are presently included in this genus viz. *M. clematidis* Wanas. et al., *M. lonicerae* (in this study) and *M. rosae* Phukhams. et al. (Index Fungorum 2019). These three species were collected from *Clematis vitalba* L. (Italy), *Lonicera maackii* (Rupr.) Maxim (Yunnan, China) and *Rosa canina* L. (Italy).

Murilentithecium lonicerae Phookamsak, Chaiwan, Wanas. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555524; *Facesoffungi number*: FoF04966, Fig. 9

Etymology: The specific epithet "*lonicerae*" refers to the host genus *Lonicera*, from which the holotype was collected.

Holotype: KUN-HKAS 102238

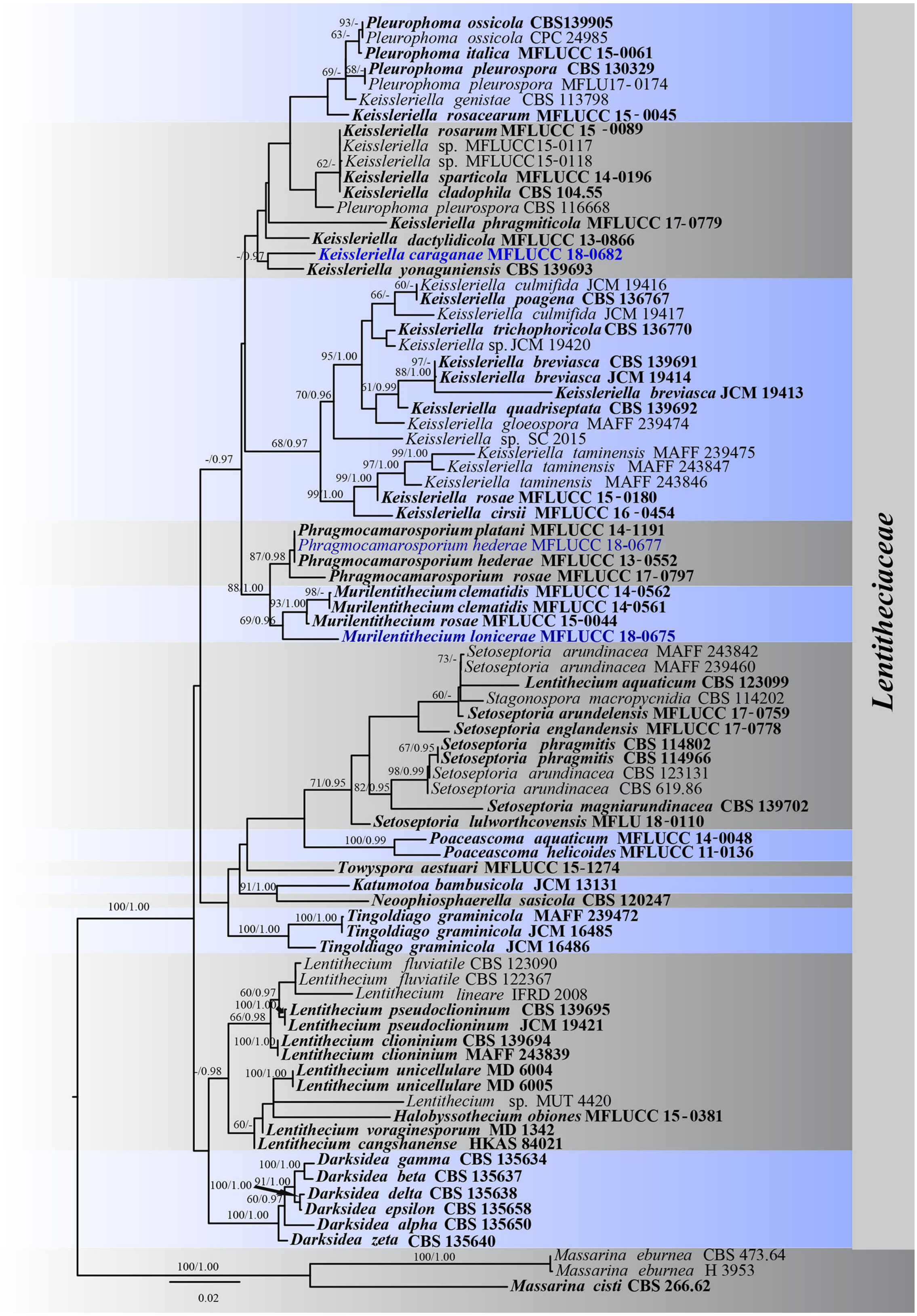
Saprobic on *Lonicera maackii*. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 95–150 µm high, 110–170 µm diam., pycnidial, semi-immersed, visible as raised, black dots on host surface, solitary, globose to subglobose, glabrous, uni-loculate, ostiolate at centre, with minute papilla, lacking periphyses. *Conidiomata walls* 5–15 µm diam., thin-walled, of unequal thickness, slightly thickened at the base, composed of 5–7 layers, of flattened, brown pseudoparenchymatous cells, slightly dark at the apex, arranged in *textura angularis* to *textura prismatica*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–15 × (3–)4–8 µm ($\bar{x}$ = 11 × 5.5 µm, n = 35), enteroblastic, phialidic, rarely annellidic, discrete, determinate, hyaline, smooth, aseptate, cylindrical to doliiform, with narrow channel, minute collarette and periclinal wall thickening, arising from the inner cavity of pycnidial wall. *Conidia* (13.5–)14–17(–18.5) × 7–10(–12) µm ($\bar{x}$ = 15.6 × 9.4 µm, n = 50), initially light brown to pale yellowish, aseptate, becoming reddish brown to dark brown, muriform, subglobose to obovoid, or turbinate, with truncate base, (1–)2–4 transverse septa, with several longitudinal sectors, not constricted at the septa, smooth-walled with minute guttules.

Culture characteristics: Colonies on PDA reaching 30–35 mm diam. after 3 weeks at 20–25 °C; colony from above, white-grey at the margin, grey at the centre; from below, white-grey at the margin, grey to dark grey at the centre, slightly radiated outwards colony; dense, circular, slightly raised to umbonate, surface smooth, with edge entire, floccose; not producing pigmentation in agar.

Material examined: CHINA, Yunnan Province, Kunming Institute of Botany, *Lonicera maackii* (Rupr.) Maxim. (*Caprifoliaceae*), 20 April 2017, R. Phookamsak, KIB035 (KUN-HKAS 102238, **holotype**), ex-type living culture, MFLUCC 18-0675 = KUMCC 18-0167 (KIB035IA), KUMCC 18-0168 (KIB035IB), KUMCC 18-0169 (KIB035IIA), KUMCC 18-0170 (KIB035IIB).

GenBank numbers: ITS = MK214370, LSU = MK214373, SSU = MK214376, TEF1-α = MK214379 (KUMCC 18-0167); ITS = MK359436, LSU = MK359441, SSU = MK359446, TEF1-α = MK359075 (KUMCC 18-0168); ITS = MK359437, LSU = MK359442, SSU = MK359447, TEF1-α = MK359076 (KUMCC 18-0169); ITS = MK359438, LSU = MK359443, SSU = MK359448, TEF1-α = MK359077 (KUMCC 18-0170).

Notes: *Murilentithecium lonicerae* can be distinguished from *M. clematidis* and *M. rosae* in having reddish brown to dark brown, subglobose to obovoid, or turbinate conidia,


93/-
Pleurophoma ossicola CBS139905
63/-
Pleurophoma ossicola CPC 24985
Pleurophoma italica MFLUCC 15-0061
69/-
68/-
Pleurophoma pleurospora CBS 130329
Pleurophoma pleurospora MFLU17-0174
Keissleriella genistae CBS 113798
Keissleriella rosacearum MFLUCC 15-0045
Keissleriella rosarum MFLUCC 15-0089
Keissleriella sp. MFLUCC15-0117
62/-
Keissleriella sp. MFLUCC15-0118
Keissleriella sparticola MFLUCC 14-0196
Keissleriella cladophila CBS 104.55
Pleurophoma pleurospora CBS 116668
Keissleriella phragmiticola MFLUCC 17-0779
Keissleriella dactylidicola MFLUCC 13-0866
-/0.97
Keissleriella caraganae MFLUCC 18-0682
Keissleriella yonaguniensis CBS 139693
60/-
Keissleriella culmifida JCM 19416
66/-
Keissleriella poagena CBS 136767
Keissleriella culmifida JCM 19417
Keissleriella trichophoricola CBS 136770
Keissleriella sp. JCM 19420
95/1.00
97/-
Keissleriella breviasca CBS 139691
88/1.00
Keissleriella breviasca JCM 19414
51/0.99
Keissleriella breviasca JCM 19413
70/0.96
Keissleriella quadriseptata CBS 139692
Keissleriella gloeospora MAFF 239474
68/0.97
Keissleriella sp. SC 2015
-/0.97
99/1.00
Keissleriella taminensis MAFF 239475
97/1.00
Keissleriella taminensis MAFF 243847
99/1.00
Keissleriella taminensis MAFF 243846
99/1.00
Keissleriella rosae MFLUCC 15-0180
Keissleriella cirsii MFLUCC 16-0454
Phragmocamarosporium platani MFLUCC 14-1191
Phragmocamarosporium hederae MFLUCC 18-0677
87/0.98
Phragmocamarosporium hederae MFLUCC 13-0552
Phragmocamarosporium rosae MFLUCC 17-0797
88/1.00
98/-
Murilentithecium clematidis MFLUCC 14-0562
93/1.00
Murilentithecium clematidis MFLUCC 14-0561
69/0.96
Murilentithecium rosae MFLUCC 15-0044
Murilentithecium lonicerae MFLUCC 18-0675
Setoseptoria arundinacea MAFF 243842
73/-
Setoseptoria arundinacea MAFF 239460
Lentithecium aquaticum CBS 123099
60/-
Stagonospora macropycnidia CBS 114202
Setoseptoria arundelensis MFLUCC 17-0759
Setoseptoria englandensis MFLUCC 17-0778
67/0.95
Setoseptoria phragmitis CBS 114802
Setoseptoria phragmitis CBS 114966
98/0.99
Setoseptoria arundinacea CBS 123131
71/0.95
82/0.95
Setoseptoria arundinacea CBS 619.86
Setoseptoria magniarundinacea CBS 139702
Setoseptoria lulworthcovensis MFLU 18-0110
100/0.99
Poaceascoma aquaticum MFLUCC 14-0048
Poaceascoma helicoides MFLUCC 11-0136
Towyspora aestuari MFLUCC 15-1274
91/1.00
Katumotoa bambusicola JCM 13131
Neoophiosphaerella sasicola CBS 120247
100/1.00
100/1.00
Tingoldiago graminicola MAFF 239472
100/1.00
Tingoldiago graminicola JCM 16485
Tingoldiago graminicola JCM 16486
Lentithecium fluviatile CBS 123090
Lentithecium fluviatile CBS 122367
Lentithecium lineare IFRD 2008
60/0.97
100/1.00
Lentithecium pseudoclioninum CBS 139695
66/0.98
Lentithecium pseudoclioninum JCM 19421
100/1.00
Lentithecium clioninium CBS 139694
Lentithecium clioninium MAFF 243839
-/0.98
100/1.00
Lentithecium unicellulare MD 6004
Lentithecium unicellulare MD 6005
Lentithecium sp. MUT 4420
Halobyssothecium obiones MFLUCC 15-0381
60/-
Lentithecium voraginesporum MD 1342
Lentithecium cangshanense HKAS 84021
100/1.00
Darksidea gamma CBS 135634
Darksidea beta CBS 135637
100/1.00
91/1.00
Darksidea delta CBS 135638
60/0.97
Darksidea epsilon CBS 135658
100/1.00
Darksidea alpha CBS 135650
Darksidea zeta CBS 135640
100/1.00
Massarina eburnea CBS 473.64
100/1.00
Massarina eburnea H 3953
Massarina cisti CBS 266.62
0.02
Lentitheciaceae

◀ **Fig. 7** Phylogram generated from maximum likelihood analysis based on the combined LSU, SSU, ITS and TEF1-α sequence dataset for taxa in *Lentitheciaceae*. Related sequences were obtained from Wanasinghe et al. (2018). Eighty-three strains are included in the combined sequence analyses, which comprise 3419 characters with gaps. Single gene analyses were also performed and topology and clade stability compared from combined gene analyses. *Massarina cisti* (CBS 266.62) and *M. eburnea* (CBS 473.64, H3953) were used as the outgroup taxa. Bootstrap support value for ML equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.95 BYPP are given above the nodes. Newly generated sequences are in blue. Type strains are in bold

with truncate base, (1–)2–4 transverse septa, with several longitudinal sectors. *Murilentithecium clematidis* has pale brown to brown, oblong to clavate conidia, with 3–5 transverse septa, and 2–5 longitudinal septa (Wanasinghe et al. 2014a; Wijayawardene et al. 2016). *Murilentithecium rosae* has yellowish brown to dark brown, ovoid conidia, with 3 transverse septa, and 1–2 longitudinal septa (Wanasinghe et al. 2018). Multigene phylogenetic analyses (Fig. 7) show that *M. lonicerae* forms a distinct lineage basal to *Murilentithecium*.

Phragmocamarosporium Wijayaw. et al.

We follow the latest treatment and updated accounts of *Phragmocamarosporium* in Wanasinghe et al. (2018). There are only three species in this genus, *P. hederae*, *P. platani* Wijayaw. et al. and *P. rosae* Wanas. et al. *Phragmocamarosporium hederae* and *P. rosae* were collected from *Hedera helix* L. and *Rosa canina* in Europe (Germany and Great Britain respectively). Whereas, *P. platani* was found on *Platanus* sp. in Asia (Guizhou, China). In this study, *P. hederae* is reported from China on a different host.

Phragmocamarosporium hederae Wijayaw., R.K. Schumach. & K.D. Hyde, Index Fungorum 370: 1 (2018), Fig. 10

Holotype: GERMANY, near Berlin, park, on a twig of *Hedera helix* L. (*Araliaceae*), 18 May 2013, Rene Klaus Schumacher, NNW GER 014/8 (MFLU 15-0165), living cultures MFLUCC 13-0552, GUCC 8.

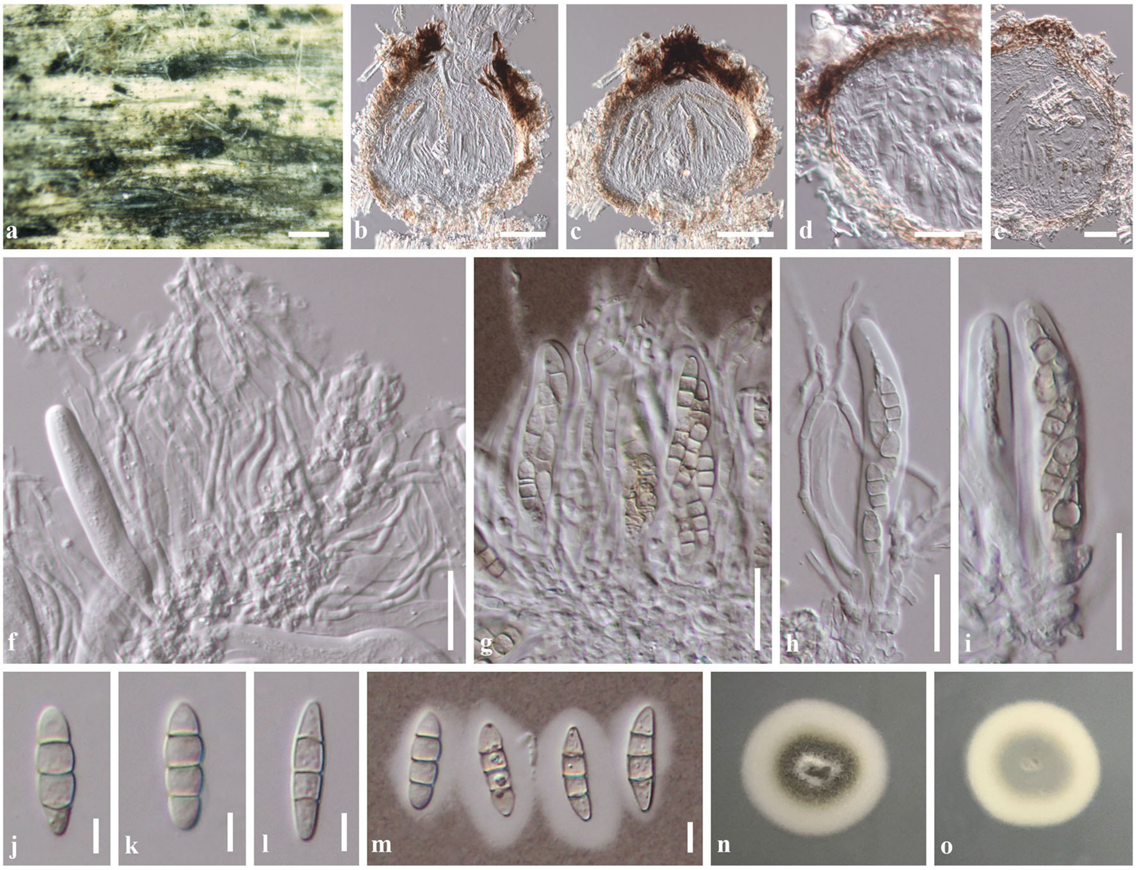


Fig. 8 ***Keissleriella caraganae*** (KUN-HKAS 102236, **holotype**). **a** Appearance of ascomata on host surface. **b, c** Section through ascomata. **d, e** Section through peridium. **f, g** Asci embedded in cellular pseudoparaphyses (g = stained in Indian ink). **h, i** Asci. **j–l** Ascospores. **m** Ascospores stained in Indian ink. **n, o** Culture on PDA after one week (n = from above, o = from below). *Scale bars* **a** = 200 µm, **b**, **c** = 50 µm, **d–i** = 20 µm, **j–m** = 5 µm

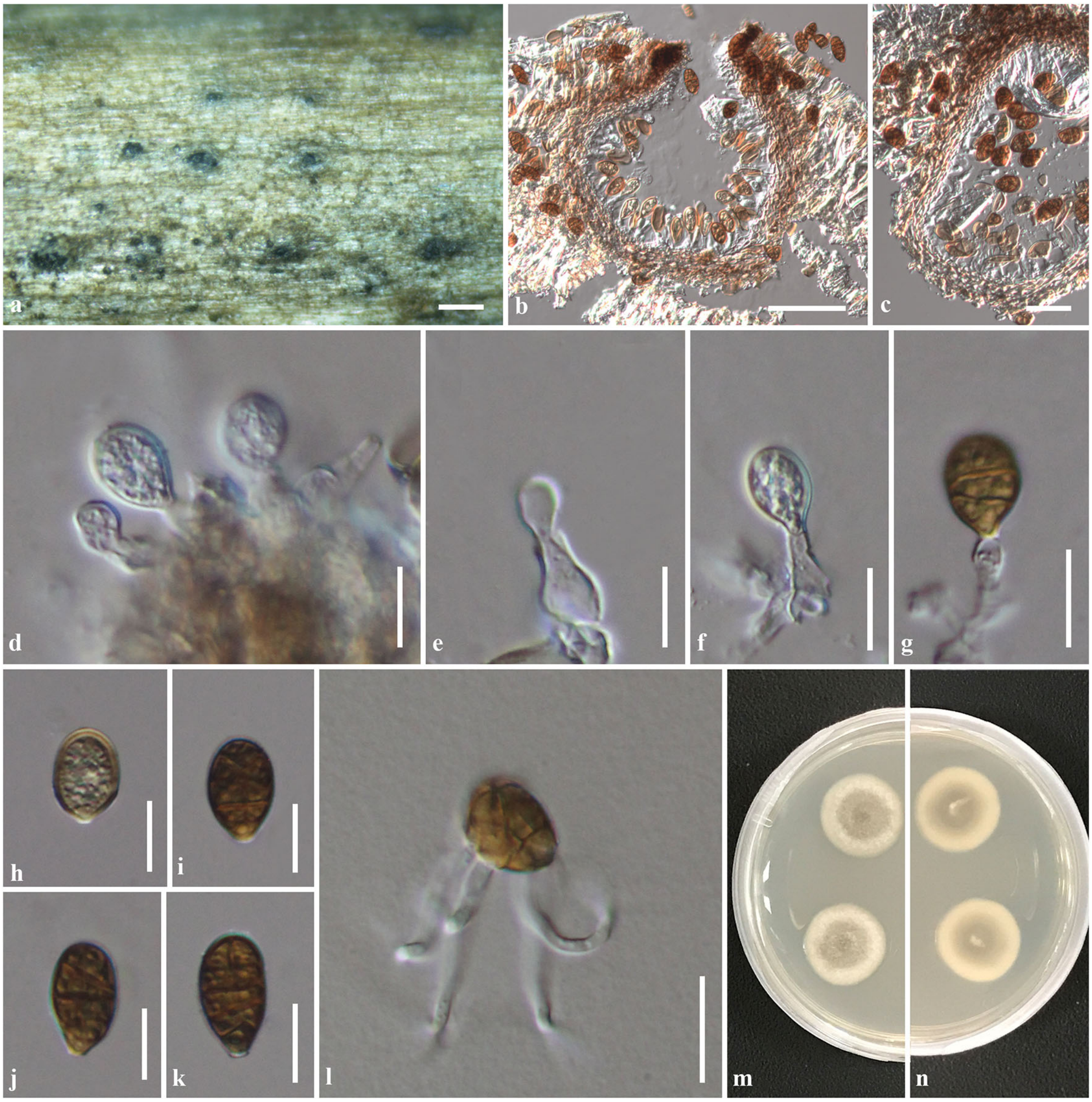


Fig. 9 ***Murilentithecium lonicerae*** (KUN-HKAS 102238, **holotype**). **a** Appearance of conidiomata on host surface. **b** Section through conidioma. **c** Section through conidioma wall. **d–g** Conidiogenous cells and conidia. **h–k** Conidia. **l** Germinating of conidium. **m, n** Culture on PDA after 1 week (**m** = from above, **n** = from below). *Scale bars* **a** = 200 µm, **b** = 50 µm, **c, l** = 20 µm, **d–k** = 10 µm

Associated with leaf spots on *Cycas* (*Cycadaceae*). **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 130–170 µm high, 180–270 µm diam., pycnidial, semi-immersed, visible as raised, black dots on host surface, scattered, solitary to gregarious, globose to subglobose, glabrous, uni-loculate, ostiolate at centre, with minute papilla, lacking periphyses. *Conidiomata walls* 10–20 µm, thin-walled, of equal thickness, composed of 3–5 layers, of flattened, brown to dark brown, pseudoparenchymatous cells, with blackened cells at the papilla, arranged in *textura angularis* to *textura prismatica*, difficult to distinguish from conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* (2.5–)3–5(–8) × (1.5–)2–5(–7) µm ($\bar{x}$ = 4.3 × 3.7 µm, n = 30), holoblastic, phialidic, hyaline, smooth, aseptate, ampulliform, arising from the inner cavity of the conidioma wall. *Conidia* (8–)10–13(–14) × 3–4 µm ($\bar{x}$ = 12 × 4.2 µm, n = 50), initially light brown, becoming reddish-brown to brown, oblong to ellipsoidal, or subclavate with truncate base, 3-septate, not constricted at the septa, smooth-walled.

Culture characteristics: Colonies on PDA reaching 10–15 mm diam. after 10 days at 25–30 °C; from above, white to cream at the margin, grey at the centre; from below, white to cream at the margin, black at the centre; medium dense, circular, slightly raised, surface slightly smooth, with edge entire, fluffy to feathery; not producing pigmentation in agar.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, associated with leaf spots on *Cycas* (*Cycadaceae*), 5 April 2017, R. Phookamsak, KIB020 (KUN-HKAS 102237), living culture, KUMCC 18-0165 (KIB020A), MFLUCC 18-0677 = KUMCC 18-0166 (KIB020B).

Known hosts and distribution: *Hedera helix* L. (*Araliaceae*; Germany) and associated with leaf spots on *Cycas* (Yunnan Province, China) (Wijayawardene et al. 2015 and this study).

GenBank numbers: ITS = MK214369, LSU = MK214372, SSU = MK214375, TEF1-α = MK214378 (KUMCC 18-0165); ITS = MK359434, LSU = MK359439, SSU = MK359444, TEF1-α = MK359073 (KUMCC 18-0166).

Notes: Multigene phylogenetic analyses (Fig. 7) show that the strain MFLUCC 18-0677 grouped with *Phragmocamarosporium hederae* and *P. platani* in *Lentitheciaceae*. A BLASTn search of LSU and SSU sequence data indicates that MFLUCC 18-0677 is identical to *P. hederae* (100% and 99% similarities, respectively). We therefore, identify our isolate as *P. hederae* and this species was collected from *Cycas* in China for the first time. Our new isolate is similar to *P. hederae* in having phragmosporous conidia. Whearas, *P. platani* has phragmosporous and muriform conidia at maturity (Wijayawardene et al. 2015). Compared to the type of *P. hederae* our new isolate has shorter and broader conidiogenous cells (8–10 × 1.5–2.5 µm in the type collection) and longer conidia (9–11 × 3–4.5 µm in the type collection). *Phragmocamarosporium platani* has smaller conidiogenous cells (1.5–3 × 1.5–2.5 µm) and narrower conidia (12–13 × 5–7.5 µm) (Wijayawardene et al. 2015). Only LSU and SSU sequence data for *P. hederae* and *P. platani* are available in GenBank, and sequences of more informative genes are needed to clarify species in this genus.

Leptosphaeriaceae M.E. Barr

Leptosphaeriaceae was introduced by Barr (1987) and is typified by *Leptosphaeria* Ces. & De Not. to accommodate species having immersed, subglobose, thick-walled ascomata containing interascal filamentous pseudoparaphyses, with bitunicate, broad asci bearing fusiform, transversely septate, hyaline to yellow-brown ascospores and coelomycetous asexual morphs in the order *Pleosporales* (Ariyawansa et al. 2015b). Ariyawansa et al. (2015b) re-circumscribed the genera in *Leptosphaeriaceae* based on morphological characteristics and multigene phylogenetic analyses, and accepted ten genera with more than 140 species. This is in agreement of the taxonomic outline of Ascomycota, provided by Wijayawardene et al. (2018a) and the notes of each genus in this family were provided by Ariyawansa et al. (2015b) and Wijayawardene et al. (2017a).

We follow the latest treatment of *Leptosphaeriaceae* in Ariyawansa et al. (2015b) and updated accounts of taxa in *Leptosphaeriaceae* in Hyde et al. (2016, 2017), Tennakoon et al. (2017) and Tibpromma et al. (2017). In this paper, we introduce four new species, *Leptosphaeria urticae*, *Plenodomus artemisiae*, *P. lijiangensis* and *Sphaerellopsis isthmospora* in *Leptosphaeriaceae*. The asexual morph of *Plenodomus sinensis* is also introduced from a fern in China and a new host record of *Sphaerellopsis paraphysata* associated with rust on living leaves of *Liriope spicata* (Thunb.) Lour (*Asparagaceae*) is reported.

Leptosphaeria Ces. & De Not.

Leptosphaeria was introduced by Cesati and De Notaris (1863) and is typified by *L. doliolum* (Pers.) Ces. & De Not. (lectotype designated by Shearer et al. 1990). The genus is characterized by semi-immersed to erumpent, coriaceous ascomata, which become superficial, a thick-walled peridium composed of scleroplectenchymatous cells, cylindrical to cylindric-clavate asci, reddish to yellowish brown, ellipsoidal to fusiform, septate ascospores and coelomycetous coniothyrium-like and phoma-like asexual morphs (Ariyawansa et al. 2015b; Dayarathne et al. 2015). Taxonomic revision of the genus was discussed in Ariyawansa et al. (2015b). Over 1600 epithets are listed for *Leptosphaeria* (Index Fungorum 2019), but few species have been confirmed by phylogenetic analysis. Most *Leptosphaeria* species lack molecular data to clarify their phylogenetic placements. Some other *Leptosphaeria sensu lato* species have been treated in different genera in *Leptosphaeriaceae* and other related families (de Gruyter et al. 2013; Ariyawansa et al. 2015b).

Leptosphaeria urticae D. Pem, E.B.G. Jones & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555597; *Facesoffungi number*: FoF04370, Fig. 11

Etymology: Name reflects the host from which the fungus was isolated.

Holotype: MFLU 18-0591

Saprobic on dead branches of *Urtica dioica*. **Sexual morph** *Ascomata* 100–130 high, 70–110 µm diam., solitary, scattered or in small groups, erumpent through host epidermis to superficial, conical to mammiform, dark brown to black, coriaceous, smooth, easily removed from the host substrate, ostiolate with minute papilla. *Ostioles* 50–70 µm diam., papillate, black, shiny, smooth. *Peridium* 25–50 µm wide, comprising two cell types, outer layer composed of small, thick-walled cells of *textura angularis* to *textura globulosa*, surface heavily pigmented termed as scleroplectenchyma, thinner at the apex, wide at sides, inner layer composed of subhyaline or light brown

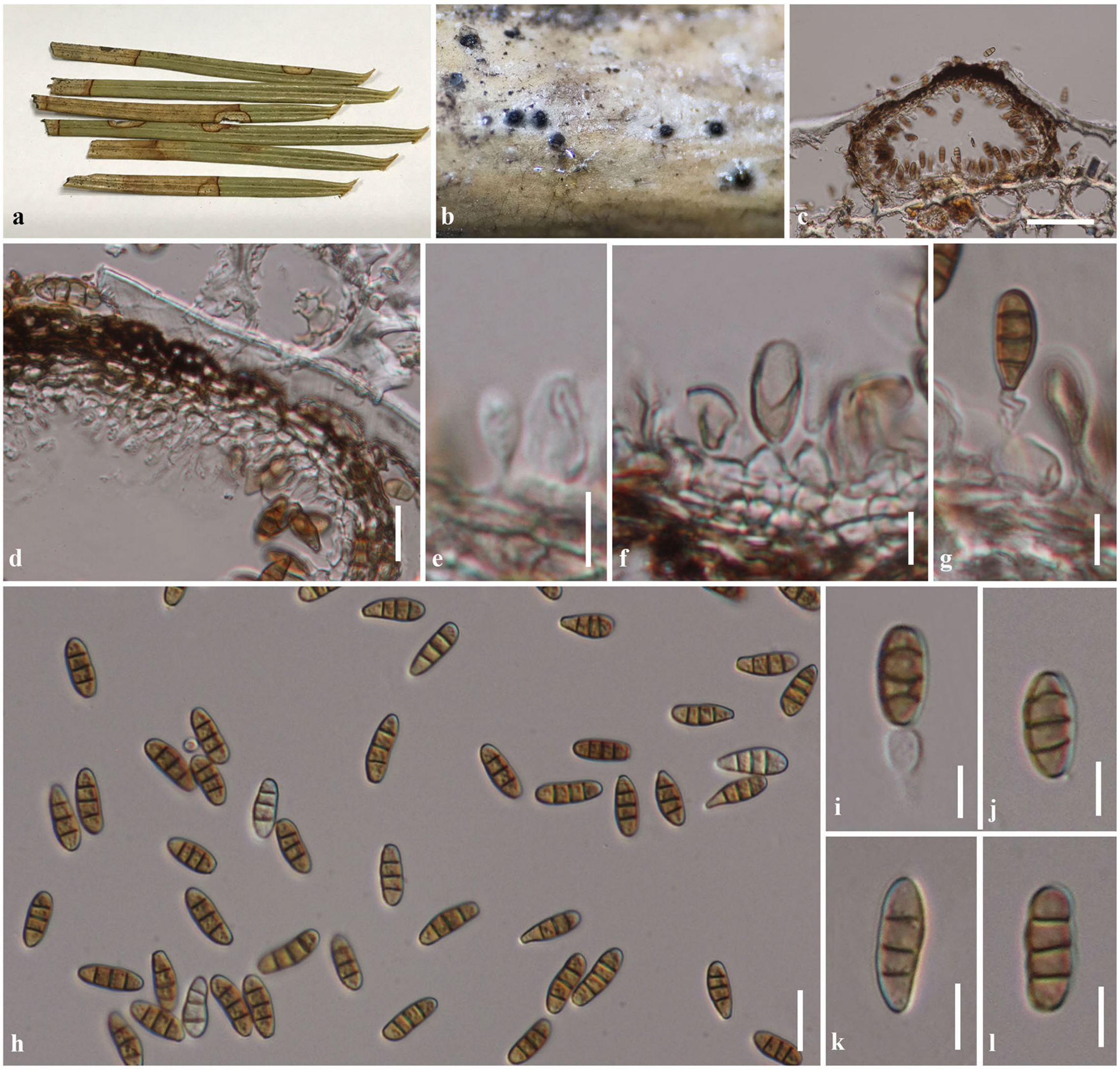


Fig. 10 ***Phragmocamarosporium hederae*** (KUN-HKAS 102237). **a** Symptom of leaf spot disease on *Cycas*. **b** Appearance of conidiomata on host surface. **c** Section through conidioma. **d** Section through conidioma wall. **e–g** Conidiogenous cells with conidia. **h–l** Conidia. *Scale bars* **c** = 50 µm, **d, h** = 10 µm, **e–g**, **i–l** = 5 µm

relatively thin-walled cells of *textura angularis*, cells near the base comparatively larger. *Hamathecium* comprising numerous, dense, 1.5–2 µm wide, filamentous, septate, cellular pseudoparaphyses, branched and anastomosing, embedded in gelatinous matrix. *Asci* 60–140 × 9–11 µm ($\bar{x}$ = 104.5 × 10 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, rounded at the apex, pedicellate, numerous, with ocular chamber. *Ascospores* 35–40 × 4–6 µm ($\bar{x}$ = 38.3 × 5.2 µm, n = 20), overlapping 1–2-seriate, initially hyaline, becoming yellowish brown at maturity, long fusiform, (8–)9-septate, constricted at the septa, narrowly rounded at both ends, smooth-walled, lacking a mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on MEA within 24 h. Colonies growing on MEA reaching 2 cm diam. in one week at 16 °C. Mycelium superficial, surface smooth, irregular, slightly raised, edge crenate, velutinous, from above white to pale yellow, reverse yellow.

Material examined: UK, Sussex, Singleton, on dead stem of *Urtica dioica* L. (*Urticaceae*), 5 April 2017, E.B Gareth Jones, 353 UK (MFLU 18-0591, **holotype**), ex-type living culture MFLUCC 17-2302.

GenBank numbers: ITS = MK123333, LSU = MK123332, SSU = MK123329, TEF1-α = MH028391.

Notes: Phylogenetic analyses of a combined LSU, SSU and ITS sequence dataset (Fig. 12) reveal that *Leptosphaeria urticae* (MFLU 18-0591) is sister to *L. italica* Dayar. et al. (MFLU 15-0174). *Leptosphaeria urticae* differs from *L. italica* in having longer asci (*L. urticae*, 60–140 × 9–11 µm versus 60–112 × 7–12 µm, *L. italica*), longer ascospores (*L. urticae*, 35–40 × 4–6 µm versus 12–18 × 4–6 µm, *L. italica*) and more ascospore septation (*L. urticae*, (8–)9-septate versus 3-septate, *L. italica*) (Dayarathne et al. 2015). Based on the NCBI BLASTn search of ITS sequence data, *L. urticae* has 96% similarity with *L. sclerotioides* (Preuss ex Sacc.) Gruyter et al. However, the two species cannot be compared as *L. urticae* is represented only by its sexual morph, whereas, *L. sclerotioides* is known only by its asexual morph (de Gruyter et al. 2013). Phylogenetic analysis indicates that these two species are not conspecific. Hence, we introduce *L. urticae* as a new species based on both morphological and molecular data.

Five *Leptosphaeria* species have been reported from *Urtica*: *L. acuta* (Fuckel) P. Karst., *L. acutiuscula* Berl., *L. atropurpurea* Petr., *L. doliolum* (Pers.) Ces. & De Not. and *L. ogilviensis* (Berk. & Broome) Ces. & De Not. (Shoemaker 1984; Farr and Rossman 2018). These species can be distinguished from each other based on ascospore septation.

Plenodomus Preuss

Plenodomus was introduced by Preuss (1851) and is typified by *P. rabenhorstii*. Subsequently, Boerema and Kesteren (1964) designated *P. lingam* (Tode) Höhn. as the type combination over *P. rabenhorstii* because the type material of *P. rabenhorstii* was lost during the World War II (de Gruyter et al. 2013; Ariyawansa et al. 2015b; Tennakoon et al. 2017). Based on molecular phylogeny, de Gruyter et al. (2013) reclassified *Phoma* section *Plenodomus* and synonymized species in *Phoma* section *Plenodomus* under the genus *Plenodomus* in *Leptosphaeriaceae*. The genus was re-circumscribed by Ariyawansa et al. (2015b) based on study of type and representative specimens coupled with molecular data. Marin-Felix et al. (2017) and Tennakoon et al. (2017) updated the accounts of *Plenodomus* based on molecular data. There are 97 epithets available in Index Fungorum (2019).

Plenodomus artemisiae A. Karunarathna, Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556118; *Facesoffungi number*: FoF05696, Fig. 13

Etymology: The specific epithet "*artemisiae*" refers to the host genus *Artemisia*, on which the type species was collected.

Holotype: KUN-HKAS 102226.

Saprobic on dead branches and stems of *Artemisia* sp. **Sexual morph** *Ascomata* 140–280 µm high, 300–450 µm diam., black, shiny on the host surface, solitary to aggregated, immersed at the base, becoming superficial, uniloculate, subglobose to irregular in shape, with truncate base, glabrous, ostiolate, papillate. *Ostioles* central, dark brown, beak-like papilla, ostiolar canal filled with periphyses. *Peridium* 10–85 µm wide, thick-walled of unequal thickness, thickened at the based, slightly thin at the apex, composed of several cell layers of dark brown scleroplectenchymatous cells, arranged in a *textura angularis* to *textura globulosa*. *Hamathecium* composed of hyaline, filamentous, 2–4 µm wide, distinctly septate pseudoparaphyses, anastomosing, embedded in a hyaline gelatinous matrix. *Asci* (64–)70–90(–100) × (9.5–)10–13 µm ($\bar{x}$ = 82.7 × 11.2 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, short, pedicellate, apically rounded with a distinct ocular chamber. *Ascospores* (28–)30–40 × (4.5–)5–6 µm ($\bar{x}$ = 34.4 × 5.5 µm, n = 30), overlapping 2–3-seriate, pale brown, fusiform, 5-septate, slightly constricted at the septa, enlarge at the third cell from above, lacking a mucilaginous sheath and appendages. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 30–33 mm diam. after 4 weeks. Colony dense, circular, low convex, surface smooth, with edge entire, floccose; from above white; from below, yellowish-grey at the edge, with white to cream margin, dark yellowish at the centre, slightly radiating outwards colony; not produced pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, on dead branches and stems of *Artemisia* sp., 20 December 2015, R. Phookamsak, AS003 (KUN-HKAS 102226, **holotype**). ex-type living culture, KUMCC 18-0151.

GenBank numbers: ITS = MK387920, LSU = MK387958, SSU = MK387928, TEF1-α = MK435600, RPB2 = MK435607 (KUMCC 18-0151).

Notes: *Plenodomus artemisiae* forms a distinct lineage and is sister to *P. salviae* Thambug. et al. (MFLUCC 13-0219) with high support (99% ML and 0.99 BYPP; Fig. 12). *Plenodomus artemisiae* can be distinguished from *P. salviae* in having shorter and broader, pale brown, fusiform ascospores, enlarged at the third cell from above. *Plenodomus salviae* has longer and thinner, yellowish brown, cylindric-fusiform ascospores (30–48 × 3.1–4.3 µm), and without the enlarged cell (Ariyawansa et al. 2015b). *Plenodomus artemisiae* is also similar to *Leptosphaeria artemisiae* (Fuckel) Auersw. in having 5-septate ascospores, with the enlarged third cell and occurring on *Artemisia*. However, *L. artemisiae* has larger ascomata and narrower ascospores (32–37 × 8.5–10; Shoemaker 1984). Furthermore, *P. artemisiae* has pale brown, fusiform ascospores, whereas, *L. artemisiae* has light reddish brown, broadly elliptical ascospores (Shoemaker 1984). Phylogenetic affinity of *L. artemisiae* could not be resolved due to lack of molecular data.

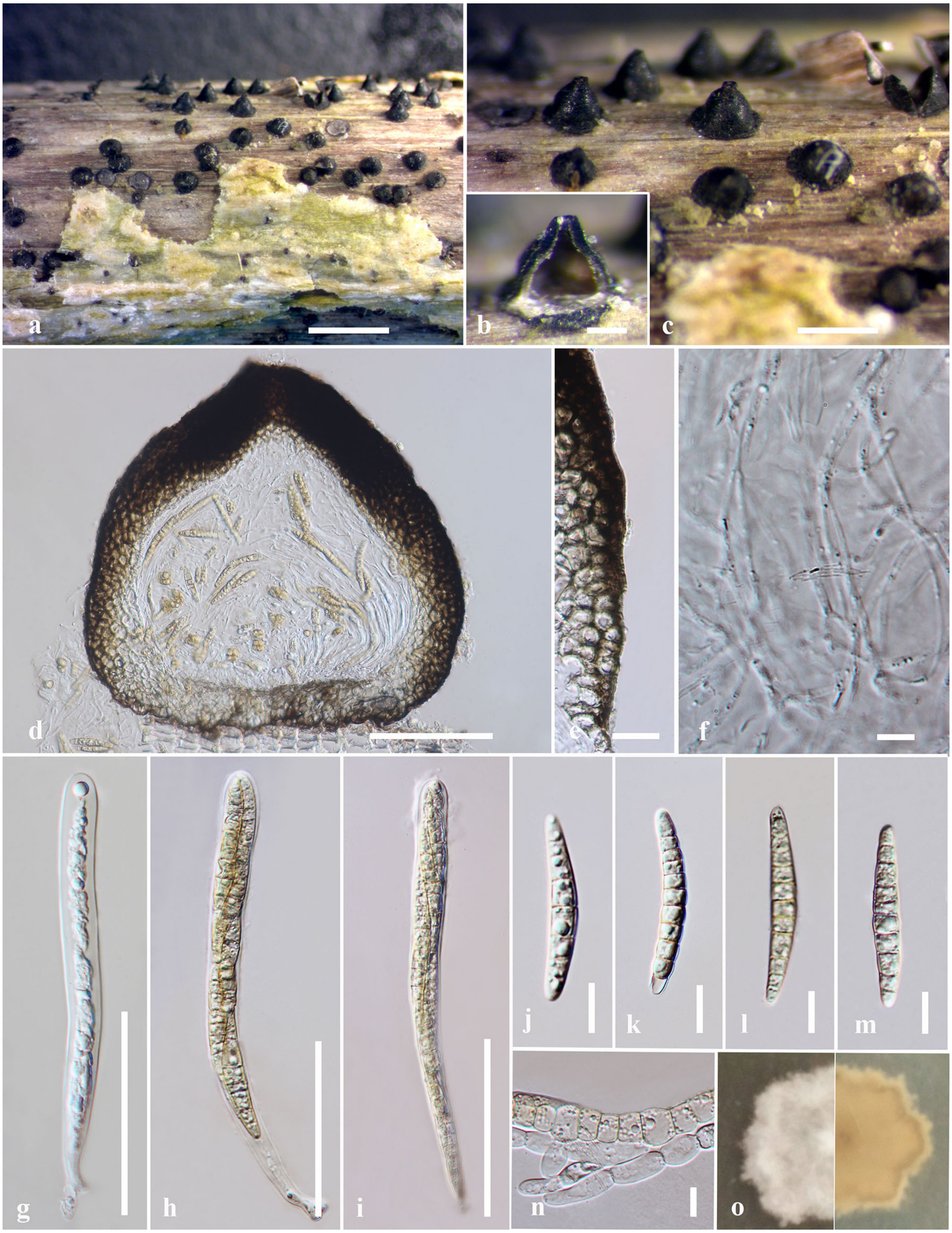


Fig. 11 ***Leptosphaeria urticae*** (MFLU 18-0591, **holotype**). **a–c** Appearance of ascomata on host surface. **d** Section through an ascoma. **e** Peridium. **f** Pseudoparaphyses. **g–i** Asci. **j–m** Ascospores. **n** Spore germination on MEA after 24 h. **o** Culture from above and below. *Scale bars* **a**, **b** = 500 µm, **c** = 200 µm, **d** = 100 µm, **e, g–i** = 50 µm, **j–m** = 10 µm, **f** = 5 µm

Plenodomus lijiangensis Phookamsak, A. Karunarathna & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556137; *Facesoffungi number*: FoF05697, Fig. 14

Etymology: The specific epithet "*lijiangensis*" refers to Lijiang prefecture-level city, of Yunnan Province, China where the holotype was collected.

Holotype: KUN-HKAS 102249

Saprobic on dead fronds of fern. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 140–290 µm high, 135–240 µm diam., pycnidial, black, scattered, gregarious, superficial, uni-loculate, varied in shape, subconical to ovoid, or subglobose, with truncate base, widest at the base, glabrous, with indistinct ostiole. *Conidiomata walls* 17–100 µm wide, thick-walled, of unequal thickness, thickened at the apex, comprising several cell layers, outer layer composed of broad, dark brown to black, scleroplectenchymatous cells of *textura angularis* to *textura globulosa*, inner layer composed of broad, hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–9 × 5–8 µm ($\bar{x}$ = 6.4 × 6.5 µm, n = 40), enteroblastic, phialidic, discrete, determinate, ampulliform to doliiform, hyaline, smooth, with minute collarette, with 1–2 apertures, and periclinal wall thickening, arising from the inner cavity of the conidioma wall. *Conidia* 3–5 × 1.7–2.3 µm ($\bar{x}$ = 4.3 × 2 µm, n = 50), hyaline, oblong to obovoid, aseptate, smooth-walled, with 1–2 guttules.

Culture characteristics: Colonies on PDA, reaching 57–58 mm diam. after 3 weeks. Colony dense, circular, flattened, slightly raised, surface smooth, with edge entire, floccose; from above white at the margin, cream at the centre, with pale grey concentric ring near the margin; from below, yellowish brown at the edge, with paler margin, dark brown to black at the centre, colony slightly radiating outwards; not producing pigmentation on agar medium. Sporulation on PDA after three months. *Conidiomata* 120–250 µm high, 130–230 µm diam., scattered, solitary to gregarious, semi-immersed in culture colony, or embedded in agar medium, perithecial, pycnidial, with short stipe (19–49 µm long), black, glabrous, globose to subglobose, lacking ostioles. *Conidiomata walls* 3–8 µm wide, thin-walled, equally thick, comprising 1–2 cell layers of dark brown to black pseudoparenchymatous cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–3 × 1.5–3 µm ($\bar{x}$ = 2.5 × 2.2 µm, n = 20), enteroblastic, phialidic, discrete, determinate, oblong to pyriform, hyaline, with minute collarette, and periclinal wall thickening, arising from the inner cavity of the conidioma wall, difficult to distinguish from the conidioma wall. *Conidia* 3–4(–4.5) × 1.5–2.5 µm ($\bar{x}$ = 3.9 × 2, n = 50), hyaline, oblong to ellipsoidal, or obovoid, aseptate, smooth-walled, with 1–2 small guttules.

Material examined: CHINA, Yunnan Province, Lijiang, Yulong, on dead fronds of fern, 1 August 2015, R. Phookamsak, LJ003 (KUN-HKAS 102249, **holotype**), ex-type living culture, KUMCC 18-0186.

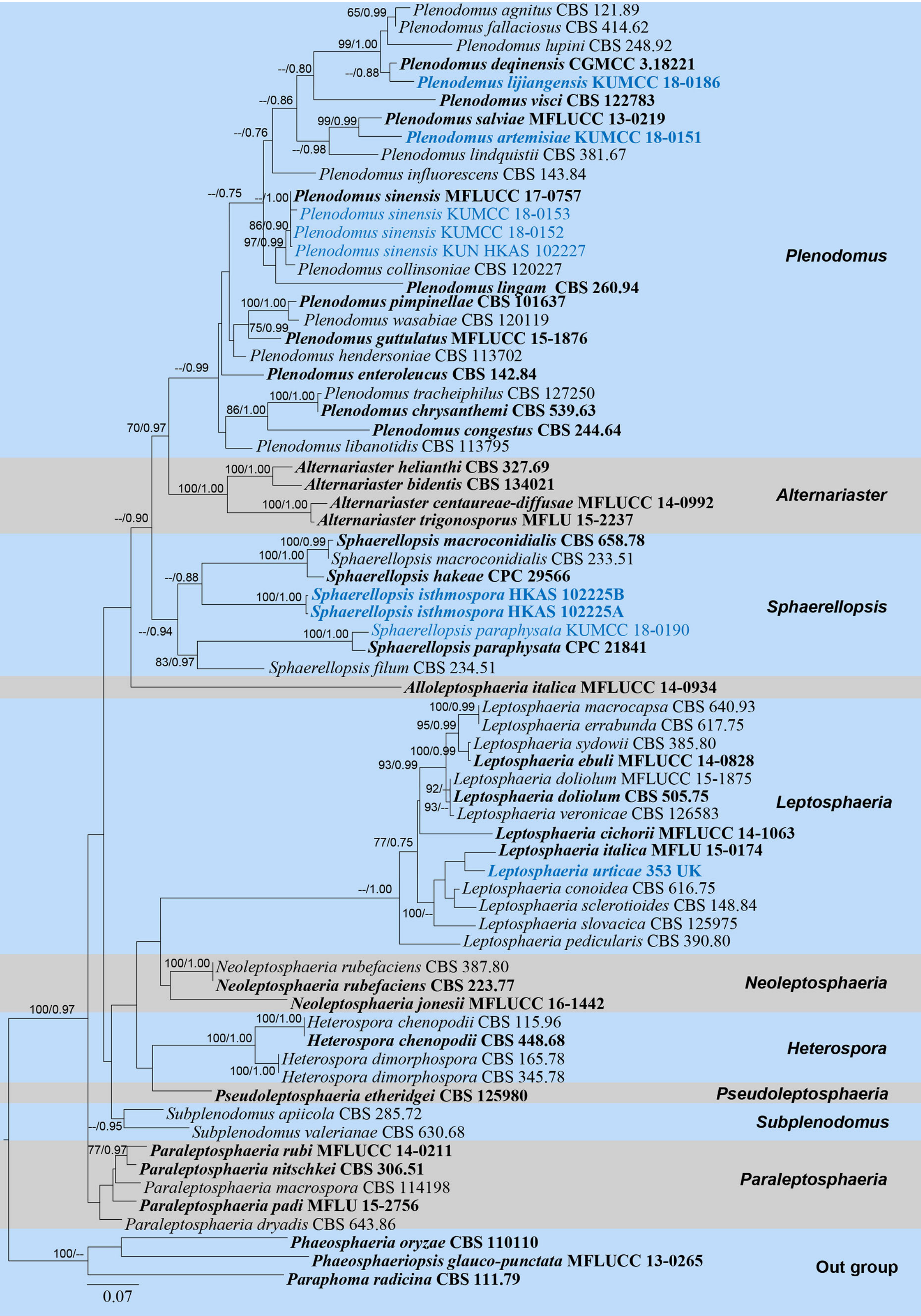
GenBank numbers: ITS = MK387921, LSU = MK387959, SSU = MK387929, TEF1-α = MK435601 (KUMCC 18-0186).

Notes: Based on the NCBI BLASTn search of ITS sequence data, *Plenodomus lijiangensis* closest match is *P. deqinensis* Qian Chen & L. Cai (CGMCC 3.18221; 98% similarity). Phylogenetic analyses of a concatenated LSU, SSU and ITS sequence dataset (Fig. 12) reveal that *P. lijiangensis* forms a sister lineage with *P. deqinensis* and groups with *P. agnitus* (Desm.) Gruyter et al., *P. fallaciosus* (Berl.) Gruyter et al. and *P. lupini* (Ellis & Everh.) Gruyter et al. *Plenodomus lijiangensis* shares a size range of conidia and conidiogenous cells with *P. deqinensis* and was also collected from Yunnan, China (Marin-Felix et al. 2017). However, *P. lijiangensis* was isolated from dead fronds of fern, while *P. deqinensis* was isolated from soil. In vitro, *P. lijiangensis* forms a globose to subglobose conidiomata, inconspicuous ostiole, with a short stipe which is similar to the asexual morph of *P. sinensis* Tennakoon et al. (Fig. 16). While, *P. deqinensis* forms globose to subglobose, slightly papillate ostiole with a narrow pore or opening via a rupture (Marin-Felix et al. 2017). A comparison of ITS sequence shows that *P. lijiangensis* differs from *P. deqinensis* in eight base positions (1.55%/517 bp). According to the guidelines in Jeewon and Hyde (2016), we introduce *P. lijiangensis* as a new species.

Plenodomus sinensis Tennakoon, Phookamsak & K.D. Hyde, in Tennakoon et al., Phytotaxa 324(1): 76 (2017), Figs. 15, 16

Holotype: CHINA, Yunnan Province, Xishuangbanna, Nabanhe, dead branch of *Tamarindus indica* (*Fabaceae*), 25 November 2015, D.S. Tennakoon, DXH 015 (MFLU 17-0767).

Saprobic on dead fronds of ferns and dead stems of *Cirsium* sp. **Sexual morph** *Ascomata* 250–290 µm high, 300–360 µm diam., black, shiny, scattered, gregarious, semi-immersed to erumpent through host epidermis, subglobose to subconical, uni-loculate, glabrous, ostiolate. *Peridium* thick-walled of unequal thickness, thickened at base, thinner toward sides and apex, composed of three type cell layers, inner layer 5–20 µm wide, comprising 2–3 strata of flattened, pale brown, thin-walled, pseudoparenchymatous cells, arranged in *textura angularis* to *textura prismatica*, middle layer 25–100 µm wide, comprising several strata, of hyaline, thick-walled, scleroplectenchymatous cells of *textura angularis* to *textura globulosa*, outer layer thin-walled, comprising 1 stratum, of black, coriaceous cells of *textura angularis*. *Hamathecium* comprising filamentous, septate, 2–4 µm wide, anastomosed pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* (75–)80–95(–107) × (8.5–)9–11(–12) µm ($\bar{x}$ = 88.1 × 10.3, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, subsessile to short pedicellate, with knob-like to truncate pedicel, apically rounded, with well-developed ocular chamber. *Ascospores*


65/0.99
Plenodomus agnitus CBS 121.89
Plenodomus fallaciosus CBS 414.62
99/1.00
Plenodomus lupini CBS 248.92
--/0.80
Plenodomus deqinensis CGMCC 3.18221
--/0.88
Plenodemus lijiangensis KUMCC 18-0186
--/0.86
Plenodomus visci CBS 122783
99/0.99
Plenodomus salviae MFLUCC 13-0219
--/0.76
Plenodomus artemisiae KUMCC 18-0151
--/0.98
Plenodomus lindquistii CBS 381.67
Plenodomus influorescens CBS 143.84
--/0.75
--/1.00
Plenodomus sinensis MFLUCC 17-0757
Plenodomus sinensis KUMCC 18-0153
86/0.90
Plenodomus sinensis KUMCC 18-0152
97/0.99
Plenodomus sinensis KUN HKAS 102227
Plenodomus collinsoniae CBS 120227
Plenodomus lingam CBS 260.94
Plenodomus
100/1.00
Plenodomus pimpinellae CBS 101637
Plenodomus wasabiae CBS 120119
75/0.99
Plenodomus guttulatus MFLUCC 15-1876
Plenodomus hendersoniae CBS 113702
--/0.99
Plenodomus enteroleucus CBS 142.84
100/1.00
Plenodomus tracheiphilus CBS 127250
86/1.00
Plenodomus chrysanthemi CBS 539.63
70/0.97
Plenodomus congestus CBS 244.64
Plenodomus libanotidis CBS 113795
100/1.00
Alternariaster helianthi CBS 327.69
100/1.00
Alternariaster bidentis CBS 134021
100/1.00
Alternariaster centaureae-diffusae MFLUCC 14-0992
Alternariaster
--/0.90
Alternariaster trigonosporus MFLU 15-2237
100/0.99
Sphaerellopsis macroconidialis CBS 658.78
100/1.00
Sphaerellopsis macroconidialis CBS 233.51
--/0.88
Sphaerellopsis hakeae CPC 29566
100/1.00
Sphaerellopsis isthmospora HKAS 102225B
Sphaerellopsis isthmospora HKAS 102225A
Sphaerellopsis
--/0.94
100/1.00
Sphaerellopsis paraphysata KUMCC 18-0190
Sphaerellopsis paraphysata CPC 21841
83/0.97
Sphaerellopsis filum CBS 234.51
Alloleptosphaeria italica MFLUCC 14-0934
100/0.99
Leptosphaeria macrocapsa CBS 640.93
95/0.99
Leptosphaeria errabunda CBS 617.75
Leptosphaeria sydowii CBS 385.80
100/0.99
93/0.99
Leptosphaeria ebuli MFLUCC 14-0828
Leptosphaeria doliolum MFLUCC 15-1875
92/-
Leptosphaeria doliolum CBS 505.75
Leptosphaeria
93/--
Leptosphaeria veronicae CBS 126583
Leptosphaeria cichorii MFLUCC 14-1063
77/0.75
Leptosphaeria italica MFLU 15-0174
Leptosphaeria urticae 353 UK
--/1.00
Leptosphaeria conoidea CBS 616.75
Leptosphaeria sclerotioides CBS 148.84
100/--
Leptosphaeria slovacica CBS 125975
Leptosphaeria pedicularis CBS 390.80
100/1.00
Neoleptosphaeria rubefaciens CBS 387.80
Neoleptosphaeria rubefaciens CBS 223.77
Neoleptosphaeria
100/0.97
Neoleptosphaeria jonesii MFLUCC 16-1442
100/1.00
Heterospora chenopodii CBS 115.96
100/1.00
Heterospora chenopodii CBS 448.68
Heterospora
Heterospora dimorphospora CBS 165.78
100/1.00
Heterospora dimorphospora CBS 345.78
Pseudoleptosphaeria etheridgei CBS 125980
Pseudoleptosphaeria
Subplenodomus apiicola CBS 285.72
Subplenodomus
--/0.95
Subplenodomus valerianae CBS 630.68
77/0.97
Paraleptosphaeria rubi MFLUCC 14-0211
Paraleptosphaeria nitschkei CBS 306.51
Paraleptosphaeria
Paraleptosphaeria macrospora CBS 114198
Paraleptosphaeria padi MFLU 15-2756
Paraleptosphaeria dryadis CBS 643.86
Phaeosphaeria oryzae CBS 110110
100/--
Phaeosphaeriopsis glauco-punctata MFLUCC 13-0265
Out group
Paraphoma radicina CBS 111.79
0.07

◀**Fig. 12** Phylogram generated from maximum likelihood analysis based on a combined LSU, SSU and ITS sequence dataset of taxa in *Leptosphaeriaceae*. The updated sequence data was derived from Tennakoon et al. (2017). Seventy strains are included in the combined sequence analyses. Single gene analyses were also performed and topology and clade stability compared from combined gene analyses. *Phaeosphaeria oryzae* (CBS 110110) and *Phaeosphaeriopsis glaucopunctata* (MFLUCC 13-0265) and *Paraphoma radicina* (CBS 111.79) were used as the outgroup taxa. Bootstrap support values for ML equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.80 BYPP are indicated at the nodes. Newly generated sequences are in blue and ex-type strains are in bold

30–39 × 4–6(–6.5) µm ($\bar{x}$ = 34.1 × 5.3, n = 40), overlapping 2–3-seriate, fusiform, initially hyaline, becoming pale brown to pale yellowish at maturity, 6-septate, widest at the third cell, slightly constricted at the septa, deeply constricted at the third septum from above, smooth-walled, inconspicuous minute appendages at both end cells. **Asexual morph** Coelomycetous. *Conidiomata* 50–120 µm high, 50–110 µm diam., pycnidial, black, shiny, scattered, gregarious, superficial, uni-loculate, globose to subglobose, with short stipe (5–10 × 7–11 µm), glabrous, ostiole central, with pore-like opening, apapillate. *Conidiomata walls* 5–10 µm wide, thin-walled, of equal thickness, comprising 2–3 cell layers, of dark brown pseudoparenchymatous cells, of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* (3–)4–7 (–8) × 4–6(–8) µm ($\bar{x}$ = 5.6 × 5.1 µm, n = 30), enteroblastic, phialidic, discrete, determinate, ampulliform to doliiform, hyaline, collarette, and periclinal wall thickening, arising from the inner cavity of the conidioma wall. *Conidia* (2.7–)3–4 × 1–2 µm ($\bar{x}$ = 3.8 × 1.4, n = 100), hyaline, oblong, slightly curved, aseptate, smooth-walled.

Culture characteristics: Colonies on PDA reaching 28–30 mm diam. after 4 weeks at room temperature. Colony dense, irregular in shape, slightly raised to low convex, surface smooth, edge undulate, with margin well-defined; from above dark grey; from below, black; not produced pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Lijiang, Yulong, on dead fronds of fern, 29 July 2015, R. Phookamsak, LJ001 (KUN-HKAS 102229, sexual morph), living culture, KUMCC 18-0153; *ibid*., Baoshan, Shuizai, Dawazi mountain, on dead fronds of fern, 22 October 2015, I.D. Goonasekara, BS010 (KUN-HKAS 102228, asexual morph), living culture, KUMCC 18-0152; Baoshan, Shuizai, Dawazi mountain, on dead stems of *Cirsium* sp. (*Asteraceae*), 22 October 2015, R. Phookamsak, BS023 (KUN-HKAS 102227).

Known hosts and distribution: *Plukenetia volubilis* L. (*Euphorbiaceae*) *Tamarindus indica* L. (*Fabaceae*) (Xishuangbanna, China) (Tennakoon et al. 2017).

GenBank numbers: ITS = MK387922, LSU = MK387960, SSU = MK387930, TEF1-α = MK435602, RPB2 = MK435608 (KUMCC 18-0153); ITS = MK387923, LSU = MK387961, SSU = MK387931, TEF1-α = MK435603 (KUMCC 18-0152); ITS = MK387924, LSU = MK387962, SSU = MK387932 (KUN-HKAS 102227).

Notes: Based on the NCBI BLASTn search of ITS sequences, our isolates (KUMCC 18-0152, KUMCC 18-0153 and KUN-HKAS 102227) match with *Plenodomus sinensis* Tennakoon et al. (MFLU 17-0757), with 99% similarity. The sexual morph of KUMCC 18-0153 and KUN-HKAS 102227 share similar size of ascomata, asci and ascospores with the type, as well as sharing similar ascospore characters with fusiform, 6-septate ascospores (Tennakoon et al. 2017). Phylogenetic analyses of a concatenated LSU, SSU and ITS sequence dataset (Fig. 12) reveal that our isolates cluster with *P. sinensis* (MFLU17-0757) with moderate support (86% ML and 0.90 BYPP).

The asexual morph of *P. sinensis*, which is reported for the first time in this study, is similar to the asexual morph of *P. lijiangensis* in having globose to subglobose conidiomata with a short stipe. However, these two species are phylogenetically distinct.

Tennakoon et al. (2017) introduced *Plenodomus sinensis* as a saprobic species occurring on *Plukenetia volubilis* and *Tamarindus indica* from Xishuangbanna, Yunnan, China (tropical rain forest climate). In this study, *P. sinensis* was found on ferns and *Cirsium* sp. from Baoshan (mild subtropical highland climate) and Lijiang (a mild, with abundant rainfall and plenty of sunshine climate), Yunnan, China. This indicates that *P. sinensis* may occur on a wide range of hosts and in different climatic regions.

Sphaerellopsis Cooke

Sphaerellopsis was introduced by Sutton (1977) to accommodate mycoparasitic taxa occurring on a wide range of rusts and is typified with *S. filum* (Biv.) B. Sutton. *Sphaerellopsis* was re-circumscribed by Trakunyingcharoen et al. (2014) and Ariyawansa et al. (2015b) based on molecular phylogeny. The link between the sexual genus *Eudarluca* Speg. and the asexual genus *Sphaerellopsis* is still debated. *Eudarluca* was synonymized under *Sphaerellopsis* by Rossman et al. (2015) based on holomorphic characters of *Eudarluca caricis* (Fr.) O.E. Erikss. However, Phookamsak et al. (2014b) re-examined the isotype specimen of *Eudarluca australis* Speg. and treated *Eudarluca* in *Phaeosphaeriaceae* according to the generic type, *E. australis* is not congeneric with *E. caricis*. *Eudarluca australis* is typical of *Phaeosphaeriaceae* in having uni-loculate ascomata, a thin-walled peridium, comprising 1–2 layers of brown, pseudoparenchymatous cells, cylindrical asci, with pale brown,

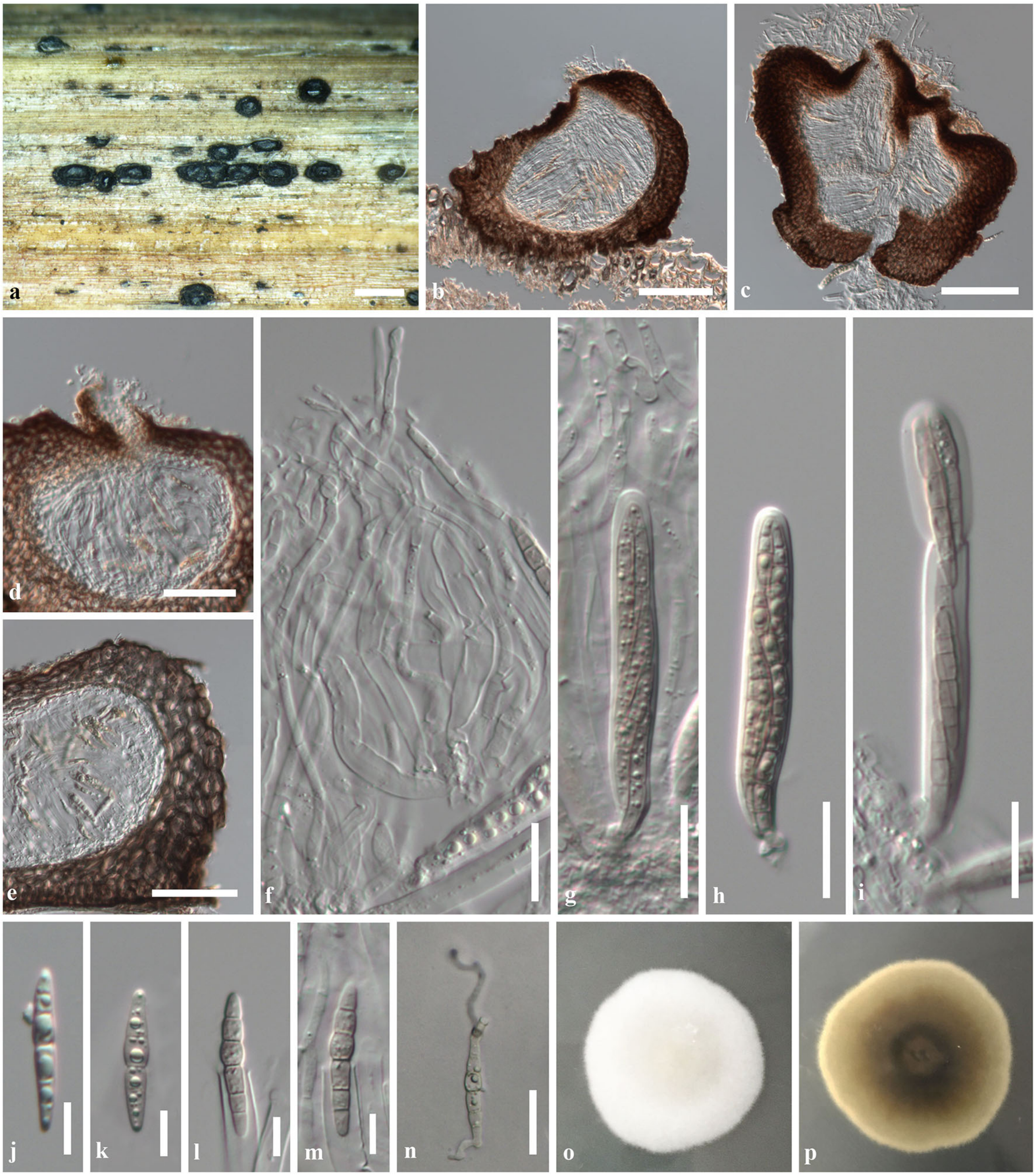


Fig. 13 ***Plenodomus artemisiae*** (KUN-HKAS 102226, **holotype**). **a** Ascomata on host. **b, c** Vertical section of ascomata. **d** Ostiole. **e** Section through peridium. **f** Pseudoparaphyses. **g–i** Asci. **j–m** Ascospores. **n** Ascospore germination. **o, p** Culture characteristics (o = from above, p = from below). *Scale bars* **a** = 500 µm, **b, c** = 100 µm, **d, e** = 50 µm, **f–i, n** = 20 µm, **j–m** = 10 µm

ellipsoidal to fusiform, (1–)2-septate ascospores and this concurs with the iconotype of *E. australis*, established by Spegazzini (1908) (Phookamsak et al. 2014b). Whereas, *E. caricis* forms black, multi-loculate ascostroma, with thick-walled peridium (Yuan et al. 1998; confirming the connection of *E. caricis* and *Sphaerellopsis filum*). Phylogenetic affinity of *Eudarluca australis* has not been proved yet.

Sphaerellopsis isthmospora A. Karunarathna, Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556138; *Facesoffungi number*: FoF05698, Fig. 17

Etymology: The specific epithet "*isthmospora*" refers to the fungus having isthmospores.

Holotype: KUN-HKAS 102225

Saprobic on dead branches of herbaceous plant. **Sexual morph** *Ascomata* 230–330 µm high, 260–510 µm diam.,

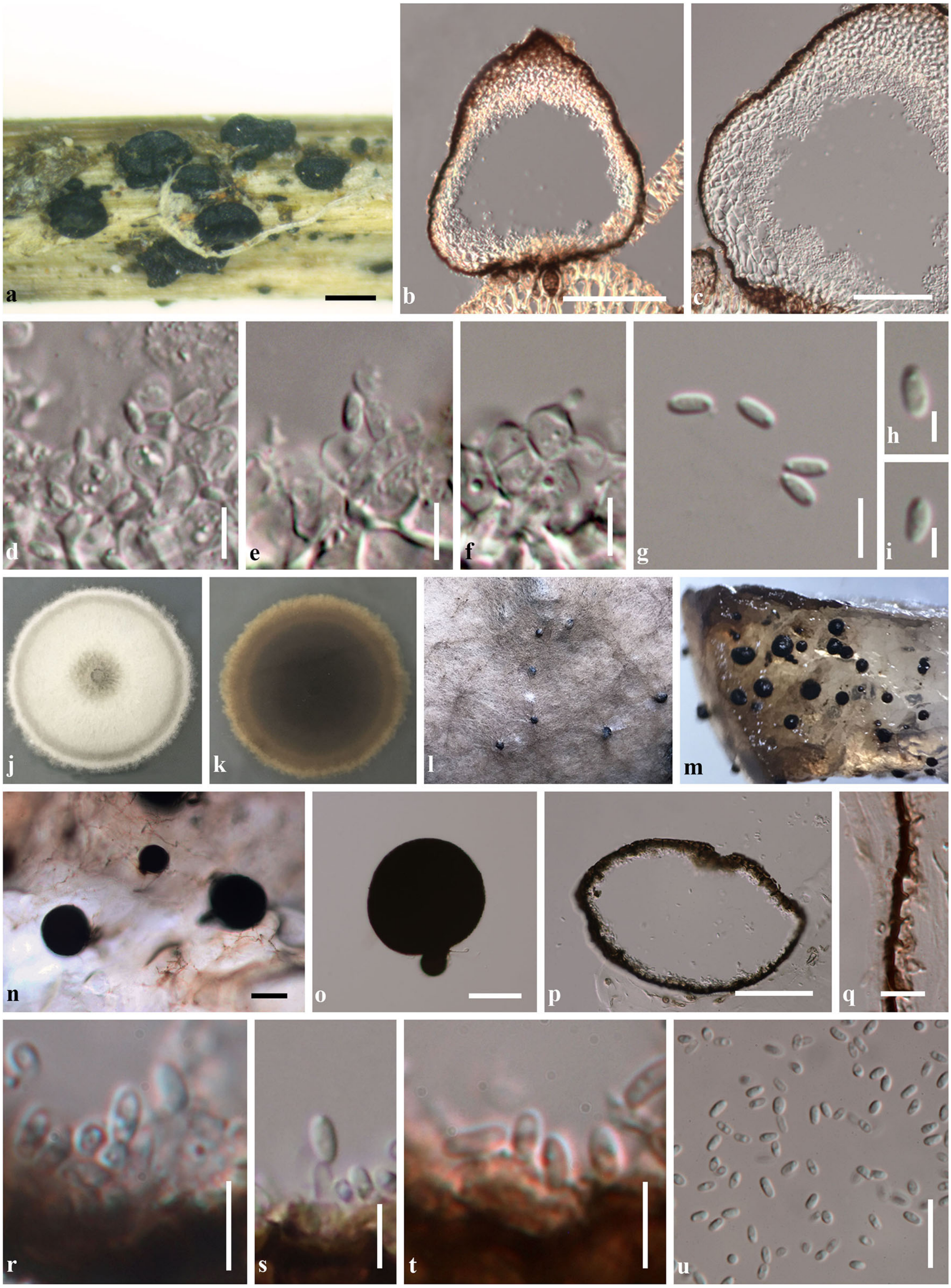


Fig. 14 ***Plenodomus lijiangensis*** (KUN-HKAS 102249, **holotype**). **a–i** Morphological characteristics on natural substrate. **l–u** Morphological characteristics in vitro. **a** Conidiomata on host. **b** Vertical section of conidioma. **c** Section through conidioma wall. **d–f** Conidiogenous cells. **g–i** Conidia. **j, k** Culture characteristics on PDA (**j** = from above, **k** = from below). **l–n** Conidiomata forming on PDA after three months. **o** Squash mount of conidioma. **p** Vertical section of conidioma. **q** Section through conidioma wall stained with congo red. **r, s** Conidiogenous cells. **t** Conidiogenous cells stained with congo red. **u** Conidia. *Scale bars* **a** = 200 µm, **b, n, o** = 100 µm, **c, p** = 50 µm, **u** = 10 µm, **g, q–t** = 5 µm, **h, i** = 2 µm

black, shiny, scattered, solitary to gregarious, erumpent through host epidermis, becoming semi-immersed to superficial, varied in shape, subglobose to mammiform, with flattened, quadrilateral, truncate base, uni-loculate, glabrous, ostiolate, minutely papillate. *Ostioles* central, with obtuse, minute papilla, dark brown to black, ostiolar canal filled with periphyses. *Peridium* 18–60 µm wide, thick-walled of unequal thickness, thicker at the sides towards the apex, with flattened base, comprising several cell layers of black, coriaceous, pseudoparenchymatous cells, arranged in *textura angularis* to *textura prismatica*. *Hamathecium* initially comprising 2–5 µm wide, hyaline, filamentous distinctly septate pseudoparaphyses, laterally becoming, 6–18 µm wide, broadly cellular, hyaline, septate catenophyses, deeply constricted at the septa. *Asci* (120–)130–150 (–165) × (15–)19–23(–28) µm ($\bar{x}$ = 141.4 × 21.6 µm, n = 20), 8-spored, bitunicate, fissitunicate, subcylindric-clavate, subsessile to short pedicellate, with truncate pedicel, apically rounded with well-developed ocular chamber. *Ascospores* (65–)75–95(–118) × 4–7 µm ($\bar{x}$ = 87.1 × 5.9 µm, n = 30), isthmosporous, overlapping 2–3-seriate, hyaline to yellowish, elongate cylindrical to subcylindric-clavate, bent at the 8th septum, 10–12-septate, slightly constricted at the septa, deeply constricted at the 8th septum, split into two part-spores; upper part 40–70(–82) µm long, 5–7-septate, cylindrical, with rounded end; lower part 28–35(–50) µm long, 2–3-septate, subcylindric-clavate, with acute end, guttulate, lacking a mucilaginous sheath. **Asexual morph** Undetermined.

Material examined: CHINA, Yunnan Province, Baoshan, Shuizai, Dawazi mountain, on dead branches of herbaceous plant, 23 October 2015, R. Phookamsak, BS012 (KUN-HKAS 102225, **holotype**).

GenBank numbers: ITS = MK387925, LSU = MK387963, SSU = MK387933, TEF1-α = MK435604 (HKAS 102225A); ITS = MK387926, LSU = MK387964, SSU = MK387934, TEF1-α = MK435605 (HKAS 102225B).

Notes: *Sphaerellopsis isthmospora* forms a phylogenetically distinct lineage, but clusters with other *Sphaerellopsis* species in *Leptosphaeriaceae* (Fig. 12). *Sphaerellopsis isthmospora* can be distinguished from other *Sphaerellopsis* species in its sexual morph having isthmosporous ascospores, with 10–12-septate, deeply constricted and bent at the 8th septum. *Sphaerellopsis filum* (sexual morph: *Eudarluca caricis*) has spindle-shaped, slightly inequilateral, 2–3-septate ascospores (Yuan et al. 1998). Based on morphological difference and phylogenetic affinity, we therefore, introduce a new species *S. isthmospora* from herbaceous plant in Baoshan, China.

Sphaerellopsis paraphysata Crous & Alfenas, in Trakunyingcharoen et al., IMA Fungus 5(2): 411 (2014)

Facesoffungi number: FoF04968, Fig. 18

Holotype: BRAZIL, Minas Gerais, Viçosa, Universidade Federal de Viçosa campus, on rust on *Pennisetum* sp., 18 November 2012, A.C. Alfenas, CBS H-21848, ex-type living culture, CPC 21841 = CBS138579.

Associated with rust on living leaves of *Liriope spicata* (Thunb.) Lour. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 105–160 µm high, 90–150 µm diam., black, pycnidial, solitary, associated with rust stromatic along the leaf veins, semi-immersed to superficial on stromata, globose to subglobose, uni-loculate, glabrous, ostiole central, with pore-like opening. *Conidiomata walls* 12–30 µm wide, composed of 2–5 layers, of dark brown pseudoparenchymatous cells of *textura angularis*. *Conidiophores* 15–21 × 2.4–3 µm ($\bar{x}$ = 18 × 2.7 µm, n = 20), arising from the basal cavity, 1–2-celled, hyaline, curved, cylindrical, or reduced to conidiogenous cells. *Conidiogenous cells* 3.5–6 × 2.5–4.5 µm ($\bar{x}$ = 4.7 × 3.5 µm, n = 20), enteroblastic, phialidic, discrete, determinate, cylindrical to ampulliform to doliiform, hyaline, 0–1-septate, smooth, thin-walled, minute collarette, with 1–2 apertures, and periclinal wall thickening. *Conidia* 14–17 × 3–5 µm ($\bar{x}$ = 15.5 × 4.5 µm, n = 20), hyaline, fusiform to ellipsoidal, mostly 1–3-septate, constricted at the central septum, smooth-walled.

Culture characteristics: Colonies on PDA reaching 25–30 mm diam. after 4 weeks at room temperature. Colony dense, irregular in shape, flattened, slightly raised, surface slightly rough, heaped and folded at the centre, with small granular and black, stromatic, edge undulate, with margin well-defined, felted at the centre, fluffy at the edge; from above white at the margin, with yellowish grey to greenish grey at the centre; from below, white to cream at the margin, black at the centre; not producing pigmentation on agar medium, sporulating on PDA after 3 weeks.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, associated with rust on living leaves of *Liriope spicata* (Thunb.) Lour (*Asparagaceae*), 6 December 2017, R. Phookamsak, KIB044 (KUN-HKAS 101483), living culture, KUMCC 18-0195.

Known hosts and distribution: Associated with rust on *Pennisetum* sp. (Brazil), on *Ravenelia macowania* on *Vachellia karroo* (South Africa), on leaves of *Phragmites* sp. (Australia), and associated with rust on living leaves of *Liriope spicata* (Yunnan, China) (Trakunyingcharoen et al. 2014; Crous et al. 2018; this study).

GenBank numbers: ITS = MK387927, LSU = MK387965, SSU = MK387935, TEF1-α = MK435606.

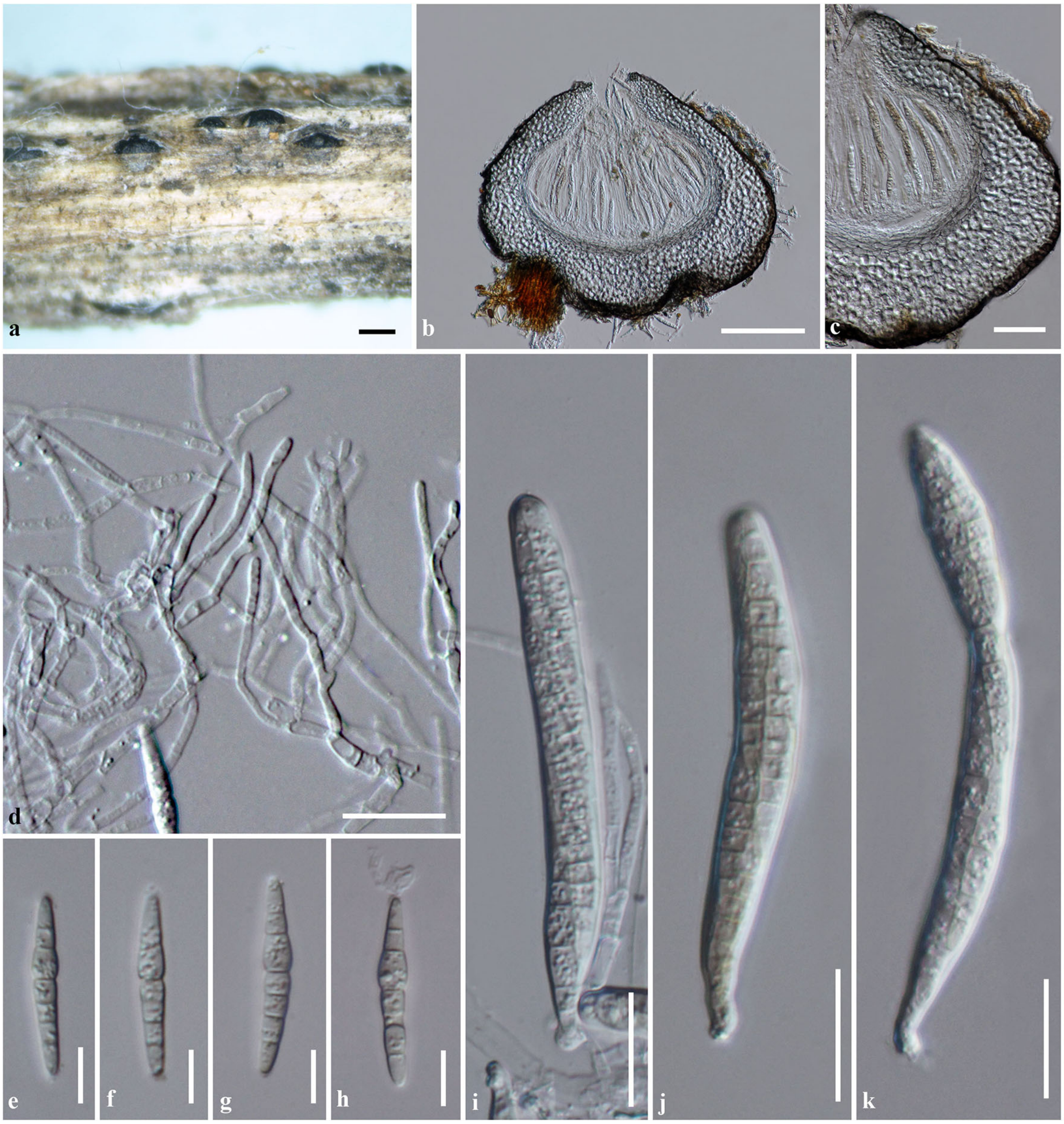


Fig. 15 ***Plenodomus sinensis*** (KUN-HKAS 102229, **sexual morph**). **a** Ascomata on host. **b** Vertical section of ascoma. **c** Section through peridium. **d** Pseudoparaphyses. **e–g** Ascospores. **h** Ascospore germination. **i–k** Asci. *Scale bars* **a** = 200 µm, **b** = 100 µm, **c** = 50 µm, **d, i–k** = 20 µm, **e–h** = 10 µm

Notes: *Sphaerellopsis paraphysata* was introduced by Trakunyingcharoen et al. (2014) based on morphological comparisons and phylogenetic analysis. We made a new collection from China associated with a rust on living leaves of *Liriope spicata*. The new isolate (KUN-HKAS 101483) is similar in morphology with *S. paraphysata* but differs from the type of *S. paraphysata* in having smaller conidiomata, presence of conidiophores and lacking paraphyses. Phylogenetic analyses of a combined LSU, SSU and ITS sequence dataset show that our strain (KUMCC 18-0195) forms a sister lineage with *S. paraphysata* (CPC 21841) with high support (100% ML and 1.00 BYPP). A comparison of ITS nucleotide base shows that our new isolate has same base pairs with the type strain of *S. paraphysata*. Thus we identify the new isolate as *S. paraphysata* and our new collection is a new host record in China.

Lophiotremataceae K. Hiray. & Kaz. Tanaka

Lophiotremataceae was introduced by Hirayama and Tanaka (2011) to accommodate the type genus *Lophiotrema* Sacc. and is typified by *L. nucula* (Fr.) Sacc. *Lophiotrema* shares morphological characters with *Lophiostoma* due to its compressed carbonaceous ascomata with crest-like apex but is distinguished by peridial

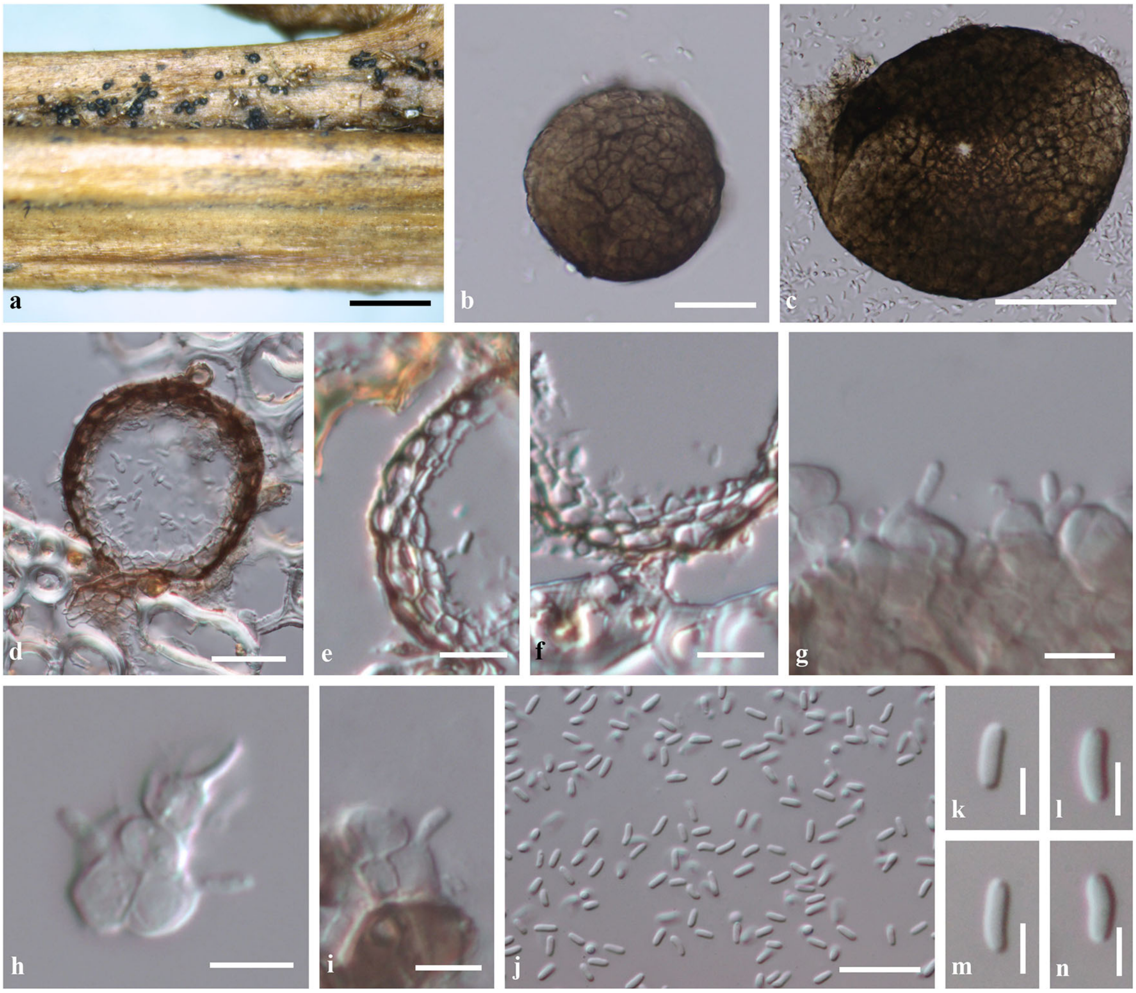


Fig. 16 ***Plenodomus sinensis*** (KUN-HKAS 102228, **asexual morph**). **a** Conidiomata on host. **b** Squash mount of conidioma. **c** Squash mount of conidioma showing ostiole. **d** Section through conidioma. **e** Section through conidioma wall. **f** Stalk of conidioma. **g–i** Conidiogenous cells. **j–n** Conidia. *Scale bars* **a** = 500 µm, **c** = 50 µm, **b, d** = 20 µm, **e, f, j** = 10 µm, **g–i** = 5 µm, **k–n** = 2 µm

structure and shape of asci (Zhang et al. 2009b, 2012; Hirayama and Tanaka 2011; Hyde et al. 2013). We follow the latest treatment and the updated accounts of *Lophiotremataceae* in Hyde et al. (2016) and Hashimoto et al. (2017). *Lophiotremataceae* comprises *Atrocalyx* A. Hashim. & Kaz. Tanaka, *Crassimassarina* A. Hashim. & Kaz. Tanaka, *Cryptoclypeus* A. Hashim. & Kaz. Tanaka, *Galeaticarpa* A. Hashim. & Kaz. Tanaka, *Lophiotrema* and *Pseudocryptoclypeus* A. Hashim. & Kaz. Tanaka (Hashimoto et al. 2017; Wijayawardene et al. 2018a). In the present study, a new species, *Lophiotrema mucilaginosis* collected on dead wood in China, is introduced.

Lophiotrema Sacc.

Lophiotrema was introduced by Saccardo (1878) and is typified by *L. nucula* (Fr.) Ces. & De Not. The genus was established to accommodate taxa in *Pleosporales*, characterized by ascomata with a slit-like ostioles, a peridium of uniform thickness, cylindrical to cylindric-clavate asci with a short stipe, hyaline, ellipsoidal to fusiform, septate ascospores and pycnidial coelomycetous asexual morphs (Hirayama and Tanaka 2011; Hirayama et al. 2014; Hashimoto et al. 2017). The genus has a long taxonomic history and has always been confused with *Lophiostoma* Ces. & De Not. and *Massarina* Sacc. in previous studies (Zhang et al. 2009b, 2012; Hirayama and Tanaka 2011; Hyde et al. 2013; Hirayama et al. 2014). However, *Lophiotrema* was re-classified based on molecular data by Hashimoto et al. (2017) and many species of *Lophiotrema sensu lato* were treated as new genera in *Lophiotremataceae*.

Lophiotrema mucilaginosis M. Raza & L. Cai, ***sp. nov.***

Index Fungorum number: IF555333; *Facesoffungi number*: FoF04941, Fig. 19

Etymology: In reference to the mucilaginous sheath around spores.

Holotype: HMAS 255437

Saprobic on dead wood. **Sexual morph** *Ascomata* 220–340 μm high, 240–400 μm diam., black, scattered, solitary, semi-immersed to erumpent through host surface, conical to mammiform, with flattened base, uni-loculate, glabrous, ostiolate, papillate. *Ostioles* 50–90 × 25–60 μm, apically with crest-like papilla, filled with periphyses, carbonaceous, with beak-like opening. *Peridium* 55–80 μm wide, outer layer thick, composed of dark, coriaceous, pseudoparenchymatous cells of *textura epidermoidea*, inner layer comprising light pigmented to hyaline cells of *textura angularis*. *Hamathecium* composed of branched, 1.5–2 μm wide, filamentous, indistinct septate, anastomosed pseudoparaphyses, embedded in a hyaline, gelatinous matrix. *Asci* (83.5–)102–144(–210) × (10.5–)13–15(–21.5) μm ($\bar{x}$ = 127.5 × 14.5 μm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate with furcate to truncate pedicel, apically rounded, with well-developed ocular chamber. *Ascospores* (31.5–)34–45.5(–48) × (5.5–)6–11(–12.5) μm ($\bar{x}$ = 39.1 × 8.6 μm, n = 40), overlapping 2-seriate, hyaline, subfusoid to

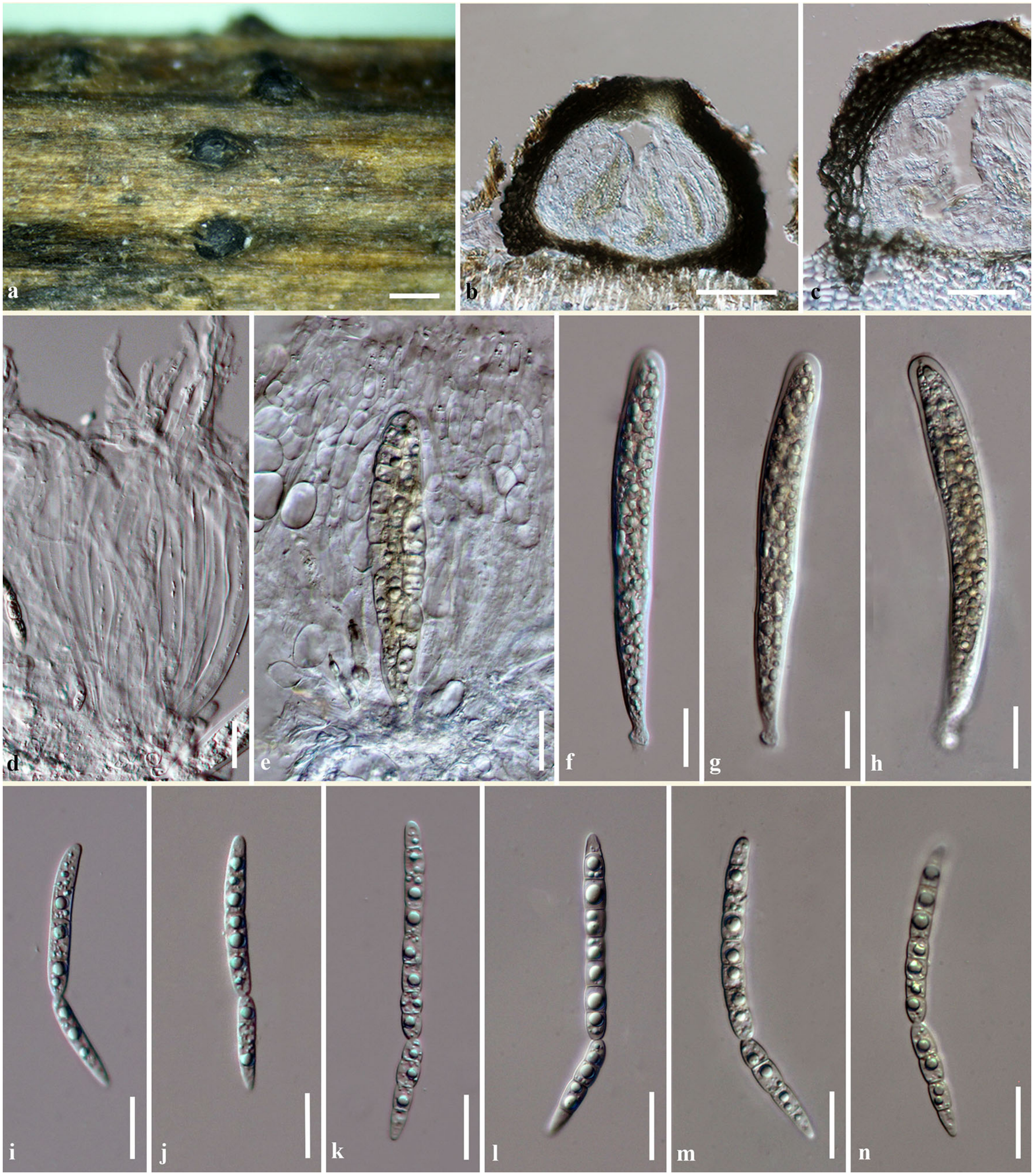


Fig. 17 ***Sphaerellopsis isthmospora*** (KUN-HKAS 102225, **holotype**). **a** Appearance of ascomata on host substrate. **b** Section through ascoma. **c** Section through peridium. **d, e** Pseudoparaphyses. **f–h** Asci. **i–n** Ascospores. *Scale bars* **a** = 500 μm, **b** = 100 μm, **c** = 50 μm, **d–n** = 20 μm

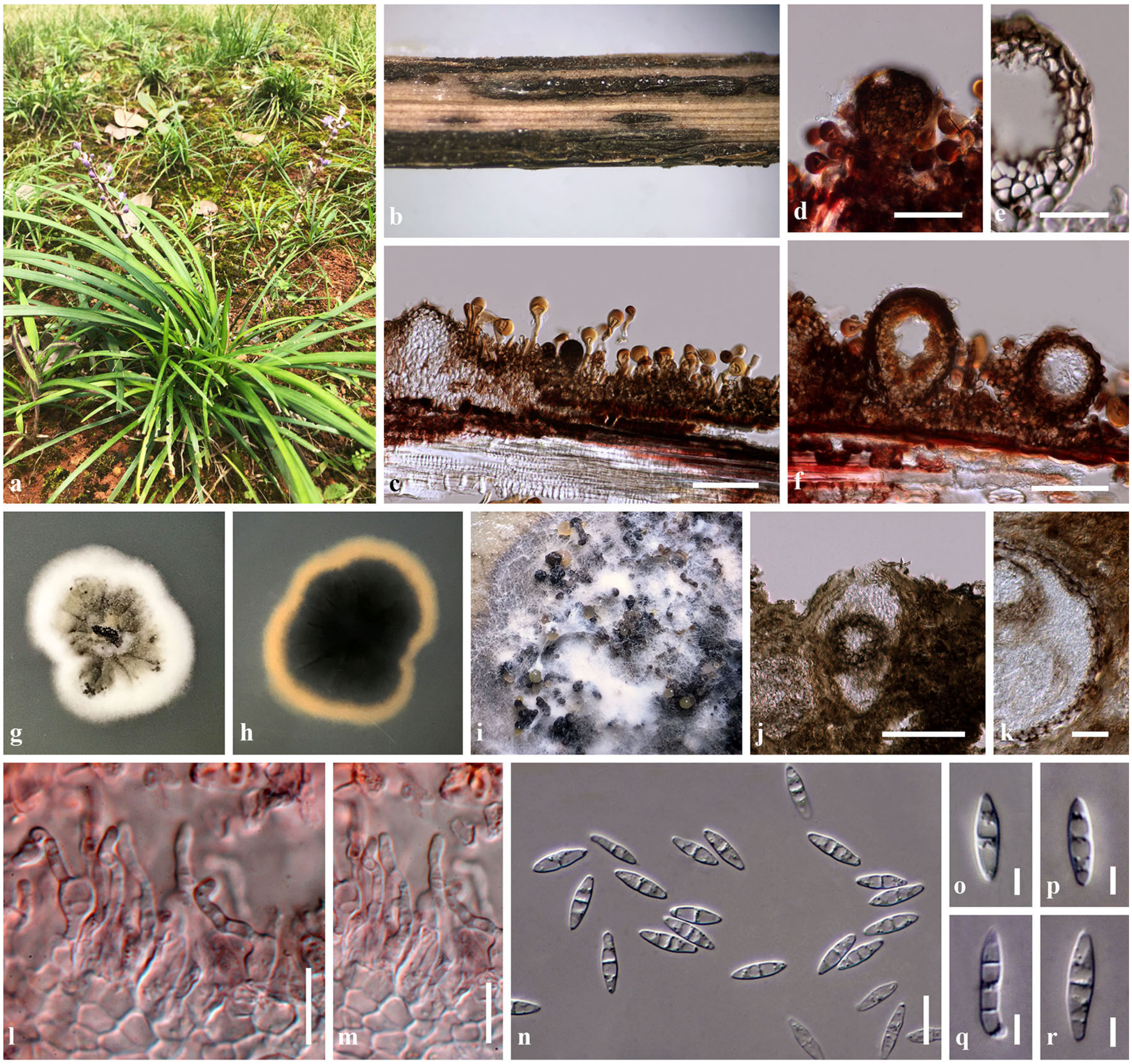


Fig. 18 ***Sphaerellopsis paraphysata*** (KUN-HKAS 101483). **a** *Liriope spicata*. **b–d** Appearance of conidiomata associated with rust on host substrate. **e** Section through conidioma wall. **f** Section through conidioma. **g, h** Culture on PDA after 2 weeks (**g** = from above, **h** = from below). **i–r** in vitro (OA). **i** Sporulation on OA after 4 weeks. **j** Section through conidioma. **k** Section through conidioma wall. **l, m** Conidiogenous cells stained in congo red. **n–r** Conidia. *Scale bars* **j** = 100 µm, **c, d, f** = 50 µm, **k** = 20 µm, **e, l, m** = 10 µm, **n** = 5 µm, **o–r** = 2 µm

fusiform, with rounded or obtuse ends, 1(–3)-septate, smooth-walled, guttulate when young, with an entire mucilaginous sheath (9–20.5 µm wide at sides). **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 2.5–3 mm diam. after 1 week at 25 ± 2 °C, circular, convex or dome-shaped, rough with entire edge, mucoid, smooth at the margin; from above, green earth at the fruiting zone, grey at the productive zone and light grey at ageing zone, dome, shining black mucoid colony; from below, light grey at the fruiting zone, light green to blackish at the productive zone, dark grey at the ageing zone; cracking and not producing pigmentation in PDA agar medium.

Material examined: CHINA, Yunnan Province, Baoshan City, Longling County, on wood litter, October 2015, M. Raza, BAP 119 (HMAS 255437, **holotype**), ex-type living culture, LC12112.

GenBank numbers: ITS = MH822889, LSU = MH822890, SSU = MH822891, RPB2 = MH822892, TEF1-α = MH822893.

Notes: Multi-loci phylogenetic analyses based on a concatenated ITS, LSU, SSU, TEF1-α and RPB2 sequence dataset show that *Lophiotrema mucilaginosis* forms a well-supported lineage (100% ML and 1.00 BYPP; Fig. 20), sister to *L. hydei* J.F. Zhang et al. and clusters with *L. neohysterioides* M.E. Barr. *Lophiotrema mucilaginosis* and *L. hydei* were collected on wood litter and herbaceous plant

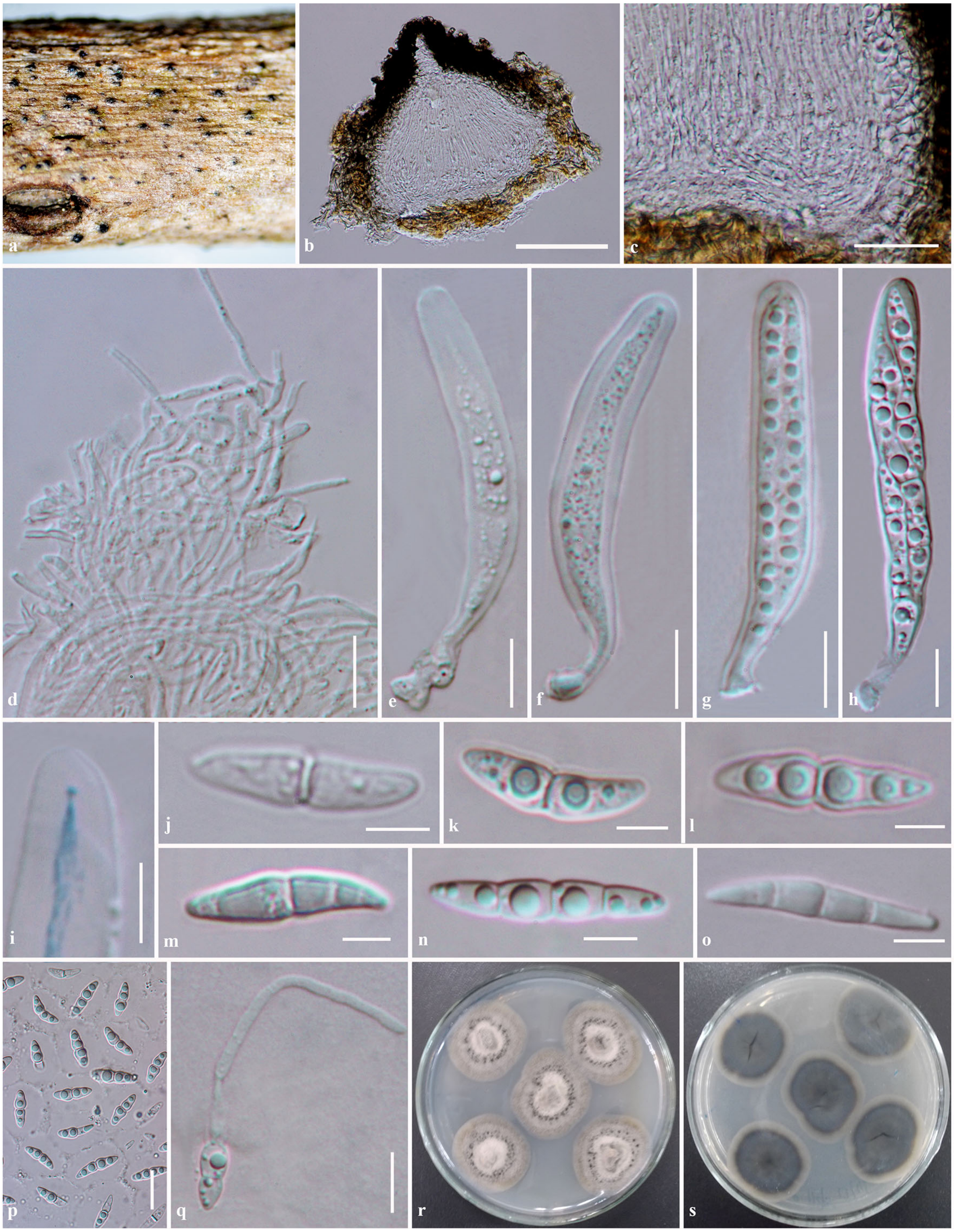


Fig. 19 ***Lophiotrema mucilaginosis*** (HMAS 255437, **holotype**). **a** Blackish ascomata on dead wood. **b** Vertical section of ascoma. **c** Peridial structure. **d** Pseudoparaphyses. **e, f** Immature asci. **g, h** Mature asci. **i** Apical ring stained with cotton blue. **j** Immature ascospores. **k–o** Mature ascospores. **p** Ascospores with mucilaginous sheath. **q** Germination of ascospore. **r, s** Culture characteristics on PDA (**r** = from above, **s** = from below). *Scale bars* **b** = 100 µm, **c** = 50 µm, **d, p, q** = 20 µm, **e–i** = 10 µm, **o** = 5, **j–n** = 2 µm

from Yunnan and Guizhou Provinces in China respectively. *Lophiotrema mucilaginosis* can be distinguished from *L. hydei* in having larger asci (78–89(–99) × 6.9–8.8 µm, *L. hydei*) and larger ascospores (23–28 × 3–4 µm, *L. hydei*) (Zhang et al. 2018). In addition, *L. mucilaginosis* has conical to mammiform ascomata,

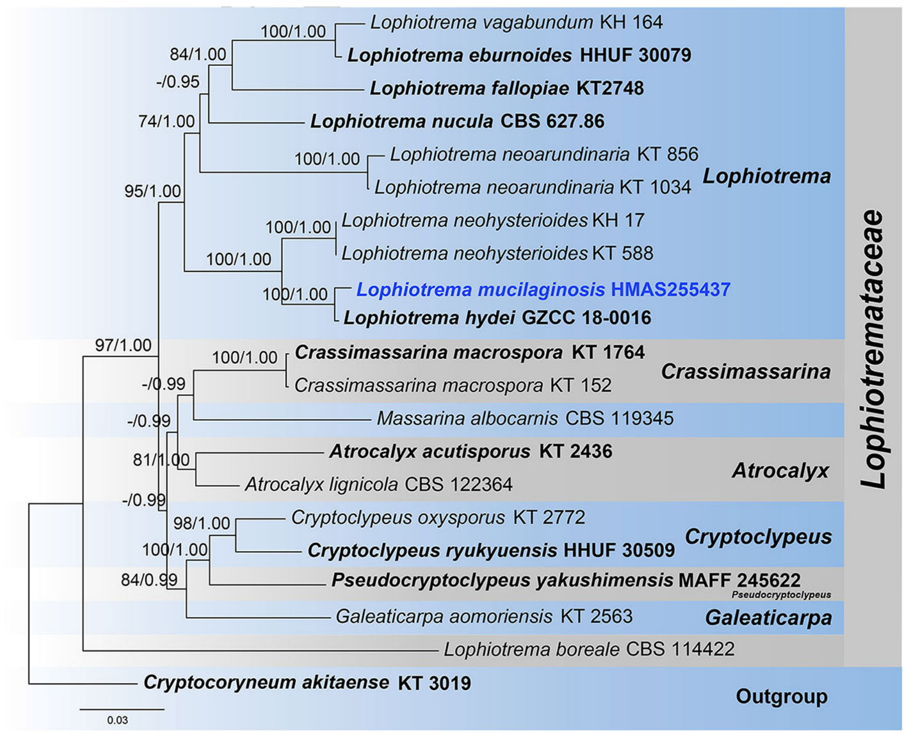


Fig. 20 Phylogenetic tree generated from maximum likelihood analysis (RAxML) based on a combined ITS, LSU, SSU, TEF1-α and RPB2 sequence dataset of genera in *Lophiotremataceae*. Maximum likelihood bootstrap support values greater than 70% and Bayesian posterior probabilities greater than 0.95 BYPP are indicated on the branches. The new isolate is in blue. The type strains are in bold. The tree is rooted with *Cryptocoryneum akitaense* (KT 3019)

with flattened base and 1(–3)-septate ascospores. Whereas, *L. hydei* has globose to subglobose ascomata and inconspicuously 0–1-septate ascospores. *Lophiotrema mucilaginosis* differs from *L. neohysterioides* by its larger asci (70–96 × 7–10 µm, *L. neohysterioides*) and larger ascospores (17–25 × 3–5 µm, *L. neohysterioides*) and presence of mucilaginous sheath surrounding the ascospores, a feature not observed in *L. neohysterioides* (Tanaka and Harada 2003a).

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

Occultibambusaceae was introduced by Dai et al. (2017a) and is typified by *Occultibambusa* D.Q. Dai & K.D. Hyde with *O. bambusae* D.Q. Dai & K.D. Hyde being the type species. The family was introduced to accommodate bambusicola-like taxa, mainly occurring on bamboo (Dai et al. 2017a; Doilom et al. 2017). Dai et al. (2017a) accepted four genera in *Occultibambusaceae* viz. *Neooccultibambusa* Doilom & K.D. Hyde., *Occultibambusa*, *Seriascoma* Phookamsak et al. and *Versicolorisporium* Sat. Hatak. et al. and this is in agreement of Wijayawardene et al. (2018a). Subsequent authors introduced new taxa in this family (Hyde et al. 2016, 2018b; Zhang et al. 2017b; Tibpromma et al. 2018). We follow the latest treatment of *Occultibambusaceae* in Dai et al. (2017a) and introduce the new genus, *Brunneofusispora* S.K. Huang & K.D. Hyde to accommodate *Brunneofusispora sinensis* and other isolates of *Massarina rubi*. The updated sequence data were retrieved from Zhang et al. (2017b).

Brunneofusispora S.K. Huang & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF555599; *Facesoffungi number*: FoF04862

Etymology: The generic epithet "*Brunneofusispora*" refers to the taxon having brown, fusiform ascospores.

Saprobic on dead wood. **Sexual morph** *Ascomata* solitary to scattered, immersed, eventually erumpent, globose to subglobose, uni-loculate, glabrous, dark brown to black, ostiolate, with long beak. *Peridium* composed of brown to hyaline pseudoparenchymatous cells of *textura angularis*. *Hamathecium* composed of numerous, filamentous, septate pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* overlapping 2-seriate, hyaline to brown, broadly fusiform, 1-septate, constricted at the septum, smooth-walled, with guttules, surrounded by a mucilaginous sheath. **Asexual morph** Undetermined.

Type species: *Brunneofusispora sinensis* S.K. Huang & K.D. Hyde

Notes: Multigene phylogenetic analyses reveal that our new taxon forms a distinct lineage, but clusters with three isolates of *Massarina rubi* (Fuckel) Sacc. (current name: *Lophiotrema rubi* (Fuckel) Y. Zhang ter et al.) in *Occultibambusaceae* (Fig. 21). We introduce a new genus *Brunneofusispora* to accommodate *B. sinensis*, which was collected from a woody plant in Yunnan, China. *Brunneofusispora* resembles *Neooccultibambusa* in occurring on woody plants and forming globose to subglobose ascomata,

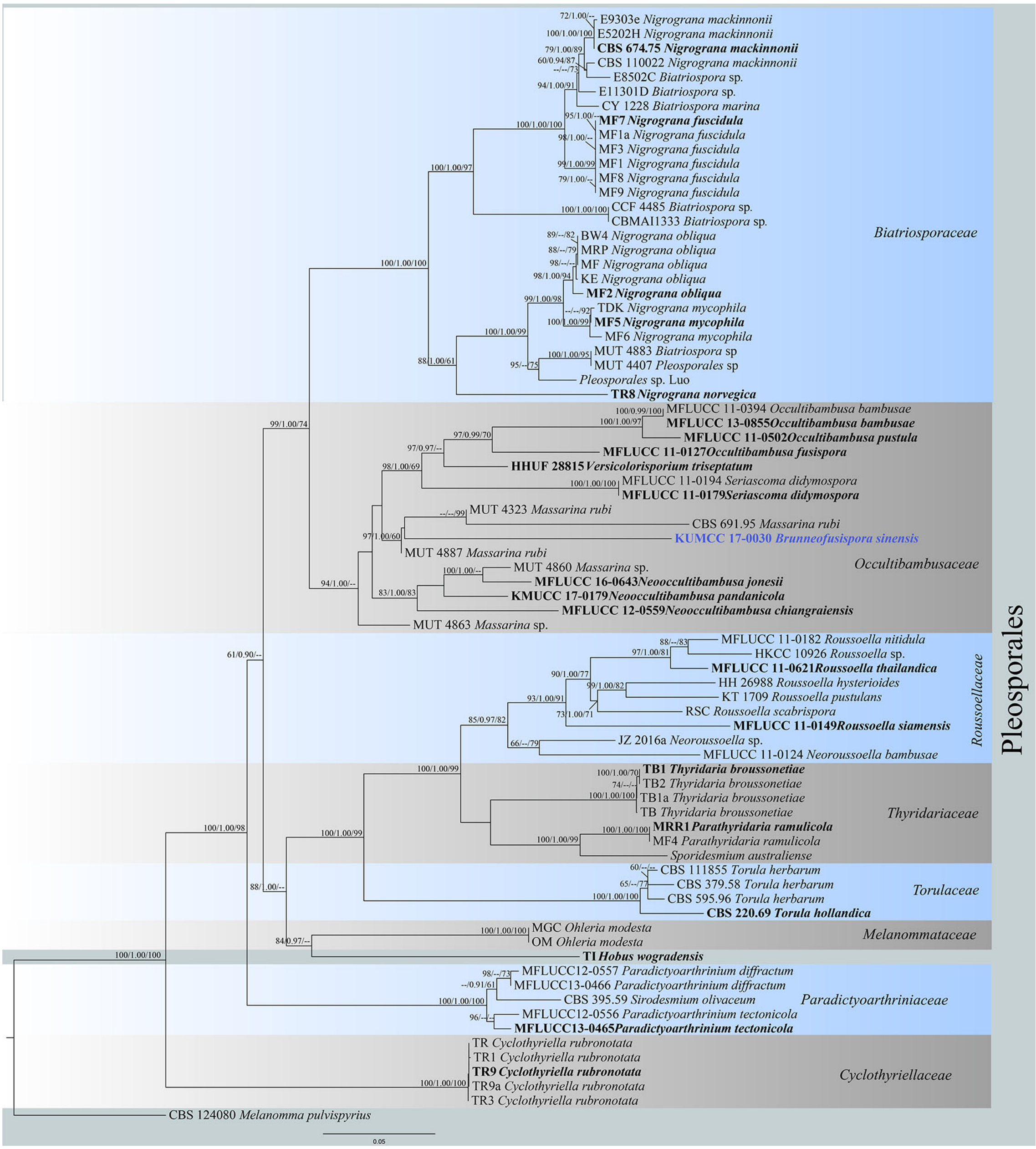


Fig. 21 Maximum likelihood phylogenetic tree generated from analysis of a combined LSU, SSU, ITS, RPB2 and TEF1-α sequence dataset for 77 taxa of representative families in *Pleosporales*. *Melanomma pulvispyrius* (CBS 124080) was selected as the outgroup taxon. ML and MP support values greater than 60% and Bayesian posterior probabilities greater than 0.90 BYPP are indicated above the nodes as ML/PP/MP. The strain numbers are noted before the species names. Isolates from this study are indicated in blue. Ex-type strains are indicated in bold

but *Brunneofusispora* differs from *Neooccultibambusa* in having a long prominent neck (Doilom et al. 2017). *Brunneofusispora* resembles *Lophiotrema* in having cylindrical, cylindric-clavate asci and fusiform ascospores, but it differs from *Lophiotrema* in having globose to subglobose ascomata, with a long prominent neck. *Lophiotrema* species have minute papilla, with crest-like or slit-like openings (Zhang et al. 2009b; Hashimoto et al. 2017).

Lophiotrema rubi (≡ *Masarina rubi*) is an orphan species in *Lophiotremataceae*, which was transferred from *Massarina* based on phylogenetic analysis by Zhang et al. (2009b). It is characterized by immersed ascomata with broadly fusiform ascospores (Saccardo 1883b; Aptroot 1998). In this study, *L. rubi* strains CBS 691.95, MUT 4323 and MUT 4887 clustered with our strain (KUMCC 17-0030) and they form an independent clade within *Occultibambusaceae* (Fig. 21). However, the morphological

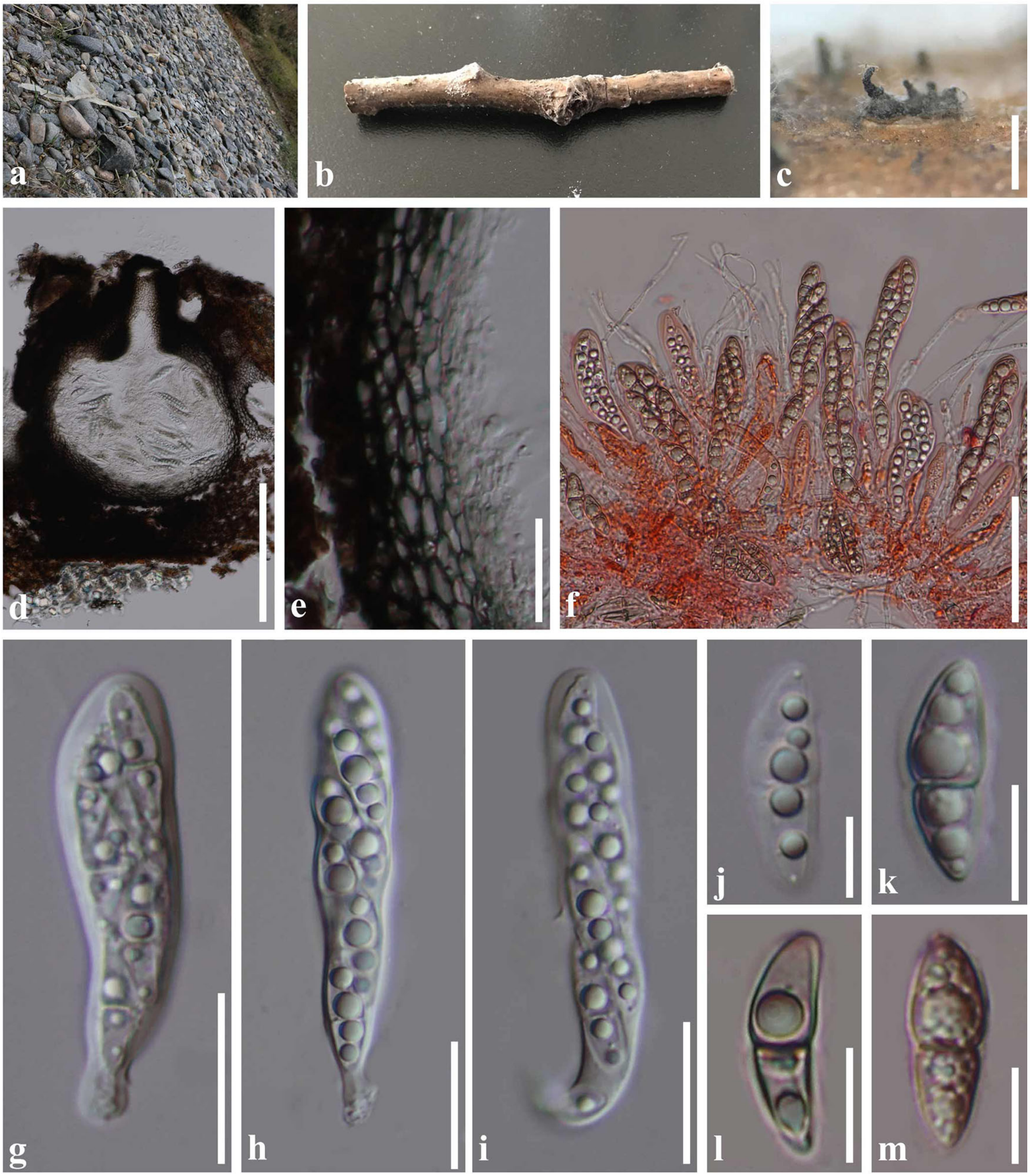


Fig. 22 ***Brunneofusispora sinensis*** (KUN-HKAS 97451, **holotype**). **a** Habitat. **b, c** Appearance of ascomata on dead wood. **d** Ascoma in vertical section. **e** Peridium. **f** Asci with pseudoparaphyses stained in congo red. **g–i** Developing stages of asci. **j–m** Ascospores (note: **l, m** stained in congo red). *Scale bars* **c** = 500 µm, **d** = 200 µm, **f** = 50 µm, **g–i** = 20 µm, **e, j–m** = 10 µm

characteristics of these strains have never been described (Zhang et al. 2009a; Gnavi et al. 2017). We therefore, tentatively include these strains of *Massarina rubi* until they are clarified base on evidence from morphology and phylogeny.

Brunneofusispora sinensis S.K. Huang & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555600; *Facesoffungi number*: FoF04863, Fig. 22

Etymology: The specific epithet "*sinensis*" refers to the country, China, where the taxon was collected.

Holotype: KUN-HKAS 97451.

Saprobic on dead wood. **Sexual morph** *Ascomata* 325–370 µm diam., perithecial, solitary to scattered, immersed, eventually erumpent, globose to subglobose, uni-loculate, glabrous, dark brown to black, ostiole, papillate with long beak. *Ostioles* central, lined with periphyses. *Peridium* 20–45 µm wide, equally thick-walled, composed of 5–8 strata, of blackened pseudoparenchymatous cells, arranged in a *textura angularis*. *Hamathecium* composed of numerous, 1.5–3.5 µm wide, filamentous, septate pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 53–110 × 9–18 µm ($\bar{x}$ = 75 × 14 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 18–22 × 5–8.5 µm ($\bar{x}$ = 20 × 7 µm, n = 50), overlapping 2-seriate, initially hyaline, becoming light brown to brown at maturity, broadly fusiform, 1-septate, constricted at the septum, smooth-walled, with guttules, surrounded by mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinated on PDA within 2 weeks at 23 °C, colony on PDA reaching 1 cm diam. after 4 weeks, irregular in shape, surface rough, with edge umbonate and well-defined margin, velvety to floccose; from above brown; from below cream, not producing pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Songming, Niulan river, on dead wood, 1 October 2016, S.K. Huang (KUN-HKAS 97451, **holotype**), ex-type living culture, KUMCC 17-0030.

GenBank numbers: ITS = MH393558, LSU = MH393557, SSU = MH393556, TEF1-α = MH395329.

Parabambusicolaceae Kaz. Tanaka & K. Hiray.

We follow the latest treatment and updated accounts of *Parabambusicolaceae* in Tanaka et al. (2015), Li et al. (2016), Phukhamsakda et al. (2016, 2018) and Wanasinghe et al. (2017). Two novel genera are introduced based on molecular phylogeny (Fig. 23) coupled with morphological characterization viz. *Lonicericola* and *Paratrimmatostroma*. In addition, a novel species *Parabambusicola thysanolaenae* is introduced.

Lonicericola Phookamsak, Jayasiri & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF556139; *Facesoffungi number*: FoF04962

Etymology: The generic epithet "*Lonicericola*" refers to the host genus *Lonicera*, from which the type species was collected.

Saprobic o dead hanging branches of *Lonicera maackii*. **Sexual morph** *Ascomata* black, scattered, solitary to gregarious, immersed under host epidermis, slightly raised, globose to subglobose, uni-loculate, glabrous, ostiolate, papillate. *Peridium* of equal thickness, composed of several layers, of flattened to broad, brown to dark brown, pseudoparenchymatous cells, arranged in *textura angularis* to *textura prismatica*. *Hamathecium* composed of numerous, filamentous, septate, anastomosed pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, broadly cylindrical to cylindric-clavate, subsessile to short pedicellate, with furcate to obtuse pedicel, apically rounded, with ocular chamber. *Ascospores* overlapping 2–3-seriate, hyaline, fusiform to vermiform, with enlarged cell, septate, constricted at the septa, smooth-walled, surrounded by distinct mucilaginous sheath. **Asexual morph** Undetermined.

Type species: *Lonicericola hyaloseptispora* Phookamsak, Jayasiri & K.D. Hyde

Notes: *Lonicericola* is similar to the sexual genera *Aquastroma* Kaz. Tanaka & K. Hiray., *Multiseptospora* Phookamsak & K.D. Hyde, *Neoaquastroma* Wanas. et al. and *Parabambusicola* Kaz. Tanaka & K. Hiray in *Parabambusicolaceae*, in having hyaline, fusiform to vermiform, multi-septate ascospores, with an entire sheath (Liu et al. 2015a; Tanaka et al. 2015). *Lonicericola* can be distinguished from these related genera based on habitat, ascomal shape, ascospore septation and multigene phylogenetic evidence. *Lonicericola* can be distinguished from *Aquastroma* based on its terrestrial habitat, broadly cylindrical to cylindric-clavate asci, with a subsessile to short pedicel and 9-septate ascospores. *Aquastroma* was found on submerged woody plant from aquatic habitat and has clavate asci, with a longer pedicel and 6–8-septate ascospores (Tanaka et al. 2015). *Lonicericola* resembles *Multiseptospora* in having globose to subglobose ascomata immersed in the host tissue. However, *Multiseptospora* has 10–11-septate ascospores, the ascomata are covered by brown to dark brown vegetative hyphal tufts, lack papilla, and have pore-like openings (Liu et al. 2015a). *Neoaquastroma* has 3–7-septate ascospores in *N. guttulatum*, 4–7-septate in *N. bauhiniae* and 5–8-septate in *N. krabiense* (Wanasinghe et al. 2017; Phukhamsakda et al. 2018). The asexual morph of *Neoaquastroma* has been reported as coelomycetous; whereas an asexual morph is not yet known for *Lonicericola*. *Parabambusicola* differs from *Lonicericola* in having hemispherical to conical ascomata, with a flattened base, and 5–6-septate ascospores as well as occurring on bamboo and stout grasses (Tanaka et al. 2015).

Multigene phylogenetic analyses reveal that *Lonicericola* forms a distinct lineage with *Aquastroma*, *Multiseptospora*, *Neoaquastroma* and *Parabambusicola* and clusters with the hyphomycetous genera *Pseudomonodictys* Doilom et al. and *Paratrimmatostroma* Jayasiri et al. with moderate support (77% ML and 0.99 BYPP). A comparison of ITS, LSU, SSU and TEF1-α sequence data indicates that *Lonicericola* differs from *Pseudomonodictys* in 97/593 bp (16.4%, ITS), 14/888 bp (1.6%, LSU), 18/1033 bp (1.7%, SSU) and 36/959 bp (3.7%, TEF1-α). However, we could not compare the morphological characteristics of *Lonicericola* with *Pseudomonodictys* and *Paratrimmatostroma* as they are represented by different morphs.

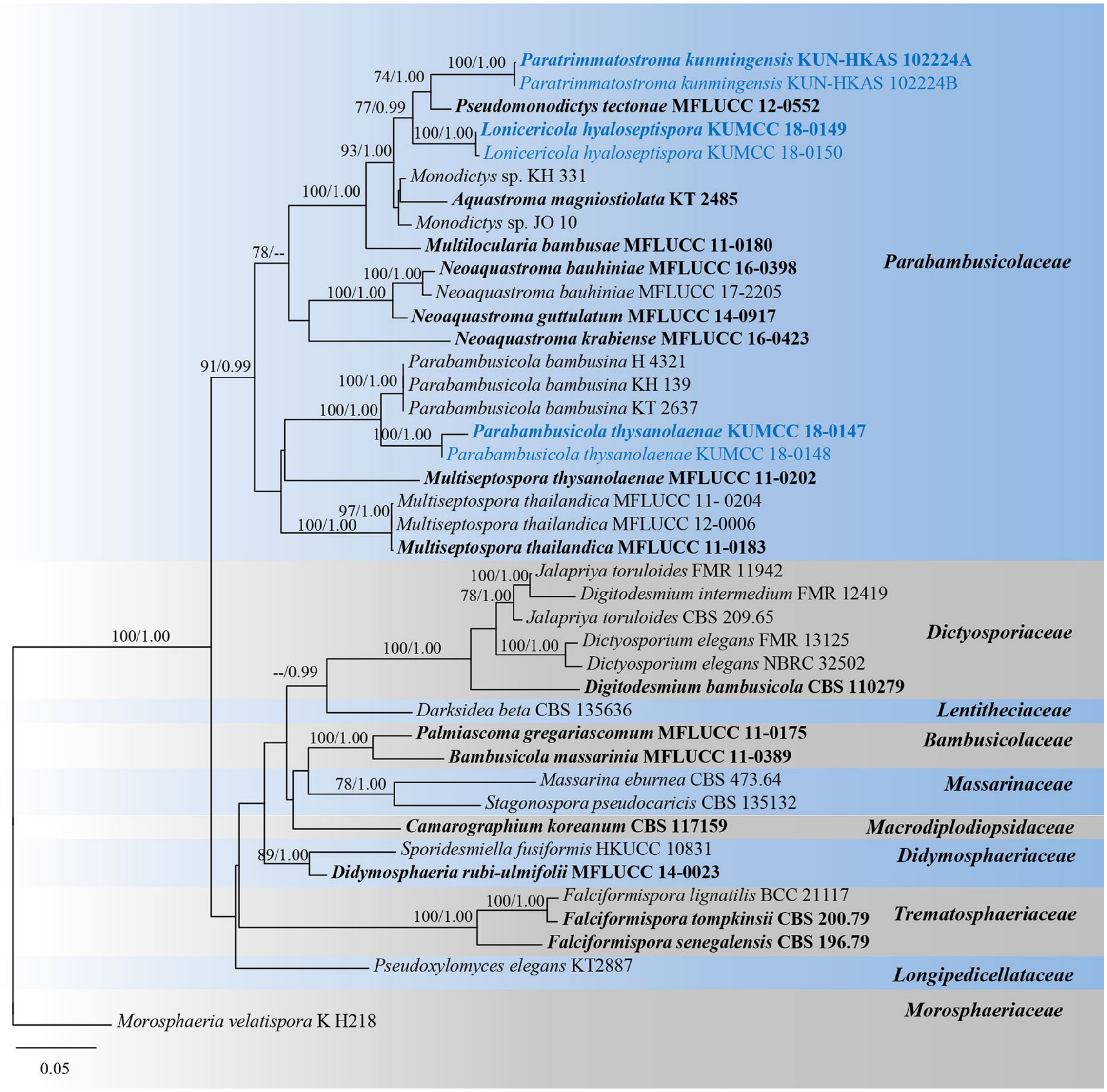


Fig. 23 Simplified phylogram showing the best RAxML tree obtained from a combined multigene (SSU, ITS, LSU and TEF1-α) analyses. Matrix of 42 taxa including related families of the family *Parabambusicolaceae* (Phukhamsakda et al. 2018). The matrix comprises 3580 characters with gaps. The best scoring RAxML tree with a final likelihood value of -14853.890740 is presented. MLBS above 70% and Bayesian posterior probabilities above 0.90 are given at each branch. The tree is rooted with *Morosphaeria velatispora* KH218 (*Morosphaeriaceae*). Type species are in bold and new isolates are in blue

Lonicericola hyaloseptispora Phookamsak, Jayasiri & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556140; *Facesoffungi number*: FoF04963, Fig. 24

Etymology: The specific epithet "*hyaloseptispora*" refers to the fungus having hyaline, multi-septate ascospores.

Holotype: KUN-HKAS 102223

Saprobic dead hanging branches of *Lonicera maackii*. **Sexual morph** *Ascomata* 170–240 µm high, 165–250 µm diam., black, scattered, solitary to gregarious, immersed under host epidermis, slightly raised, globose to subglobose, uni-loculate, glabrous, ostiolate, papillate. *Ostioles* centrally located, oblong, with minute papilla, with pore-like opening, filled with hyaline periphyses. *Peridium* 8–25 µm wide, of equal thickness, composed of several layers, of flattened to broad, brown to dark brown, pseudoparenchymatous cells, arranged in *textura angularis* to *textura prismatica*. *Hamathecium* composed of numerous, 2–3.5 µm wide, filamentous, septate, anastomosed pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* (90–)100–120(–145) × (24–)25–30(–33) µm ($\bar{x}$ = 115.1 × 27 µm, n = 30), 8-spored, bitunicate, fissitunicate, broadly cylindrical to cylindric-clavate, subsessile to short pedicellate, with furcate to obtuse pedicel, apically rounded, with ocular chamber clearly visible when

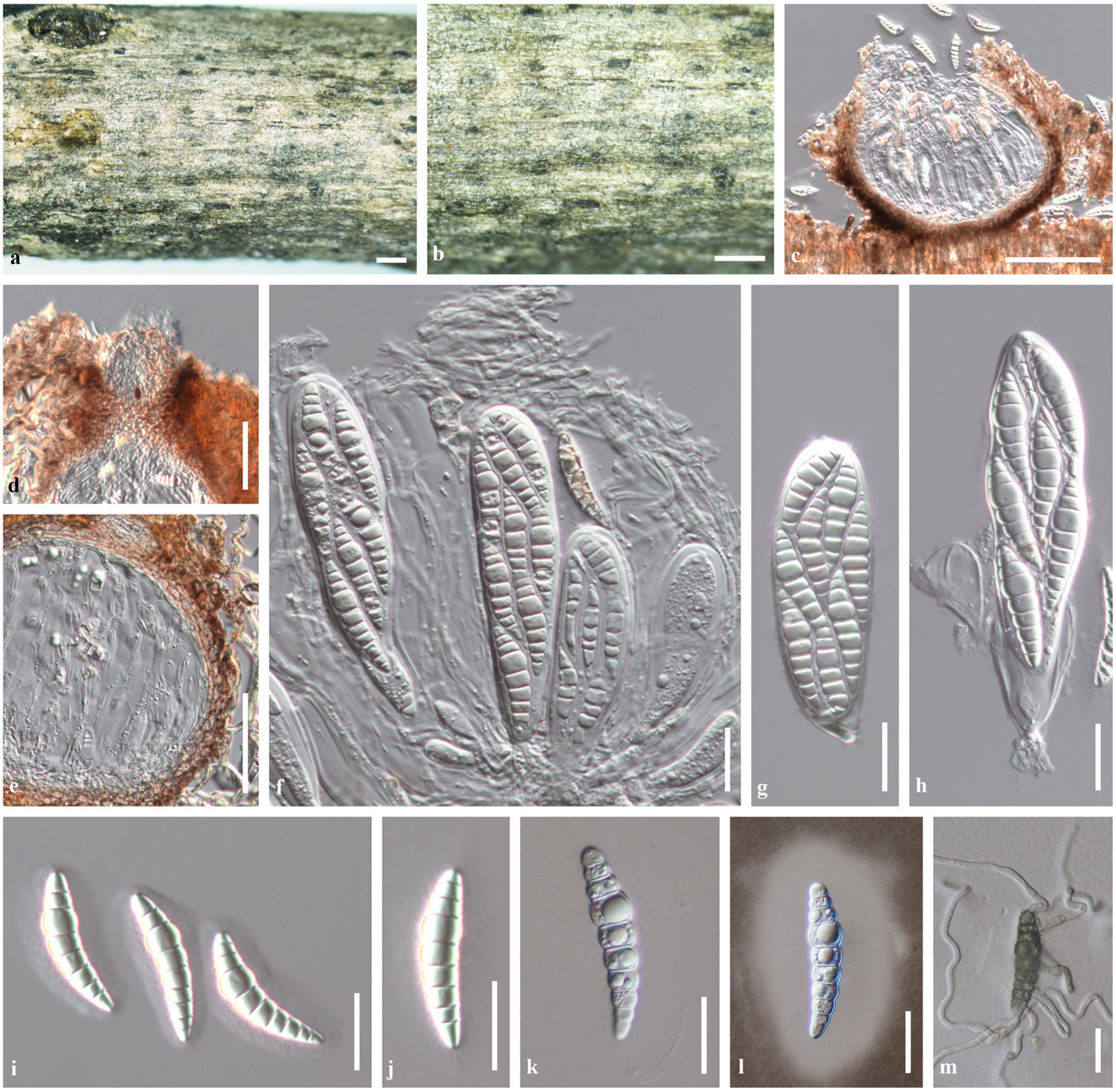


Fig. 24 ***Lonicericola hyaloseptispora*** (KUN-HKAS 102223, **holotype**). **a, b** Appearance of ascomata on host substrate. **c** Section through ascoma. **d** Ostiole with papilla immersed in the host. **e** Section through peridium. **f** Asci immersed in hyaline, cellular pseudoparaphyses. **g, h** Asci. **i–k** Ascospores. **l** Ascospore stained with Indian ink. **m** Germinating ascospore. *Scale bars* **a**, **b** = 500 µm, **c** = 100 µm, **d, e** = 50 µm, **f–m** = 20 µm

young. *Ascospores* overlapping 2–3-seriate, hyaline, becoming brown when release from the asci, fusiform to vermiform, enlarged at the 4th cell from the apex (4–10 × 9–12 µm, l/w), (8–)9-septate, constricted at the septa, smooth-walled, with small to large guttules, surrounded by entire mucilaginous sheath (3.5–13 µm wide). **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 50–55 mm diam. after 3 weeks at room temperature (20–30 °C). Colony dense, circular, flattened, slightly raised, surface smooth, with entire edge, floccose to fluffy; from above dark grey to brown; from below, black; not producing pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Kunming, Kunming Institute of Botany, on dead hanging branches of *Lonicera maackii*, 20 April 2017, R. Phookamsak, KIB034 (KUN-HKAS 102223, **holotype**), ex-type living culture KUMCC 18-0149 (KIB034A), KUMCC 18-0150 (KIB034B).

GenBank numbers: ITS = MK098191, LSU = MK098197, SSU = MK098203, (KUMCC 18-0149); ITS = MK098194, LSU = MK098200, SSU = MK098206, TEF1-α = MK098210 (KUMCC 18-0150).

Parabambusicola Kaz. Tanaka & K. Hiray

We follow the latest treatment and updated accounts of *Parabambusicola* in Tanaka et al. (2015). Previously, only

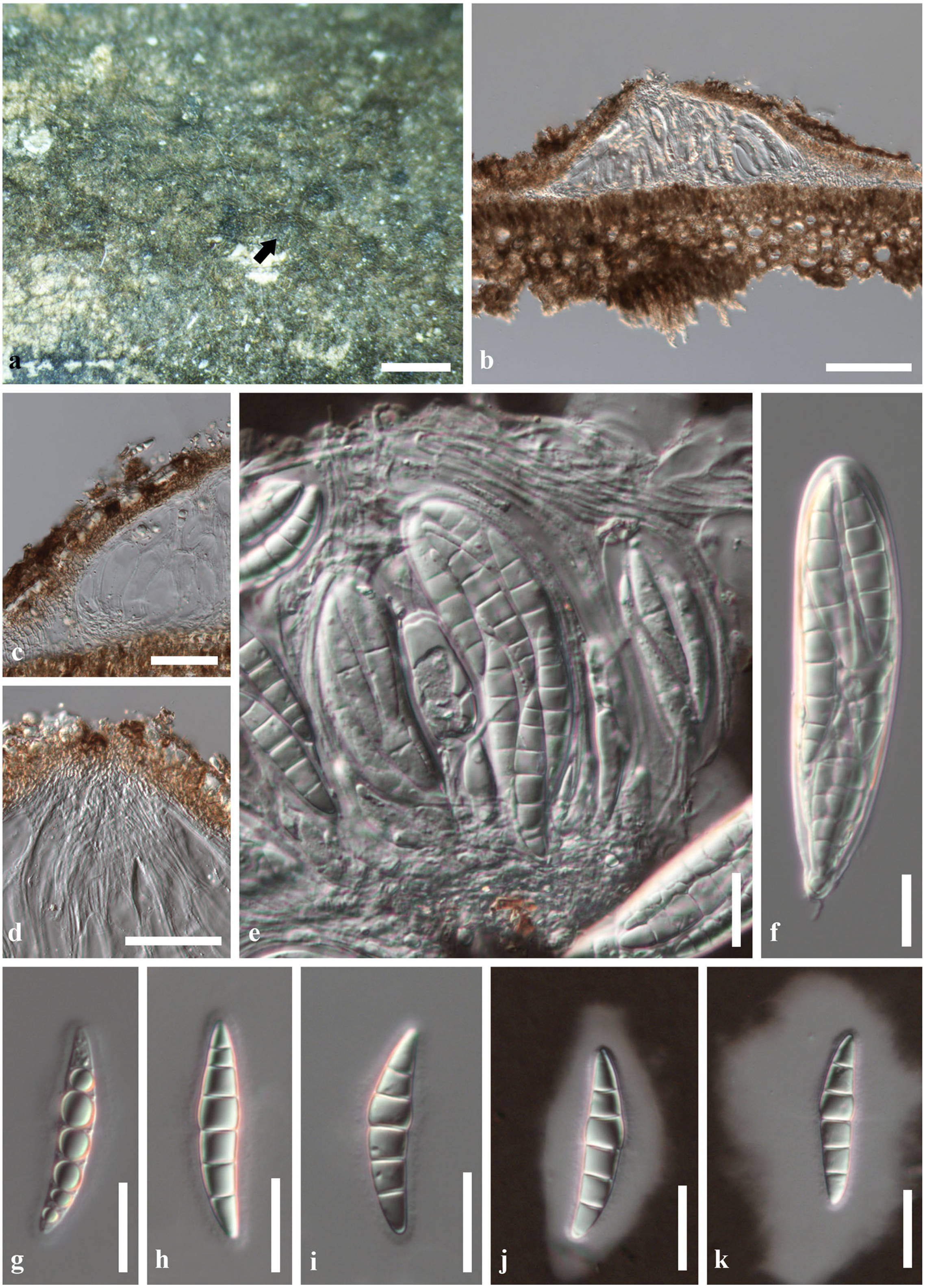


Fig. 25 ***Parabambusicola thysanolaenae*** (KUN-HKAS 102222, **holotype**). **a** Appearance of ascomata on host substrate. **b** Section through ascoma. **c** Section through peridium. **d** Ostiole. **e** Asci immersed in hyaline, cellular pseudoparaphyses, stained in Indian ink. **f** Ascus. **g–i** Ascospores. **j, k** Ascospores stained in Indian ink. *Scale bars* **a** = 500 µm, **b** = 100 µm, **c, d** = 50 µm, **e–k** = 20 µm

P. bambusina was accommodated in this genus (Index Fungorum 2019). We introduce the second species, *P. thysanolaenae*, collected from *Thysanolaena maxima* in Yunnan, China.

Parabambusicola thysanolaenae Goonas., Jayasiri, Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555596; *Facesoffungi number*: FoF04964, Fig. 25

Etymology: Named after the host from which the fungus was isolated.

Holotype: KUN-HKAS 102222

Saprobic on dead stems of *Thysanolaena maxima*, appearing as raised, dome-shaped areas on host surface, covered by brown, vegetative hyphae. **Sexual morph** *Ascomata* 130–170 µm high, 430–600 µm wide, mostly clustered together, sometimes solitary, immersed under host epidermis, raised, becoming semi-immersed, globose in surface view, hemispherical with a flattened base in cross section, uni-loculate, glabrous, ostiole central, with pore-like opening. *Peridium* 25–60 µm wide, lateral walls composed of numerous layers of inner, hyaline, flattened cells to outer, pale brown to brown, *textura angularis* cells and pale brown to brown, globular or polygonal cells showing no conspicuous layers at the base, intermixed with host tissue. *Hamathecium* composed of numerous, 1.5–3 µm wide, filamentous, septate pseudoparaphyses, anastomosing above the asci, embedded in a hyaline gelatinous matrix. *Asci* (50–)80–120 × (10–)25–33 µm ($\bar{x}$ = 107 × 28 µm, n = 30), 8-spored, bitunicate, fissitunicate, broadly cylindrical to cylindric-clavate, subsessile, rounded at the apex, with inconspicuous ocular chamber, clearly visible when young. *Ascospores* 45–55 × 7.5–11 µm ($\bar{x}$ = 46.5 × 9 µm, n = 35), overlapping 2–3-seriate, hyaline, fusiform to vermiform, narrower towards the lower cell, enlarged at the 4th cell from apex, slightly curved, 5–(6–7)-septate, primary septum mostly median, constricted at the septa, smooth-walled, with an entire sheath, large guttules present when immature. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 30–32 mm diam. after 3 weeks at room temperature (20–30 °C). Colony dense, circular, flattened, surface smooth, with entire edge, velvety to floccose; from above greenish grey to dark green, paler at the edge; from below, black; produced dark brown pigmentation around colony on agar medium. Colonies on MEA reaching 28–30 diam. after 3 weeks at room temperature (20–30 °C). Colony dense, circular, flattened, surface smooth, with entire edge, floccose to cottony; from above cream to pale yellowish; from below, yellowish brown, paler at the edge; not producing pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Mengla County, Xishuangbanna Tropical Botanical Garden (XTBG), on dead stems of *Thysanolaena maxima* (Roxb.) Kuntze (*Poaceae*), 22 April 2017, R. Phookamsak, IS003 (KUN-HKAS 102222, **holotype**), ex-type living culture, KUMCC 18-0147 (IS003A), KUMCC 18-0148 (IS003B).

GenBank numbers: ITS = MK098190, LSU = MK098199, SSU = MK098205, TEF1-α = MK098209 (KUMCC 18-0147); ITS = MK098193, LSU = MK098198, SSU = MK098202, TEF1-α = MK098211 (KUMCC 18-0148).

Notes: *Parabambusicola thysanolaenae* shares similar peridial and ascal characters with *P. bambusina* (Teng) Kaz. Tanaka & K. Hiray. but can be distinguished by having larger ascomata (300–500 × 150–300 µm in *P. bambusina*), absence of a beak-like structure and wider peridium (10–20 µm in *P. bambusina*). Ascospores of *P. thysanolaenae* are 5-septate and shorter than the 3–5-septate ascospores of *P. bambusina* (54.7 × 8.4 µm, Tanaka and Harada 2003b). Phylogenetically *P. thysanolaenae* clusters with *P. bambusina* forming a well-separated lineage (100% ML and 1.00 BYPP; Fig. 23).

Paratrimmatostroma Jayasiri, Phookamsak, D.J. Bhat & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF556153; *Facesoffungi number*: FoF04960

Etymology: With reference to similar morphology of genus "*Trimmatostroma*"

Saprobic on dead fronds of a fern. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Sporodochia* effuse or confluent, visible as black powdery, superficial mass on host substrate, flattened, light brown, with a membranous base, composed of pseudoparenchymatous cells of *textura angularis*. *Mycelium* immersed, composed of septate, pale brown, branched hyphae. *Conidiophores* macronematous, or semi-macronematous, mononematous, prostrate, or erect, usually short, oblong to cylindrical, straight or flexuous, arising as lateral branches from creeping hyphae, septate, branched or unbranched, slightly constricted at the septa so as to give a monilioid appearance, pale brown, smooth-walled. *Conidiogenous cells* holoblastic, mono- to polyblastic, integrated, terminal, brown, smooth-walled. *Conidia* solitary, acropleurogenous, dark brown, paler at the apical cell, branched, straight or flexuous, variable in shape, helicoid, cylindrical, sigmoid, or reniform, solitary, tapering near apex and base, rounded at tip, septate, constricted at the septa, smooth and thick-walled.

Type species: *Paratrimmatostroma kunmingensis* Jayasiri, Phookamsak, D.J. Bhat & K.D. Hyde

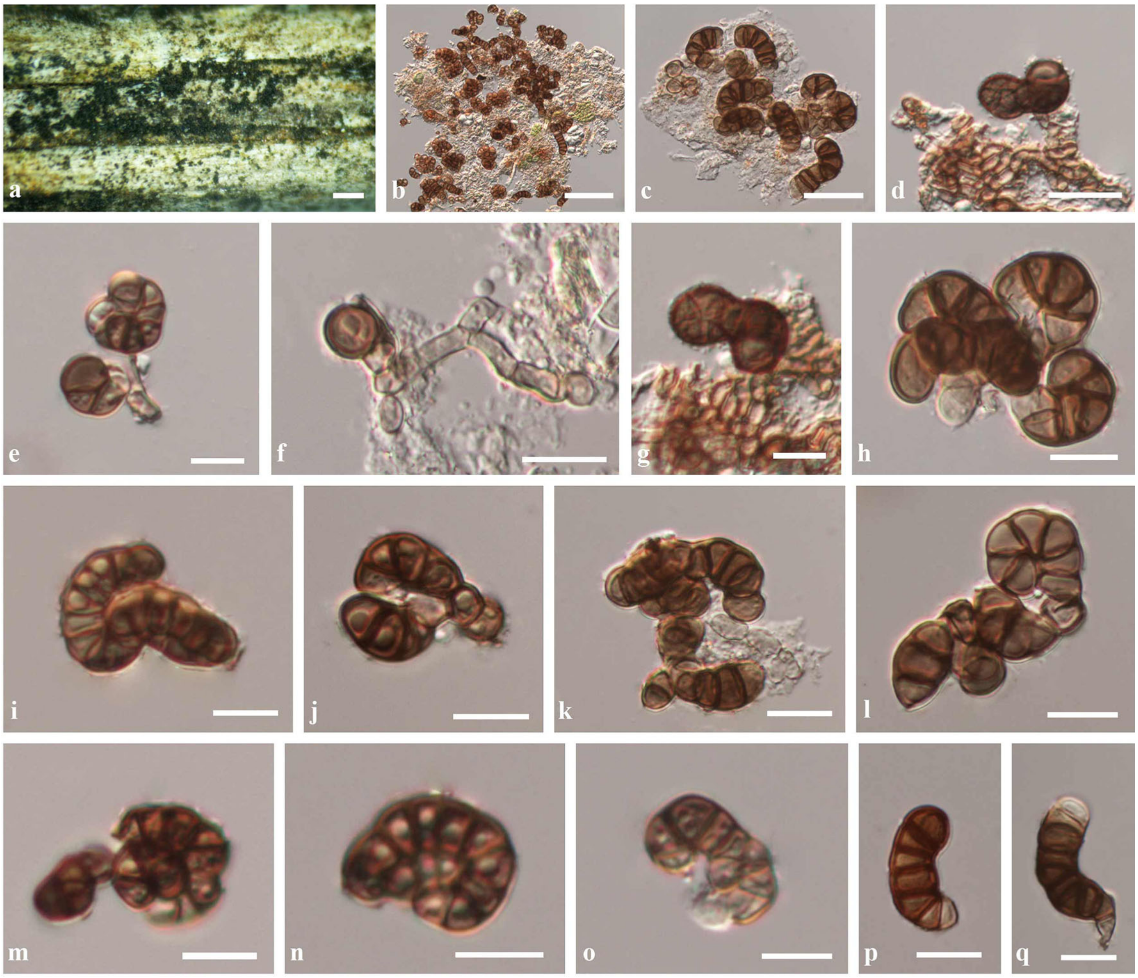


Fig. 26 ***Paratrimmatostroma kunmingensis*** (KUN-HKAS102224, **holotype**). **a** Appearance of sporodochia on host substrate. **b, c** Sporodochia. **d–g** Conidiophores with attached conidia. **h–q** Conidia. *Scale bars* **a** = 200 µm, **b** = 50 µm, **d–q** = 10 µm

Notes: Paratrimmatostroma is similar to *Trimmatostroma* Corda in forming effuse to confluent sporodochia, semi-macronematous, mononematous conidiophores, integrated, terminal conidiogenous cells, and branched, straight or flexuous, septate, pigmented conidia, which are variable in shape (Ellis 1971; Crous et al. 2007a). However, they are phylogenetically distinct in that *Paratrimmatostroma* belongs to *Parabambusicolaceae* (*Pleosporales*, Dothideomycetes), whereas *Trimmatostroma* was recently treated in *Mollisiaceae* Rehm (*Helotiales*, Leotiomycetes) (Crous et al. 2007a; Wijayawardene et al. 2018a). Multigene phylogenetic analyses show that *Paratrimmatostroma* forms a well-resolved clade (74% ML and 1.00 BYPP; Fig. 23), and clusters with *Pseudomonodictys* and *Lonicericola*. *Paratrimmatostroma* is distinct from *Pseudomonodictys* in forming sporodochia on the host substrate and having branched, straight or flexuous conidia, with variable conidial shape. *Pseudomonodictys* has muriform, top-shaped to ellipsoidal conidia and does not form sporodochia on host substrate (Ariyawansa et al. 2015a). *Paratrimmatostroma* was found on a fern in Yunnan, China (nonflowering vascular plants in the low-latitude monsoon climate), whereas, *Pseudomonodictys* was collected from teak in Thailand (flowering plant in tropical climate). A comparison of ITS, LSU, SSU and TEF1-α sequence dataset indicates that *Paratrimmatostroma* differs from *Pseudomonodictys* in 64/540 bp (11.8%, ITS), 23/857 bp (2.7%, LSU), 22/1060 bp (2.1%, SSU) and 41/928 bp (4.4%, TEF1-α). Based on phylogenetic analysis and morphological distinctiveness, we introduce *Paratrimmatostroma* as a new genus to accommodate a single species, *P. kunmingensis*.

Paratrimmatostroma kunmingensis Jayasiri, Phookamsak, D.J. Bhat & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556152; *Facesoffungi number*: FoF04961, Fig. 26

Etymology: The specific epithet "*kunmingensis*" refers to Kunming City, Yunnan Province, China, where the type was collected.

Holotype: KUN-HKAS 102224

Saprobic on dead fronds of a fern. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Sporodochia* effuse or confluent, visible as black powdery, superficial mass on host substrate, flattened, light brown, with a membranous base, composed of pseudoparenchymatous cells of *textura angularis*. *Mycelium* immersed, composed of septate, pale brown, branched hyphae. *Conidiophores* (6–)15–30(–50) × 2–4 µm ($\bar{x}$ = 19.2 × 3.2 µm, n = 20), macronematous or semi-macronematous, mononematous, prostrate, or erect, usually short, oblong to cylindrical, straight or flexuous, arising as lateral branches from creeping hyphae, septate, branched or unbranched, slightly constricted at the septa so as to give a monilioid appearance, pale brown, smooth-walled. *Conidiogenous cells* 3–10(–15) × 2–4.5 µm ($\bar{x}$ = 7.1 × 3.1 µm, n = 30), holoblastic, mono- to polyblastic, integrated, terminal, brown, smooth-walled. *Conidia* solitary, acropleurogenous, dark brown, paler at the apical cell, branched, straight or flexuous, variable in shape, helicoid [(8–)10–20(–27) × (6–)10–20 µm ($\bar{x}$ = 16.8 × 13.7 µm, n = 40)], cylindrical to sigmoid, or reniform [(8.5–)15–50 × 6–8(–10) µm ($\bar{x}$ = 29.7 × 7.7 µm, n = 50)], solitary, tapering near apex and base, rounded at tip, multi-septate, 6–13-septate at maturity, constricted at the septa, smooth and thick-walled.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, on dead fronds of a fern, 1 April 2017, R. Phookamsak, KIB025 (KUN-HKAS 102224, **holotype**).

GenBank numbers: ITS = MK098192, LSU = MK098196, SSU = MK098204, TEF1-α = MK098208 (KUN-HKAS 102224A); ITS = MK098195, LSU = MK098201, SSU = MK098207 (KUN-HKAS 102224B).

Periconiaceae (Sacc.) Nann.

Periconiaceae has long been unused and placed as members of *Massarinaceae* Munk until Tanaka et al. (2015) revised *Massarineae* and placed it as a distinct family based on phylogenetic analysis (Tanaka et al. 2015; Hyde et al. 2017, 2018b). We follow the latest treatment and updated accounts of *Periconiaceae* in Tanaka et al. (2015), Hyde et al. (2017, 2018b), Liu et al. (2017b) and Thambugala et al. (2017). We report *Periconia cortaderiae* Thambug. & K.D. Hyde from *Caragana arborescens* Lam. (*Fabaceae*) in Yunnan, China for the first time.

Periconia Tode

Periconia was introduced by Tode (1791) to accommodate hyphomycetous species having macronematous conidiophores and 1-celled, pigmented, verruculose to echinulate conidia and is typified by *P. lichenoides* Tode (Tanaka et al. 2015; Thambugala et al. 2017). The genus was re-circumscribed by Tanaka et al. (2015) and this was followed by subsequent authors (Hyde et al. 2017, 2018b; Liu et al. 2017b; Thambugala et al. 2017). We follow the latest treatment of *Periconia* in Tanaka et al. (2015). The updated phylogenetic analyses were retrieved from Thambugala et al. (2017) and Hyde et al. (2018b) (Fig. 27).

Periconia cortaderiae Thambug. & K.D. Hyde, in Thambugala et al., Mycosphere 8(4): 734 (2017), Fig. 28

Holotype: THAILAND, Chiang Rai, Mae Fah Luang University, on dead stems and leaves of *Cortaderia* sp. (*Poaceae*), 21 December 2014, K.M. Thambugala, KM 035 (MFLU16–2579), ex-type living culture MFLUCC 15–0457, ICMP 21414

Saprobic on dead, hanging branches of *Caragana arborescens*. **Sexual morph** Undetermined. **Asexual morph** *Colonies* on the substratum superficial, numerous, effuse, black, floccose. *Mycelium* immersed on the substrate, composed of septate, branched, smooth, dark hyphae. *Conidiophores* 100–225 × 8.5–11 µm, macronematous, mononematous, septate, branched, erect, mostly slightly flexuous to curved, dark brown, forming sphaerical heads at apex, arising from a stromatic base. *Conidiogenous cells* 4.5–5.2 × 4.1–5.6 µm ($\bar{x}$ = 4.9 × 5.1 µm, n = 20), mono- to polyblastic, discrete, terminal, globose, light brown. *Conidia* (5.5–)6–9(–12) × (4.5–)5–8 µm ($\bar{x}$ = 7.8 × 6.4 µm, n = 50), solitary or catenate, in acropetal chains, subglobose to globose, occasionally ellipsoidal to cylindrical, light brown to moderately brown, verruculose.

Culture characteristics: Colonies on PDA reaching 68–74 mm diam. after 3 weeks at room temperature (20–30 °C). Colony medium sparse, circular, flattened, surface smooth, edge entire, velvety to woolly; from above, sectoring, with a part of cream to pale yellowish and yellowish-green to dark grey, with small white tufts in another part; from below, pale yellowish at the margin, sectoring at the centre, with a part of yellowish to orange-yellow and dark brown in another part; not producing pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, on dead hanging branches of *Caragana arborescens* (*Fabaceae*), 2 April 2017, R. Phookamsak, KIB017 (KUN-HKAS 102240), living culture, KUMCC 18-0174 = MFLUCC18-0667 (KIB017A), KUMCC 18-0175 = MFLUCC18-0668 (KIB017B).

Known hosts and distribution: On dead stems and leaves of *Cortaderia* sp. (*Poaceae*, Thailand) and *Caragana arborescens* (*Fabaceae*, Yunnan, China; in this study).

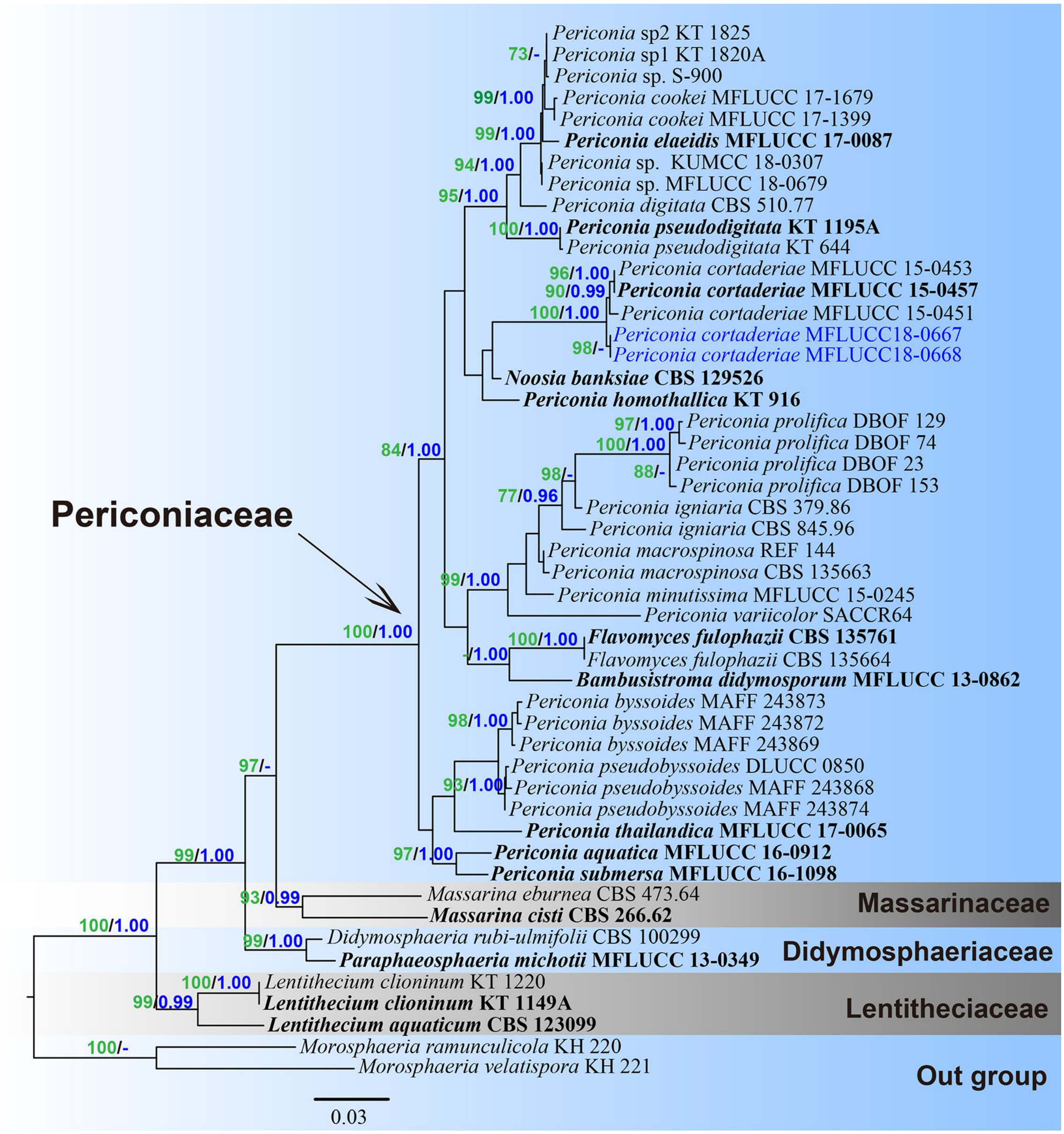


Fig. 27 Phylogram generated from the best scoring of the RAxML tree based on combined ITS, LSU and TEF1-α sequence dataset of taxa in *Periconiaceae* and other related families (*Massarinaceae*, *Didymellaceae* and *Lentitheciaceae*). Taxa in *Morosphaeriaceae*, *Morosphaeria ramunculicola* (KH 220) and *M. velatispora* (KH 221) were selected as the outgroup taxa. Bootstrap support values for maximum likelihood (green) equal to or greater than 70% and the Bayesian posterior probabilities (blue) equal or higher than 0.95 are indicated above the nodes. Ex-type and ex-epitype strains are in bold. Newly generated sequences are indicated in blue

GenBank numbers: ITS = MH892348, LSU = MH892401 (MFLUCC 18-0667); ITS = MH892349, LSU = MH892402, TEF1-α = MH908964 (MFLUCC18-0668).

Notes: Phylogenetic analyses of a concatenated LSU, ITS and TEF1-α sequence datset show that our strains (MFLUCC 18-0667 and MFLUCC 18-0668) form a well-resolved clade, clustering with *Periconia cortaderiae* (100% ML and 1.00 BYPP; Fig. 27). A comparison of ITS and TEF1-α nucleotide base pair indicates that our strains are identical to the type strain of *P. cortaderiae*, which is not significantly different (2/520 bp in ITS and 4/830 bp in TEF1-α). We therefore, identify our isolates as *P. cortaderiae* and report its occurrence on *Caragana arborescens* in Yunnan, China for the first time. Our isolate has shorter conidiophores (400–800 µm high, holotype) and slightly larger conidia (4–6.6 × 4.1–7.1 µm, holotype) (Thambugala et al. 2017). *Periconia* species are morphologically variable in different hosts and geographic distributions, but the molecular data of informative genes can

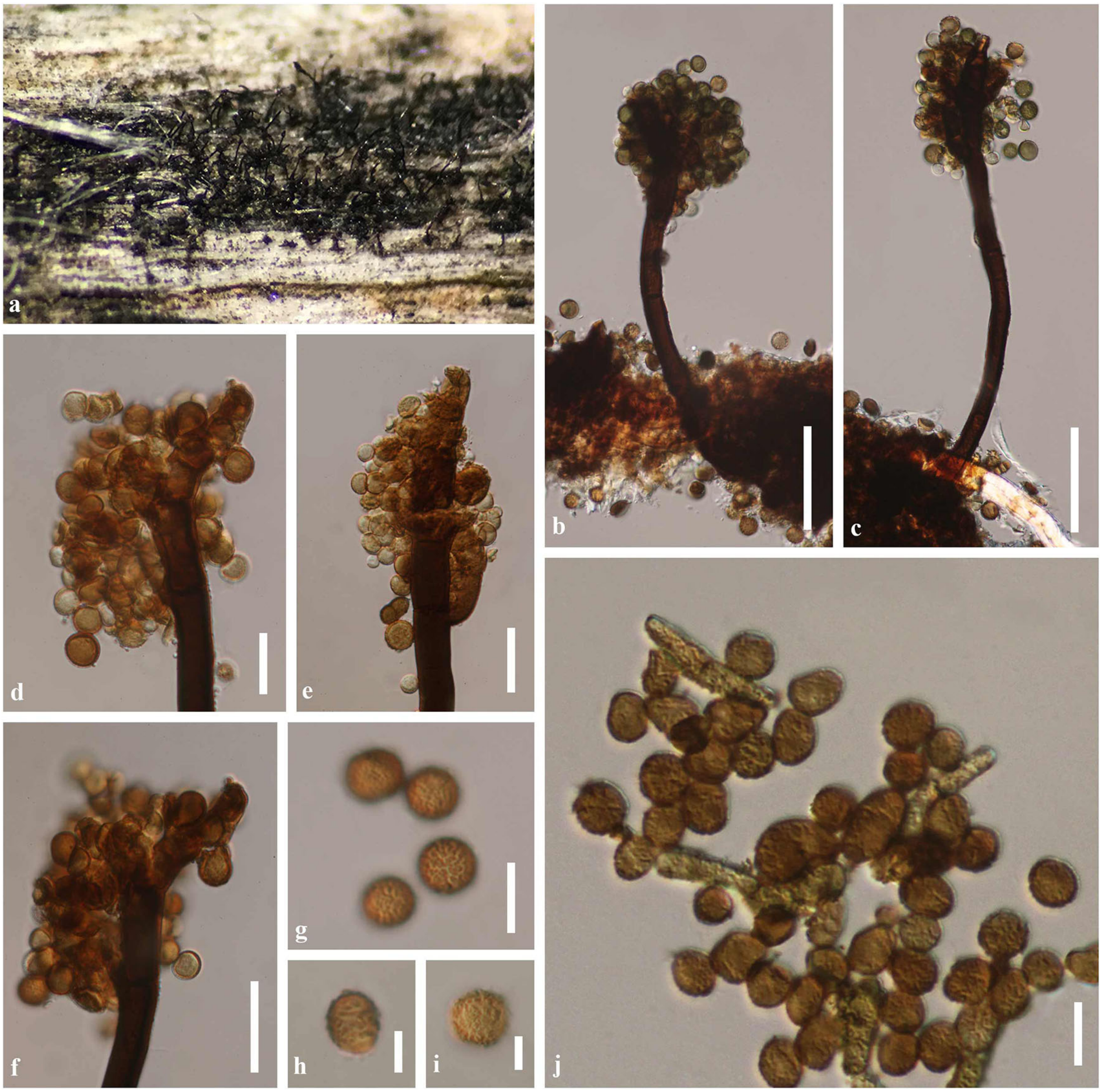


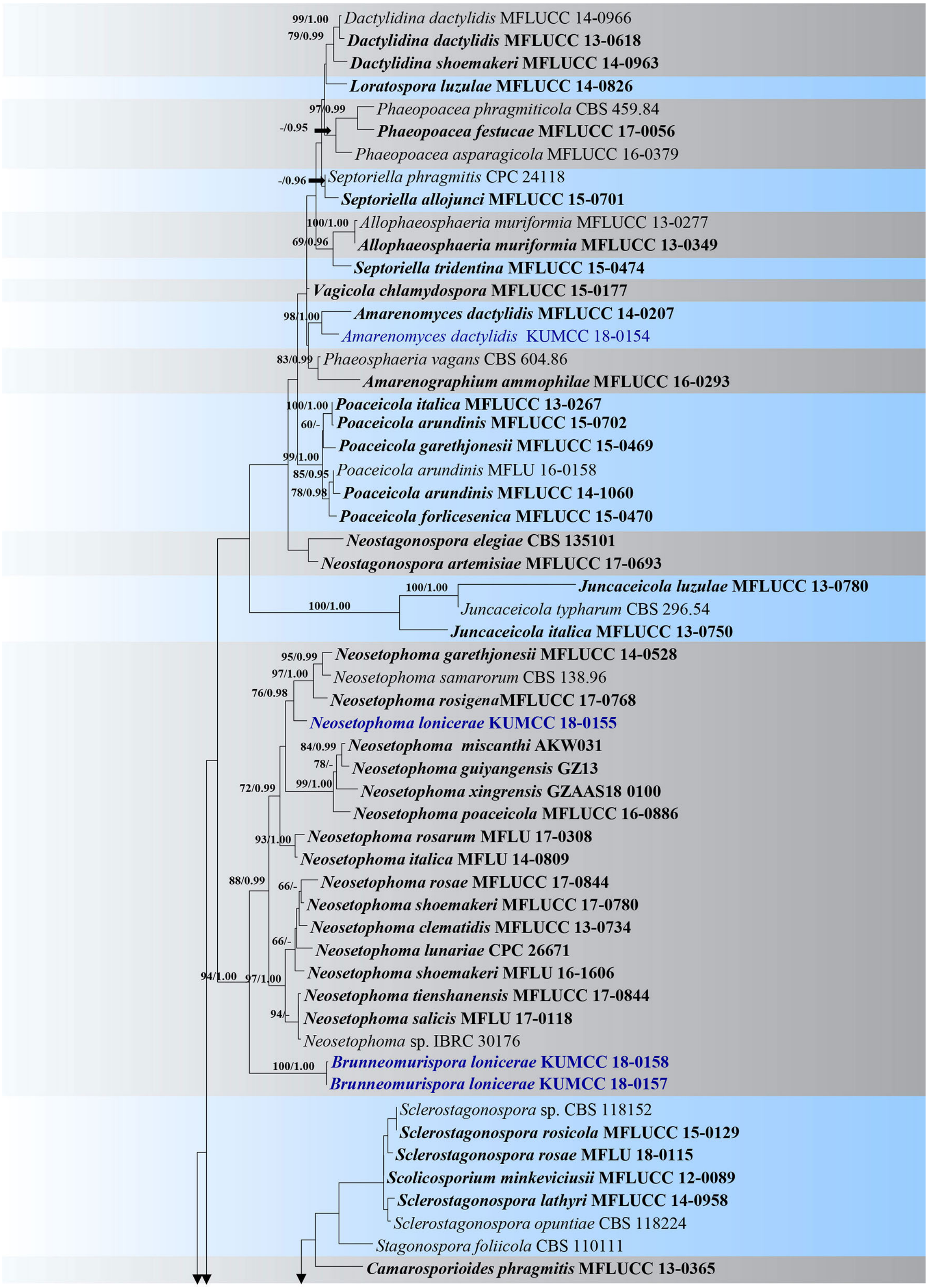
Fig. 28 ***Periconia cortaderiae*** (KUN-HKAS102240). **a** Appearance of fungal colonies on host substrate. **b, c** Conidiophores. **d–f** Conidiophores and conidiogenous cells. **g–j** Conidia. *Scale bars* **b, c** = 50 µm, **d–f** = 20 µm, **g, j** = 10 µm, **h, i** = 5 µm

clarify their conspecificity. Therefore, more informative genes such as RPB2 and TUB2 are needed in further studies of this genus.

Phaeosphaeriaceae M.E. Barr

Phaeosphaeriaceae was introduced by Barr (1979) to accommodate fungal taxa which mainly occurr on monocotyledons, but are also found on some herbaceous plants (Phookamsak et al. 2014b, 2017). Many additional genera have been introduced in this family since Phookamsak et al. (2014b) re-circumscribed the genera in *Phaeosphaeriaceae*. Wijayawardene et al. (2018a) listed 52 genera in *Phaeosphaeriaceae*. Wanasinghe et al. (2018), Bakhshi et al. (2019) and Maharachchikumbura et al. (2019) introduced other seven genera in this family, and 59 genera are now accepted in *Phaeosphaeriaceae* based on molecular phylogeny coupled with morphological characteristics (Wanasinghe et al. 2018; Wijayawardene et al. 2018a). We follow the latest treatment and updated accounts of *Phaeosphaeriaceae* in Phookamsak et al.

Fig. 29 Phylogram generated from maximum likelihood analysis ▶ based on a concatenated LSU, SSU, TEF1-α and ITS sequence dataset of *Phaeosphaeriaceae*. Updated sequence data were obtained from GenBank (http://www.ncbi.nlm.nih.gov/) and retrieved from Hyde et al. (2018b) and Wanasinghe et al. (2018). One hundred and fifty-two strains are included in the analysis. *Staurosphaeria rhamnicola* (MFLUCC 17-0813 and MFLUCC 17-0814) were selected as the outgroup taxon. Bootstrap support values for maximum likelihood (left) equal to or greater than 60% and Bayesian posterior probabilities (right) equal or higher than 0.95 are indicated above the nodes. Newly generated sequences are in blue. Type strains are indicated in bold


99/1.00
Dactylidina dactylidis MFLUCC 14-0966
79/0.99
Dactylidina dactylidis MFLUCC 13-0618
Dactylidina shoemakeri MFLUCC 14-0963
Loratospora luzulae MFLUCC 14-0826
97/0.99
Phaeopoacea phragmiticola CBS 459.84
-/0.95
Phaeopoacea festucae MFLUCC 17-0056
Phaeopoacea asparagicola MFLUCC 16-0379
-/0.96
Septoriella phragmitis CPC 24118
Septoriella allojunci MFLUCC 15-0701
100/1.00
Allophaeosphaeria muriformia MFLUCC 13-0277
69/0.96
Allophaeosphaeria muriformia MFLUCC 13-0349
Septoriella tridentina MFLUCC 15-0474
Vagicola chlamydospora MFLUCC 15-0177
98/1.00
Amarenomyces dactylidis MFLUCC 14-0207
Amarenomyces dactylidis KUMCC 18-0154
83/0.99
Phaeosphaeria vagans CBS 604.86
Amarenographium ammophilae MFLUCC 16-0293
100/1.00
Poaceicola italica MFLUCC 13-0267
60/-
Poaceicola arundinis MFLUCC 15-0702
Poaceicola garethjonesii MFLUCC 15-0469
99/1.00
85/0.95
Poaceicola arundinis MFLU 16-0158
78/0.98
Poaceicola arundinis MFLUCC 14-1060
Poaceicola forlicesenica MFLUCC 15-0470
Neostagonospora elegiae CBS 135101
Neostagonospora artemisiae MFLUCC 17-0693
100/1.00
Juncaceicola luzulae MFLUCC 13-0780
100/1.00
Juncaceicola typharum CBS 296.54
Juncaceicola italica MFLUCC 13-0750
95/0.99
Neosetophoma garethjonesii MFLUCC 14-0528
97/1.00
Neosetophoma samarorum CBS 138.96
76/0.98
Neosetophoma rosigenaMFLUCC 17-0768
Neosetophoma lonicerae KUMCC 18-0155
84/0.99
Neosetophoma miscanthi AKW031
78/-
Neosetophoma guiyangensis GZ13
72/0.99
99/1.00
Neosetophoma xingrensis GZAAS18 0100
Neosetophoma poaceicola MFLUCC 16-0886
93/1.00
Neosetophoma rosarum MFLU 17-0308
Neosetophoma italica MFLU 14-0809
88/0.99
66/-
Neosetophoma rosae MFLUCC 17-0844
Neosetophoma shoemakeri MFLUCC 17-0780
Neosetophoma clematidis MFLUCC 13-0734
66/-
Neosetophoma lunariae CPC 26671
94/1.00
97/1.00
Neosetophoma shoemakeri MFLU 16-1606
Neosetophoma tienshanensis MFLUCC 17-0844
94/-
Neosetophoma salicis MFLU 17-0118
Neosetophoma sp. IBRC 30176
100/1.00
Brunneomurispora lonicerae KUMCC 18-0158
Brunneomurispora lonicerae KUMCC 18-0157
Sclerostagonospora sp. CBS 118152
Sclerostagonospora rosicola MFLUCC 15-0129
Sclerostagonospora rosae MFLU 18-0115
Scolicosporium minkeviciusii MFLUCC 12-0089
Sclerostagonospora lathyri MFLUCC 14-0958
Sclerostagonospora opuntiae CBS 118224
Stagonospora foliicola CBS 110111
Camarosporioides phragmitis MFLUCC 13-0365

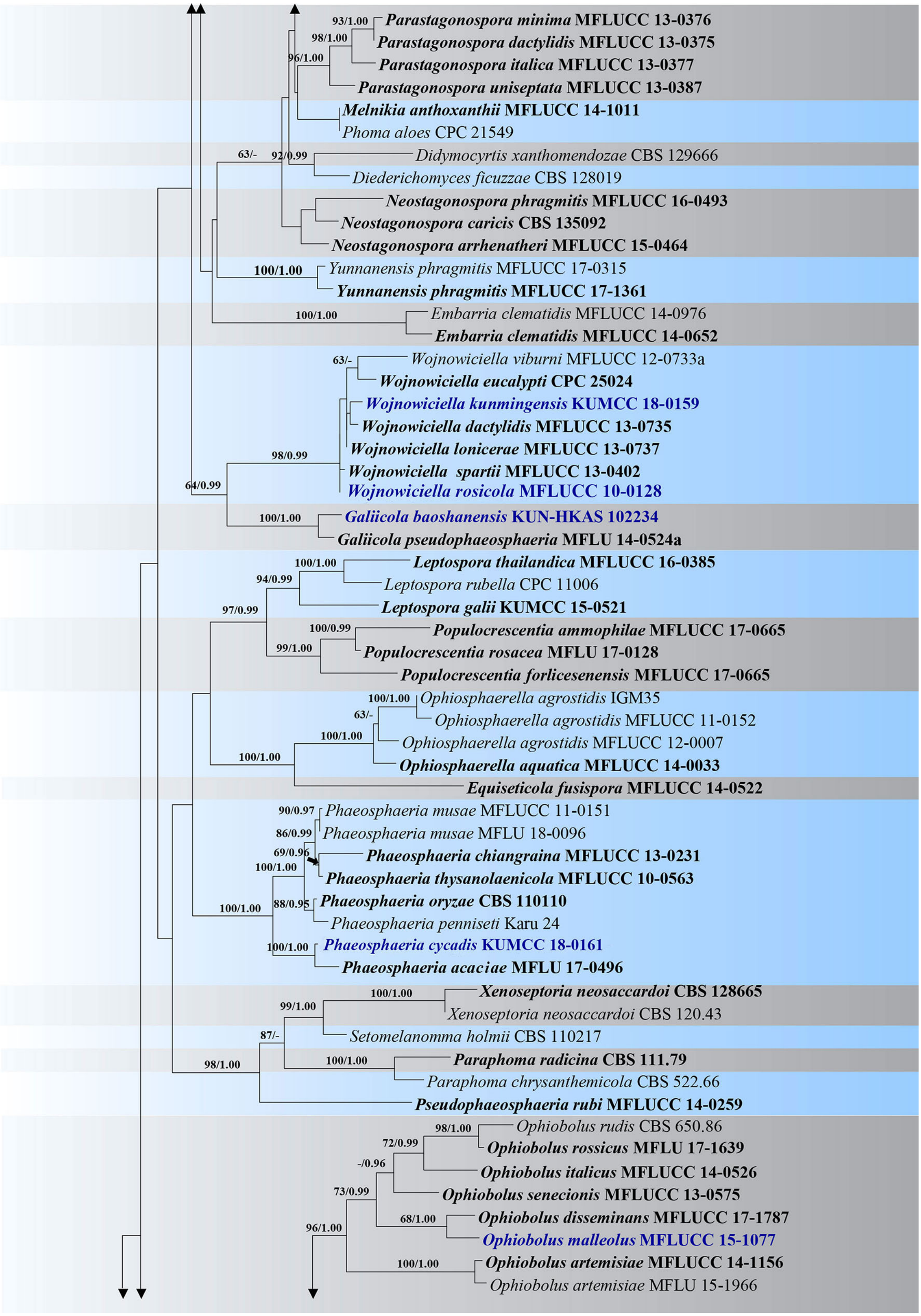


Fig. 29 continued

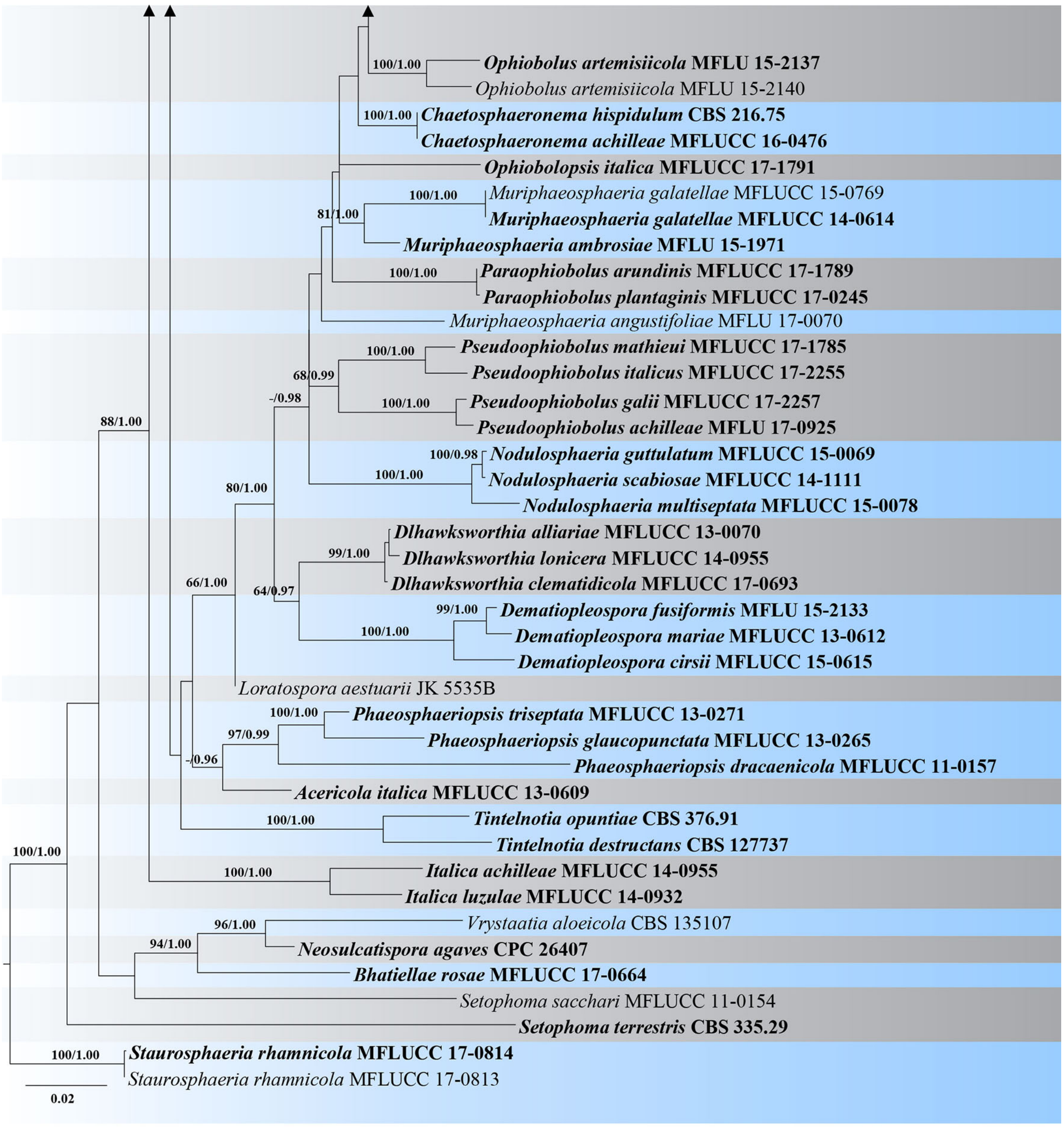


Fig. 29 continued

(2014b), Hyde et al. (2018b) and Wanasinghe et al. (2018). A new genus *Brunneomurispora* is introduced to accommodate a single species, *B. lonicerae*. Five new species are also introduced viz. *Galiicola baoshanensis*, *Neosetophoma lonicerae*, *Ophiobolus malleolus*, *Phaeosphaeria cycadis* and *Wojnowiciella kunmingensis*. Furthermore, *Wojnowicia rosicola* W.J Li et al. is transferred to *Wojnowiciella*. *Amarenomyces dactylidis* Mapook et al. is reported from a fern in China for the first time. An updated phylogenetic analysis (Fig. 29) was performed following previous phylogenies derived from Hyde et al. (2018b) and Wanasinghe et al. (2018).

Amarenomyces O.E. Erikss.

Amarenomyces was introduced by Eriksson (1981) and is typified by *A. ammophilae* (Lasch) O.E. Erikss., occurring on marine grass (*Ammophila arenaria* L., *Poaceae*). The genus is characterized by immersed to erumpent, globose to subglobose ascomata, thin-walled peridium, multi-layered endotunica, broadly cylindrical asci, with subsessile, knob-like pedicel and large, pigmented, septate, thick-walled and sheathed ascospores (Phookamsak et al.

2014b). Eriksson (1981) placed the genus in *Botryosphaeriaceae* Theiss. & Syd.; however, Zhang et al. (2009a) treated the genus as a synonym of *Phaeosphaeria* I. Miyake in *Phaeosphaeriaceae* based on molecular phylogeny. Phookamsak et al. (2014b) re-circumscribed the genera in *Phaeosphaeriaceae* based on multigene phylogenetic analyses coupled with morphological studies and thus, *Amarenomyces* was re-instated. Hyde et al. (2017) introduced a second species, *A. dactylidis* Mapook et al., collected from dead aerial stems of *Dactylis glomerata* L. in Italy. Only two species are presently accommodated in this genus.

Amarenomyces dactylidis Mapook, Camporesi & K.D. Hyde, in Hyde et al., Fungal Divers 87: 78 (2017), Fig. 30

Holotype: ITALY, Forlì-Cesena Province, Camposonaldo-Santa Sofia, on dead aerial stems of *Dactylis glomerata* (*Poaceae*), 10 January 2014, E. Camporesi, MFLU 17-0498, ex-type living culture MFLUCC 14-0207.

Saprobic on dead fronds of a fern. **Sexual morph** *Ascomata* 170–230 µm high, 160–260 µm diam., scattered, solitary, semi-immersed to superficial, visible as raised, black dots on the host surface, globose to subglobose, uniloculate, glabrous, ostiole central, with minute, papilla (20–45 × 25–55 µm, l/w), lacking periphyses. *Peridium* 13–23 µm wide, thin-walled of equal thickness, composed of 5–6 cell layers, of flattened to broad, pseudoparenchymatous cells; outer layer comprising brown to dark brown cells of *textura angularis*; inner layer comprising flattened, hyaline to pale brown cells, of *textura angularis* to *textura prismatica*. *Hamathecium* composed of numerous, 1.8–4.5 µm wide, filamentous, septate, pseudoparaphyses, anastomosing above the asci, embedded in a hyaline gelatinous matrix. *Asci* (70–)75–95(–113) × (9.5–)10–13(–14) µm ($\bar{x}$ = 88.9 × 12 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, with furcate pedicel, apically rounded, with well-developed ocular chamber. *Ascospores* (19–)(23–)25–28(–32) × 4.5–6 µm ($\bar{x}$ = 26.1 × 5.5 µm, n = 50), overlapping 1–2-seriate, yellowish brown to brown, fusiform to subcylindrical, slightly narrower towards the end cells, asymmetrical, 7–8-septate, slightly constricted at the septa, enlarged at the 5th or 6th cell from above, flattened at the 2nd to 4th, or 5th cells, smooth-walled, surrounded by a distinct mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 35–38 mm diam. after 3 weeks at room temperature (20–30 °C). Colony dense, irregular in shape, flattened to slightly raised, surface smooth, with edge undulate, velvety to floccose; from above, initially white, with pale grey at the centre, becoming greenish grey after 4 weeks; from below, white to pale yellowish at the margin, dark brown at the centre, becoming black after 4 weeks; not producing pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Baoshan, Shuizai, Dawazi mountain, on dead fronds of a fern, 22 October 2015, I.D. Goonasekara, BS008 (KUN-HKAS 102230), living culture, KUMCC 18-0154.

Known hosts and distribution: On dead aerial stems of *Dactylis glomerata* (*Poaceae*, Italy) and on dead fronds of a fern (Yunnan, China) (Hyde et al. 2017; this study).

GenBank numbers: ITS = MK356371, LSU = MK356345, SSU = MK356359.

Notes: Multigene phylogenetic analyses show that the new strain KUMCC 18-0154 is sister to *Amarenomyces dactylidis* (MFLUCC 14-0207) with high support (98% ML and 1.00 BYPP). A comparison of ITS nucleotide base pairs shows that KUMCC 18-0154 is identical (1/541 bp) to *A. dactylidis* and thus, we identify our new isolate as *A. dactylidis*. Our isolate (KUN-HKAS 102230) shares a size range of the ascomata, asci and ascospores as well as the ascospore septation with the type (MFLU 17-0498). Although, our isolate is slightly larger in ascomata, asci and ascospores, but ITS sequence data showed that they are conspecific (Hyde et al. 2017). Therefore, *A. dactylidis* is reported from a fern in Yunnan, China for the first time.

Brunneomurispora Phookamsak, Wanas. & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF556165; *Facesoffungi number*: FoF05699

Etymology: The generic epithet "*Brunneomurispora*" refers to the fungus having brown, muriform ascospores.

Saprobic on *Lonicera maackii*. **Sexual morph** *Ascomata* scattered, solitary or in groups, semi-immersed to erumpent, globose to subglobose, or irregular in shape, uniloculate, glabrous, ostiolate, papillate. *Peridium* slightly thick, composed of several layers, of small, flattened to broad, dark brown, pseudoparenchymatous cells of *textura angularis* to *textura prismatica*. *Hamathecium* composed of numerous, broad, filamentous, septate, anastomosed pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, broadly cylindrical to cylindric-clavate, or clavate, short pedicellate, apically rounded, with inconspicuous ocular chamber. *Ascospores* overlapping 1–2-seriate, dark brown, muriform, fusiform to ellipsoidal, asymmetrical, slightly larger in the upper part, constricted at the central septum, smooth-walled, lacking mucilaginous sheath. **Asexual morph** Undetermined.

Type species: *Brunneomurispora lonicerae* Phookamsak, Konta, Wanas. & K.D. Hyde

Notes: Phylogenetic analyses of a concatenated LSU, SSU, TEF1-α and ITS sequence dataset (Fig. 29) show that our new strains (KUMCC 18-0157 and KUMCC 18-0158) form a well-separated lineage basal to *Neosetophoma* Gruyter et al. with high support (94% ML and 0.99 BYPP). Our new isolate is distinct from *Neosetophoma* in having dark brown muriform ascospores. While, the sexual morph of *Neosetophoma* has phragmosporous, brown, fusiform ascospores (Tibpromma et al. 2017; Hyde et al. 2018b). Hence, we introduce a new genus *Brunneomurispora* herein to accommodate *B. lonicerae* which was isolated from *Lonicera maackii* in Yunnan, China.

Brunneomurispora resembles *Embarria* Wanas. et al. and *Hydeomyces* Maharachch. et al. in having immersed to erumpent, globose or subglobose ascomata, with a minute papilla, clavate asci, with dark brown, muriform, asymmetrical ascospores and ascospores that are constricted at the central septum (Wanasinghe et al. 2018; Maharachchikumbura et al. 2019). However, *Brunneomurispora* can be distinguished from *Embarria* in its peridium structure comprising several layers of brown, small, flattened to broad pseudoparenchymatous cells and its ascospores being 4–6 transverse septa, with 1–2 longitudinal septa, sectored, and lacking a mucilaginous sheath. *Embarria* has a thin-walled peridium, comprising large, 2–3 cell layers of pseudoparenchymatous cells and its ascospores are 4–6 transverse septa, with a single longitudinal septum, surrounded by a thick mucilaginous sheath (Wanasinghe et al. 2018). *Hydeomyces* differs from *Brunneomurispora* in having thicker peridium (35–60 µm thick), smaller, cylindrical asci (70–85 × 9–17 µm) and smaller, 1-seriate, muriform ascospores, with 2–4 transverse septa and 1 longitudinal septum (10–15 × 5–6.5 µm) (Maharachchikumbura et al. 2019). *Hawksworthiana lonicerae* Wanas. et al. was also isolated from *Lonicera* in Italy. This species differs from *Brunneomurispora lonicerae* in having cylindrical to cylindric-clavate asci, with yellowish brown, ellipsoidal, muriform, 3 transverse septa, with 1 longitudinal septum ascospores (Wanasinghe et al. 2018).

Many genera in *Phaeosphaeriaceae* are characterized by dictyosporous ascospores viz. *Allophaeosphaeria* Ariyaw. et al., *Dactylidina* Wanas. et al., *Dematiopleospora* Wanas. et al., *Embarria*, *Galiicola* Tibpromma et al., *Hawksworthiana* Wanas. et al., *Hydeomyces* Maharachch. et al., *Italica* Wanas. et al., *Muriphaeosphaeria* Phukhams. et al., *Populocrescentia* Wanas. et al. and *Yunnanensis* Karun. et al. (Wanasinghe et al. 2014b, 2018; Ariyawansa et al. 2015a; Liu et al. 2015a; Phukhamsakda et al. 2015; Karunarathna et al. 2017; Maharachchikumbura et al. 2019). These genera are represented by a single or a few species and have very little morphological differences in their sexual morphs. However, they always form distinct clades, separate from each other, as well as the asexual morphs of some different genera. Furthermore, *Poaceicola* and *Populocrescentia* are heterogeneous, forming both phragmosporous and dictyosporous ascospores (Wanasinghe et al. 2018). More sampling of taxa in these genera are needed for a better understanding.

Brunneomurispora lonicerae Phookamsak, Konta, Wanas. & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF556166; *Facesoffungi number*: FoF05700, Fig. 31

Etymology: The specific epithet "*lonicerae*" refers to the host genus *Lonicera*, from which the fungus was collected.

Holotype: KUN-HKAS 102232

Saprobic on dead hanging branches of *Lonicera maackii*. **Sexual morph** *Ascomata* 170–280 µm high, 230–330 µm diam., scattered, solitary, or in groups, semi-immersed to erumpent, visible as raised, black dot on the host surface, globose to subglobose, occasionally irregular in shape, uni-loculate, glabrous, ostiole central, with minute, mammiform papilla, lacking periphyses. *Peridium* 15–40 µm wide, of unequal thickness, composed of several layers, of small, flattened to broad, pseudoparenchymatous cells; outer layer comprising brown to dark brown cells of *textura angularis*; inner layer comprising flattened, hyaline cells of *textura angularis* to *textura prismatica*. *Hamathecium* composed of numerous, 2–5.5 µm wide, filamentous, septate, anastomosed pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* (67–)80–110(–132) × (13–)16–20(–24) µm ($\bar{x}$ = 98 × 18.8 µm, n = 25), 8-spored, bitunicate, fissitunicate, broadly cylindrical to cylindric-clavate, or clavate, short pedicellate, with truncate pedicel, apically rounded, with inconspicuous ocular chamber, clearly seen when immature. *Ascospores* (12–)14–18(–20)(–23) × (4–)5–8(–13) µm ($\bar{x}$ = 17 × 7.7 µm, n = 50), overlapping 1–2-seriate, dark brown, muriform, fusiform to ellipsoidal, with acute or rounded ends, or acute at the upper cells, asymmetrical, slightly larger in the upper part, straight, sometimes bent, mostly 4–6 transverse septa, with 1–2 longitudinal septa in each cell, becoming many sectors, constricted at the central septum, smooth-walled, lacking a mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 28–30 mm diam. after 1 week at room temperature (20–30 °C). Colony medium dense, circular, flattened, surface smooth, with edge entire, velvety to woolly; from above, white to cream at the margin towards the centre, with sectored, greenish grey to dull green or light green at the centre; from below, cream to pale yellowish at the margin, yellowish at the middle, brown-green at the centre; not producing pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, on dead hanging branches of *Lonicera maackii*, 20 April 2017, R. Phookamsak, KIB030 (KUN-HKAS 102232, **holotype**),

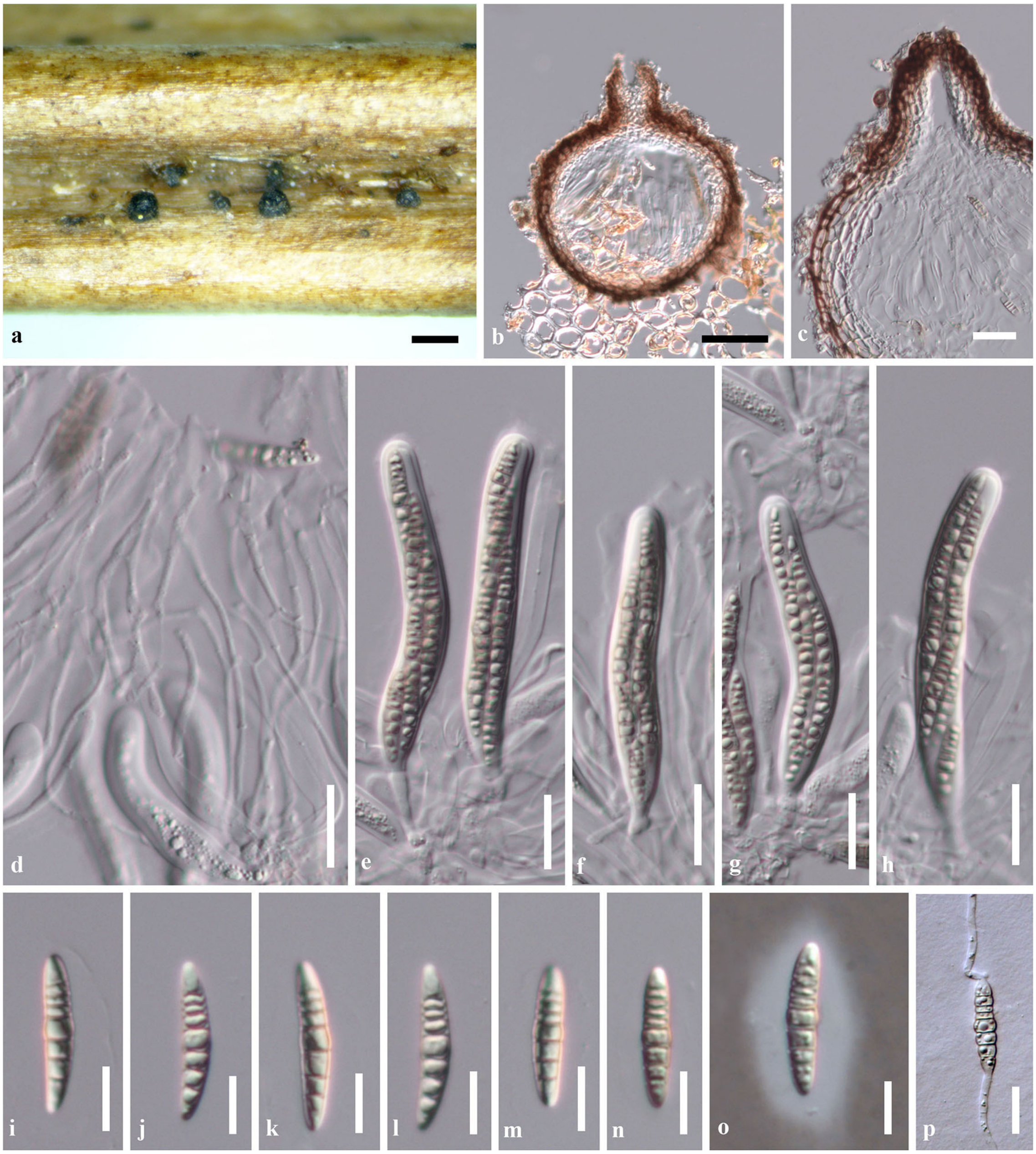


Fig. 30 ***Amarenomyces dactylidis*** (KUN-HKAS 102230). **a** Appearance of ascomata on host. **b** Section through ascoma. **c** Section through peridium. **d** Cellular pseudoparaphyses. **e–h** Asci. **i–n** Ascospores. **o** Ascospore stained with Indian ink. **p** Ascospore germination. *Scale bars* **a** = 200 µm, **b** = 50 µm, **c–h** = 20 µm, **i–p** = 10 µm

ex-type living culture KUMCC 18-0157 (KIB030A), KUMCC 18-0158 (KIB030B).

GenBank numbers: ITS = MK356372, LSU = MK356346, SSU = MK356360, TEF1-α = MK359064, RPB2 = MK359079 (KUMCC 18-0157); ITS = MK356373, LSU = MK356347, SSU = MK356361, TEF1-α = MK359065 (KUMCC 18-0157).

Galiicola Tibpromma et al.

Galiicola was introduced by Ariyawansa et al. (2015a) to accommodate a single species *G. pseudophaeosphaeria* Tibpromma et al. which was found as a saprobe on *Galium* in Italy. The genus is characterized by semi-immersed to erumpent, globose to subglobose ascomata, fissitunicate, cylindric-clavate asci, orange-brown, elongate fusiform ascospores with 4–5 transverse septa, some with 1–2 longitudinal septa; its asexual morph has not been found (Ariyawansa et al. 2015a). We introduce a second species, *G. baoshanensis* which is represented by its asexual morph.

Galiicola baoshanensis Phookamsak, Wanas. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556167; *Facesoffungi number*: FoF05701, Fig. 32

Etymology: The specific epithet "*baoshanensis*" refers to Baoshan prefecture-level city of Yunnan Province, China, where the holotype was collected.

Holotype: KUN-HKAS 102234

Saprobic on dead branches of herbaceous plant. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous, amarenographium-like. *Conidiomata* 90–125 µm high, 90–120 µm diam., pycnidial, scattered, solitary, immersed to semi-immersed, uni-loculate, globose to subglobose, glabrous, dark brown, visible as small black dot on the host surface, ostiolate, apapillate, with pore-like opening. *Conidiomata walls* 8–25 µm wide, thin-walled, composed of flattened to broad, brown to dark brown pseudoparenchymatous cells, arranged in a *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–7(–12) × (2–)3–6 µm ($\bar{x}$ = 5.7 × 4.7 µm, n = 30), enteroblastic, phialidic, discrete, determinate, ampulliform to doliiform, occasionally cylindrical, unbranched, aseptate, hyaline, smooth, minute collarette with periclinal wall thickening, arising from the inner cavity of the conidioma wall, difficult to distinguish from the conidioma wall. *Conidia* (30–)35–45 × (10–)11–14(–15.5) µm ($\bar{x}$ = 39.6 × 12.9 µm, n = 50), muriform, brown to dark brown, paler at the end cells, ellipsoidal to broadly fusiform, or subclavate, apex rounded, base truncate or obtuse, 8–9 transverse septa, with 2–4 longitudinal septa, not constricted at the septa, rough-walled, echinulate, lacking mucilaginous sheath surrounding conidia.

Material examined: CHINA, Yunnan Province, Baoshan, Shuizai, Dawazi mountain, on dead branches of herbaceous plant, 23 October 2015, R. Phookamsak, BS018 (KUN-HKAS 102234, **holotype**).

GenBank numbers: ITS = MK356374, LSU = MK356348, SSU = MK356362, TEF1-α = MK359066.

Notes: Multigene phylogenetic analyses of a combined LSU, SSU, TEF1-α and ITS sequence dataset show that *Galiicola baoshanensis* forms a sister lineage with the generic type of *Galiicola*, *G. pseudophaeosphaeria* with high support (100% ML and 1.00 BYPP; Fig. 29). A comparison of TEF1-α sequences indicates that *G. baoshanensis* differs from *G. pseudophaeosphaeria* in 14/730 bp (1.9%). However, we could not compare the morphological characters of *G. baoshanensis* with *G. pseudophaeosphaeria* as they are represented by different morphs. *Galiicola baoshanensis* is introduced as the asexual species in *Galiicola* for the first time.

Galiicola baoshanensis is similar to *Amarenographium ammophilae* Wanas. et al. in having conidia that are muriform, clavate, ellipsoidal, ovoid or fusoid conidia, with rounded apex, acute or truncate base, and 7–9 transverse septa (Wijayawardene et al. 2016). However, *G. baoshanensis* can be distinguished from *A. ammophilae* in having brown to dark brown conidia, with 2–4 longitudinal septa and lacking appendages at the apex and the base. Whereas, *A. ammophilae* has yellowish brown to brown conidia, with 1–3 longitudinal septa and appendages at the apex and the base (Wijayawardene et al. 2016). A comparison of ITS and TEF1-α sequences indicates that *G. baoshanensis* differs from *A. ammophilae* in 71/570 bp (12.5%) and 58/899 bp (6.5%), respectively. Muti-gene phylogenetic analyses also supported their distinctiveness (Fig. 29).

Neosetophoma Gruyter et al.

We follow the latest treatment and updated accounts of *Neosetophoma* in Hyde et al. (2018b) and Wanasinghe et al. (2018). Seventeen species are known in this genus (Hyde et al. 2018b; Index Fungorum 2019).

Neosetophoma lonicerae Phookamsak, Wanas. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556168; *Facesoffungi number*: FoF05702, Fig. 33

Etymology: The specific epithet "*lonicerae*" refers to the host genus *Lonicera*, from which the holotype was collected.

Holotype: KUN-HKAS 102231

Saprobic on *Lonicera maackii*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 110–160 µm high, 80–160 µm diam., pycnidial, scattered, solitary to gregarious, immersed to semi-immersed, uniloculate, globose to subglobose, glabrous, dark brown to black, visible as small black dot on the host surface, associating with other fungal taxa, ostiole central, occasionally near the centre, minutely mammiform papilla. *Conidiomata walls* 5–12 µm wide, equally thin-walled, composed of 2–3 cell layers, of broad, brown to dark brown pseudoparenchymatous cells, arranged in a *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.5–7 × (3–)5–10 µm ($\bar{x}$ = 6.2 × 6.7 µm, n = 20), enteroblastic, phialidic, discrete, determinate, ampulliform to doliiform, unbranched, aseptate, hyaline, smooth, minute collarette with periclinal wall thickening, arising from the inner cavity of the conidioma wall. *Conidia* (8.5–)9–12(–14) × 4–5 µm ($\bar{x}$ = 11 × 4.8 µm, n = 50), yellowish brown, ellipsoidal, 1–3-septate, not constricted at the septa, smooth-walled, lacking mucilaginous sheath surrounding conidia.

Culture characteristics: Colonies on PDA reaching 33–35 mm diam. after 3 weeks at room temperature (20–30 °C). Colony medium dense, circular, flattened to raised, surface slightly rough with hyphal tufts, edge entire, velvety to fluffy; from above, white to white yellowish at the margin, light green to yellowish green at the centre; from below, radiating outwards colony, white to cream at

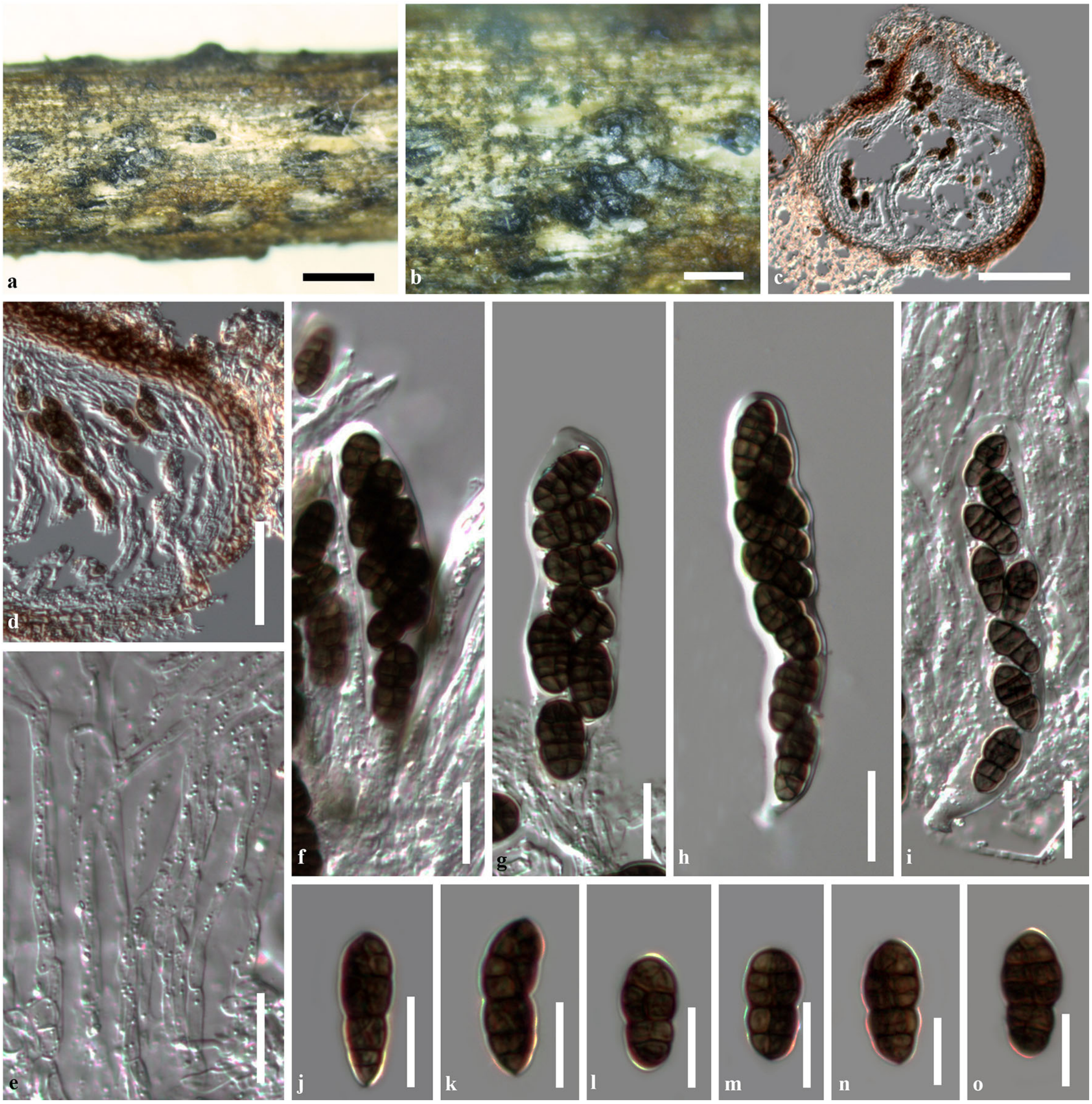


Fig. 31 ***Brunneomurispora lonicerae*** (KUN-HKAS 102232, **holotype**). **a** Appearance of ascomata on host. **b** Close up of ascoma on host. **c** Section through ascoma. **d** Section through peridium. **e** Cellular pseudoparaphyses. **f–i** Asci. **j–o** Ascospores. *Scale bars* **a** = 500 µm, **b** = 200 µm, **c** = 100 µm, **d** = 50 µm, **e–i** = 20 µm, **j–o** = 10 µm

the margin, dark green to black at the middle, orangish brown at the centre; producing yellowish pigment on agar medium.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, on dead hanging branches of *Lonicera maackii*, 20 April 2017, R. Phookamsak, KIB033 (KUN-HKAS 102231, **holotype**), ex-type living culture, KUMCC 18-0155 (KIB033A), KUMCC 18-0156 (KIB033B).

GenBank numbers: ITS = MK356375, LSU = MK356349, SSU = MK356363, TEF1-α = MK359067 (KUMCC 18-0155); ITS = MK356376, LSU = MK356350, SSU = MK356364, TEF1-α = MK359068 (KUMCC 18-0156).

Notes: In the NCBI BLASTn search of ITS sequence, *Neosetophoma lonicerae* has a closest match with fungal endophyte species (M16-3161) with 100% similarity and is closely related to *N. italica* W.J. Li et al., *N. rosarum* R.H. Perera et al., *N. samarorum* (Desm.) Gruyter et al. and *N. rosigena* Wanas. et al. with 98% similarity. Multigene phylogenetic analyses based on a combined LSU, SSU, TEF1-α and ITS sequence dataset show that *N. lonicerae* forms a separate lineage, clustering with *N. rosigena*, *N. samarorum* and *N. garethjonesii* Tibpromma et al. with moderate support (76% ML and 0.98 BYPP; Fig. 29). A comparison of ITS nucleotide base pairs shows that *N. lonicerae* differs from *N. rosigena*, *N. samarorum* and *N. garethjonesii* in 14/555 bp (2.5%), 15/555 bp (2.7%) and

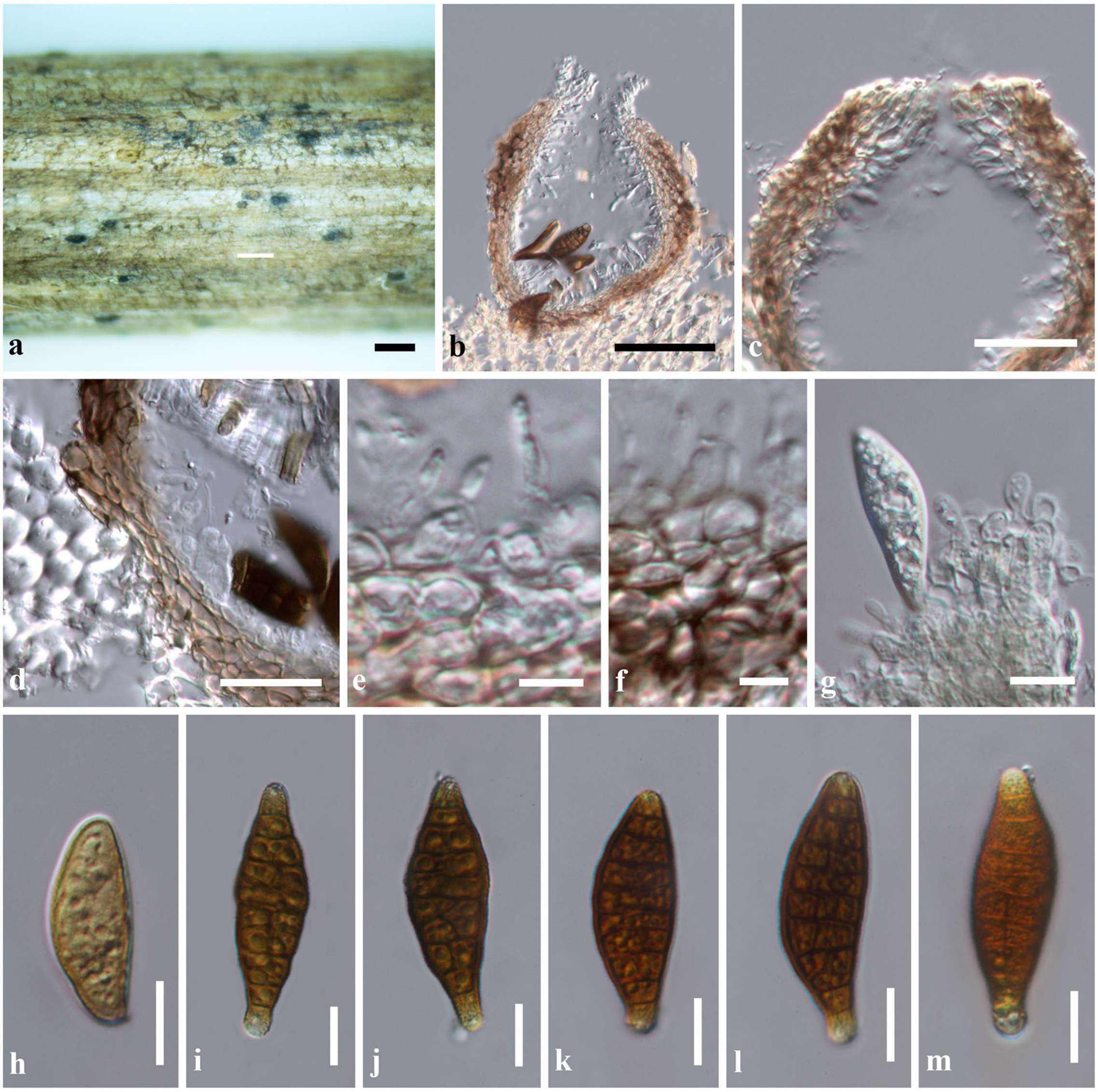


Fig. 32 ***Galiicola baoshanensis*** (KUN-HKAS 102234, **holotype**). **a** Appearance of conidiomata on host. **b** Section through conidioma. **c** Ostiole with pore-like opening. **d** Section through conidioma wall. **e–g** Conidiogenous cells. **h** Conidium when immature. **i–m** Conidia. *Scale bars* **a** = 200 µm, **b** = 50 µm, **d** = 20 µm, **c, g–m** = 10 µm, **e, f** = 5 µm

16/522 bp (3%), respectively. We therefore, introduce *N. lonicerae* as a new species following the guidelines of Jeewon and Hyde (2016).

Neosetophoma lonicerae is similar to some other *Neosetophoma* species in having pale brown to brown, oblong to ellipsoidal, or subfusoid, 1–3-septate conidia; such as in *N. iranianum* Papizadeh et al., *N. italica*, *N. rosae* R.H. Perera et al., *N. rosarum* and *N. shoemakeri* Senwanna et al. However, they can be distinguished based on their conidial size, host occurrence and phylogenetic distance (Liu et al. 2015a; Karunarathna et al. 2017; Hyde et al. 2018b; Wanasinghe et al. 2018).

Ophiobolus Riess

We follow the latest treatment and updated accounts of *Ophiobolus* in Phookamsak et al. (2017).

Ophiobolus malleolus S.K. Huang, Bulgakov & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554782; *Facesoffungi number*: FoF04686, Fig. 34

Etymology: The specific name "*malleolus*" refers to the hammer-shaped at top of the ascospores.

Holotype: MFLU 15-2230.

Saprobic on dead stems of *Cirsium arvense* (*Asteraceae*). **Sexual morph** *Ascomata* 230–270 µm high, 265–310 µm diam., scattered, solitary to gregarious, immersed, eventually erumpent, uni-loculate, globose to subglobose,

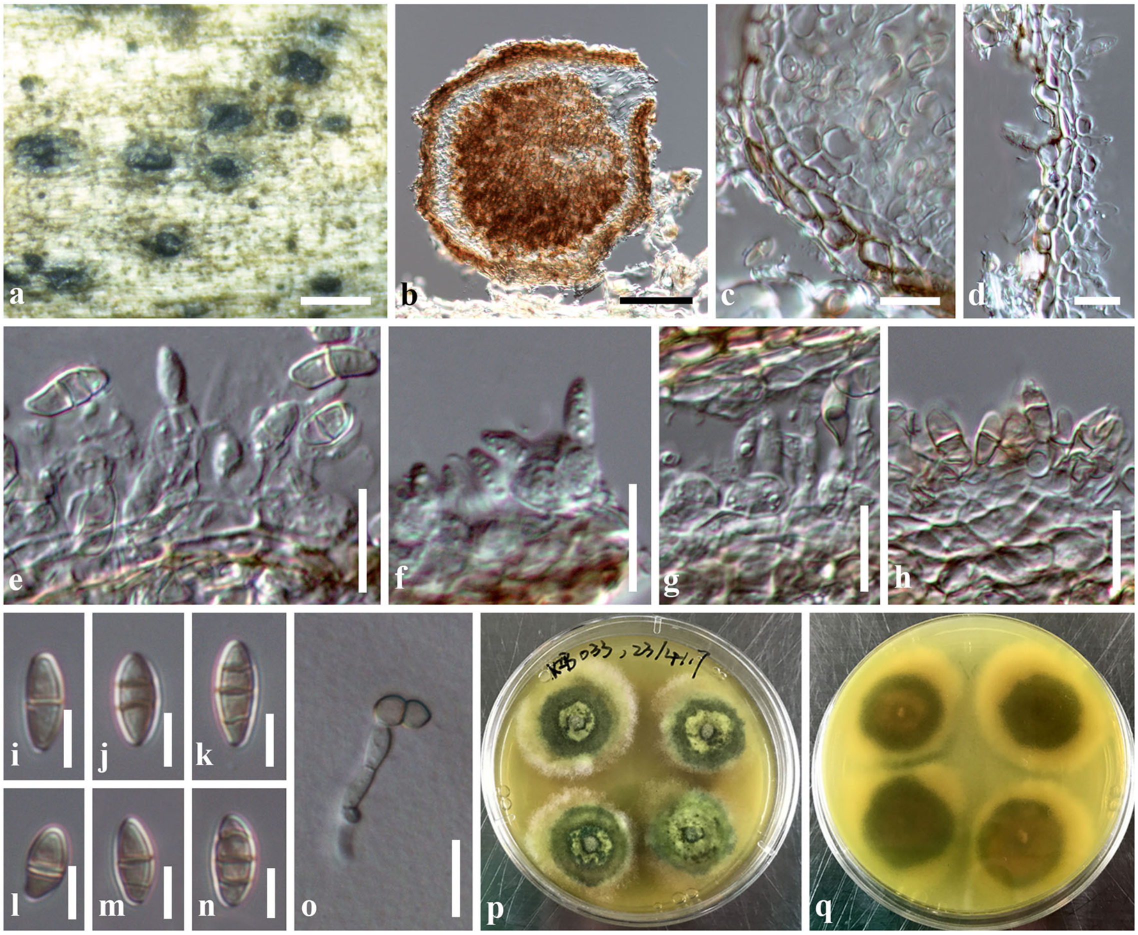


Fig. 33 ***Neosetophoma lonicerae*** (KUN-HKAS 102231, **holotype**). **a** Appearance of conidiomata on host. **b** Section through conidioma. **c, d** Section through conidioma wall. **e–h** Conidiogenous cells. **i–n** Conidia. **o** Germinated conidium. **p, q** Culture characteristics on PDA (**p** = from above, **q** = from below). *Scale bars* **a** = 200 µm, **b** = 50 µm, **c–h, o** = 10 µm, **i–n** = 5 µm

dark brown to black, papillate. *Ostiole* central, short papilla, filled with periphyses. *Peridium* 25–60 µm wide, thick-walled, composed of several cell layers of brown to dark brown cells, paler to hyaline towards the inner layers, outer layer comprising black, coriaceous stratum, arranged in a *textura angularis*. *Hamathecium* composed of numerous, 1–3 µm wide, filamentous, septate pseudoparaphyses, anastomosing at the apex, embedded in a gelatinous matrix. *Asci* 125–155 × 12–15 µm ($\bar{x}$ = 140 × 12.5 µm, n = 20), 8-spored, bitunicate, cylindric-clavate, subsessile to short pedicellate, with knob-like or truncate pedicel, rounded at the apex, with a distinct ocular chamber. *Ascospores* 100–112 × 2.5–4.5 µm ($\bar{x}$ = 107.5 × 3.5 µm, n = 50), fasciculate, in parallel or spiral, initially hyaline, becoming brown at maturity, guttulate, filiform, enlarged at the first cell with hammer-like, tapering towards the end cell, up to 15 septa, curved, slightly constricted at the septa at maturity, smooth-walled, with apical mucilaginous cap. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on PDA, colony reaching 10 mm diam. after 2 weeks at room temperature (20–30 °C). Colony dense, irregular in shape, flattened to umbonate, surface smooth, with edge erose, velvety to floccose; from above, cream; from below, cream to pale yellowish; not producing pigmentation on agar medium.

Material examined: RUSSIA, Rostov region, Krasnosulinsky District, Donskoye forestry, arboretum (47.8547249°N, 40.2318907°E), on dead stems of *Cirsium arvense* (*Asteraceae*), 28 June 2015, T.S. Bulgakov, T-526 (MFLU 15-2230, **holotype**), ex-type living culture, MFLUCC 15-1077.

GenBank numbers: ITS = MH399730, LSU = MH399731, SSU = MH399729.

Notes: Multigene phylogenetic analyses reveal a close phylogenetic affinity between *Ophiobolus malleolus* and *O. disseminans* (Fig. 29, 68% ML and 1.00 BYPP). *Ophiobolus malleolus* is distinct from *O. disseminans* in its ascospores being filiform with an enlarged at the apical cell similar to a hammer-like, with apical mucilaginous cap, and not splitting into two part spores. *Ophiobolus disseminans* has filiform ascospores with two swollen cells near the centre, lacks an apical mucilaginous cap, and splits into two part spores at the central septum (Phookamsak et al. 2014b, 2017).

Ophiobolus anguillides (Cooke) Sacc. also has filiform ascospores enlarged hammer-like at the apical cell and an apical mucilaginous cap. However, *O. anguillides* has larger ascomata and ascospores (500–600 µm diam., and 120–130 × 2.5–3 µm; Shoemaker 1976). *Ophiobolus anguillides* has been reported from many hosts, mainly on *Artemesia* in Europe and North America (Shoemaker 1976; Farr and Rossman 2018). However, the species has never been reported from *Cirsium arvense*. Unfortunately, there is no molecular data available for *O. anguillides*.

Phaeosphaeria I. Miyake

We follow the latest treatment and updated accounts of *Phaeosphaeria* in Phookamsak et al. (2014b), Hyde et al. (2017) and Tibpromma et al. (2017). More than 200 epithets are listed under *Phaeosphaeria* in Index Fungorum (2019); however, the phylogenetic affinities of few species have been confirmed based on molecular data. Some species listed under *Phaeosphaeria* have already been transferred to other related genera in *Phaeosphaeriaceae* and other related families (Phookamsak et al. 2014b; Ariyawansa et al. 2015a; Tennakoon et al. 2016).

Phaeosphaeria cycadis Wanas., Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556169; *Facesoffungi number*: FoF05703, Fig. 35

Etymology: The specific name "*cycadis*" refers to the host family *Cycadaceae*, of which the holotype was collected.

Holotype: KUN-HKAS 102235

Associated with leaf spots on *Cycas* sp. (*Cycadaceae*). **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* (60–)100–160 µm high, (60–) 135–200 µm diam., pycnidial, visible as black dot on host surface, scattered to clustered, solitary to gregarious, semi-immersed to erumpent, uni-loculate, subglobose to ampulliform, or irregular in shape, ostiolate, with minute papilla. *Conidiomata walls* 10–20(–30) µm wide, composed of 4–5 cell layers, of brown to dark brown pseudoparenchymatous cells, of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* (3.5–)4.5–8 × 4–8 (–10) µm ($\bar{x}$ = 6.4 × 5.7 µm, n = 30), ampulliform to broadly conical, gradually tapering toward the apex, holoblastic, phialidic, hyaline, smooth-walled, with periclinal wall thickening, arising from the inner cavity of the conidioma wall. *Conidia* (10–)12–14(– 16) × 3–5 µm ($\bar{x}$ = 12.9 × 3.9 µm, n = 50), pale brown to light yellowish, oblong to ellipsoidal, or subcylindrical, (0–)1–2-septate, truncate to obtuse base, with obtuse apex, not constricted at the septa, smooth-walled.

Culture characteristics: Colonies on PDA reaching 50–52 mm diam. after 3 weeks at room temperature (20–30 °C). Colony dense, irregular in shape, flattened, surface slightly smooth, edge undulate, with entire margin, cottony to floccose, slightly sparse near the margin; from above, white to cream, slightly radiated outwards colony; from below, slightly radiating, cream at the margin, pale brown to yellowish-brown at the centre, sectering with golden brown; not producing pigmentation on agar medium.

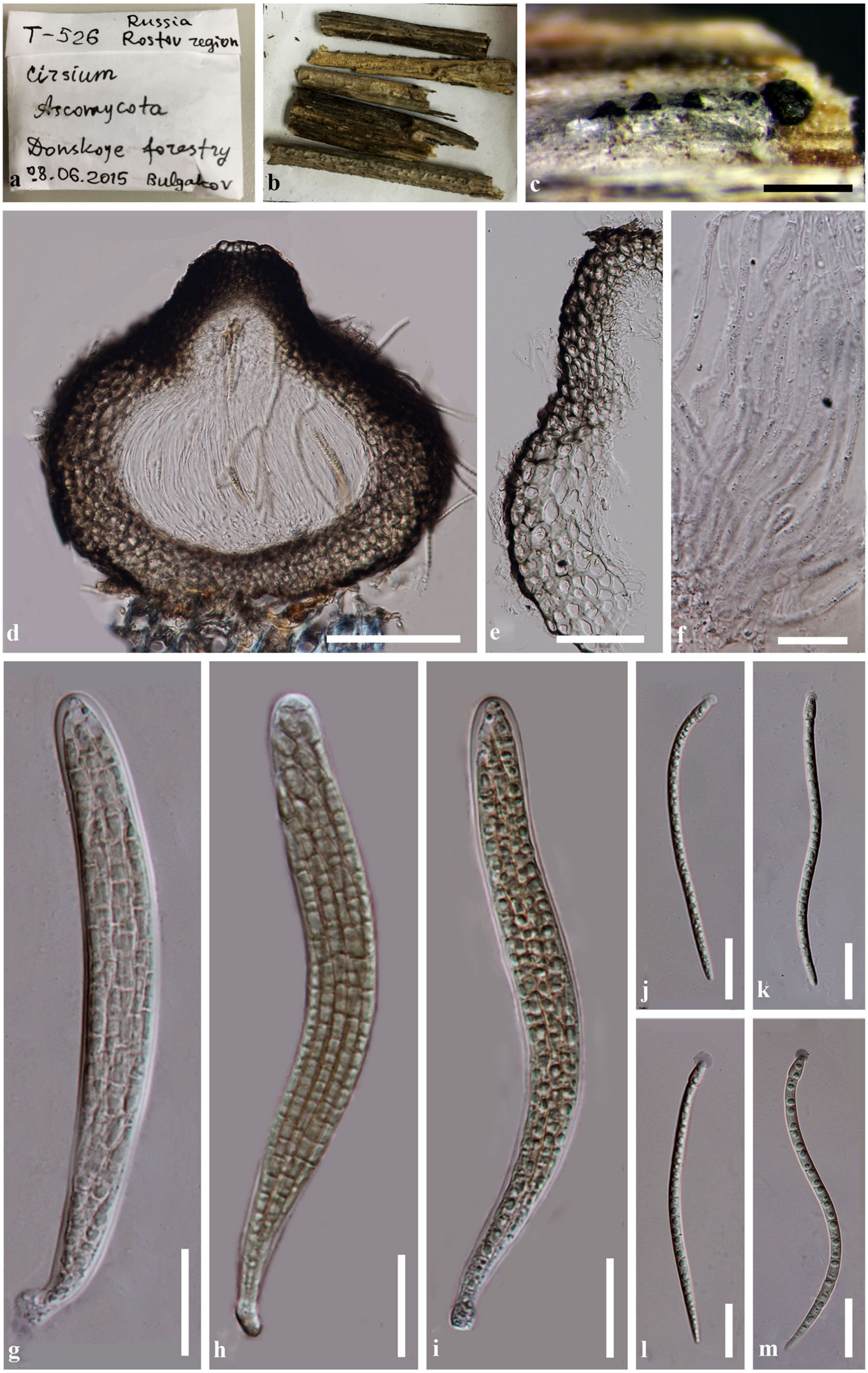
Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, associated with leaf spots on *Cycas* sp. (*Cycadaceae*), 5 April 2017, R. Phookamsak, KIB022 (KUN-HKAS 102235, **holotype**), ex-type living culture, KUMCC 18-0161 (KIB022A), KUMCC 18-0162 (KIB022B).

GenBank numbers: ITS = MK356378, LSU = MK356352, SSU = MK356366, TEF1-α = MK359069 (KUMCC 18-0161); ITS = MK356379, LSU = MK356353, SSU = MK356367, TEF1-α = MK359070 (KUMCC 18-0162).

Notes: In the NCBI BLASTn search of ITS sequences, *Phaeosphaeria cycadis* most closely matches *P. acaciae* Tennakoon et al. with 99% similarity. Multigene phylogenetic analyses based on a combined LSU, SSU, TEF1-α and ITS sequence dataset show that *P. cycadis* forms a sister lineage with *P. acaciae* with high support (100% ML and 1.00 BYPP; Fig. 29). The ITS gene could not clarify the novelty of *P. cycadis* in this study as the species is not significantly different from *P. acaciae* in a comparison of ITS sequences (5/452 bp). Phookamsak et al. (2014b) mentioned that *Phaeosphaeria* contains species complexes that cannot be resolved based only on the ITS gene and that a combination of protein coding genes, such as TEF1-α and RPB2, is necessary to clarify species in this genus. Based on morphological characteristics, *P. cycadis* differs from *P. acaciae* in having larger conidia (*P. cycadis*, (10–)12–14 (– 16) × 3–5 µm versus 8–12 × 2.4–3.5 µm, *P. acaciae*; Hyde et al. 2017), with (0–)1–2 conidial septa and is associated with leaf spots on *Cycas* sp. *Phaeosphaeria acaciae* has 1–3 conidial septa and occurs on dead stems of *Acacia* sp. as a saprobe (Hyde et al. 2017). Furthermore, *P. acaciae* produced a pink pigment on PDA, but this is absent in *P. cycadis*. We therefore, introduce *P. cycadis* as a new species in this study based on its morphological distinctiveness.

Wojnowiciella Crous et al.

Wojnowiciella was introduced by Crous et al. (2015b) and is typified by *W. eucalypti* Crous et al. Crous et al. (2015a) treated *Wojnowicia* as a synonym of *Septoriella*


T-526
Russia
Rostov region
Cirsium
Ascomycota
Donskoye forestry
28.06.2015
Bulgakov
a
b
c
d
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j
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◀**Fig. 34** ***Ophiobolus malleolus*** (MFLU 15-2230, **holotype**) **a** Herbarium label. **b** Appearance of ascomata on *Cirsium arvense* stems. **c** Ascomata on host. **d** Ascoma in vertical section. **e** Peridium. **f** Pseudoparaphyses. **g–i** Developing stages of the asci. **j–m** Ascospores (note: **m** stained in Indian ink). *Scale bars* **c** = 500 µm, **d** = 100 µm, **e** = 50 µm, **f–m** = 20 µm

Oudem. based on nomenclature study and this is in agreement of Wijayawardene et al. (2017a). Subsequently, all identified *Wojnowicia* species in *Phaeosphaeriaceae* were synonymized under *Wojnowiciella* (Crous et al. 2015b; Hernandez-Restrepo et al. 2016). *Wojnowiciella* can be distinguished from *Wojnowicia* Sacc. in having apapillate, glabrous conidiomata and dark brown conidia (Crous et al. 2015b). *Wojnowicia* was introduced by Saccardo (1892) and is characterized by setose conidiomata (Crous et al. 2015a; Wijayawardene et al. 2016). Seven species are accommodated in this genus (Index Fungorum 2019).

Wojnowiciella kunmingensis Phookamsak, Wanas. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556170; *Facesoffungi number*: FoF05704, Fig. 36

Etymology: The specific epithet "*kunmingensis*" refers to Kunming Institute of Botany, Kunming City, Yunnan Province, China, where the holotype was collected.

Holotype: KUN-HKAS 102233

Saprobic on *Lonicera maackii*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 110–190 µm high, 110–190 µm diam., pycnidial, scattered, solitary to gregarious, immersed, slightly raised, visible as small black dot on host surface, uni-loculate, globose to subglobose, glabrous, dark brown to black, ostioles central, apapillate, with pore-like opening. *Conidiomata walls* 5–12 µm wide, thin-walled, of equal thickness, composed of 1–3 cell layers, of flattened, dark brown, pseudoparenchymatous cells, arranged in a *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* (3–)4–6.5(–9) × (2.5–)3.5–6(–8) µm l/w ($\bar{x}$ = 5 × 5.3 µm, n = 40), holoblastic, phialidic, discrete, determinate, ampulliform to doliiform, unbranched, aseptate, hyaline, smooth, arising from the inner cavity of the conidioma wall. *Conidia* (16–)18–24(–27.5) × 4–6(–7) µm l/w ($\bar{x}$ = 22 × 5.6 µm, n = 50), dark brown, subcylindrical to fusiform, or reniform, slightly curved, with acute to rounded apex, and rounded to truncate base, 3–7-septate, not constricted at the septa, thick-walled, smooth-walled, with guttules, having flattened, mucous caps at both ends.

Culture characteristics: Colonies on PDA reaching 35–38 mm diam. after 2 weeks at room temperature (20–30 °C). Colony medium dense, slightly irregular in shape, flattened to slightly raised, surface slightly rough with greyish-green hyphal tufts, edge undulate, with entire margin, floccose; from above, slightly radiating, white to cream at the margin, pale brown at the middle, separated from the margin with brown to dark green concentric ring near the edge, greyish green to dark green at the centre; from below, white to cream margin, brown to dark brown at the centre; not producing pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, on dead hanging branches of *Lonicera maackii*, 20 April 2017, R. Phookamsak, KIB031 (KUN-HKAS 102233, **holotype**), ex-type living culture, KUMCC 18-0159 (KIB031A), KUMCC 18-0160 (KIB031B).

GenBank numbers: ITS = MK356380, LSU = MK356354, SSU = MK356368, TEF1-α = MK359071 (KUMCC 18-0159); ITS = MK356381, LSU = MK356355, SSU = MK356369, TEF1-α = MK359072, RPB2 = MK359078 (KUMCC 18-0160).

Notes: In the NCBI BLASTn search of ITS sequences, *Wojnowiciella kunmingensis* most closely matches *W. dactylidis* (Wijayaw. et al.) Hern.-Restr. & Crous, *W. spartii* (W.J. Li et al.) Hern.-Restr. & Crous and *Wojnowicia italica* Qing Tian et al. with 99% similarity. ITS and TEF1-α genes could not resolve the novelty of the *Wojnowiciella* species in this study. A comparison of ITS and TEF1-α nucleotide bases shows that *Wojnowiciella kunmingensis* is not significantly different from *W. dactylidis* and other *Wojnowiciella* species as well as *Wojnowicia italica*. However, a comparison of RPB2 sequence data shows that *Wojnowiciella kunmingensis* differs from *W. dactylidis* and *Wojnowicia italica* in 21/856 bp (2.4%) and 20/954 bp (2.1%), respectively.

Multigene phylogenetic analyses based on a combined LSU, SSU, TEF1-α and ITS sequence data show that *Wojnowiciella kunmingensis* forms a sister lineage with *W. dactylidis* and clusters with other *Wojnowiciella* species (Fig. 29). However, *W. kunmingensis* differs from *W. dactylidis* in having 3–7-septate conidia, while *W. dactylidis* has 7–11-septate conidia (Liu et al. 2015a). *Wojnowiciella leptocarpi* Crous et al. also has 3–7-septate conidia, with mucous caps at both ends. However, *W. kunmingensis* has longer conidia ((16–)18–24(–27.5) × 4–6(–7) µm versus 26–36 × 4–6 µm; Hernandez-Restrepo et al. 2016), that are brown to dark brown, and smooth-walled. The conidia of *W. leptocarpi* are orange brown, thick-walled, and verruculose (Hernandez-Restrepo et al. 2016). A comparison of RPB2 sequence data shows that *W. kunmingensis* differs from *W. leptocarpi* in 29/851 bp (3.4%). *Wojnowiciella lonicerae* (Wijayaw. et al.) Hern.-Restr. & Crous was also collected from *Lonicera*, but it has 8–11-septate conidia (Liu et al. 2015a).

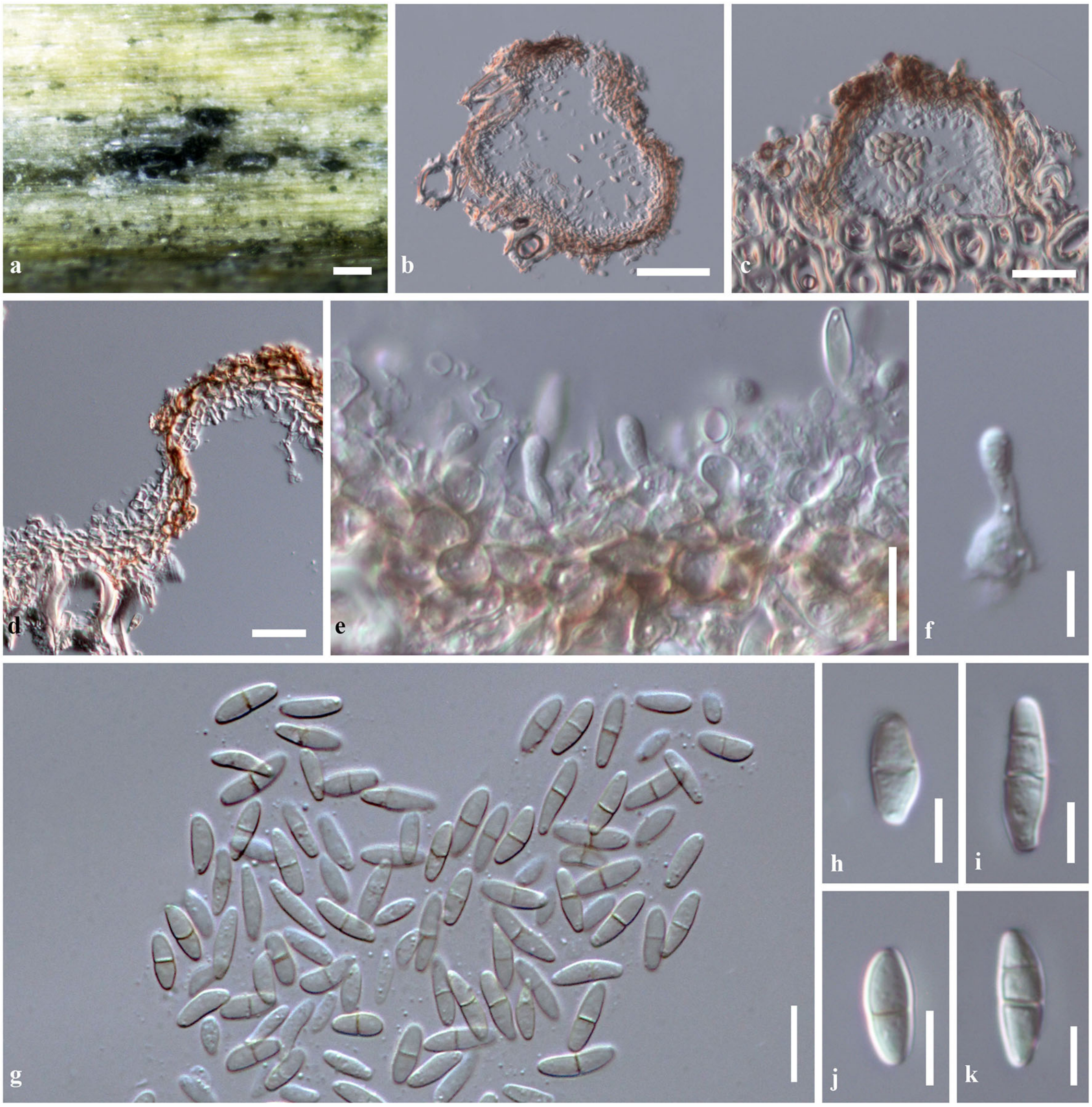


Fig. 35 ***Phaeosphaeria cycadis*** (KUN-HKAS 102235, **holotype**). **a** Appearance of conidiomata on host. **b, c** Section through conidiomata. **d** Section through conidioma wall. **e, f** Conidiogenous cells. **g–k** Conidia. *Scale bars* **a** = 100 µm, **b** = 50 µm, **c, d** = 20 µm, **e, g** = 10 µm, **f, h–k** = 5 µm

Wojnowiciella rosicola (W.J. Li et al.) Wanas., Phookamsak & K.D. Hyde, ***comb. nov.***

Index Fungorum number: IF556171; *Facesoffungi number*: FoF05705

Basionym: *Wojnowicia rosicola* W.J. Li, Camporesi & K.D. Hyde, in Wanasinghe et al., Fungal Divers.: https://doi.org/10.1007/s13225-018-0395-7, [144] (2018)

Holotype: ITALY, Arezzo [AR], Montemezzano, on dead aerial branch of *Rosa* sp. (*Rosaceae*), 25 August 2014, E. Camporesi, IT 2200 (MFLU 17-2785); ex-type living culture, MFLUCC 15-0128.

Morphological description: See Wanasinghe et al. (2018) (Fig. 93, pp. 144–147).

Notes: *Wojnowiciella rosicola* was introduced by Wanasinghe et al. (2018) as *Wojnowicia rosicola* W.J. Li et al. The species clustered with other *Wojnowiciella* species in *Phaeosphaeriaceae* that were previously treated in *Wojnowicia* and recently treated as a synonym of *Wojnowiciella* by Crous et al. (2015a, b) and Hernandez-Restrepo et al. (2016). Based on morphological characteristics and phylogenetic analyses, the species is congeneric with *Wojnowiciella*. We therefore, treat *W. rosicola* as a new combination.

Pseudoastrosphaeriellaceae Phookamsak & K.D. Hyde

Pseudoastrosphaeriellaceae was introduced by Phookamsak et al. (2015b) to accommodate a monotypic genus

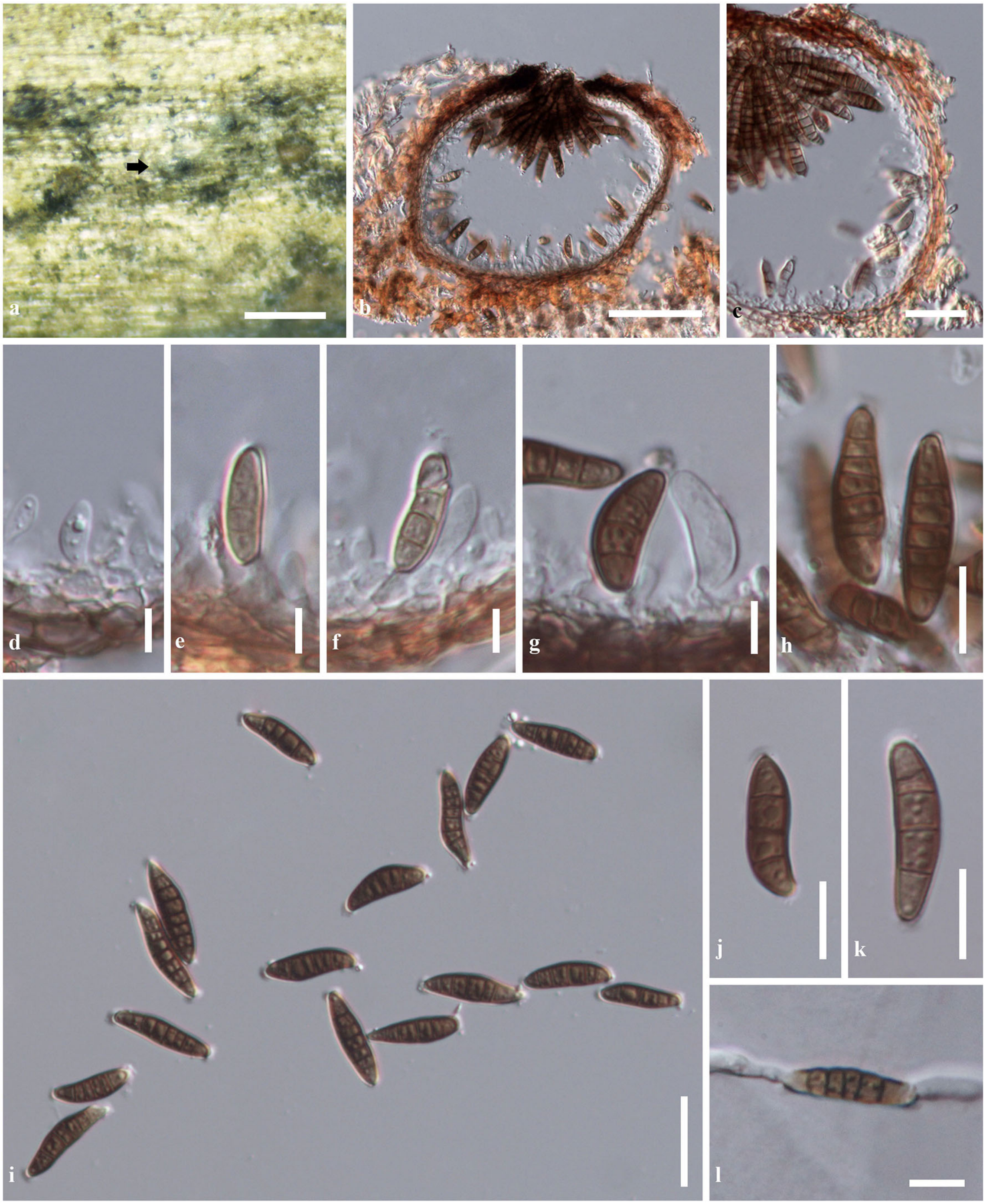


Fig. 36 ***Wojnowiciella kunmingensis*** (KUN-HKAS 102233, **holotype**). **a** Appearance of conidiomata on host. **b** Section through conidioma. **c** Section through conidioma wall. **d–g** Conidiogenous cells. **h–k** Conidia. **l** Germinated conidium. *Scale bars* **a** = 200 µm, **b** = 50 µm, **c, i** = 20 µm, **h, j–l** = 10 µm, **d–g** = 5 µm

Pseudoastrosphaeriella. This family is characterized by hemispherical to lenticular ascostromata, globose to subglobose ascomata with a flattened or rounded base, immersed beneath host epidermis, erumpent through host surface by a papilla, with short to long necks, trabeculate pseudoparaphyses, short pedicellate, cylindric-clavate to clavate asci, and hyaline or brown, septate ascospores and coelomycetous asexual morphs (Phookamsak et al. 2015b). Based on close morphological characteristics and phylogenetic support, Hyde et al. (2017) accommodated *Carinispora* K.D. Hyde in *Pseudoastrosphaeriellaceae* and this was followed by Wijayawardene et al. (2018a). In this study, we introduce a new genus *Pseudoastrosphaeriellopsis* typified by *P. kaveriana* in *Pseudoastrosphaeriellaceae* based on molecular phylogeny coupled with morphological characteristics.

Pseudoastrosphaeriellopsis Devadatha, Wanas., Jeewon & V.V. Sarma, ***gen. nov.***

Index Fungorum number: IF555790; *Facesoffungi number*: FoF05706

Etymology: Generic epithet in resemblance to *Pseudoastrosphaeriella*

Saprobic on decaying stems and twigs of *Avicennia marina* and *Suaeda monoica*, black spots, with short necks on host surface. **Sexual morph** *Ascomata* light brown, solitary to gregarious, immersed to erumpent, globose to subglobose with a rounded base, uni-loculate, coriaceous, brown, short papillate, ostiolate. *Ostioles* central, cylindrical, straight to oblique, with ostiolar canal lined by hyaline periphyses. *Peridium* thin- to thick-walled, unequally thickened, composed of two layers, inner stratum with hyaline to pale brown compressed cells of *textura angularis*, outer stratum with compact brown polygonal cells of *textura angularis*, fused with the host tissue. *Hamathecium* composed of numerous, filamentous, septate, branched, hyaline pseudoparaphyses. *Asci* 8-spored, bitunicate, cylindric-clavate to clavate, with a short, thick pedicel, apically rounded and thickened with an ocular chamber. *Ascospores* overlapping 1–2-seriate, brown, fusiform to broadly fusiform, slightly curved with round to acute ends, slightly constricted at the 3rd septum and rarely at other septa, broader in the middle and tapering towards the ends, septate, with hyaline apical and terminal ends, smooth-walled, lacking guttules and mucilaginous sheath. **Asexual morph** Undetermined.

Type species: *Pseudoastrosphaeriellopsis kaveriana* Devadatha, Wanas., Jeewon & V.V. Sarma

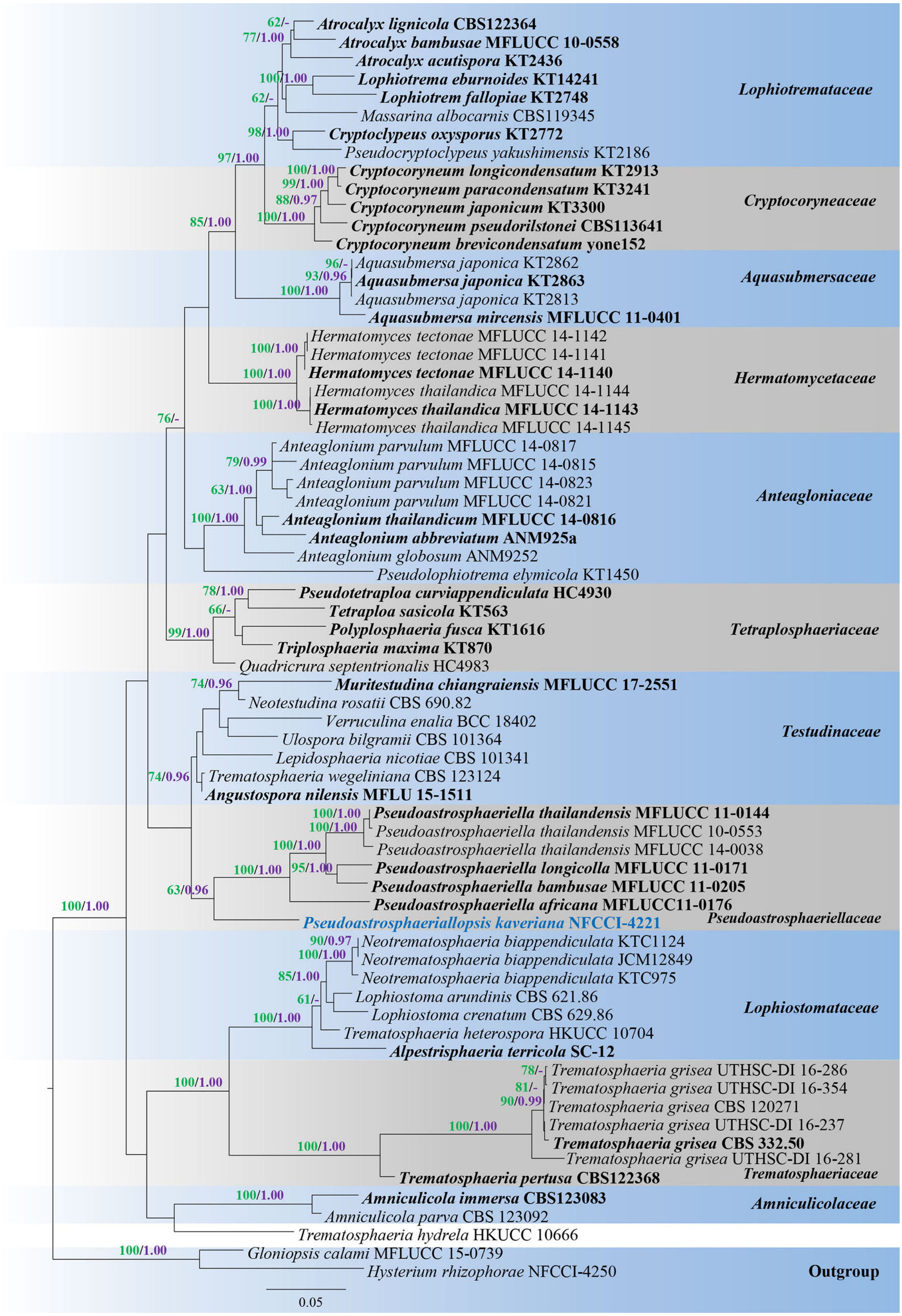
Notes: The genus *Pseudoastrosphaeriella* Phookamsak et al. was introduced by Phookamsak et al. (2015b) to accommodate *P. aequatoriensis* (K.D. Hyde & J. Fröhl.) Phookamsak & K.D. Hyde, *P. africana* (D. Hawksw.) Phookamsak & K.D. Hyde, *P. bambusae* Phookamsak & K.D. Hyde, *P. longicolla* Phookamsak & K.D. Hyde, *P. papillata* (K.D. Hyde & J. Fröhl.) Phookamsak & K.D. Hyde and *P. thailandensis* Phookamsak et al. based on morphology and multigene phylogenetic analyses. Some of the species were previously treated in *Astrosphaeriella* Syd. & P. Syd. Maximum likelihood tree (Fig. 37) generated based on a combined LSU, SSU, ITS, RPB2 and TEF1-α dataset reveals that our new taxon clusters within *Pseudoastrosphaeriellaceae* sister to *Pseudoastrosphaeriella* with 63% ML and 0.95 BYPP statistical support. Tree topologies generated under ML and Bayesian criteria from combined datasets were congruent, whereas maximum parsimonious tree was varied, which showed that our taxon forms a clade between *Testudinaceae* Arx and *Tetraplosphaeriaceae* Kaz. Tanaka & K. Hiray. without any statistical support. Further comparison of LSU nucleotides between our taxon and *Pseudoastrosphaeriella thailandensis* (GenBank: KT955478) resulted in 62/871 (7.1%) base pair differences which confirms its placement as a new genus in *Pseudoastrosphaeriellaceae*.

Pseudoastrosphaeriellopsis shares morphological similarity with *Pseudoastrosphaeriella* in having immersed ascomata underneath the host epidermis, erumpent, uniloculate, coriaceous, brown, and short papillate asci, with trabeculate pseudoparaphyses (Phookamsak et al. 2015b). However, *Pseudoastrosphaeriellopsis* can be distinguished from *Pseudoastrosphaeriella* in having globose to subglobose ascomata, immersed in host tissue, with fusiform to broadly fusiform ascospores.

Pseudoastrosphaeriellopsis kaveriana resembles *Neotrematosphaeria biappendiculata* (Kaz. Tanaka et al.) Thambug. et al., but differs in having immersed ascomata, with pore-like ostiole, and ascospores lacking appendages, whereas, the latter has semi-immersed ascomata, with crest-like ostiole, and ascospores with appendages at both ends (Thambugala et al. 2015). *Biappendiculispora japonica* Thambug. et al. differs from *Pseudoastrosphaeriellopsis kaveriana* in having slit-like ostioles, bulbous pedicels and 7–9 transverse septa ascospores with appendages (Thambugala et al. 2015). *Pseudoastrosphaeriellopsis kaveriana* also shares similarities with *Trematosphaeria wegeliniana* L. Holm & K. Holm, *T. hydrophila* Sacc. and *T. crassisepta* Kaz. Tanaka et al. in having 5-septate ascospores and overlapping ascospore dimensions, but is clearly distinct in having immersed ascomata beneath the host epidermis, short papilla and light brown, fusiform to broadly fusiform, slightly curved ascospores (Tanaka et al. 2015). *Trematosphaeria wegeliniana* and *T. hydrophila* lack a detailed description from type material and their taxonomic position remains unclear (Tanaka et al. 2015).

Thambugala et al. (2015) transferred *Trematosphaeria terricola* G.S. Gong to *Alpestrisphaeria terricola* (G.S. Gong) Thambug. & K.D. Hyde and *Trematosphaeria biappendiculata* (KTC 1124) to the new genus *Neotrematosphaeria biappendiculata* based on their morphological resemblance to *Lophiostomataceae* and multigene phylogeny. Our combined multiloci phylogenetic analysis also reveals that taxonomic position of some species in *Trematosphaeria* remains unclear and this needs further collection and revision.

Pseudoastrosphaeriellopsis kaveriana Devadatha, Wanas., Jeewon & V.V. Sarma, ***sp. nov.***


62/-
77/1.00
Atrocalyx lignicola CBS122364
Atrocalyx bambusae MFLUCC 10-0558
Atrocalyx acutispora KT2436
100/1.00
Lophiotrema eburnoides KT14241
62/-
Lophiotrem fallopiae KT2748
Massarina albocarnis CBS119345
98/1.00
Cryptoclypeus oxysporus KT2772
Pseudocryptoclypeus yakushimensis KT2186
Lophiotremataceae
97/1.00
100/1.00
Cryptocoryneum longicondensatum KT2913
99/1.00
Cryptocoryneum paracondensatum KT3241
88/0.97
Cryptocoryneum japonicum KT3300
85/1.00
100/1.00
Cryptocoryneum pseudorilstonei CBS113641
Cryptocoryneum brevicondensatum yone152
Cryptocoryneaceae
96/-
Aquasubmersa japonica KT2862
93/0.96
Aquasubmersa japonica KT2863
100/1.00
Aquasubmersa japonica KT2813
Aquasubmersa mircensis MFLUCC 11-0401
Aquasubmersaceae
Hermatomyces tectonae MFLUCC 14-1142
100/1.00
Hermatomyces tectonae MFLUCC 14-1141
100/1.00
Hermatomyces tectonae MFLUCC 14-1140
Hermatomyces thailandica MFLUCC 14-1144
100/1.00
Hermatomyces thailandica MFLUCC 14-1143
Hermatomyces thailandica MFLUCC 14-1145
Hermatomycetaceae
76/-
Anteaglonium parvulum MFLUCC 14-0817
79/0.99
Anteaglonium parvulum MFLUCC 14-0815
63/1.00
Anteaglonium parvulum MFLUCC 14-0823
Anteaglonium parvulum MFLUCC 14-0821
100/1.00
Anteaglonium thailandicum MFLUCC 14-0816
Anteaglonium abbreviatum ANM925a
Anteaglonium globosum ANM9252
Pseudolophiotrema elymicola KT1450
Anteagloniaceae
78/1.00
Pseudotetraploa curviappendiculata HC4930
66/-
Tetraploa sasicola KT563
99/1.00
Polyplosphaeria fusca KT1616
Triplosphaeria maxima KT870
Quadricrura septentrionalis HC4983
Tetraplosphaeriaceae
74/0.96
Muritestudina chiangraiensis MFLUCC 17-2551
Neotestudina rosatii CBS 690.82
Verruculina enalia BCC 18402
Ulospora bilgramii CBS 101364
Lepidosphaeria nicotiae CBS 101341
74/0.96
Trematosphaeria wegeliniana CBS 123124
Angustospora nilensis MFLU 15-1511
Testudinaceae
100/1.00
Pseudoastrosphaeriella thailandensis MFLUCC 11-0144
100/1.00
Pseudoastrosphaeriella thailandensis MFLUCC 10-0553
100/1.00
Pseudoastrosphaeriella thailandensis MFLUCC 14-0038
100/1.00
95/1.00
Pseudoastrosphaeriella longicolla MFLUCC 11-0171
Pseudoastrosphaeriella bambusae MFLUCC 11-0205
63/0.96
Pseudoastrosphaeriella africana MFLUCC11-0176
100/1.00
Pseudoastrosphaeriallopsis kaveriana NFCCI-4221
Pseudoastrosphaeriellaceae
90/0.97
Neotrematosphaeria biappendiculata KTC1124
100/1.00
Neotrematosphaeria biappendiculata JCM12849
85/1.00
Neotrematosphaeria biappendiculata KTC975
61/-
Lophiostoma arundinis CBS 621.86
Lophiostoma crenatum CBS 629.86
100/1.00
Trematosphaeria heterospora HKUCC 10704
Alpestrisphaeria terricola SC-12
Lophiostomataceae
78/-
Trematosphaeria grisea UTHSC-DI 16-286
81/-
Trematosphaeria grisea UTHSC-DI 16-354
100/1.00
90/0.99
Trematosphaeria grisea CBS 120271
Trematosphaeria grisea UTHSC-DI 16-237
100/1.00
Trematosphaeria grisea CBS 332.50
100/1.00
Trematosphaeria grisea UTHSC-DI 16-281
Trematosphaeria pertusa CBS122368
Trematosphaeriaceae
100/1.00
Amniculicola immersa CBS123083
Amniculicola parva CBS 123092
Amniculicolaceae
Trematosphaeria hydrela HKUCC 10666
100/1.00
Gloniopsis calami MFLUCC 15-0739
Hysterium rhizophorae NFCCI-4250
Outgroup
0.05

◀**Fig. 37** Phylogram generated from maximum likelihood analysis based on LSU, SSU, ITS, RPB2 and TEF1-α sequence dataset of representative families in *Pleosporales* showing phylogenetic affinities of *Pseudoastrosphaeriellopsis kaveriana*. *Gloniopsis calami* (MFLUCC 15-0739) and *Hysterium rhizophorae* (NFCCI-4250) were selected as the outgroup taxa. Bootstrap support values for maximum likelihood (green), equal to or greater than 60% and Bayesian posterior probabilities (purple) equal to or greater than 0.95 are given above each branch, respectively. The new isolate is in blue. Type strains are in bold

Index Fungorum number: IF555791; *Facesoffungi number*: FoF05707, Fig. 38

Etymology: Specific epithet in reference to the river Kaveri.

Holotype: AMH-9912

Saprobic on decaying stems and twigs of *Avicennia marina* and *Suaeda monoica*, black spots ascomata, with short necks on host surface. **Sexual morph** *Ascomata* 225–335 µm high, 220–345 µm diam., immersed to erumpent, globose to subglobose, solitary to gregarious, coriaceous, brown, short papillate, ostiolate. *Ostioles* 110–165 µm long, 50–90 µm diam., central, cylindrical, straight to oblique, with ostiolar canal lined by hyaline periphyses. *Peridium* 15–25 µm wide, less developed at the base compared to the sides and top, composed of two layers, inner stratum with 3–5 layers of hyaline to pale brown compressed cells of *textura angularis*, outer stratum with compact brown polygonal cells of *textura angularis*, fused with the host cells and fungal tissue. *Hamathecium* composed of numerous, 1–3 µm wide, filamentous, septate, branched, hyaline pseudoparaphyses, embedded in a gelatinous matrix, anastomosing between and above the asci. *Asci* 85–145 × 15–18 µm ($\bar{x}$ = 108 × 17 µm, n = 40), 8-spored, bitunicate, cylindric-clavate to clavate, with a short, thick pedicel, apically rounded and thickened, with an ocular chamber. *Ascospores* 25–40 × 5–10 µm ($\bar{x}$ = 34 × 7 µm, n = 50), overlapping 1–2-seriate, brown, fusiform to broadly fusiform, slightly curved with round to acute ends, broader in the middle and tapering towards the ends, 5-septate, slightly constricted at the 3rd septum and rarely at other septa, smooth-walled, hyaline at both ends, from the central septum upper half is shorter and lower half is longer, lacking guttules and mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinated on SWA within 24 h, germ tubes arising from terminal ends of the ascospore. Colonies on MEA reaching 30–45 mm diam. after 25 days of incubation at room temperature, pale olive buff to olive buff, reverse brown, velvety, surface raised, irregular, with light yellow exudates.

Material examined: INDIA, Tamil Nadu, Tiruvarur, Muthupet mangroves (10.4°N 79.5°E), on decaying stems and twigs of *Avicennia marina* (Forssk.) Vierh. (*Acanthaceae*), 28 November 2015, B. Devadatha, AMH-9912 (**holotype**); **isotype** at Pondicherry University, Puducherry), ex-type living culture, NFCCI-4221; *ibid.* on stems and twigs of *Suaeda monoica* Forssk. ex J.F. Gmel), 28 November 2015, B. Devadatha, PUHD33.

GenBank numbers: ITS = MG947599, LSU = MG947595, SSU = MG947598, TEF1-α = MG968955, RPB2 = MG948547.

Roussoellaceae Jian K. Liu et al.

We follow the latest treatment and updated accounts of *Roussoellaceae* in Liu et al. (2014), Dai et al. (2017a), Tibpromma et al. (2017), Hyde et al. (2018b), Jayasiri et al. (2019) and Jiang et al. (2019). Phylogenetic affinities of the family were discussed by Jaklitsch and Voglmayr (2016) where *Roussoellaceae* was treated as a synonym of *Thyridariaceae*. However, Tibpromma et al. (2017) reinstated *Roussoellaceae* based on multigene phylogenetic analysis which showed *Roussoellaceae* is a well-resolved family in *Pleosporales* and this was concurred by Wanasinghe et al. (2018), Wijayawardene et al. (2018a), Jayasiri et al. (2019) and Jiang et al. (2019). Seven genera were accepted in this family based on molecular data and morphological characteristics (Wijayawardene et al. 2018a).

Taxonomic status of genera in *Roussoellaceae* is doubtful and needs to be clarified due to taxa in these genera have similar conidial characters and phylogeny has always shown that they are monophyletic (Liu et al. 2014; Dai et al. 2017a; Tibpromma et al. 2017; Hyde et al. 2018b; Jiang et al. 2019). However, *Neoroussoella* Phookamsak et al. and *Roussoellopsis* I. Hino & Katum. are distinct from *Roussoella* but these two genera usually cluster with *Roussoella* species (Liu et al. 2014; Phookamsak et al. 2014a; Dai et al. 2017a; Tibpromma et al. 2017; Hyde et al. 2018b; Jiang et al. 2019). Wanasinghe et al. (2018) introduced *Pseudoneoconiothyrium* (Phukhams. et al.) Phukhams. et al. and *Pararoussoella* to accommodate roussoella-like taxa in *Thyridariaceae*. We use increased taxon sampling in our phylogenetic analysis (Fig. 39) and show that the two genera erected by Wanasinghe et al. (2018), cluster with *Roussoella* species in *Roussoellaceae*.

Jayasiri et al. (2019) clarified *Neoroussoella* based on multigene phylogenetic analysis coupled with morphological characteristics, *N. entadae* Jayasiri et al. and *N. leucaenae* Jayasiri et al. were introduced. *Roussoella solani* Crous & M.J. Wingf. was transferred to *Neoroussoella* as *N. solani* (Crous & M.J. Wingf.) Jayasiri & K.D. Hyde. In addition, *Roussoella mukdahanensis* Phookamsak et al. was transferred to *Pararoussoella* as *P. mukdahanensis* (Phookamsak et al.) Jayasiri & K.D. Hyde. In this study, *Neoroussoella heveae* Senwanna et al. and *Roussoella elaeicola* Konta & K.D. Hyde are introduced as novel species based on morphological characteristics coupled with multigene phylogenetic analysis. In addition, *Neoroussoella leucaenae* is described on *Hevea brasiliensis* Müll.Arg. from Thailand for the first time.

Neoroussoella J.K. Liu et al.

We follow the latest treatment and updated accounts of *Neoroussoella* in Jayasiri et al. (2019).

Neoroussoella heveae Senwanna, Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555287; *Facesoffungi number*: FoF04825, Fig. 40

Etymology: Name refers to the host genus *Hevea*, from which the fungus was collected.

Holotype: MFLU 17-1983

Saprobic on Para rubber (*Hevea brasiliensis*). **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 90–130 µm high, 115–180 µm diam., pycnidial, immersed, visible as small, brown to black dots on the host surface, solitary, scattered, globose, uni-loculate, glabrous, ostiole not observed. *Conidiomata walls* 7–15 µm wide, thick-walled, composed of several cell layers of dark brown to black, pseudoparenchymatous cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–7 × 2–5 µm ($\bar{x}$ = 5.2 × 3.4 µm, n = 15), lining the inner cavity, difficult to distinguish from pycnidial wall, enteroblastic, phialidic, integrated, simple, short, hyaline, ampulliform to doliiform, thin-walled, smooth. *Conidia* 2.5–5 × 2–4 µm ($\bar{x}$ = 4 × 3, n = 50), globose or subglobose to ellipsoidal, initially hyaline, becoming brown to dark brown, aseptate, with one or two guttules, rough-walled, verruculose.

Culture characteristics: Colonies on MEA reaching 20–25 mm diam. after 2 weeks at 25–30 °C, colony from above, circular, medium dense, edge entire, velvety to woolly, white at the margin, white to yellowish in the middle, geenish grey to grey at the centre; from below, white at the margin, greenish grey at the centre, with concentric rings radiate.

Material examined: THAILAND, Phayao Province, Muang District, Mae Ka, on twig of *Hevea brasiliensis* (*Euphorbiaceae*), 5 December 2016, C. Senwanna, RBPY018 (MFLU 17-1983, **holotype**), ex-type living culture, MFLUCC 17-0338.

GenBank numbers: ITS = MH590693, LSU = MH590689, SSU = MH590691.

Notes: *Neoroussoella heveae* is introduced based on morphological and phylogenetic evidence. Our strain forms a separate lineage, clusters with *Neoroussoella* species (78% ML; Fig. 39). *Neoroussoella heveae* differs from the asexual morph of *Neoroussoella* species in having verruculose conidia, whereas, other *Neoroussoella* species have smooth-walled conidia.

Neoroussoella leucaenae Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 1–186 (2019), Fig. 41

Holotype: THAILAND, Krabi Province, Mueang Krabi District, on decaying pod carpel of *Leucaena* sp. (*Fabaceae*), 31 August 2017, S.C. Jayasiri, C 356 (MFLU 18-2159; MFLU 18-2160, isotype), ex-type living culture MFLUCC 18-1544, KUMCC 18-0266.

Saprobic on dead twigs of *Hevea brasiliensis*. **Sexual morph** *Ascomata* 130–195 µm high, 150–170 µm diam., visible as raised, aggregated, small, dark brown to black dots on the host surface, immersed, erumpent through host epidermis by minute papilla, scattered, solitary, sometimes gregarious, globose to subglobose, occasionally irregular in shape, uni-loculate, glabrous, ostiole central with minute papilla. *Peridium* (7–)10–18 µm, composed of several layers, of hyaline to dark brown pseudoparenchymatous cells, inner layer comprising flattened, hyaline to brown cells, arranged in a *textura prismatica* to *textura angularis*, outer layer comprising thick, dark brown to black cells, arranged in a *textura angularis*. *Hamathecium* composed of dense, 1–3 µm wide, hyaline, septate, filamentous, anastomosed pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* (35–)42–68(–75) × 4–5(–6) µm ($\bar{x}$ = 53 × 5.5, n = 15), 8-spored, bitunicate, cylindrical, with a short pedicel, apically rounded, with an indistinct ocular chamber. *Ascospores* 7–10(– 15) × 3–4.5(– 6.5) µm ($\bar{x}$ = 9.4 × 4.4, n = 40), overlapping 1-seriate, hyaline when young and medium to dark brown when mature, ellipsoidal to ovoid, with rounded ends, 1-septate, constricted at the septum, rough-walled, with two guttules, and longitudinal striations. **Asexual morph** See Jayasiri et al. (2019).

Culture characteristics: Colonies on PDA reaching 15–25 mm diam. after 3 weeks at 25–30 °C, circular, medium dense, edge entire, velvety; from above, light grey at the margin, white to light grey at the centre; from below, white at the margin, light to dark brown at the centre.

Material examined: THAILAND, Phayao Province, Muang District, Mae Ka, on dead twigs of *Hevea brasiliensis*, 3 January 2017, C. Senwanna, RBPY028 (MFLU 17-1985), living culture, MFLUCC 17-0346.

Known hosts and distribution: On decaying pod carpel of *Leucaena* sp. and *Pterocarpus* sp., *Hevea brasiliensis* (Thailand) (Jayasiri et al. 2019; this study).

GenBank numbers: ITS = MH590694, LSU = MH590690, SSU = MH590692, TEF1-α = MH590688.

Notes: *Neoroussoella leucaenae* (MFLU 17-1985) is found on Para rubber in Thailand for the first time. Phylogenetically our strain (MFLUCC 17-0346; Fig. 39) clusters with the type strain of *N. leucaenae* (MFLUCC 18-1544) and strain MFLUCC 17-0927 with moderate support (76% ML and 1.00 BYPP; Fig. 39). There is different only one and three nucleotide base positions in ITS

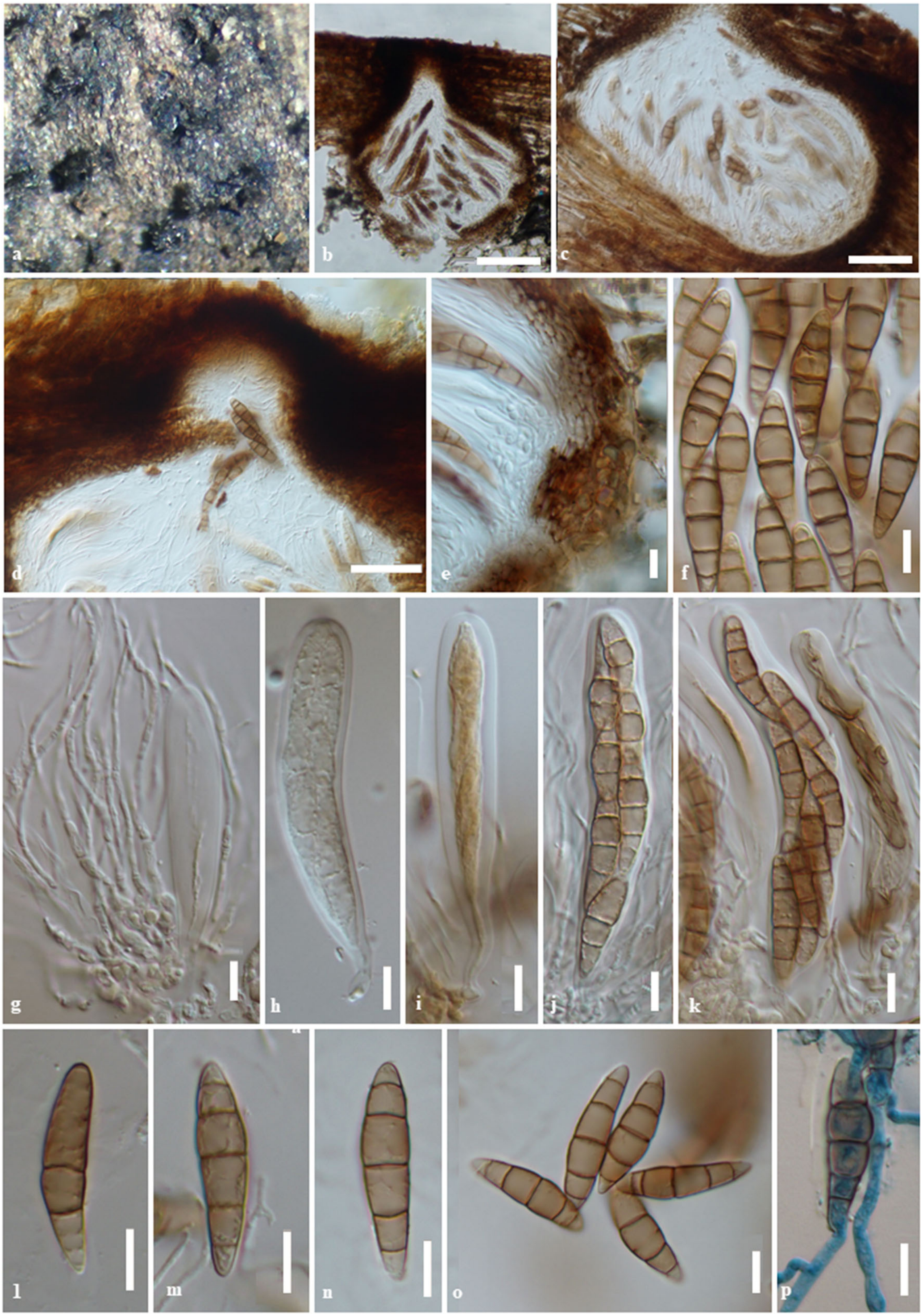


Fig. 38 ***Pseudoastrosphaeriellopsis kaveriana*** (AMH-9912, **holotype**). **a** Ascomata semi-immersed and released ascospores on the decaying wood of *Avicennia marina*. **b, c** Longitudinal sections of ascoma. **d** Ostiole. **e** Section of peridium comprising hyaline to pale brown cells of *textura angularis*. **g** Cellular pseudoparaphyses. **h–k** Immature and mature asci. **f, l–o** Ascospores. **p** Germ tubes developed from terminal ends of ascospore. *Scale bars* **b** = 100 µm, **c, d** = 50 µm, **e–p** = 10 µm

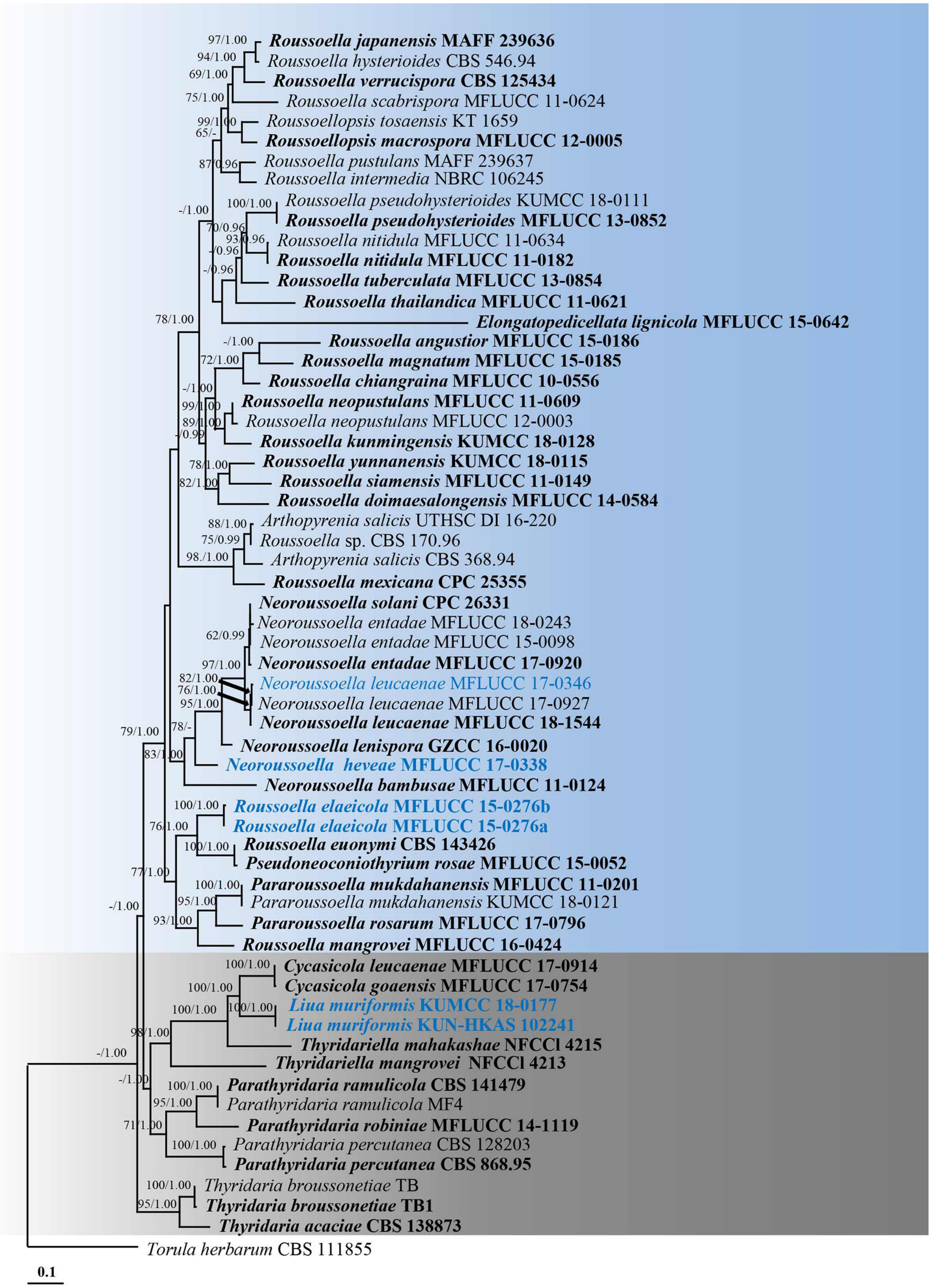


Fig. 39 Maximum likelihood phylogenetic tree based on a combined LSU, SSU, ITS, TEF1-α and RPB2 sequence dataset. The tree is rooted to *Torula herbarum* (CBS 111855). Bootstrap support values for ML (left) equal to or greater than 60% and the Bayesian posterior probabilities (right), equal to or greater than 0.95 BYPP are indicated above the nodes. Ex-type strains are in bold and the newly generated sequences are indicated in blue

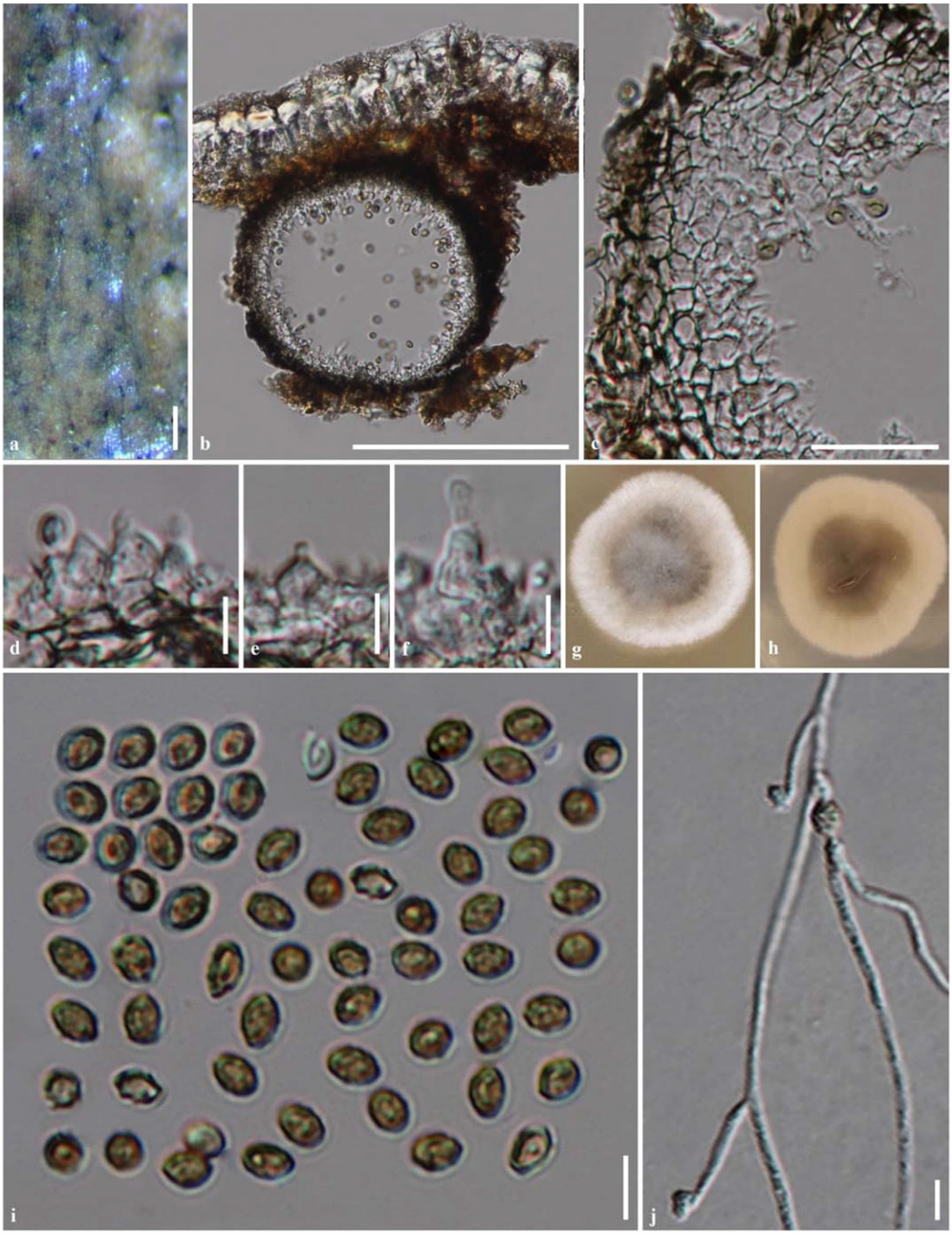


Fig. 40 ***Neoroussoella heveae*** (MFLU 17-1983, **holotype**). **a** Conidiomata immersed in host substrate. **b** Section through the conidioma. **c** Conidioma wall. **d–f** Conidiogenous cells. **g, h** Colony on MEA (**g** = from above, **h** = from below). **i** Conidia. **j** Germinated conidium. *Scale bars* **a** = 200 µm, **b** = 100 µm, **c** = 20 µm, **d–j** = 5 µm

and TEF1-α among *N. leucaenae* strains MFLUCC 18-1544, MFLUCC 17-0927 and MFLUCC 17-0346, which confirms that they are conspecific.

Roussoella Sacc.

We follow the latest treatment and updated accounts of *Roussoella* in Liu et al. (2014), Tibpromma et al. (2017), Hyde et al. (2018b) and Jiang et al. (2019).

Roussoella elaeicola Konta & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555291; *Facesoffungi number*: FoF04834, Fig. 42

Etymology: Name reflects the host genus *Elaeis*.

Holotype: MFLU 15-0022

Saprobic on dead petiole of *Elaeis guineensis*. **Sexual morph** *Ascomata* 315–410 µm high, 325–350 µm diam., solitary, immersed in host tissue, erumpent through the host surface with minute papilla, globose to subglobose, uni-loculate, ostiole central with papilla, lacking periphyses. *Peridium* 25–70 µm wide, thin-walled, composed of several layers of small, compressed, hyaline to light brown pseudoparenchymatous cells of *textura angularis*, outer layers fusing with the host. *Hamathecium* composed of dense, 0.9–2.8 µm broad, filamentous, septate, trabeculate pseudoparaphyses, embedded in mucilage. *Asci* 70–140 × 6–9 µm ($\bar{x}$ = 100 × 8 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, pedicellate, rounded apex with an indistinct ocular chamber. *Ascospores* 10–15 × 3–6 µm ($\bar{x}$ = 12 × 4 µm, n = 30), slightly overlapping 1-seriate, hyaline to light brown when immature, ellipsoid with obtuse ends, becoming dark brown at maturity, 1-septate, with large guttules in each cell, constricted at the septum, rough-walled with poroid ornamentation, surrounded by mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinated on MEA within 24 h with germ tube was produced from both cells. Colony on MEA, at first whitish, felty, azonate, with fluffy margin, after incubation for 3–4 weeks appear circular, with fluffy, dense, pale brown mycelium in the middle and dense mycelium in the outer ring on the surface with smooth margin; from below, brown to dark brown in the middle and pale brown to yellow at the margin hyphae, septate, branched, and smooth.

Material examined: THAILAND, Chiang Rai Province, on dead petiole of *Elaeis guineensis* (*Arecaceae*), 25 November 2014, S. Konta, HR02d (MFLU 15-0022, **holotype**), ex-type living culture, MFLUCC 15-0276.

GenBank numbers: ITS = MH742329, LSU = MH742326 (MFLUCC 15-0276a); ITS = MH742330, LSU = MH742327 (MFLUCC 15-0276b); LSU = MH742328, SSU = MH742331 (MFLUCC 15-0276c).

Notes: Roussoella elaeicola (MFLU 15-0022) is introduced as a novel species and it was collected from oil palm (*Elaeis guineensis*) in Chiang Rai, Thailand for the first time. Multigene phylogenetic analyses show that *R. elaeicola* has a close relationship with *R. euonymi* Crous & Akulov and *Pseudoneoconiothyrium rosae* Phukhams et al. (Fig. 39) which were collected from *Euonymus europaeus* L. (*Celastraceae*) in Ukraine and on dead aerial spines of *Rosa canina* L. (*Rosaceae*) in Italy, respectively (Crous et al. 2018; Wanasinghe et al. 2018). However, we could not compare the morphological characteristics of our new species with these two species as *Roussoella euonymi* and *Pseudoneoconiothyrium rosae* are only known as asexual morph species, while our new taxon is represented by the sexual morph. One of the distinctive characters of *Roussoella elaeicola* is the distinctive trabeculate pseudoparaphyses (*sensu* Liew et al. 2000). A comparison of ITS nucleotide base pairs indicates that *Roussoella elaeicola* differs from *R. euonymi* and *Pseudoneoconiothyrium rosae* in 37/513 bp (7.2%) and 38/514 bp (7.4%). *Roussoella elaeicola* can be distinguished from other *Roussoella* species by its ascospores having poroid ornamentation, similar to *R. scabrispora* (Liu et al. 2014). However, *R. elaeicola* and *R. scabrispora* form a distinct lineage in *Roussoellaceae*.

Sulcatisporaceae Kaz. Tanaka & K. Hiray.

Sulcatisporaceae was introduced by Tanaka et al. (2015) to accommodate three genera: *Magnicamarosporium* Kaz. Tanaka & K. Hiray., *Neobambusicola* Crous & M.J. Wingf. and *Sulcatispora* Kaz. Tanaka & K. Hiray. and is typified by *Sulcatispora*. The family is characterized by globose to subglobose, ostiolate, papillate ascomata, a thick-walled peridium with a poorly developed base, and trabeculate, anastomosed pseudoparaphyses, bitunicate, clavate asci, and hyaline, broadly fusiform, 1-septate ascospores with an entire sheath. The asexual morphs are coelomycetous, with ellipsoid to subglobose, hyaline to dark brown, muriform or phragmosporous conidia (Crous et al. 2014b; Tanaka et al. 2015; Phukhamsakda et al. 2017). Five species from three genera are accommodated in this family. We introduce a new species, *Neobambusicola brunnea* (MFLU 18-1393) based on a phylogenetic analysis of a combined LSU and ITS sequence dataset (Fig. 43).

Neobambusicola Crous & M.J. Wingf.

Neobambusicola was introduced as a monotypic genus by Crous et al. (2014b) and is typified by *N. strelitziae* Crous & M.J. Wingf., isolated from leaves of *Strelitzia nicolai* in South Africa. The genus was represented by its asexual morph and is characterized by erumpent, globose, dark brown, ostiolate conidiomata, a thin-walled of peridium, subcylindrical to ampulliform, phialidic conidiogenous cells and hyaline to olivaceous, fusoid-ellipsoid, smooth-walled, 1-septate conidia with hyaline, smooth, guttulate to granular, aseptate, subglobose to subcylindrical microconidia (Crous et al. 2014b). Crous et al. (2014b) treated the genus in *Bambusicolaceae*. Tanaka et al. (2015) introduced a new family *Sulcatisporaceae* to accommodate *Neobambusicola*, *Magnicamarosporium* and *Sulcatispora*. Only *Neobambusicola strelitziae* was accommodated in *Neobambusicola*, but we introduce a second species *N. brunnea* which is represented by the sexual morph.

Neobambusicola brunnea Y. Chen & Norphanphoun, *sp. nov.*

Index Fungorum number: IF555293; *Facesoffungi number*: FoF05708, Fig. 44

Etymology: The specific epithet "*brunnea*" refers to the brownish ascospores.

Holotype: MFLU 18-1393

Saprobic on dead stem of herbage. **Sexual morph** *Ascomata* 80–205 µm high, 90–260 µm diam., semi-immersed, blackish, irregular in shape, scattered on surface of stem, uni-loculate, glabrous, ostiolate, apapillate. *Ostioles* 35.5–68 µm diam., dark, circular and sunken at the apex of ascoma. *Peridium* 30–40 µm thick, two layered, thick-walled, outer layer irregular, comprising dark brown cells of *textura angularis* and inner layer slightly, irregular of light brown cells. *Hamathecium* comprising 1–2 µm wide, filamentous, branched or simple, septate, anastomosed, cellular pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* 70–90 × 8–10 µm ($\bar{x}$ = 83.6 × 9 µm, n = 10), 4- or 8-spored, bitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded, with an ocular chamber. *Ascospores* 11–18 × 5–6 µm ($\bar{x}$ = 12.9 × 5.8 µm, n = 20), 1-seriate, brown to dark brown, oblong to ellipsoidal, with rounded ends, 1-septate, slightly constricted at the septum, smooth-walled, with small guttules. **Asexual morph** Undetermined.

Material examined: CHINA, Guizhou Province, Qiandongnan Miao and Dong Autonomous Prefecture, Huangping District, on dead stem of herbage, 10 September 2017, Y. Chen, QDN001 (MFLU 18-1393, **holotype**).

GenBank numbers: ITS = MH644792, LSU = MH644791.

Notes: DNA was extracted directly from the ascomata, and a phylogenetic analysis of combined ITS and LSU sequence dataset shows that *Neobambusicola brunnea* is closely related to *N. strelitziae* with moderate support (87% ML; Fig. 43). A comparison of ITS and LSU pair wise shows that *N. brunnea* differs from *N. strelitziae* in 31 and 40 base positions, respectively. Therefore, *N. brunnea* is introduced as a novel species and this is the first report of the sexual morph of *Neobambusicola*.

Thyridariaceae Q. Tian & K.D. Hyde

Thyridariaceae was introduced by Hyde et al. (2013) to accommodate the genus *Thyridaria* Sacc. and is typified by *T. broussonetiae* (Sacc.) Traverso. The familial concept was solitary or gregarious, immersed to erumpent, globose, coriaceous ascomata, in valsoid configurations, with stromatic, pigmented, prosenchymatous tissues and ostioles with a disc-like ostiolar canal. Asci are fissitunicate, cylindrical to subclavate, pedicellate, with trabeculate pseudoparaphyses and ascospores are pigmented, ellipsoidal to fusiform and verruculose, with transverse eusepta or distosepta, and form coelomycetous *Cyclothyrium* asexual morphs (Hyde et al. 2013; Jaklitsch and Voglmayr 2016). Jaklitsch and Voglmayr (2016) excluded *Cyclothyrium* from *Thyridariaceae* and the genus was tentative placed in *Pleosporales*, genera *incertae sedis* (Wijayawardene et al. 2018a). Furthermore, they also synonymized *Roussoellaceae* under *Thyridariaceae* and accepted *Neoroussoella*, *Thyridaria*, *Roussoella*, *Roussoellopsis* and *Parathyridaria* Jaklitsch & Voglmayr. However, Tibpromma et al. (2017) reinstated *Roussoellaceae* and this was followed by subsequent authors (Hyde et al. 2018b; Wanasinghe et al. 2018; Wijayawardene et al. 2018a; Jayasiri et al. 2019; Jiang et al. 2019). Recently, Wanasinghe et al. (2018) introduced three new genera in *Thyridariaceae* viz. *Cycasicola* Wanas et al., *Pseudoneoconiothyrium* and *Pararoussoella* Wanas et al. However, in the present study *Pseudoneoconiothyrium* and *Pararoussoella* cluster with other *Roussoella* species in *Roussoellaceae*. Devadatha et al. (2018) also introduced a new genus *Thyridariella* Devadatha et al. in *Thyridariaceae*. *Thyridariella* clustered with *Cycasicola* in our study (Fig. 39). However, these two genera are represented by different morphs and we therefore, treat them as different genera until a link between these two genera is proven. In this study, we introduce a novel genus *Liua* to accommodate a novel species *Liua muriformis* in *Thyridariaceae* based on morphological distinctiveness and phylogenetic support.

Liua Phookamsak & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF556175; *Facesoffungi number*: FoF05709

Etymology: In honour of Jian-Kui Liu, for his excellent work on taxonomic revision of Dothideomycetes.

Saprobic on *Lonicera maackii*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* pycnidial, scattered, solitary, immersed, slightly raised, visible as small black dot on host surface, uni-loculate, globose to subglobose, glabrous, dark brown to black, ostioles central, apapillate, with pore-like opening. *Conidiomata walls* thin-walled, of equal thickness, composed of 3–5 cell layers, of flattened, brown to dark brown, pseudoparenchymatous cells, arranged in a *textura angularis* to *textura prismatica*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, phialidic, discrete, determinate, ampulliform to cylindrical, unbranched, aseptate, occasionally 1–2-septate, hyaline, smooth, arising from the inner cavity of the conidioma wall. *Conidia* phragmosporous to muriform, dark brown, oblong to ellipsoidal, or obovoid, (2–)3-transversely septate, with (0–)3 longitudinal septa, slightly constricted at the septa, smooth-walled.

Type species: *Liua muriformis* Phookamsak, H.B. Jiang & K.D. Hyde

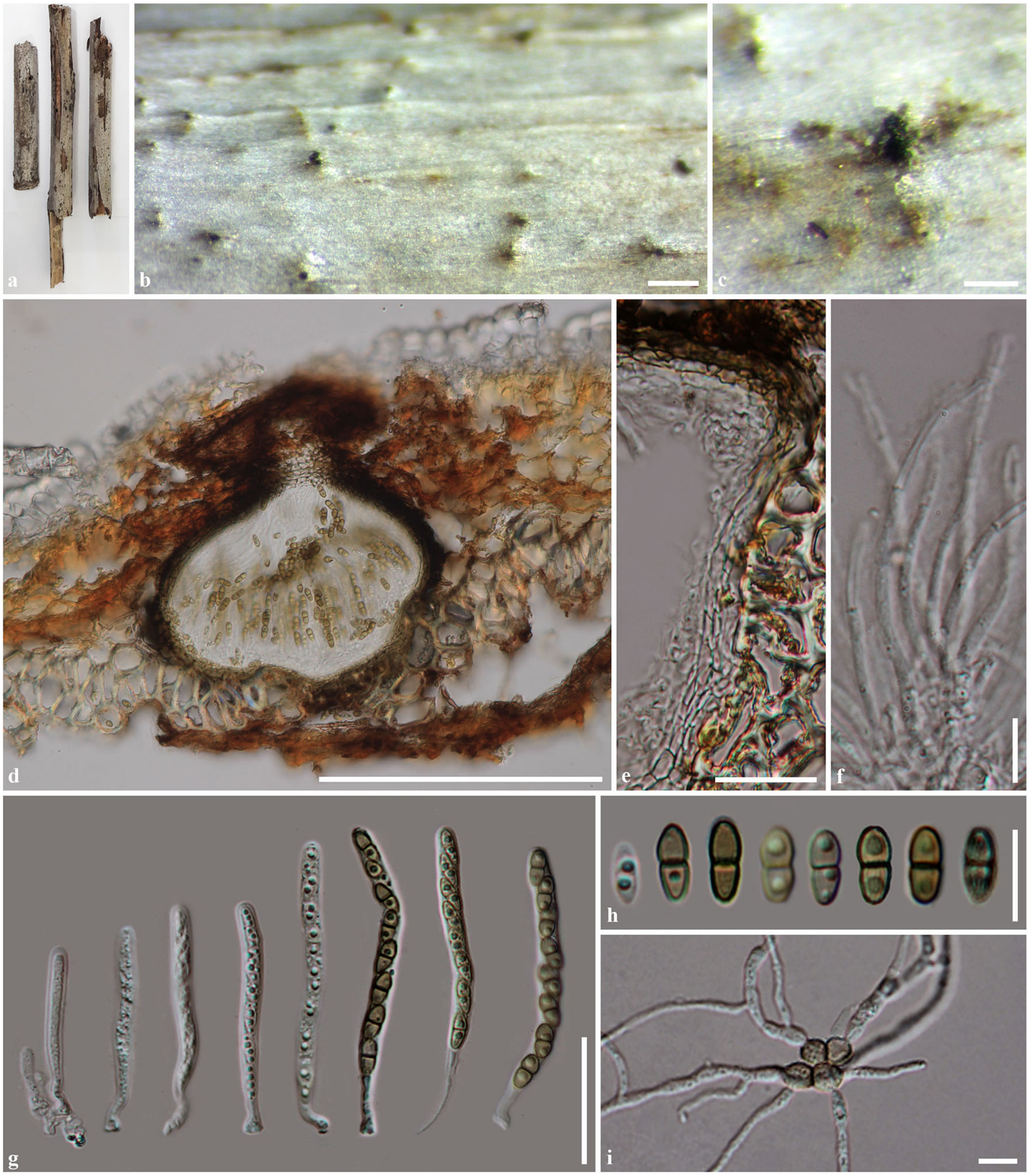
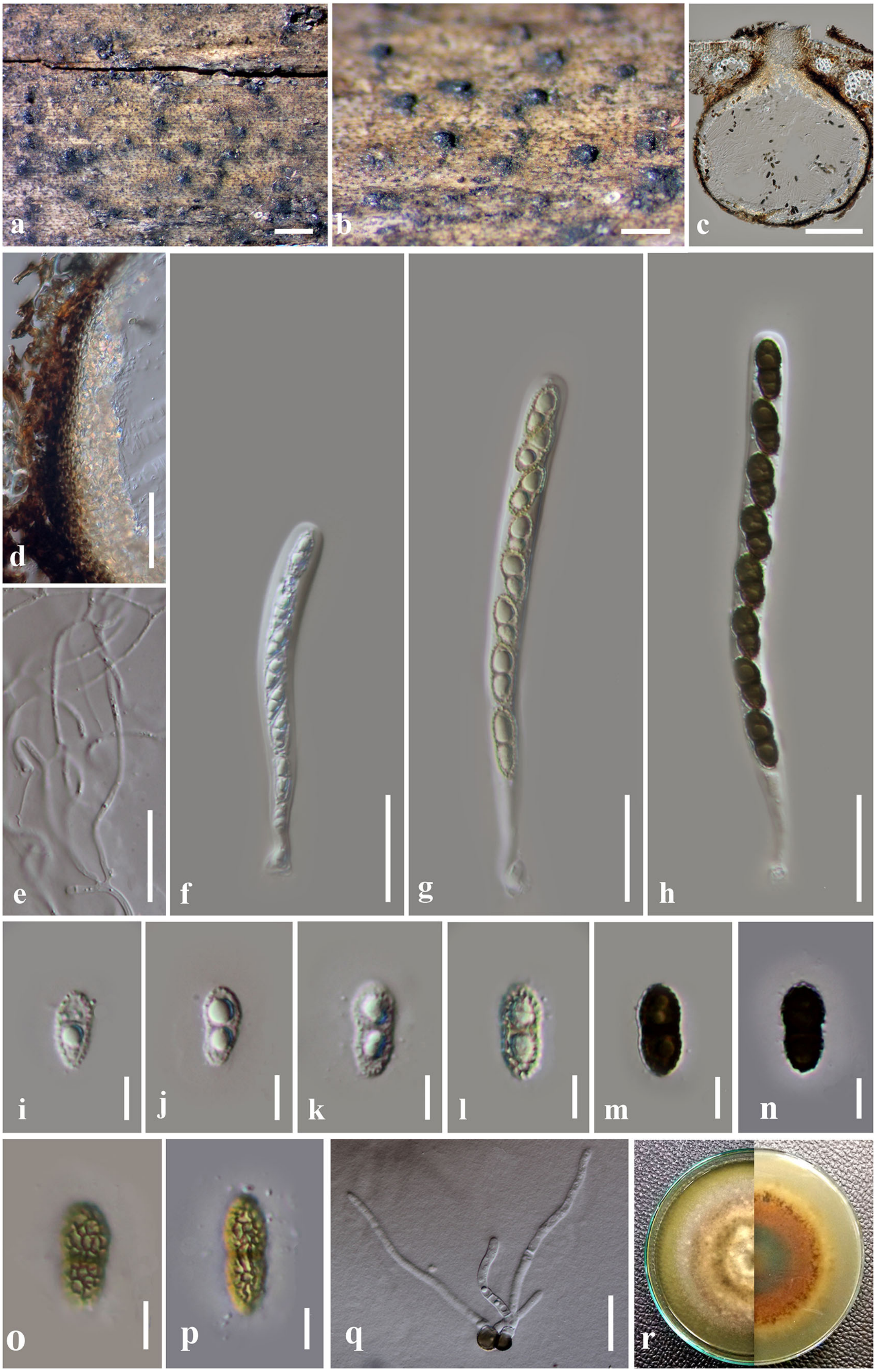


Fig. 41 ***Neoroussoella leucaenae*** (MFLU 17-1985). **a–c** Habit on substrate. **d** Section through ascoma. **e** Peridium. **f** Pseudoparapyses. **g** Asci. **h** Ascospores. **i** Germinated ascospores. *Scale bars* **b–d** = 200 µm, **g** = 30 µm, **e** = 20 µm, **f, h, i** = 10 µm

Notes: In the NCBI BLASTn search of ITS sequences, *Liua muriformis* most closely matches with leaf litter ascomycete (strain its072) with 95% similarity and *Cycasicola goaensis* Wanas. et al. (MFLU 17-0581) with 93% similarity. Multigene phylogenetic analyses based on a combined LSU, SSU, ITS, TEF1-α and RPB2 sequence dataset show that *L. muriformis* forms a sister clade with *C. goaensis* and *C. leucaenae* Jayasiri et al. with high support (100% ML and 1.00 BYPP) and clusters with other two *Thyridariella* species in *Thyridariaceae*. *Liua muriformis* differs from *C. goaensis* and *C. leucaenae* in having dark brown, muriform or phragmosporous conidia, whereas, *C. goaensis* and *C. leucaenae* have pale yellowish, aseptate conidia (Wanasinghe et al. 2018; Jayasiri et al. 2019).

Fig. 42 ***Roussoella elaeicola*** (MFLU 15-0022, **holotype**). **a**, **b** Ascomata on host substrate. **c** Section of ascoma. **d** Peridium. **e** Pseudoparaphyses. **f–h** Asci. **i–l** Immature ascospores. **m, n** Mature ascospores. **o, p** Ascospores with poroid ornamentation. **q** Germinated ascospore. **r** Culture characteristic on MEA from above and below. *Scale bars* **a**, **b** = 1000 µm, **c** = 100 µm, **d** = 50 µm, **e–h**, **q** = 20 µm, **i–p** = 5 µm ▶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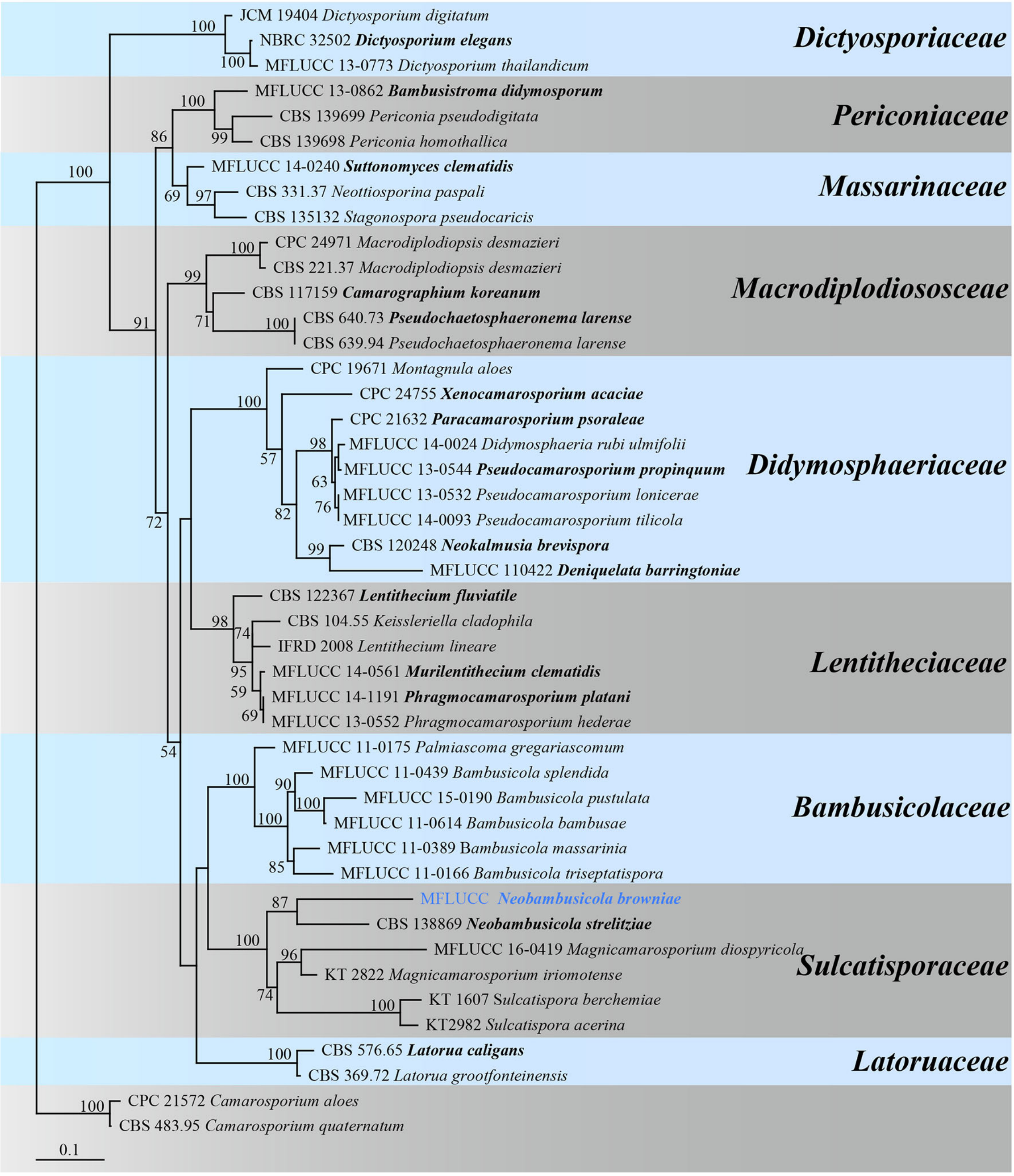


Fig. 43 Phylogram generated from RAxML analysis based on a combined LSU and ITS sequence dataset. Tree is rooted with *Camarosporium aloes* (CPC 21572) and *C. quaternatum* (CBS 483.95). Bootstrap values ≥ 50% are indicated at the nodes. The new species is indicated in blue. Ex-type strains are indicated in bold

Therefore, we introduce *Liua* as a new genus to accommodate *L. muriformis* based on its morphological distinct with *Cycasicola*.

Liua muriformis Phookamsak, H.B. Jiang & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556176; *Facesoffungi number*: FoF05710, Fig. 45

Etymology: The specific epithet "*muriformis*" refers to the holotype having muriform ascospores

Holotype: KUN-HKAS 102241

Saprobic on *Lonicera maackii*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 80–150 µm high, 110–190 µm diam., pycnidial, scattered, solitary, immersed, slightly raised, visible as small black dot on host surface, uni-loculate, globose to subglobose, glabrous, dark brown to black, ostioles central, apapillate, with pore-like opening. *Conidiomata walls* 7–17 µm wide, thin-walled, of equal thickness, composed of 3–5 cell layers, of flattened, brown to dark brown, pseudoparenchymatous cells, arranged in a *textura angularis* to *textura prismatica*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* (3–)5–12.5(–17.5) × (2–)5–10 µm l/w ($\bar{x}$ = 8.2 × 5.4 µm, n = 30), holoblastic, phialidic, discrete, determinate, ampulliform to cylindrical, unbranched, aseptate, occasionally 1–2-septate, hyaline, smooth, arising from the inner cavity of the conidioma wall. *Conidia* (12.5–)13–15(–17) × 7–9(–10) µm l/w ($\bar{x}$ = 14.4 × 8.2 µm, n = 50), phragmosporous to muriform, dark brown, oblong to ellipsoidal, or obovoid, (2–)3-transversely septate, with (0–)3 longitudinal septa, slightly constricted at the septa, smooth-walled.

Culture characteristics: Colonies on PDA, reaching 30–32 mm diam. after 3 weeks at room temperature (20–30 °C). Colony dense, circular, flattened to slightly raised, surface rough, radially furrowed at the centre, smooth at the margin, with edge entire, velvety; from above, greyish green at the margin, pale yellowish to yellowish green at the centre; from below, dark green to greenish grey; not producing pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, on dead hanging branches of *Lonicera maackii*, 20 April 2017, R. Phookamsak, KIB032 (KUN-HKAS 102241, **holotype**), ex-type living culture, KUMCC 18-0177.

GenBank numbers: ITS = MK433599, LSU = MK433598, SSU = MK433595, TEF1-α = MK426798, RPB2 = MK426799 (KUMCC 18-0177); ITS = MK433600, LSU = MK433592 (KUN-HKAS 102241, KIB0032F).

Dothideomycetes, orders *incertae sedis*

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

Asterinaceae Hansf.

Asterinaceae was introduced by Hansford (1946) to accommodate obligate biotrophic, or epiphytic fungi which formed web-like, black colonies on the upper and lower surfaces of leaves, or stems, with or without appressoria of external mycelium, superficial, dimidiate ascomata with radiating star-like openings, fissitunicate asci, cylindrical, 2–6-celled, yellowish to brown ascospores and forming both coelomycetous and hyphomycetous asexual morphs (Hyde et al. 2013; Hongsanan et al. 2014, 2016; Guatimosim et al. 2015). Twenty-one genera are accepted in the family (Wijayawardene et al. 2018a). Updated molecular phylogeny and their evolutionary relationships based on molecular clock evidence were provided by Hongsanan et al. (2016) and Liu et al. (2017a).

Lembosia Lév.

The genus *Lembosia* was described by Léveillé (1845), based on the type species, *L. tenella* Lév. The genus is characterized by having lirelliform or V–Y-shaped ascomata, opening by a longitudinal fissure, 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 (Hongsanan et al. 2014). More than 260 epithets are listed under *Lembosia* in Index Fungorum (2019). However, few species have molecular data. In this manuscript we introduce the new species *Lembosia brigadeirensis* (Fig. 46).

Lembosia brigadeirensis Firmino, A.R. Machado & O.L. Pereira, ***sp. nov.***

MycoBank number: MB822355; *Facesoffungi number*: FoF04108, Fig. 47

Etymology: Name derived from the mountain range where the fungus was collected, Serra do Brigadeiro.

Holotype: VIC 44208

Epiphyllous on *Epidendrum* sp. **Sexual morph** *Colonies* 4–6 mm diam., amphigenous, circular to irregular, single to confluent, dark brown, black. *Hyphae* 4–5 µm diam., straight to flexuous, irregularly branched, brown, septate, hyphal cells cylindrical, smooth. *Appressoria* 5.5–7.5 × 6–8 µm, few, entire to lobate, sessile, lateral, alternate to unilateral, never opposed, globose, unicellular, straight, brown, penetration peg central on the appressorial cell. *Ascomata* 530–1180 × 140–230 µm, superficial, hysterothecia, lirelliform, V–Y-shaped, mostly linear, on the top of mycelial mat, single to confluent, fringed at margins, massed in the centre of the colony, opening by longitudinal fissures, dark brown to black, wall of *textura radiate* to *irregulata*, cells isodiametric to cylindrical. *Pseudoparaphyses* up to 2.5 µm wide, cylindrical, filiform, septate, unbranched, hyaline. *Asci* 30–47.5 × 15–22 µm, 8-spored, bitunicate, fissitunicate, subclavate to cylindrical, disposed as an upright palisade layer. *Ascospores* 17.5–19.5 × 5.5–8 µm, cylindrical to oblong-clavate, ends rounded, straight or slightly arched, 1-septate, constricted at the median septum, hyaline, becoming brown at maturity, smooth-walled. **Asexual morph** Undetermined.

Material examined: BRAZIL, Minas Gerais, Araponga, Parque Estadual da Serra do Brigadeiro, on leaves of *Epidendrum* sp. (*Orchidaceae*), 10 September 2014, A.L. Firmino (VIC 44208, **holotype**).

GenBank numbers: ITS = MF667946, LSU = MF664531.

Notes: *Lembosia brigadeirensis* is a distinct species when compared with many other *Lembosia* species reported on *Orchidaceae* (Léveillé 1845; Horne 1905; Sydow 1939; Silva and Pereira 2008; Hosagoudar et al. 2009; Firmino and Pereira 2014). *Lembosia brigadeirensis* is

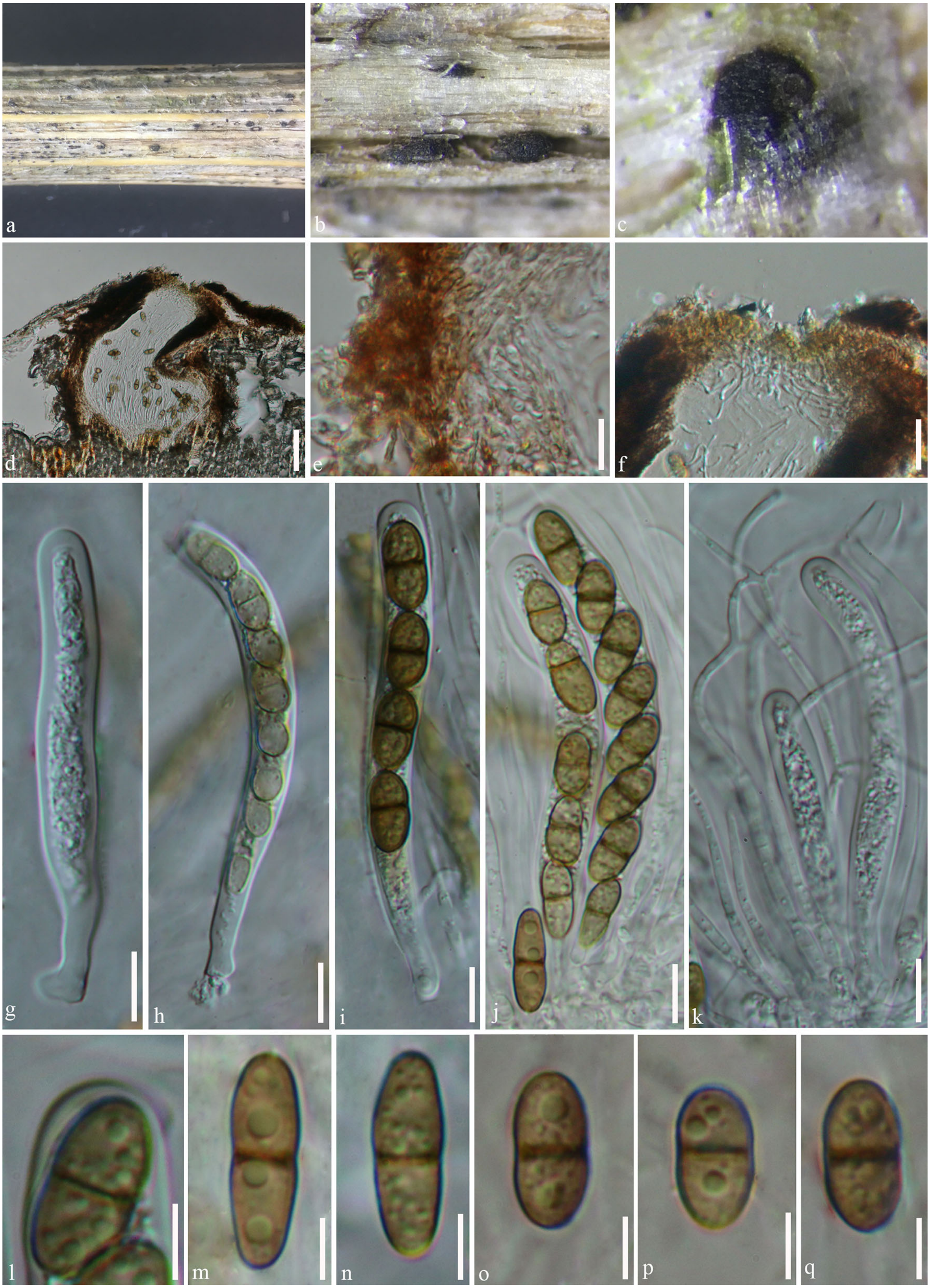


Fig. 44 ***Neobambusicola brunnea*** (MFLU 18-1393, **holotype**). **a–c** Appearance of ascomata semi-immersed in the host. **d–f** Vertical section of ascoma. **g–j** Mature asci with ascospores. **k** Hamathecium. **l** Apex of the ascus. **m–q** Ascospores. *Scale bars* **d** = 50 µm, **f** = 20 µm, **e, g–k** = 10 µm, **l–q** = 5 µm

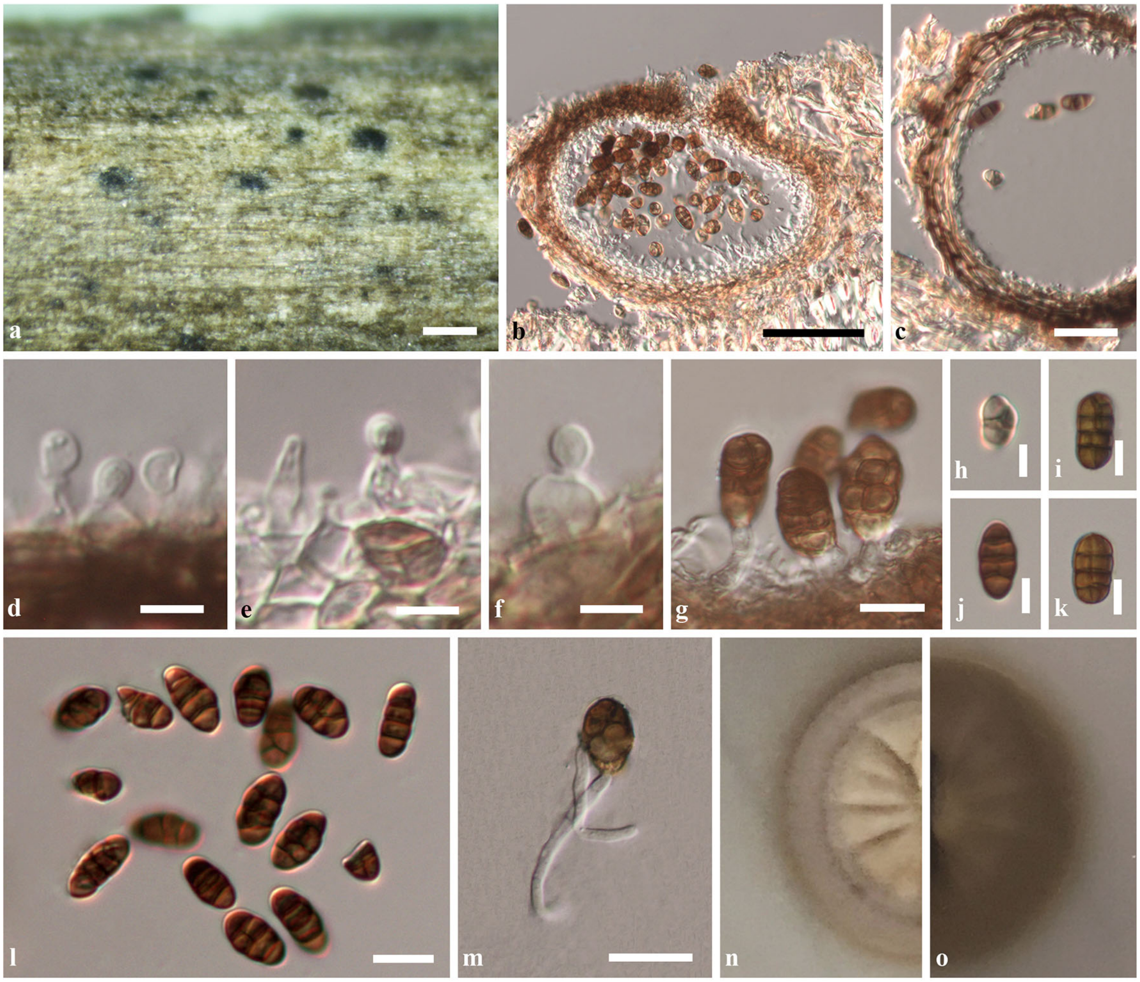


Fig. 45 ***Liua muriformis*** (KUN-HKAS 102241, **holotype**). **a** Appearance of conidiomata on host. **b** Section through conidioma. **c** Section through conidioma wall. **d–g** Conidiogenous cells. **h–l** Conidia. **m** Germinated conidium. **n, o** Culture characteristics on PDA (n = from above, o = from below). *Scale bars* **a** = 200 µm, **b** = 50 µm, **c** = 20 µm, **l, m** = 10 µm, **d–k** = 5 µm

most similar to *L. sertiferae* Syd., which has epiphyllous colonies, lobate appressoria, ellipsoid to oblong asci, and fusiform to oblong ascospores (Firmino and Pereira 2014). *Lembosia bezerrae* Firmino & O.L. Pereira has epiphyllous colonies, smaller appressoria, saccate to ovoid asci, and fusiform and smaller ascospores than *L. brigadeirensis* (Firmino and Pereira 2014). *Lembosia epidendri* Meir. Silva & O.L. Pereira has narrow hyphae, wider appressoria, smaller hysterothecia, saccate to ovoid asci, branched pseudoparaphyses, and larger and fusiform ascospores (Silva and Pereira 2008; Firmino and Pereira 2014). *Lembosia dendrochili* Lév. differs from *L. brigadeirensis* in having smaller hysterothecia, and larger asci (Léveillé 1845; Firmino and Pereira 2014). *Lembosia rolfsii* W.T. Horne differs from *L. brigadeirensis* in the subcuticular mycelium and conidia on superficial mycelium, and probably belonging to *Maheshwaramyces* (Hosagoudar et al. 2009; Firmino and Pereira 2014).

Based on LSU sequence data, *Lembosia brigadeirensis* is 97% similarity to *Prillieuxina baccharidincola* (Rehm) Petr. (GenBank no. KP143735), 95% similarity to *Asterina melastomatis* Lév. (GenBank no. KP143739) and 94% similarity to *Alysidiella suttonii* Cheew. & Crous (GenBank no. HM628777). Based on ITS sequence data, *L. brigadeirensis* is 88% similarity to *Blastacervulus eucalypti* H.J. Swart (GenBank no. GQ303271), *Alysidiella suttonii* (GenBank no. HM628774), and *Heteroconium kleinzeense* Crous & Z.A. Pretorius (GenBank no. EF110616). Phylogenetic analysis of LSU sequence dataset (Fig. 46) shows that *Lembosia brigadeirensis* forms a sister lineage with *Prillieuxina baccharidincola* (VIC42817) with high support (100% BYPP). *Lembosia* differs from *Prillieuxina* G. Arnaud and *Asterina* Lév. in having elliptical to cylindrical ascomata with longitudinal fissure. *Alysidiella* Crous and *Blastacervulus* H.J. Swart are asexual morph genera belonging to the same family as *Lembosia* (*Asterinaceae*), but with no known connection to a sexual morph. *Heteroconium* Petr. is also an asexual morph, but belonging to *Herpotrichiellaceae* (*Chaetothyriales*).

Botryosphaeriales Schoch et al.

Botryosphaeriaceae Theiss. & P. Syd.

Botryosphaeriaceae can be found as endophytes, saprobes and plant pathogens on various substrates worldwide (Liu et al. 2012b; Slippers et al. 2013; Dissanayake et al. 2016; Phillips et al. 2018; Jayawardena et al. 2019). The family comprises 28 genera and more than 190 species (Phillips et al. 2018; Tibpromma et al. 2018; Wijayawardene et al. 2018a). We follow the latest treatments and updated accounts in Dissanayake et al. (2016), Hyde et al. (2016), Yang et al. (2017), Phillips et al. (2018), Wanasinghe et al. (2018) and Jayawardena et al. (2019). Phylogenetic analyses based on a combined ITS, LSU, TEF1-α and TUB2 sequence dataset are provided for the genera *Dothiorella* (Fig. 48) and *Sphaeropsis* (Fig. 51).

Dothiorella Sacc.

We follow the latest treatment and updated accounts of *Dothiorella* in Yang et al. (2017). Updated phylogenetic analysis was retrieved from Dissanayake et al. (2017) and Wanasinghe et al. (2018).

Dothiorella acericola Phookamsak, Tennakoon & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556178; *Facesoffungi number*: FoF05711, Fig. 49

Etymology: The specific epithet "*acericola*" refers to the host genus *Acer*, on which the holotype was collected.

Holotype: KUN-HKAS 102213

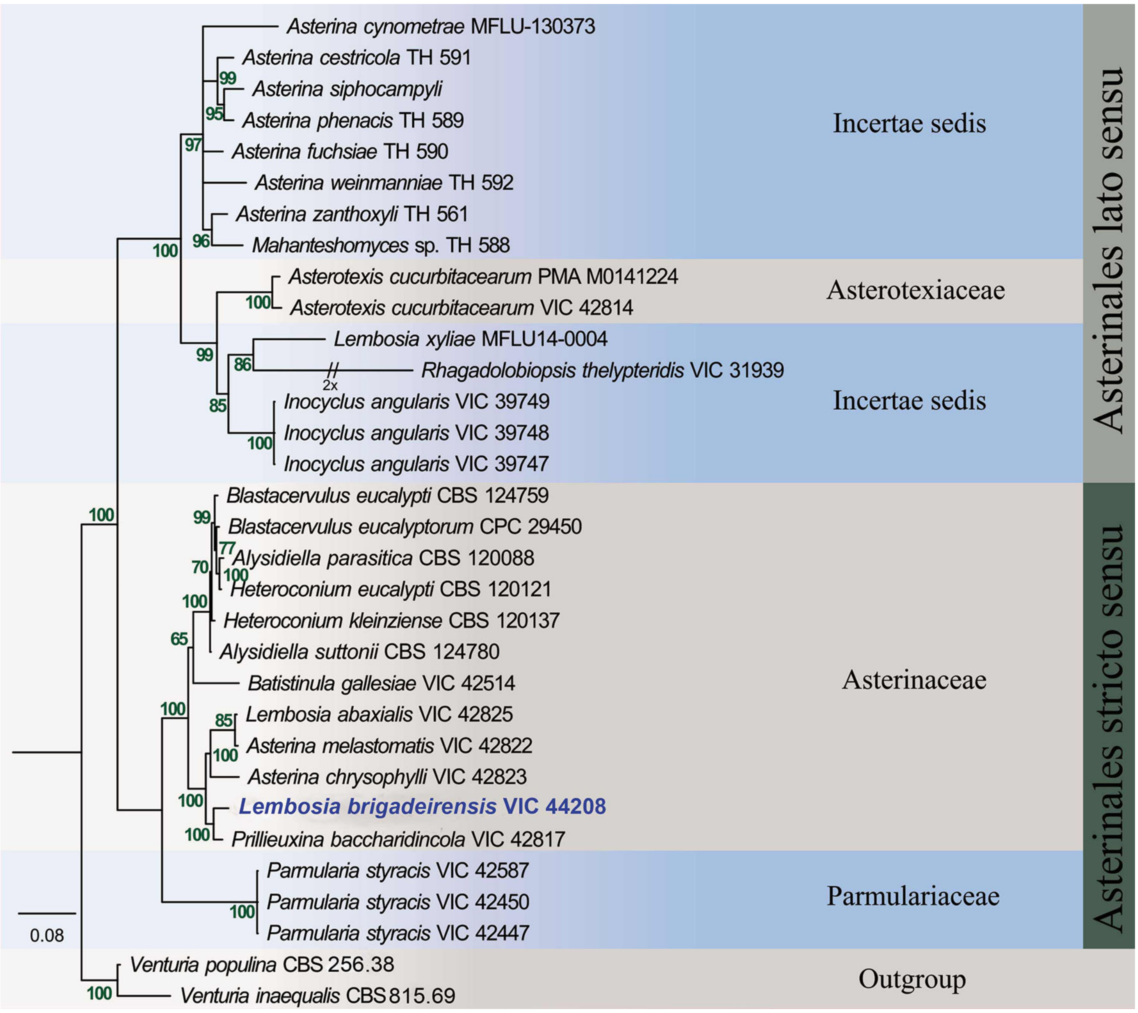


Fig. 46 Phylogenetic tree was obtained by Bayesian inference methods using the sequences of the LSU region. The posterior probability values are indicated at the nodes. Strain numbers are indicated after species names. New sequence is in blue bold. The analyses included 30 strains including representative genera of *Asterinales sensu stricto* and *Asterinales sensu lato*. The tree is rooted with *Venturia populina* (CBS 256.38) and *V. inaequalis* (CBS 815.69)

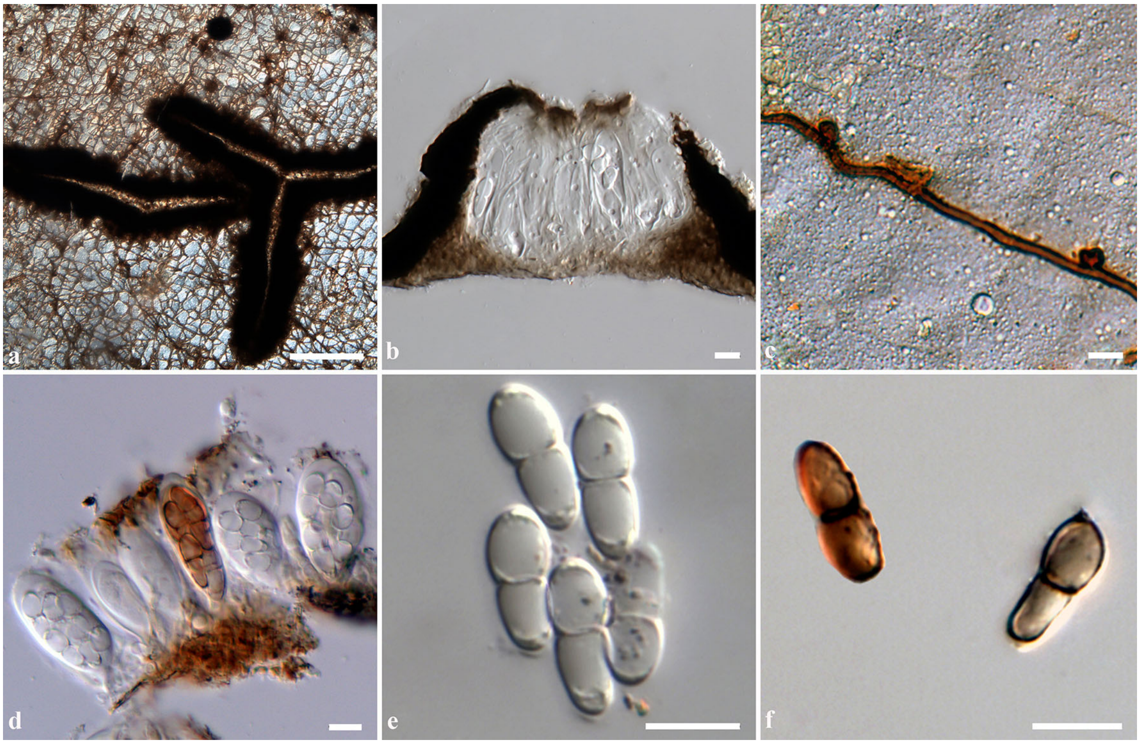


Fig. 47 ***Lembosia brigadeirensis*** (VIC 44208, **holotype**). **a** Colony with open hysterothecia and surface mycelium. **b** Cross section of the ascomata. **c** Globose to lobate unicelular appressoria. **d** Parallel bitunicate asci. **e** Immature hyaline ascospores. **f** Brown and smooth ascospores. *Scale bars* **a** = 200 µm, **b**–**f** = 10 µm

Saprobic on dried twigs of *Acer palmatum*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 220–360 µm high, 190–310 µm diam., pycnidial, aggregated, clustered, semi-immersed to erumpent, dark brown to black, globose to subglobose, uni- to biloculate, ostiole central, with minute papilla. *Conidiomata walls* 15–40 µm wide, composed of several layers of broad to flattened, dark brown to black, pseudoparenchymatous cells of *textura angularis* to *textura prismatica*, with flattened, hyaline cells towards the inner layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* (7–)9–15(–24) × 3–6(–7) µm l/w ($\bar{x}$ = 13.2 × 4.5 µm, n = 30), holoblastic, phialidic, discrete, determinate, ampulliform to cylindrical, unbranched, aseptate, hyaline, smooth, arising from the inner cavity of the conidioma wall. *Conidia* 17–22(–23) × 7–10(–13) µm l/w ($\bar{x}$ = 20.8 × 9.2 µm, n = 50), dark brown, oblong to ellipsoidal, 1-septate, slightly constricted at the septum, smooth-walled.

Culture characteristics: Colonies on PDA reaching 70–73 mm diam. after 1 week at 20–30 °C; initially medium sparse to dense, circular, or slightly irregular in shape, surface smooth, with edge entire to lobate; from above, initially white, becoming white-grey to grey; from below, grey to pale yellowish; not producing pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Kunming, Panlong, Ciba, on dead hanging twigs of *Acer palmatum* Thunb. (*Sapindaceae*), 28 November 2015, R. Phookamsak, COE009 (KUN-HKAS 102213, **holotype**), ex-type living culture KUMCC 18-0137.

GenBank numbers: ITS = MK359449, TEF1-α = MK361182.

Notes: In the NCBI BLASTn search of ITS and TEF1-α sequences, *Dothiorella acericola* is most similar to *D. viticola* A.J.L. Phillips & J. Luque, with 99% and 98% similarities, respectively. Phylogenetic analyses of a combined ITS and TEF1-α sequence dataset show that *D. acericola* is sister to *Spencermartinsia alpina* Y. Zhang ter & Ming Zhang and distinct from *D. viticola* (Fig. 48). *Dothiorella acericola*, *Spencermartinsia alpina* and *S. yunnana* Zhang ter & Ming Zhang were collected from Yunnan, China, but they are phylogenetically distant (Zhang et al. 2016). *Dothiorella acericola* has the same size range of conidia as *Spencermartinsia alpina* and *S. yunnana* (Zhang et al. 2016). A comparison of TEF1-α nucleotide bases shows that *D. acericola* differs from *Spencermartinsia alpina* and *S. yunnana* in 11/225 bp (4.9%) and 13/225 bp (5.8%), respectively. Therefore, we introduce a new species, *D. acericola* in this study based on the guidelines of Jeewon and Hyde (2016). Yang et al. (2017) treated *Spencermartinsia* as a synonym of

Dothiorella. *Spencermartinsia alpina* and *S. yunnana* should perhaps be transferred to the genus *Dothiorella.*

Dothiorella sarmentorum (Fr.) A.J.L. Phillips, A. Alves & J. Luque, Mycologia 97(2): 522 (2005)

Facesoffungi number: FoF04836, Fig. 50

Saprobic on a wide range of hosts. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 300–440 µm high, 215–300 µm diam., stromatic, solitary or scattered in small groups, immersed, uni-loculate, individual or aggregated, black, with globose to subglobose, ostiole. *Conidiomata walls* comprising several layers; outer layers thick-walled, dark brown cells of *textura angularis*; inner layers of thin-walled, lightly pigmented or hyaline cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining inner the conidioma cavity, holoblastic, hyaline, subcylindrical, proliferating at the same level giving rise to periclinal thickenings. *Conidia* 18–23 × 8–10 µm ($\bar{x}$ = 21 × 9.4 µm, n = 30), ovoid, with a broadly rounded apex and truncate base, initially hyaline to lightly pigmented and aseptate, becoming dark brown, 1-septate, slightly constricted at the septum, smooth-walled.

Material examined: RUSSIA, Rostov region, Shakhty City, Alexandrovsky Park, on dead twigs of *Platycladus orientalis* (L.) Franco (*Cupressaceae*), 14 March 2016, T.S. Bulgakov (MFLU 16-1627).

Known hosts: *Acer platanoides* L., *Aesculus hippocastanum* L., *Armeniaca vulgaris* Lam., *Cedrus atlantica* (Endl.) Manetti ex Carrière, *Chamaecyparis lawsoniana* (A. Murray) Parl., *Cornus sanguinea* L., *Coronilla emerus* L., *Crataegus* sp., *Cryptomeria japonica* (L.f.) D.Don, *Cupressus lusitanica* Mill., *Eriobotrya japonica* (Thunb.) Lindl., *Euonymus europaeus* L., *Forsythia europaea* Degen & Bald., *Malus pumila* Miller, *Menispermum canadense* L., *Paliurus spina-christi* Mill., *Persica vulgaris* Mill., *Pistacia* spp., *Populus nigra* L., *Prunus* spp., *Pyrus communis* L., *Quercus* spp., *Salix* sp., *Thuja* spp., *Ulmus* spp., *Vitis* spp. (Farr and Rossman 2018).

Known distribution: Iran, Italy, Netherlands, New Zealand, Norway, Poland, Portugal, Serbia, Spain, Sweden, UK (Great Britain), Ukraine, the USA (California, Florida, Oregon, Washington) (Farr and Rossman 2018).

GenBank numbers: ITS = MH571673, TEF1-α = MH628155.

Notes: *Dothiorella sarmentorum* was introduced by Phillips et al. (2005). This species is a cosmopolitan distribution including many economical important trees (Phillips et al. 2005, 2013; Dissanayake et al. 2017). We isolated *D. sarmentorum* from *Platycladus orientalis* (*Cupressaceae*) for the first time (Farr and Rossman 2018). The morphological characters such as conidia shape, size and colour are similar to the type as described. However, we could not obtain a living culture from the isolated spores. Therefore, the morphology of the species is based only on characters on the host. Phylogenetic analyses of a combined ITS and TEF1-α sequence dataset (Fig. 48) show that our isolate (MFLU 16-1627) clusters with the type strain of *D. sarmentorum* (IMI63581b) and strain CBS 115038.

Sphaeropsis Sacc.

Sphaeropsis was introduced by Saccardo (1880b) to accommodate diplodia-like taxa and is typified by *S. visci* (Alb. & Schwein.) Sacc. with *Phaeobotryosphaeria* sexual morph (Phillips et al. 2008, 2013; Dissanayake et al. 2016; Wijayawardene et al. 2017a). *Sphaeropsis* has a cosmopolitan distribution on various hosts (Farr and Rossman 2018). The genus is characterized by pseudothecial, brown to black, uni-loculate ascomata, thick endotunica, bitunicate asci, with cellular pseudoparaphyses, brown, aseptate ascomata and asexual morph forms with stromatic conidiomata, with paraphyses and oval, oblong or clavate, aseptate conidia (Phillips et al. 2013). More than 600 species are listed under *Sphaeropsis* in Index Fungorum (2019). However, Phillips et al. (2013) re-circumscribed the genus and only five species were accepted based on morphological characteristics of the sexual and asexual morph connections and phylogenetic evidence (Phillips et al. 2008, 2013; Doilom et al. 2015, 2017; Dissanayake et al. 2016; Wijayawardene et al. 2017a). In this study, we report a new host record of *S. eucalypticola* from *Bauhinia purpurea* (L.) Benth. in Thailand.

Sphaeropsis eucalypticola A.J.L. Phillips, in Phillips et al., Stud Mycol 76: 158 (2013)

Facesoffungi number: FoF00169, Fig. 52

Holotype: THAILAND, Chiang Rai Province, Muang District, on dead twig of *Eucalyptus* sp., 8 August 2011, M. Doilom, MFLU 12-0753.

Saprobic on dead twigs. **Sexual morph** *Ascostromata* 250–350 µm high, 170–250 µm diam. (ascostromata with papilla, not including subiculum or hypostroma), black, convex on host tissue, appearing through cracks in bark, scattered or clustered in small to large groups on a subiculum or hypostroma, 185–260 µm high at the base, aggregated, initially immersed, becoming erumpent, when cut horizontally locules visible as white contents and dark ascospore dots, uni-loculate or multi-loculate, globose to subglobose or flask-shaped. *Papilla* 60–95 µm long, 65–85 µm diam., ostiole with periphyses. *Peridium* 35–80 µm wide, thick-walled, composed of several layers of dark brown to black, coriaceous cells of *textura angularis*. *Hamathecium* comprising 2.5–4 µm wide, hyphae-like, hyaline, numerous, septate pseudoparaphyses, constricted at the septa. *Asci* 102–175 × 22–32 µm ($\bar{x}$ = 130 × 27 µm, n = 15), 8-spored, bitunicate, fissitunicate, cylindric-clavate or clavate, with a short or long pedicel, apically rounded

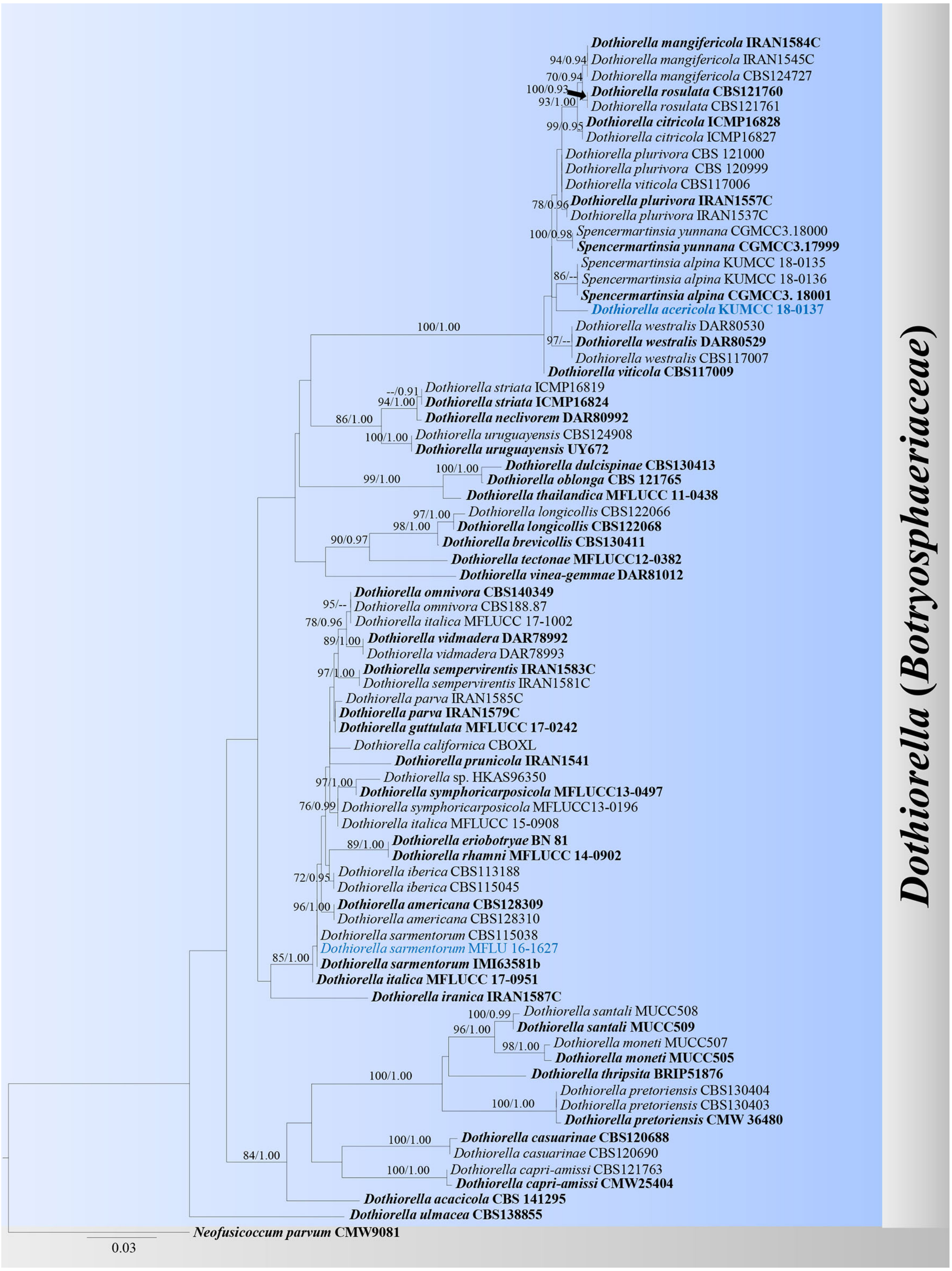


Fig. 48 Phylogenetic tree generated from maximum likelihood (RAxML) based on a combined ITS and TEF1-α. Maximum likelihood bootstrap value ≥ 70% and Bayesian posterior probabilities ≥ 0.95 BYPP are given at the nodes. The ex-type strains are in bold. The newly generated sequences are in blue. The tree is rooted with *Neofusicoccum parvum* (CMW9081)

with an ocular chamber. *Ascospores* 27–33 × 11–14 µm ($\bar{x}$ = 30 × 13 µm, n = 20), overlapping 2-seriate, hyaline when young, becoming pale brown or reddish brown when mature, ellipsoidal to ovoid, aseptate, sometime 2-septate, broader in the centre, with an apiculus at both ends, thick-walled, echinulate. **Asexual morph** Undetermined.

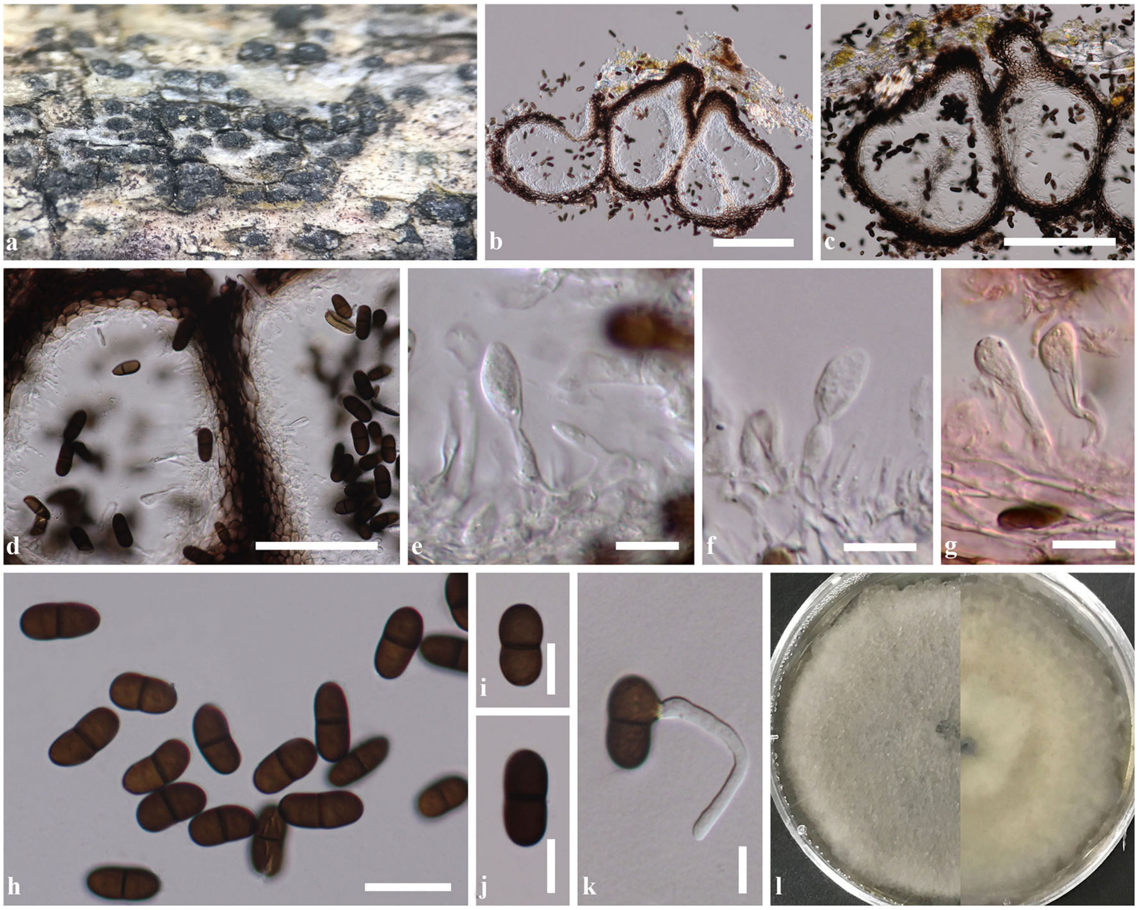


Fig. 49 ***Dothiorella acericola*** (KUN-HKAS 102213, **holotype**). **a** Appearance of conidiomata on host. **b, c** Section through conidiomata. **d** Section through conidioma wall. **e–g** Conidiogenous cells (g = stained with congo red). **h–j** Conidia. **k** Germinated conidium. **l** Culture characteristics on PDA from above and below. *Scale bars* **b, c** = 200 µm, **d** = 50 µm, **h** = 20 µm, **e–g, i–k** = 10 µm

Culture characteristics: Ascospores germinating on PDA after 5–10 h. Germ tubes produced from germ pore of ascospores. Colonies on PDA, reaching the edge of the Petri dish after 5 days, flat or effuse, undulate, initially white, after 3 days becoming brownish grey to olive.

Material examined: THAILAND, Chiang Rai Province, Muang District, Tha Sud Subdistrict, Mae Fah Luang University campus grounds, on dead twigs of *Bauhinia purpurea* L. (*Leguminosae*), 14 March 2012, M. Doilom, MKBB031 (MFLU 18-1857), living culture, MFLUCC 12-0171.

Known hosts and distribution: *Eucalyptus* sp., *Bauhinia purpurea*, *Tectona grandis* L.f. (Thailand) (Liu et al. 2012b; Phillips et al. 2013; Doilom et al. 2017).

GenBank numbers: ITS = MK108956, TEF1-α = MK108958, TUB2 = MK108957.

Notes: A new isolate of *Sphaeropsis eucalypticola* (MFLUCC 12–0171) was collected from dead twigs of *Bauhinia purpurea* in Thailand. This new isolate shares a close phylogenetic affinity to the type of *S. eucalypticola* (100% ML, 100% MP and 1.00 BYPP) in our combined phylogeny of ITS, TEF1-α and TUB2 sequence data (Fig. 51). *Sphaeropsis eucalypticola* has been reported from *Eucalyptus* sp. and *Tectona grandis* in Thailand (Liu et al. 2012b; Doilom et al. 2017), but it has not been previously reported from *Bauhinia purpurea* (Fig. 52).

Microthyriales G. Arnaud

Microthyriales, genera *incertae sedis*

Parazalerion Madrid, Gené & Cano, ***gen. nov.***

MycoBank number: MB824747; *Facesoffungi number*: FoF04480

Etymology: The name reflects the superficial morphological similarity between this genus and species of *Zalerion sensu lato*

Saprobic in soil. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Vegetative hyphae* septate, branched, subhyaline to light olivaceous. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* subcylindrical to narrowly clavate, smooth-walled, light olivaceous. *Conidia* produced terminally or laterally on

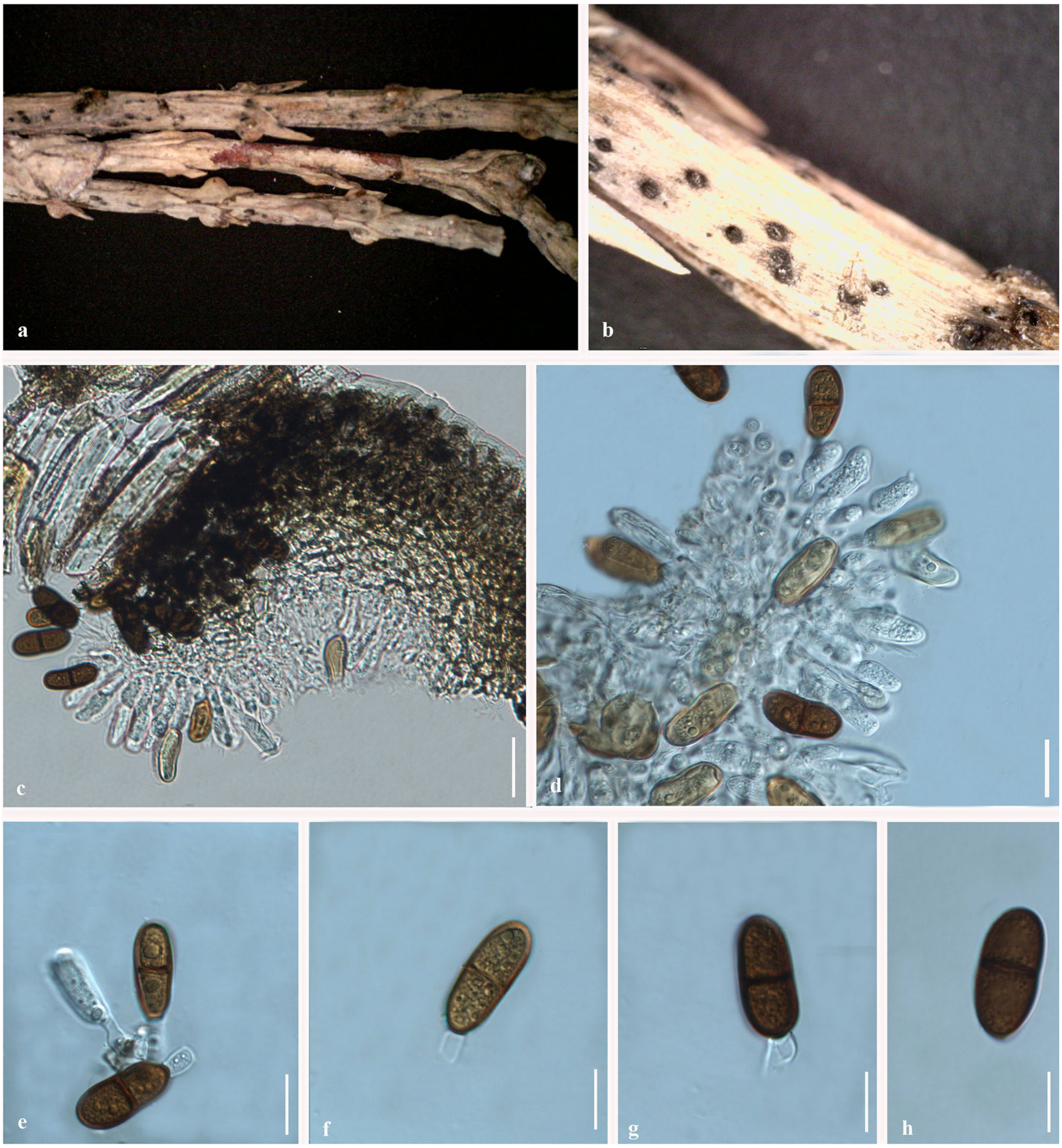


Fig. 50 ***Dothiorella sarmentorum*** (MFLU 16-1627). **a**, **b** Appearance of conidiomata on host surface. **c** Section through conidioma wall. **d, e** Conidiogenous cells. **f–h** Conidia. *Scale bars* **c, d** = 20 µm, **e–h** = 10 µm

undifferentiated hyphae, or on short conidiophores. *Conidial filament* curved, sinuous or irregularly coiled, multiseptate, light olivaceous brown to mid brown, slightly to strongly constricted at the septa; groups of conidia often appear compactly intertwined, forming irregularly shaped masses of cells.

Type species: *Parazalerion indica* Madrid, Gené & Cano

Notes: *Parazalerion* is introduced as a novel monotypic conidial genus of Ascomycota. Morphologically, it resembles the marine genus *Zalerion* R.T. Moore & Meyers (Sordariomycetes, genera *incertae sedis*) in the production of irregularly coiled, dematiaceous, multi-septate conidia which often form knots of cells (Ellis 1976; Goos 1985; Campbell et al. 2005). The new genus, however, was found in a terrestrial habitat and is phylogenetically related to *Spirosphaera minuta* Hennebert (Fig. 53), which belongs in Dothideomycetes, relatively close to *Microthyriaceae* (Voglmayr et al. 2011). Furthermore, knots of cells originate from a single conidial filament in *Zalerion*, whereas in *Parazalerion* they originate from the intertwining of groups of conidia (Fig. 54). This particular development of knots of cells also distinguish *Parazalerion* from other similar genera, including *Cirrenalia* Meyers &

R.T. Moore, *Cumulospora* I. Schmidt, *Glomerulispora* Abdel-Wahab & Nagah., *Halazoon* Abdel-Aziz et al., *Hiogispora* Abdel-Wahab & Nagah., *Hydea* K.L. Pang & E.B.G. Jones, *Matsusporium* E.B.G. Jones & K.L. Pang, *Moheitospora* Abdel-Wahab et al., *Moleospora* Abdel-Wahab et al. and *Moromyces* Abdel-Wahab et al. (Ellis 1971; Abdel-Wahab et al. 2010). The LSU-based phylogenetic tree demonstrates that *Parazalerion* is phylogenetically clearly distinct from those hyphomycete genera (Fig. 53).

The closest match in the BLASTn search with ITS + LSU sequences of *Parazalerion indica* strain CBS 125443 is *Spirosphaera minuta* strain CBS 476.66 (GenBank no. HQ696659, 92% similarity, 92% query coverage). In our study, *Spirosphaera minuta* and *Parazalerion indica* appeared as sister taxa in the LSU-based phylogenetic tree (Fig. 53) and this relationship received 97% bootstrap support. Since the type species of *Spirosphaera*, *S. floriformis* Beverw., is a phylogenetically distant species belonging to *Helotiales* (Voglmayr et al. 2011), *Spirosphaera minuta* apparently needs to be reallocated to a different genus. Its definitive phylogenetic position deserves further study, but the fungus is also clearly different from *Parazalerion*. It occurs on submerged plant material and produces more or less globose conidia formed by a complexly coiled hyaline, branching filament (Hennebert 1968). *Spirosphaera* is a polyphyletic genus that needs to be revised. Another member of this genus, *S. cupreorufescens* Voglmayr is a member of *Pleosporales* (Voglmayr et al. 2011) and also needs to be segregated from *Spirosphaera sensu stricto*.

Parazalerion indica Madrid, Gené & Cano, ***sp. nov.***

MycoBank number: MB824748; *Facesoffungi number*: FoF04481, Fig. 54

Etymology: Refers to the country where this fungus was collected, India.

Holotype: IMI 397928

Saprobic in soil. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Vegetative hyphae* 1–1.5 µm wide, septate, branched, subhyaline to light olivaceous, smooth- and thin-walled. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.5–5 × 1.5–2 µm, subcylindrical to narrowly clavate, smooth-walled, light olivaceous. *Conidia* produced terminally or laterally on undifferentiated hyphae, or on short conidiophores. *Conidial filament* curved, sinuous or irregularly coiled, with 1–3(–6) usually thick and dark septa, light olivaceous brown to mid brown, thick-walled, smooth to verruculose, slightly to strongly constricted at the septa, 8–19(–26) µm long, 4–5.5 µm wide at the widest part, with an obtuse apex; groups of conidia often appearing tightly intertwined, forming compact, irregularly shaped, light olivaceous brown to dark brown, 8–23 µm wide masses of cells.

Culture characteristics: Colonies reaching 21 mm. diam. on OA and 25 mm. diam. on PCA and PDA after 14 days at 25 °C. On OA light grey and floccose at the centre, light brown to dark brown and almost glabrous towards the periphery, with a fimbriate margin; reverse dark brown at the centre, light brown towards the periphery. On PCA white to cream, funiculose at the centre, almost glabrous towards the periphery, with a fimbriate margin; reverse concolorous with obverse. On PDA velvety to floccose, cream to dark brown, with a fimbriate margin; reverse concolorous with obverse. No diffusible pigments observed in any of the tested media.

Material examined: INDIA, Delhi, isolated from soil, 2 February 1997, H.C. Gugnani (IMI 397928, **holotype**), ex-type living cultures CBS 125443, FMR 9690.

GenBank numbers: ITS + LSU = MH100803.

Muyocopronales Mapook et al.

Muyocopronaceae K.D. Hyde

Muyocopronaceae was invalidly introduced by Luttrell (1951) [as 'Myiocopronaceae'], and is typified by *Muyocopron* Speg. with *M. corrientinum* Speg. as the type species. The genus was introduced to accommodate epiphytic fungi, characterized by black, superficial, dimidiate-scutate, subcarbonaceous, ostiolate ascomata, without mycelium and bitunicate, ovoid to obclavate asci, containing subglobose to ellipsoidal, hyaline ascospores (Mapook et al. 2016; Tibpromma et al. 2016). *Muyocopron* has long historical discussion of its taxonomic placement (Saccardo 1883a; von Arx and Müller 1954, 1975; Eriksson and Hawksworth 1993; Lumbsch and Huhndorf 2007; 2010), until Hyde et al. (2013) re-defined the family *Muyocopronaceae* to accommodate *Muyocopron*. Mapook et al. (2016) introduced the order *Muyocopronales* to accommodate this family based on molecular data coupled with morphological characteristics. Only *Muyocopron* is accommodated in the family with more than 60 epithets listed (Hyde et al. 2013; Mapook et al. 2016; Tibpromma et al. 2016; Wijayawardene et al. 2018a; Index Fungorum 2019). In this study, a new host and geographical records of *Muyocopron lithocarpi* Mapook et al. is reported (Figs. 55, 56).

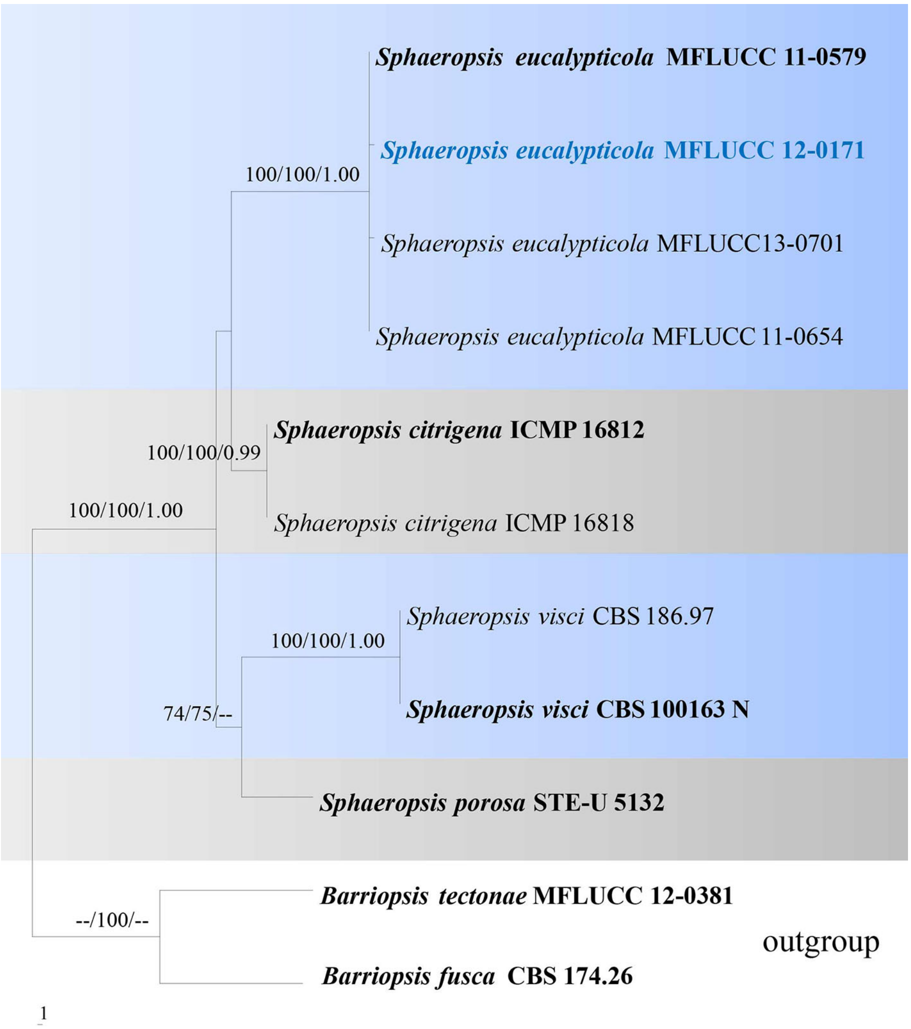
Muyocopron Speg.

We follow the latest treatment and updated accounts of *Muyocopron* in Mapook et al. (2016) and Tibpromma et al. (2016).

Muyocopron lithocarpi Mapook, Boonmee & K.D. Hyde, in Mapook et al., Phytotaxa 265(3): 235 (2016), Fig. 56

Holotype: THAILAND, Chiang Rai Province, on fallen leaves of *Lithocarpus lucidus* (*Fagaceae*), 30 September

Fig. 51 Phylogram generated from parsimonious tree based on combined ITS, TEF1-α and TUB2 sequence dataset. The tree is rooted to *Barriopsis tectonae* (MFLUCC 12-0381) and *B. fusca* (CBS 174.26). Maximum parsimony and maximum likelihood bootstrap values ≥ 70% and Bayesian posterior probabilities ≥ 0.95 are given at the nodes. The ex-type strains are in bold. The newly generated sequence is in blue bold



2014, A. Mapook (MFLU 15-1133), ex-type living culture MFLUCC 14-1106.

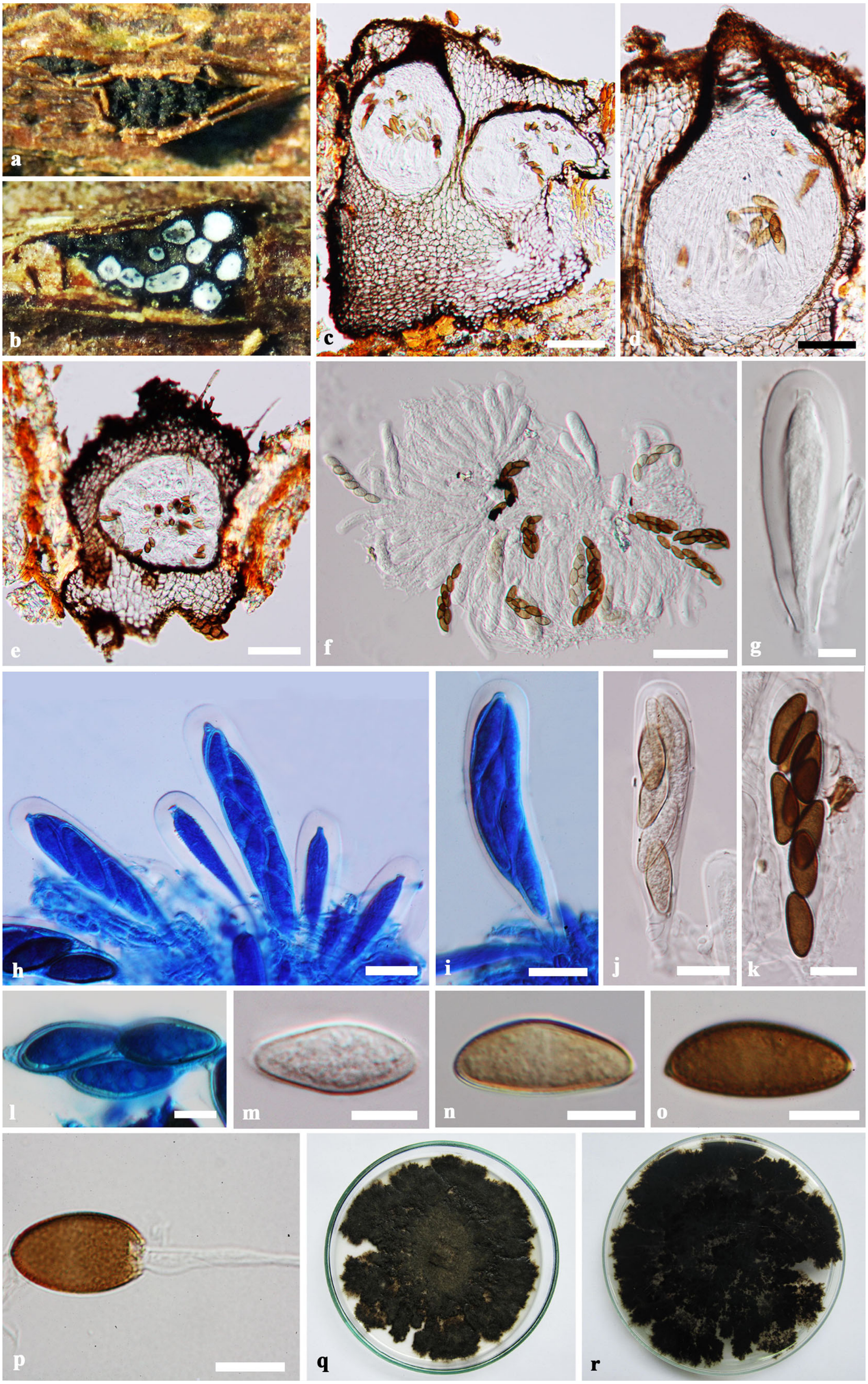
Saprobic on dead stems of herbaceous plant. **Sexual morph** *Ascostromata* dry, black, circular, raised to umbonate on the host surface, without a subiculum, easily removed from the host, clustered, gregarious, or in groups of 2–3 locules, ostiolate. *Ascomata* 55–110 µm high, 175–380 µm diam., clustered, gregarious or in groups, superficial, black, with a central irregular ostiole. *Peridium* 10–27 µm wide, slightly thick-walled of unequal thickness, poorly developed at the base, slightly thick at the sides towards the apex, comprising two types of cell layers; outer layer composed of black carbonaceous, brittle cells, inner layer composed of hyaline to brown, pseudoparenchymatous cells of *textura angularis* to *textura prismatica*. *Hamathecium* comprising numerous, 2–3 µm wide, filiform, septate, anastomosed pseudoparaphyses. *Asci* (41–)47–78(–85) × (18–)21–28(–29) µm ($\bar{x}$ = 59.6 × 24.5 µm, n = 45), 8-spored, bitunicate, ovoid to obclavate, or ampulliform, short pedicellate, apically rounded, apex thick with small ocular chamber. *Ascospores* (12–)14–19(–20) × (7–)8–10(–12) µm ($\bar{x}$ = 17.2 × 9.8 µm, n = 60), overlapping 1–3-seriate, hyaline, subglobose to obovoid, with obtuse ends, 1-celled, rough-walled with small granules, and 1–3 large guttules. **Asexual morph** Undetermined.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Jinghong, Nabanhe, on dead stems of herbaceous plant, 21 November 2015, R. Phookamsak, XB016 (KUN-HKAS 102243).

Known hosts and distribution: *Lithocarpus lucidus*, *Peltophorum* sp. (Thailand); *Cercis chinensis* (Guizhou, China) (Mapook et al. 2016; Jayasiri et al. 2019).

GenBank numbers: LSU = MK447738, SSU = MK447740.

Notes: In molecular phylogenetic analysis our isolate clusters with *Muyocopron lithocarpi* Mapook et al. (Fig. 55). The morphology of our isolate is similar to *M. lithocarpi* described by Mapook et al. (2016), although our isolate has larger asci than in the original description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◀**Fig. 52** ***Sphaeropsis eucalypticola*** (MFLU 18-1857). **a** Ascostromata on dead twig of *Bauhinia purpurea*. **b** Ascostromata cut through horizontally showing the white contents with dark spots corresponding to asci with ascospores. **c–e** Vertical section of ascostromata. **f** Immature and mature asci with immature and mature ascospores. **g–i** Immature asci. **j, k** Asci with ascospores**. l, m** Immature ascospores. **n, o** Ascospores. **p** Germinated ascospore. **q, r** Colony on PDA after 2 months (**q** = above view, **r** = below view). *Notes* **h, i, l** stained in lactophenol cotton blue. *Scale bars* **c, e, f** = 100 µm. **d** = 50 µm. **g, l–p** = 10 µm. **h–k** = 20 µm

(41–85 × 18–29 µm versus 45–65 × 15–28 µm) (Mapook et al. 2016). The species was collected from herbaceous plant in Yunnan, China for the first time.

Tubeufiales Boonmee & K.D. Hyde

Tubeufiaceae M.E. Barr

We follow the latest treatment and updated accounts of *Tubeufiaceae* in Brahmanage et al. (2017), Chaiwan et al. (2017), Liu et al. (2018), Lu et al. (2018a, b), Phookamsak et al. (2018), Tibpromma et al. (2018) and Jayasiri et al. (2019). There are 27 genera accommodated in this family based on molecular data coupled with morphological characteristics (Lu et al. 2018b; Tibpromma et al. 2018; Wijayawardene et al. 2018a; Jayasiri et al. 2019). In this study, a new species *Pseudohelicomyces menglunicus* is introduced from a rotten seed coat in Yunnan, China (Fig. 57).

Pseudohelicomyces Y.Z. Lu et al.

We follow the latest treatment and updated accounts of *Pseudohelicomyces* in Lu et al. (2018b) and Jayasiri et al. (2019).

Pseudohelicomyces menglunicus J.F. Li, Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555770; *Facesoffungi number*: FoF05763, Fig. 58

Etymology: The specific epithet "*menglunicus*" refers to the Menglun Town, Xishuangbanna, Yunnan, China, where the holotype was collected.

Holotype: KUN-HKAS 85795

Saprobic on seed coat. **Sexual morph** Undetermined. **Asexual morph** *Mycelium* immersed on the substrate, composed of septate, branched, smooth, thin-walled, subhyaline to dark brown hyphae. *Conidiophores* (106–)130–220 × 9–13(–13.5) µm, macronematous or micronematous, paler towards the apex, hyaline to light brown, thin-walled, smooth, septate, branched, straight or flexuous, cylindrical, tapering towards the apex. *Conidiogenous cells* (20–) 23.5–32(–36) × (4–)4.5–5.5(–6) µm ($\bar{x}$ = 4.5 × 5.3 µm, n = 10), holoblastic, integrated, intercalary and sometimes terminal, determinate or sympodial, occasionally small and discrete, denticulate, denticles cylindrical, often narrow, hyaline, smooth. *Conidia* (18–)20–33(–34) × (21.5–)25–30(–40) µm ($\bar{x}$ = 22.5 × 27.2 µm, n = 20), pleurogenous or acropleurogenous, solitary, simple, subhyaline to paler yellowish brown, septate, slightly constricted at the septa, planate to cochleate, smooth, thin-walled, hygroscopic.

Culture characteristics: Conidia germinating on PDA within 14 h and germ tubes produced from all cells. Colonies growing on PDA, hairy, brown to dark brown, reaching 5 mm in 15 days at 23 °C, mycelium partly superficial, partly immersed, slightly effuse, radially striate, with irregular edge, subhyaline to dark brown; conidia sporulating within 15 days on PDA.

Material examined: CHINA, Yunnan Province, Xishuangbanna, on unidentified seed, 15 August 2014, J.F. Li, H-26 (KUN-HKAS 85795, **holotype**), ex-type living culture, MFLUCC14-0689.

GenBank numbers: ITS = MK335914, SSU = MK335915, TEF1-α = MK335916.

Notes: *Pseudohelicomyces menglunicus* resembles species of *Helicosporium* Nees and *Neohelicosporium* Y.Z. Lu et al. in morphological characters, but is obviously unique in conidiophores and conidia. *Pseudohelicomyces menglunicus* differs from *Helicosporium* and *Neohelicosporium* species in having flexuose, branched and hyphae-like conidiophores, and smooth-walled conidia. In the phylogenetic analysis (Fig. 57), *P. menglunicus* forms a separated lineage, sister to *P. aquaticus* Y.Z. Lu et al. with moderate support (76% ML and 0.97 BYPP). Jayasiri et al. (2019) introduced a new sexual morph species, *P. quercus* Jayasiri et al. on fruit of *Quercus* sp. from Thailand. The species also formed a clade with *P. aquaticus* and *P. menglunicus* (pre-analysis, data not shown). A comparison of ITS and TEF1-α nucleotide bases shows that *P. menglunicus* differs from *P. quercus* in 37/569 bp (6.5%) of ITS and 28/912 bp (3.1%) of TEF1-α. Hence, *P. menglunicus* is introduced as a new asexual morph species.

Class Eurotiomycetes O.E. Erikss. & Winka

We follow the latest treatment and updated account of Eurotiomycetes in Gueidan et al. (2014) and Geiser et al. (2015). The outline and notes of the genera in Eurotiomycetes was provided by Wijayawardene et al. (2017a, 2018a).

Subclass Chaetothyriomycetidae Doweld

Chaetothyriales M.E. Barr

Cyphellophoraceae Réblová & Unter.

Cyphellophoraceae was introduced by Réblová et al. (2013) to accommodate a monotypic genus *Cyphellophora* G.A. de Vries and is typified by *C. laciniata* G.A. de Vries

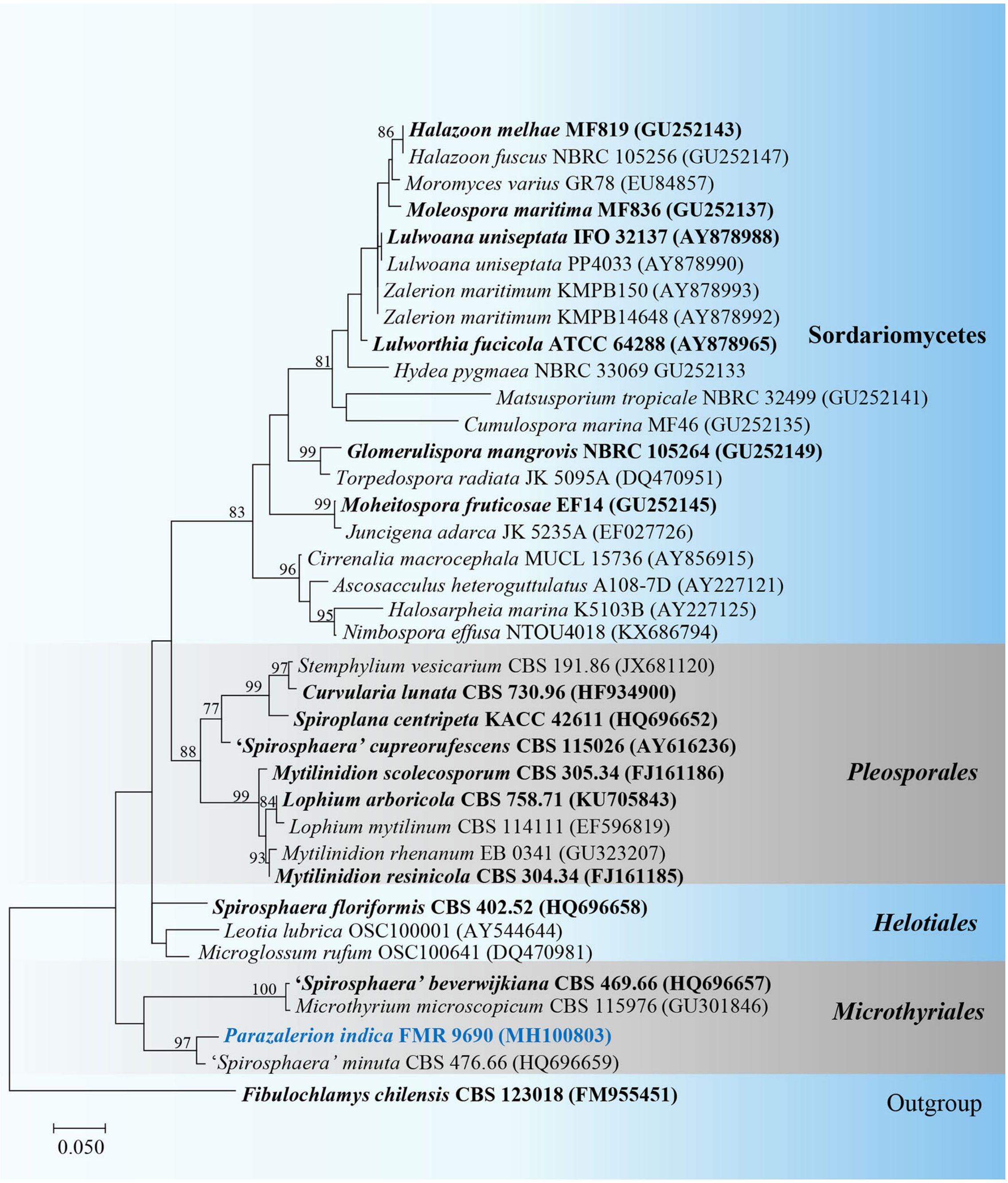


Fig. 53 Maximum likelihood tree based on partial LSU region, showing the phylogenetic relationships of *Parazalerion* and other ascomycetes including morphologically similar hyphomycetous genera. Bootstrap support values > 70% are shown near the internodes. The tree is rooted to *Fibulochlamys chilensis* (*Agaricales*). The original isolate numbers and GenBank accession numbers of LSU sequences are noted after the species names. Ex-type strains are indicated in bold

which was isolated from human skin in Switzerland. Taxa have been reported as pathogens or endophytes on plants, or as soil borne, as well as infection on humans and animals (i.e., nails and skin) (Réblová et al. 2013; Feng et al. 2014; Gao et al. 2015; Yang et al. 2018a). Twenty-six epithets are listed in Index Fungorum (2019) with 23 possible species are accepted in this genus.

Cyphellophora G.A. de Vries

Most *Cyphellophora* species have been reported in their asexual morph. However, Yang et al. (2018a) reported the sexual morph of *Cyphellophora* on living leaves of *Alnus nepalensis* D. Don (*Betulaceae*) from China for the first time. We introduce a new sexual species, *C. filicis*, which was collected from dead fronds of a fern in Thailand. The

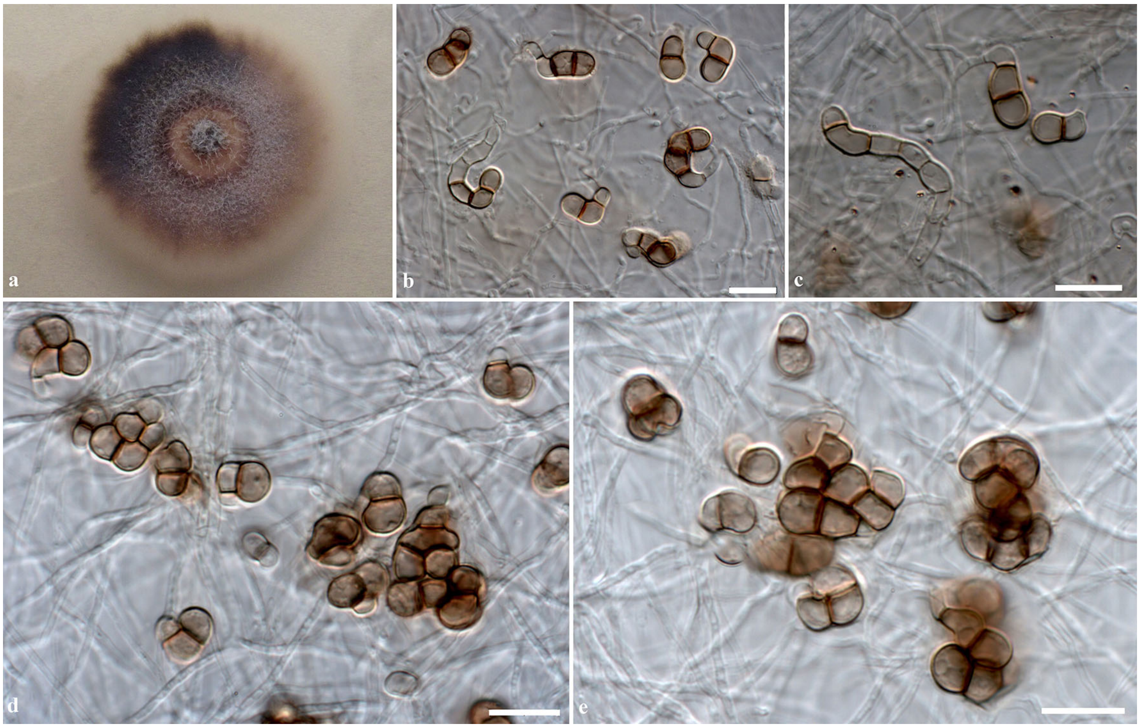


Fig. 54 ***Parazalerion indica*** (CBS 125443, **holotype**). **a** Colony on PDA after 14 days at 25 °C. **b, c** Conidiogenous cells and conidia. **d, e** Conidia and knots of cells. *Scale bars* **a–e** = 10 μm

new species is introduced based on its morphological distinctiveness and phylogenetic support (Fig. 59).

Cyphellophora filicis Hongsanan, Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556179; *Facesoffungi number:* FoF05712, Fig. 60

Etymology: The specific epithet "*filicis*" (Latin: fern) refers to the host, from which the holotype was collected.

Holotype: KUN-KHAS 102220

Saprobic on dead fronds of a fern, without dark superficial hyphae, appearing as black dots on host surface. **Sexual morph** *Ascomata* 40–60 μm high, 55–75 μm diam., immersed in host tissue, becoming erumpent, solitary, subglobose to globose, dark brown, uni-loculate, glabrous, ostiolate, with minute papilla. *Peridium* 3–10 μm wide, thin-walled, composed of 2–5 layers of flattened, brown pseudoparenchymatous cells of *textura angularis*. *Asci* 30–50 × (10–)12–15(–19) μm ($\bar{x}$ = 41.5 × 13.6 μm, n = 30), 8-spored, bitunicate, ovoid to ampulliform, short pedicellate, with an ocular chamber. *Ascospores* (15–)17–20(–22) × (3–)4–5(–6) μm ($\bar{x}$ = 18.6 × 4.7 μm, n = 30), overlapping 2–3-seriate, hyaline, ellipsoidal to fusiform, inconspicuously 3-septate, not constricted at the septa, narrowly round at the ends, sometimes curved at the middle, with a guttule in each cell. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 34–36 mm diam. after 3 weeks at 20–25 °C, colonies circular, dense, flat, slightly raised, surface dull, with edge entire, woolly to velvety; from above, dark grey at the margin, white-grey at the centre, separating from the margin by convex, concentric ring; from below dark greenish at the margin, with green yellowish at the centre; not producing pigmentation in agar.

Material examined: THAILAND, Chiang Rai Province, Doi Pui, on dead fronds of a fern, 2 February 2017, R. Phookamsak, DP002 (KUN-KHAS 102220, **holotype**), ex-type living culture, KUMCC 18-0144 (DP002A), KUMCC18-0145 (DP002B).

GenBank numbers: ITS = MK404056, LSU = MK404052, SSU = MK404054 (KUMCC 18-0144); ITS = MK404057, LSU = MK404053, SSU = MK404055 (KUMCC18-0145).

Notes: The phylogenetic tree (Fig. 59) shows that *Cyphellophora filicis* is closely related to a fungus in *Chaetothyriales* (T222) that is associated with ants nest and their runway galleries (Nepel et al. 2014). It is also related to *C. fusarioides* (B. Sutton & C.K. Campb.) Decock, *C. laciniata* G.A. de Vries, *C. suttonii* (Ajello et al.) Decock and *C. vermispora* A. Walz & de Hoog, but as a distinct new species in *Cyphellophora* (Fig. 59). We could not compare morphological characters of our new species and those *Cyphellophora* species due to the fact that *C. filicis* is

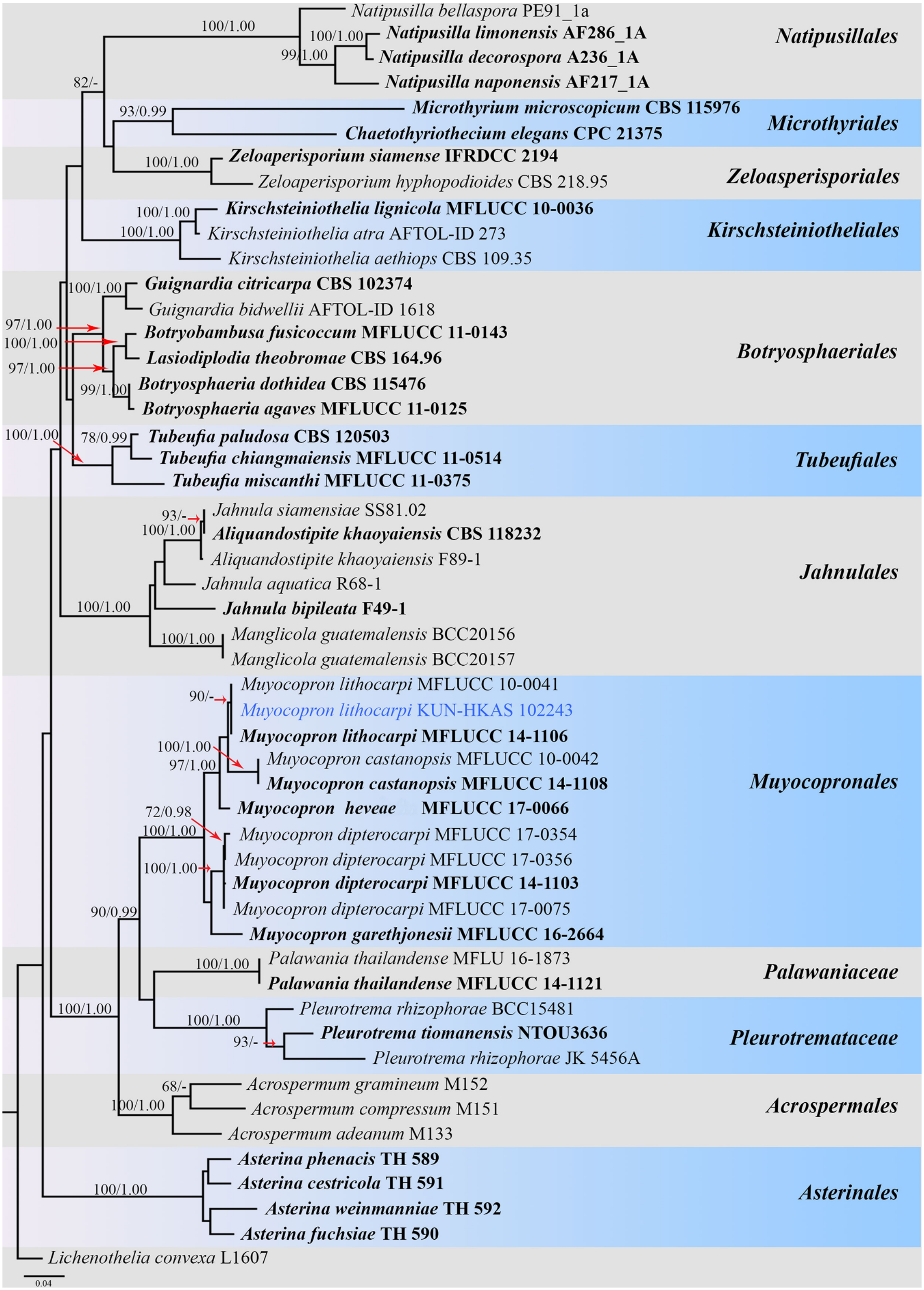


Fig. 55 RAxML tree based on a combined LSU and SSU sequence dataset. Bootstrap support values for ML equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.95 BYPP are defined as ML/BYPP above the nodes. The tree is rooted to *Lichenothelia convexa* (L1607). Newly generated sequence is in blue and ex-type strains are in bold

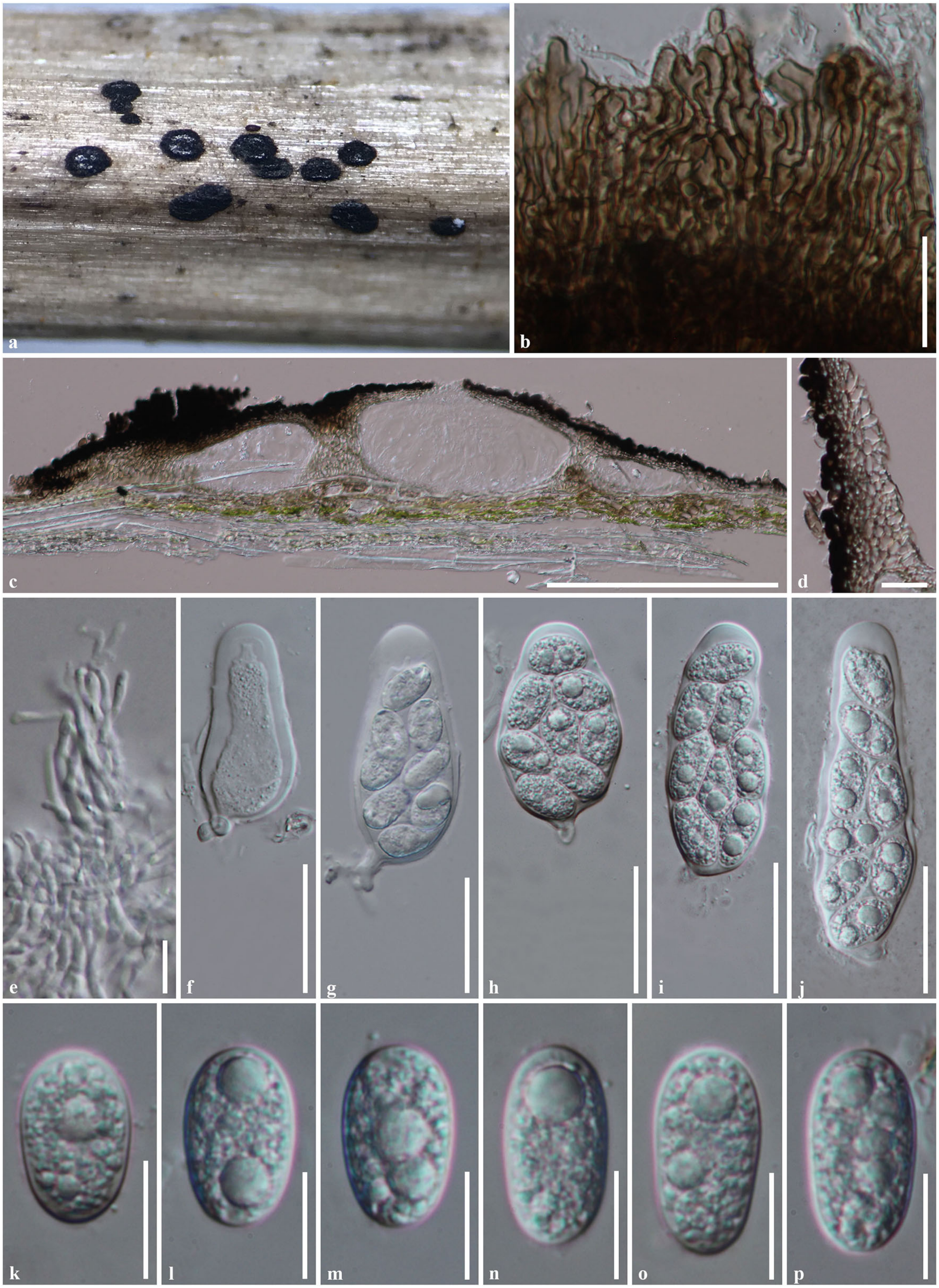
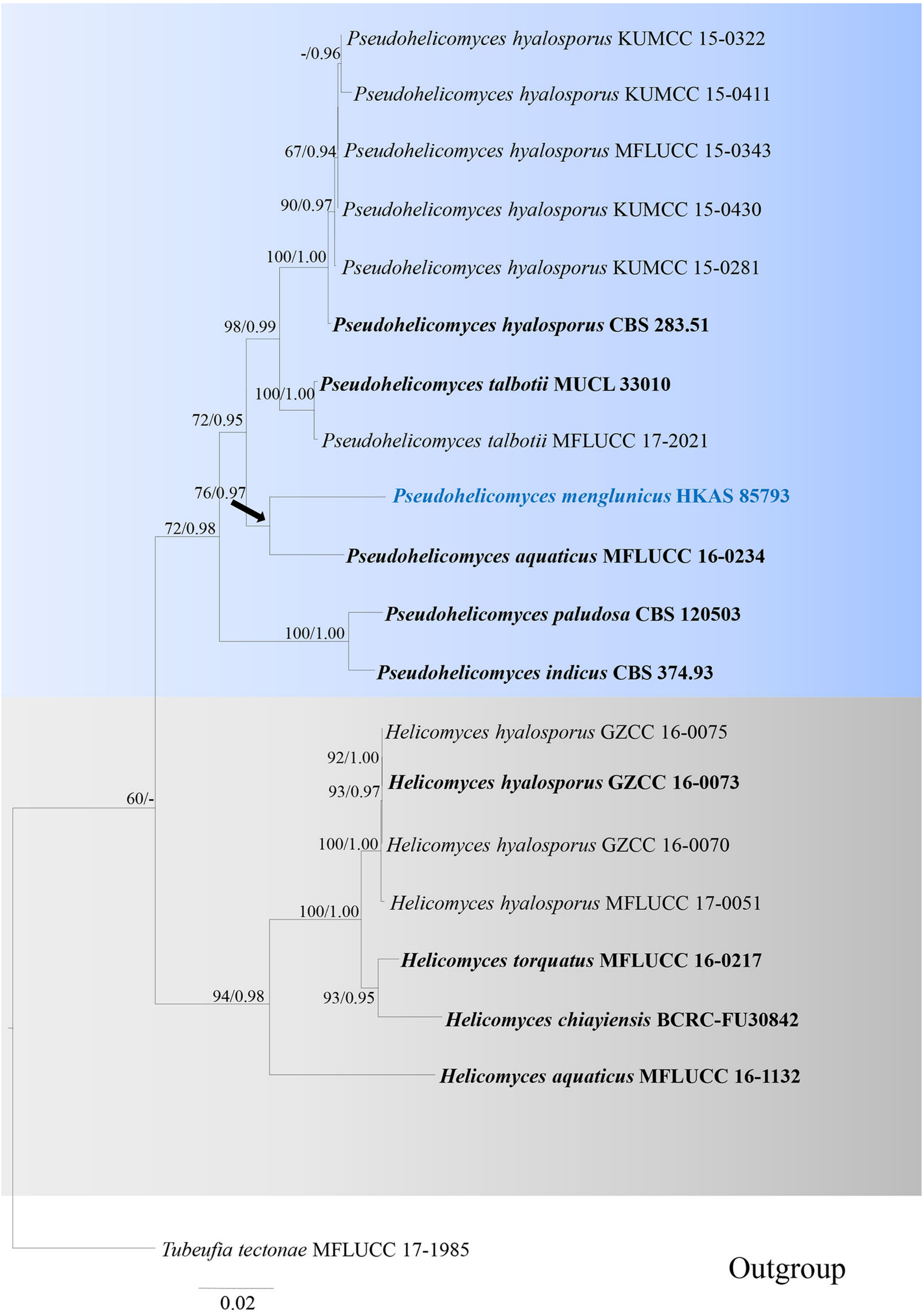


Fig. 56 ***Muyocopron lithocarpi*** (KUN-HKAS 102243). **a** Ascomata on host substrate. **b** Squash mounts showing upper wall of ascoma. **c** Section through the ascostroma. **d** Peridium. **e** Pseudoparaphyses. **f–j** Development of asci. **k–p** Ascospores. *Scale bars* **c** = 200 μm, **f–j** = 30 μm, **b, d** = 20 μm, **e, k–p** = 10 μm



-/0.96
Pseudohelicomyces hyalosporus KUMCC 15-0322
Pseudohelicomyces hyalosporus KUMCC 15-0411
67/0.94
Pseudohelicomyces hyalosporus MFLUCC 15-0343
90/0.97
Pseudohelicomyces hyalosporus KUMCC 15-0430
100/1.00
Pseudohelicomyces hyalosporus KUMCC 15-0281
98/0.99
***Pseudohelicomyces hyalosporus* CBS 283.51**
100/1.00
***Pseudohelicomyces talbotii* MUCL 33010**
72/0.95
Pseudohelicomyces talbotii MFLUCC 17-2021
76/0.97
Pseudohelicomyces menglunicus HKAS 85793
72/0.98
***Pseudohelicomyces aquaticus* MFLUCC 16-0234**
***Pseudohelicomyces paludosa* CBS 120503**
100/1.00
***Pseudohelicomyces indicus* CBS 374.93**
Helicomyces hyalosporus GZCC 16-0075
92/1.00
***Helicomyces hyalosporus* GZCC 16-0073**
93/0.97
60/-
100/1.00
Helicomyces hyalosporus GZCC 16-0070
Helicomyces hyalosporus MFLUCC 17-0051
100/1.00
***Helicomyces torquatus* MFLUCC 16-0217**
94/0.98
93/0.95
***Helicomyces chiayiensis* BCRC-FU30842**
***Helicomyces aquaticus* MFLUCC 16-1132**
Tubeufia tectonae MFLUCC 17-1985
Outgroup
0.02

◀ **Fig. 57** Phylogram generated from the best scoring of the RAxML tree based on a combined ITS, LSU, TEF1-α and RPB2 sequence dataset of *Pseudohelicomyces* and related genus *Helicomyces* in *Tubeufiaceae*. *Tubeufia tectonae* (MFLUCC 17-1985) was selected as the outgroup taxon. Bootstrap support values for maximum likelihood (left) equal to or greater than 60% and the Bayesian posterior probabilities (right) equal or higher than 0.90 BYPP are indicated above the nodes. Ex-type and ex-epitype strains are in bold. Newly generated sequences are indicated in blue

sexual morph species, while those other species in *Cyphellophora* were found as asexual morph. The first record of the sexual characters in *Cyphellophora* (*C. jingdongensis*) was provided by Yang et al. (2018a). However, *C. jingdongensis* differs from *C. filicis* in growing on honey dew excretions from insects, with dark superficial mycelium, scattered, superficial ascomata, without short necks, ellipsoidal to cylindrical asci and 1–3-septate fusoid ascospores. Thus, we introduce *C. filicis* as a new species based on the sexual morph characters and phylogenetic evidence (Figs. 59, 60).

Herpotrichiellaceae Munk

The family *Herpotrichiellaceae* was introduced by Munk (1953) and placed in the order *Chaetothyriales* (Barr 1976; Réblová et al. 2013; Gueidan et al. 2014; Wijayawardene et al. 2018a). The family is characterized by small, superficial, inconspicuous, setose ascomata, fissitunicate asci and greenish grey to brown, phragmosporous or dictyosporous ascospores (Munk 1953; Hyde et al. 2016). Species of this family can be saprobes on decaying wood, bark and leaves and are also found as pathogens on humans and living plants, as well as parasites on fungi or lichens worldwide (Crous et al. 2007b; Untereiner et al. 2011; Wijayawardene et al. 2017a). Fifteen genera are accepted in this family (Wijayawardene et al. 2018a).

Capronia Sacc.

Capronia is a poorly understood ascomycete genus characterized by very small, setose ascomata, lacking paraphyses, fissitunicate asci, and septate, or muriform, hyaline or pigmented ascospores (Munk 1957a, b; Müller et al. 1987; Untereiner et al. 2011; Friebes 2012). Species of this genus are associated with a wide range of hosts as saprobes on rotting wood or bark and decaying stems and leaves of herbaceous plants, or pathogenic on plants as well as parasites on other fungi, or lichens (Untereiner 2000; Untereiner et al. 2011; Wijayawardene et al. 2017a). We introduce a new species *Capronia camelliae-yunnanensis*, collected on *Camellia yunnanensis* in China (Figs. 61, 62).

Capronia camelliae-yunnanensis M. Raza, Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: IF555356; *Facesoffungi number*: FoF04884, Fig. 62

Etymology: Named after the epithet of *Camellia yunnanensis*, the host of which the holotype was collected.

Holotype: HMAS 255435

Saprobic on *Camellia yunnanensis*. **Sexual morph** *Ascomata* 175–200 µm high, 215–220 µm diam., scattered or clustered, solitary, superficial on decorticated bark of host, with papilla, globose to subglobose, lodged on a basal subiculum, which form loose hyphae penetrating the underlying cells, setose around the surface of the wall, setae up to 30 µm long. *Peridium* 20–30 µm wide, thick-walled, of equal thickness, composed of several layers of small, pseudoparenchymatous cells, inner layers comprising hyaline cells, arranged in a *textura angularis*, outer layers comprising brown to dark brown becoming blackened cells of *textura prismatica*. *Hamathecium* composed of dense, 3–5 µm wide, broad, filamentous paraphyses with indistinct septate, not constricted at the septa, embedded in a gelatinous matrix. *Asci* (51–)57–78(–80) × (5–)6–10(–12) µm ($\bar{x}$ = 67.8 × 8.7 µm, n = 40), 8-spored, bitunicate, fissitunicate, broadly cylindrical, short pedicellate with knob-like pedicel, apically broad rounded, with a blunt ocular chamber. *Ascospores* (10–)13–17(–19) × (2–)3–5 µm ($\bar{x}$ = 15.1 × 4.5 µm, n = 40), overlapping 1–3-seriate, hyaline and aseptate when young, becoming light brown to yellowish, ellipsoidal to fusiform, muriform, with 3–7 transverse septa and 1–3 longitudinal septa, slightly constricted at the septa, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 15–20 mm diam. after 5 weeks at 25 ± 2 °C, colonies circular, umbonate, smooth to woolly with entire edge, velvety, smooth at the margin; from above, light green at the fruiting zone, whitish green at the productive zone and ageing zone; from below, light green at the fruiting zone, dark green to blackish at the productive zone, grey at the ageing zone; not producing pigmentation in PDA.

Material examined: CHINA, Yunnan Province, Baoshan City, Longling County, on decorticated bark of *Camellia yunnanensis* Cohen Stuart (*Theaceae*), October 2015, M. Raza, HMAS 255435 (**holotype**), ex-type living culture, CGMCC3.19061.

GenBank numbers: ITS = MH807377, LSU = MH807378, SSU = MH807379.

Notes: Capronia *camelliae-yunnanensis* forms a well-supported clade, sister to *C. pilosella* (P. Karst.) E. Müll. et al. (100% ML and 1.00 BYPP; Fig. 61). *Capronia camelliae-yunnanensis* differs from *C. pilosella* in the shape and size of the ascospores (*C. camelliae-yunnanensis*, (10–)13–17(–19) × (2–)3–5 µm versus 12–14 × 4–4.5 µm, *C. pilosella*; Karsten 1873). *Capronia pilosella* has phragmosporous, fusoid to clavate-fusoid, 3-septate ascospores

Fig. 58 ***Pseudohelicomyces menglunicus*** (KUN-HKAS 85793, **holotype**). **a, b** Colonies on rotten seed coat. **c** Conidiophores with conidiogenous cells. **d**, **e** Conidiophores. **f** Conidiophores bearing conidia. **g** Conidiogenous cells. **h**–**r** Conidia. **s** Germinated conidium. *Scale bars* **a** = 0.5 cm, **b, d, e** = 100 μm, **f, s** = 50 μm, **c, g–r** = 20 μm

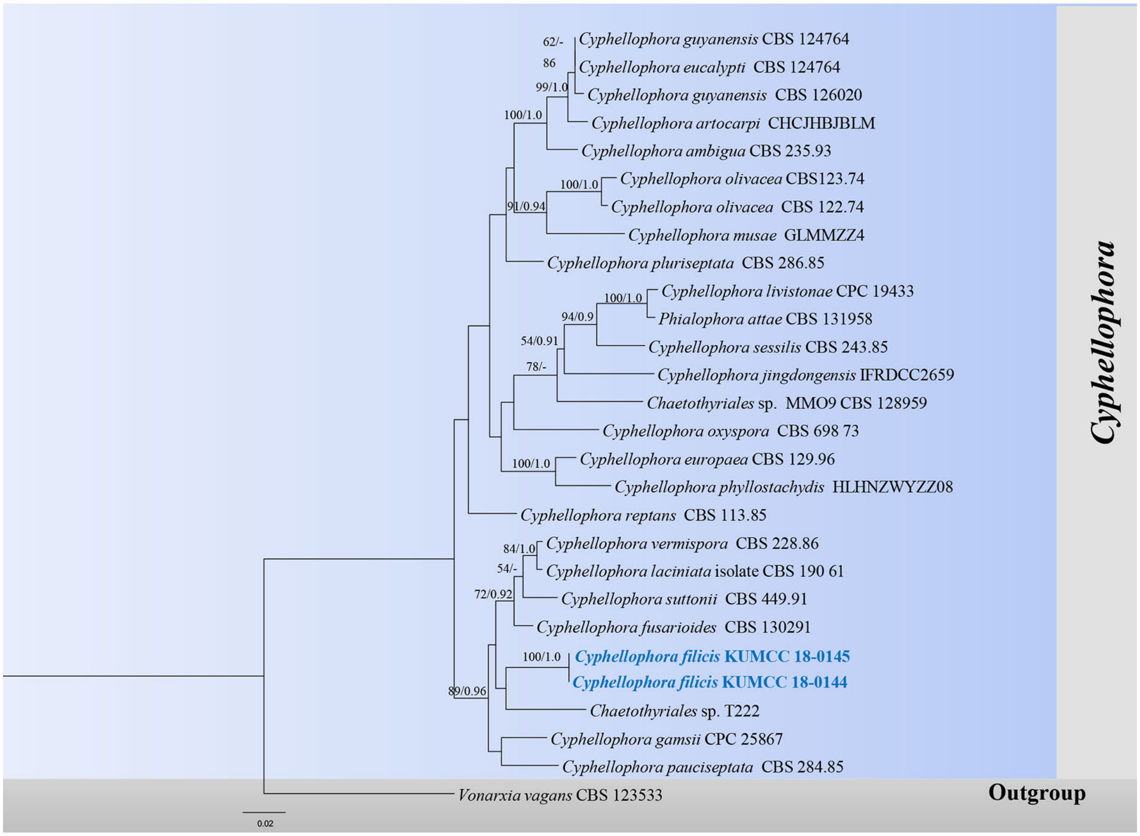


Fig. 59 RAxML phylogenetic tree generated from a combined ITS, LSU and SSU sequence dataset. Bootstrap support values equal or above 50% and Bayesian values equal or above 0.90 BYPP are shown at each node. *Vonarxia vagans* (CBS 123533) was used as the outgroup taxon. Newly generated sequences are in blue

(Karsten 1873; Müller et al. 1987), while *C. camelliae-yunnanensis* has muriform, ellipsoidal to fusiform, ascospores with 3–7 transverse septa and 1–3 longitudinal septa.

Subclass Eurotiomycetidae Geiser & Lutzoni

Eurotiales G.W. Martin ex Benny & Kimbr.

Trichocomaceae E. Fisch.

The family *Trichocomaceae* was introduced by Fischer (1897). This is a large saprobic family in nature with the most well-known genera including *Aspergillus* P. Micheli ex Haller, *Penicillium*, and *Paecilomyces* Bainier. Species belonging to this family have the ability to produce secondary metabolites (mycotoxins or extrolites), and enzymes (Pitt and Hocking 2009; Samson et al. 2010; Houbraken et al. 2011).

Penicillium Link

The genus *Penicillium* was first described by Link in 1809. Species of *Penicillium* are well known and found abundantly in the soil, air, indoor environments and in contaminated foods (Frisvad and Samson 2004; Samson et al. 2010). According to Houbraken and Samson (2011), the genus *Penicillium* was divided into four subgenera: *Aspergilloides* Dierckx, *Furcatum* Pitt., *Penicillium*, and *Biverticillium* Dierckx, and 25 sections. Among the sections of *Penicillium*, section *Citrina* was introduced by Houbraken and Samson (2011) based on phylogenies derived from RPB1, RPB2, Tsr1, and Cct8 sequence data. Currently, section *Citrina* contains 40 species (Houbraken et al. 2011; Visagie et al. 2014a, b). Members of section *Citrina* are found in soil, leaf litter, indoor environments, and food (Pitt 1979; Pitt and Hocking 2009; Samson et al. 2010). The species of section *Citrina* are characterized by the production of relatively small conidia, symmetrically biverticillate conidiophores and ampulliform phialides. They are also known for their ability to produce a variety of extrolites, including mycotoxins, citrinin, and citreoviridin (Houbraken et al. 2011). While, evaluating fungal diversity in soil samples in Korea, a new species was isolated and is described here based on morphological characteristics and phylogenetic analyses (Fig. 63).

Penicillium dokdoense Hyang B. Lee & T.T.T. Nguyen, ***sp. nov.***

Index Fungorum number: IF554459; *Facesoffungi number*: FoF013606, Fig. 64

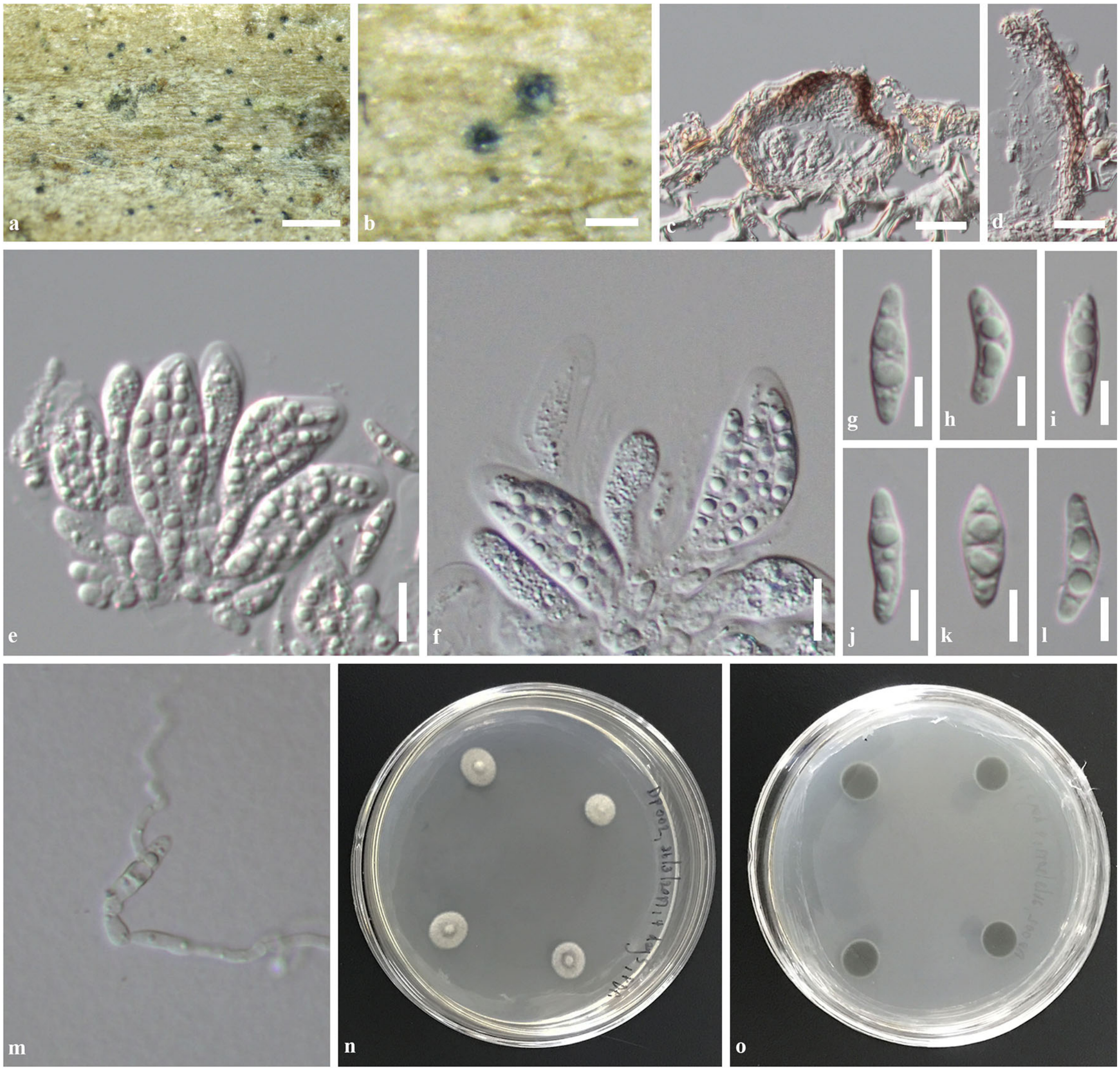


Fig. 60 ***Cyphellophora filicis*** (KUN-KHAS 102220, **holotype**). **a, b** Appearance of ascomata on host surface. **c** Section through ascoma. **d** Section through peridium. **e, f** Asci embedded in a hyaline gelatinous matrix. **g–l** Ascospores. **m** Ascospore germination. **n, o** Culture characteristics on PDA (n = from above, o = from below). *Scale bars* **a** = 500 µm, **b** = 100 µm, **c, d** = 20 µm, **e, f** = 10 µm, **g–l** = 5 µm

Etymology: Named after the place where it was collected, Dokdo Island

Holotype: CNUFC-DDS11-1

Sexual morph Undetermined. **Asexual morph** Hyphomycetous. *Colonies* grow slowly on CYA, reaching 23.5–26 mm diam. at 25 °C in 7 days, grey-green, floccose in centre, soluble pigment absent, margin entire; reverse yellowish white with yellow-brown in centre. *Conidiophores* mostly biverticillate, sometimes monoverticillate, or divaricate, stipes smooth, vary greatly in length, septate, 2–3.5 µm wide. *Metulae* cylindrical, 2–5 per stipe, 10.5–17.5 × 2.5–4.2 µm. *Phialides* ampulliform, 3–9 per metula, 6.7–11.5 × 2–3.5 µm. *Conidia* roughened, globose to subglobose, or ellipsoidal, and dark blue-green, 2–3.5 × 2–3 µm.

Culture characteristics: The isolate grew over a wide range of temperatures with varying growth rates on MEA, CYA, YES and CREA. The average growth rates of CNUFC-DDS11-1 on MEA, CYA, YES, and CREA medium at 25 °C were 34.5, 24.5, 22, and 14.5 mm per 7 days, respectively. Optimal growth was observed around 25 °C, slow growth was observed below 10 °C, and no growth at 37 °C.

Material examined: REPUBLIC OF KOREA, from soil in Dokdo Island in the East Sea of Korea, June 2014, CNUFC-DDS11-1 (**holotype**); **isotype** in Korean

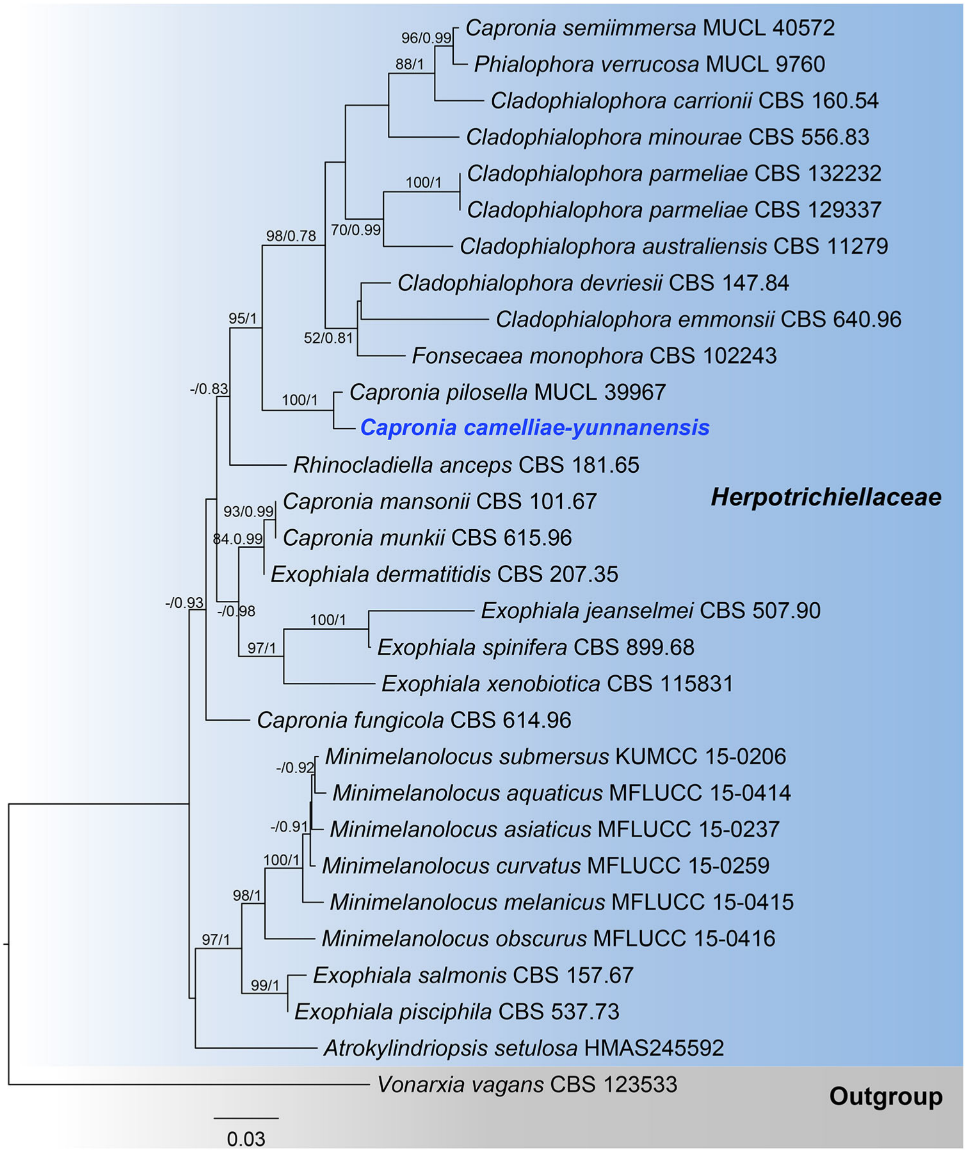


Fig. 61 Phylogenetic tree generated from maximum likelihood (RAxML) based on a combined ITS, LSU and SSU sequence dataset of *Herpotrichiellaceae*. Maximum likelihood bootstrap support values greater than 50% and Bayesian posterior probabilities greater than 0.75 BYPP are indicated on the notes. The new isolate is in blue. The tree is rooted with *Vonarxia vagans* (CBS 123533)

Collection for Type Cultures (KCTC, Daejeon, Korea), ex-type living culture, JMRC:SF:013606.

GenBank numbers: ITS = MG906868, TUB2 = MH243037, CMD = MH243031 (CNUFC-DDS11-1); ITS = MG906869, TUB2 = MH243038, CMD = MH243032 (CNUFC-DDS11-2).

Notes: The data from combined sequence analyses of the two loci (Fig. 63) reveal that *Penicillium dokdoense*, *P. terrigenum* Houbraken et al., *P.* cf. *terrigenum* and *P. copticola* Houbraken et al. are closely related. *Penicillium dokdoense* shares several similarities with *P. terrigenum* as its growth on CREA is poor with no acid production, but this species differs from *P. terrigenum* in terms of reverse colour on CYA and YES, and colony features on CYA. Furthermore, *P. dokdoense* produces globose to subglobose, or ellipsoid conidia and biverticillate, monoverticillate, or divaricate conidiophores, in contrast to the mostly ellipsoid conidia and biverticillate sporangiophores of *P. terrigenum*. *Penicillium terrigenum* and *P. copticola* grew at a similar range of temperatures from 25 °C to 30 °C, whereas *P. dokdoense* grew slowly. *Penicillium dokdoense* grows and sporulates at 35 °C, while, *P.* cf. *terrigenum* does not grow above 30 °C. At 5 °C, *P. dokdoense* and *P. copticola* were both capable of growth, whereas *P. terrigenum* was not. When grown on CYA, colonies of *P. dokdoense* are weakly wrinkled, while colonies of *P. terrigenum* are strongly wrinkled. The results of morphological and comparative sequence analyses of *P. dokdoense* indicate that it is a distinct species from *P. terrigenum*, *P.* cf. *terrigenum*, and *P. copticola*. Thus, *P. dokdoense* is proposed.

Class Lecanoromycetes O.E. Erikss. & Winka

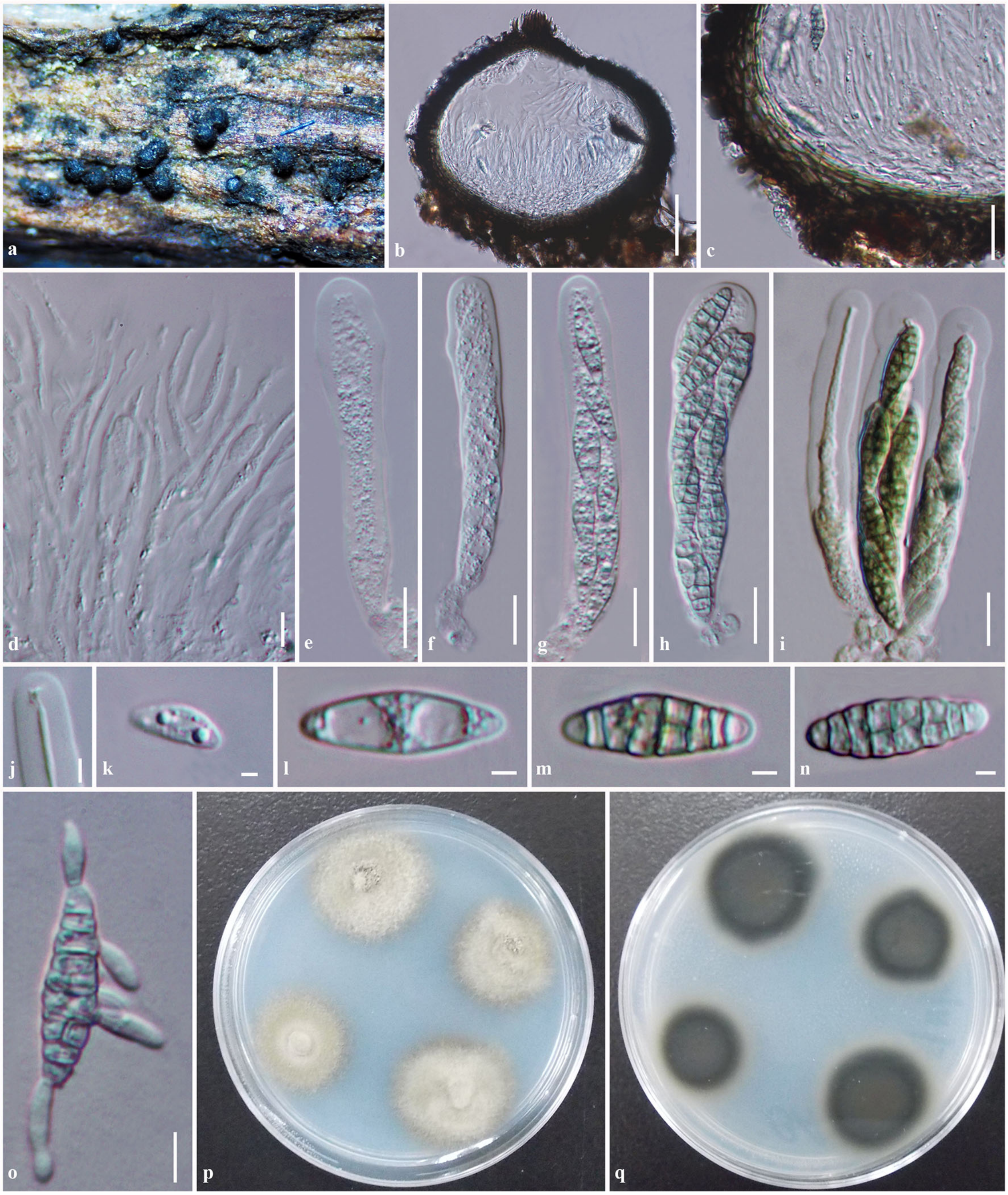


Fig. 62 ***Capronia camelliae-yunnanensis*** (HMAS 255435, **holotype**). **a** Blackish ascomata on decorticated bark of *Camellia yunnanensis*. **b** Vertical section of ascoma. **c** Peridial structure. **d** Paraphyses. **e–h** Asci. **i** Asci stained with Melzer's reagent. **j** Apical ring stained with Melzer's reagent. **k, l** Immature ascospores. **m, n** Mature ascospores. **o** Germinated ascospore. **p, q** Culture characteristics on PDA (**p** = from above, **q** = from below). *Scale bars* **b** = 50 μm, **c, d** = 20 μm, **e–i** = 10 μm, **o** = 5, **j–n** = 2 μm

We follow the latest treatment and updated accounts of Lecanoromycetes in Miadlikowska et al. (2014) and Kraichak et al. (2018). The updated outline and notes of the genera in Lecanoromycetes was provided by Wijayawardene et al. (2017a, 2018a).

Lecanoromycetes, families *incertae sedis*

Micropeltidaceae Clem. & Shear

The family *Micropeltidaceae* was introduced by Clements and Shear (1931) as 'Micropeltaceae' and is typified by *Micropeltis* Mont. with *M. applanata* Mont. as the type species. The family comprises foliar, biotrophic epiphytes, which are mostly found on the lower leaf surface as small black dots. *Micropeltidaceae* species are characterized by superficial, flattened, black-blue or greenish to black thyriothecia, easily removed from the host surface, poorly developed at the base, the wall comprising interwoven hyphae, with a central ostiole and ascospores are septate and hyaline (Clements and Shear 1931; Wu et al. 2011; Hyde et al. 2013; Hongsanan et al. 2015; Hongsanan and Hyde 2017). *Micropeltis phetchaburiensis* sp. nov. is introduced based on its morphological characteristics coupled with phylogenetic analyses of a combined LSU and SSU sequence dataset (Fig. 65). The new species was collected from living leaves in Thailand.

Micropeltis Mont.

We follow the latest treatment and updated account of *Micropeltis* in Hongsanan and Hyde (2017).

Micropeltis phetchaburiensis Dayarathne, Hongsanan & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555294; *Facesoffungi number*: FoF04841, Fig. 66

Etymology: Name reflects Phetchaburi Province in Thailand, from where the species was collected.

Holotype: MFLU 18-1408

Epiphytic appearing as small black dots, superficial, on the upper surface of living leaves, superficial hyphae absent. **Sexual morph** *Thyriothecia* 75–90 × 140–160 µm diam. ($\bar{x}$ = 80 × 150 µm, n = 5), solitary, superficial on

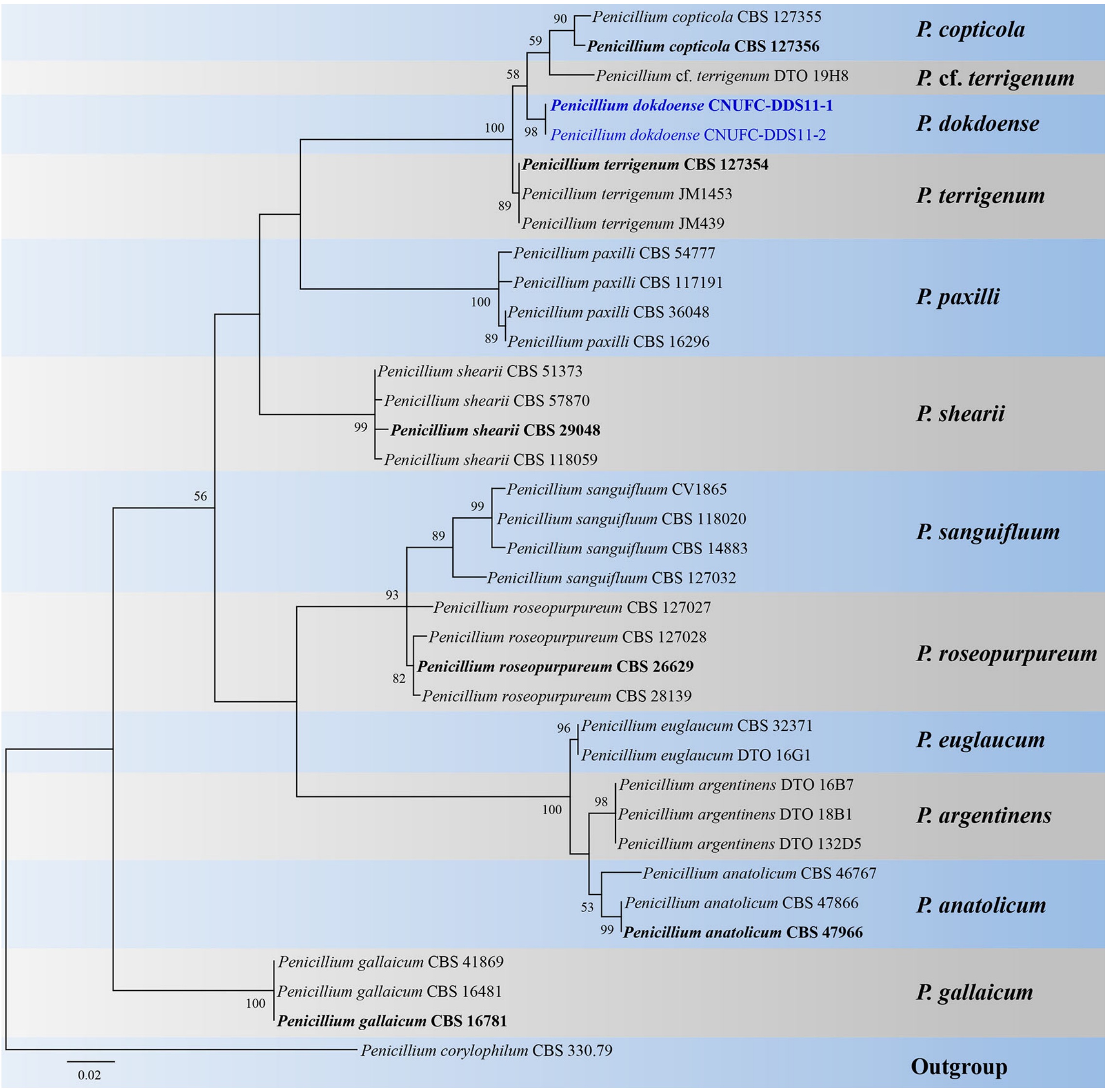


Fig. 63 Phylogenetic tree based on maximum likelihood analysis of a combined beta tubulin (TUB2) and calmodulin (CMD) dataset for *Penicillium dokdoense* and related species within the sect. *Citrina*. Sequence of *Penicillium corylophilum* was used as outgroup taxon. Numbers at the nodes indicate the bootstrap values (≥ 50%) from 1000 replications. The bar indicates the number of substitutions per position. New taxa are in blue and ex-type strains in bold

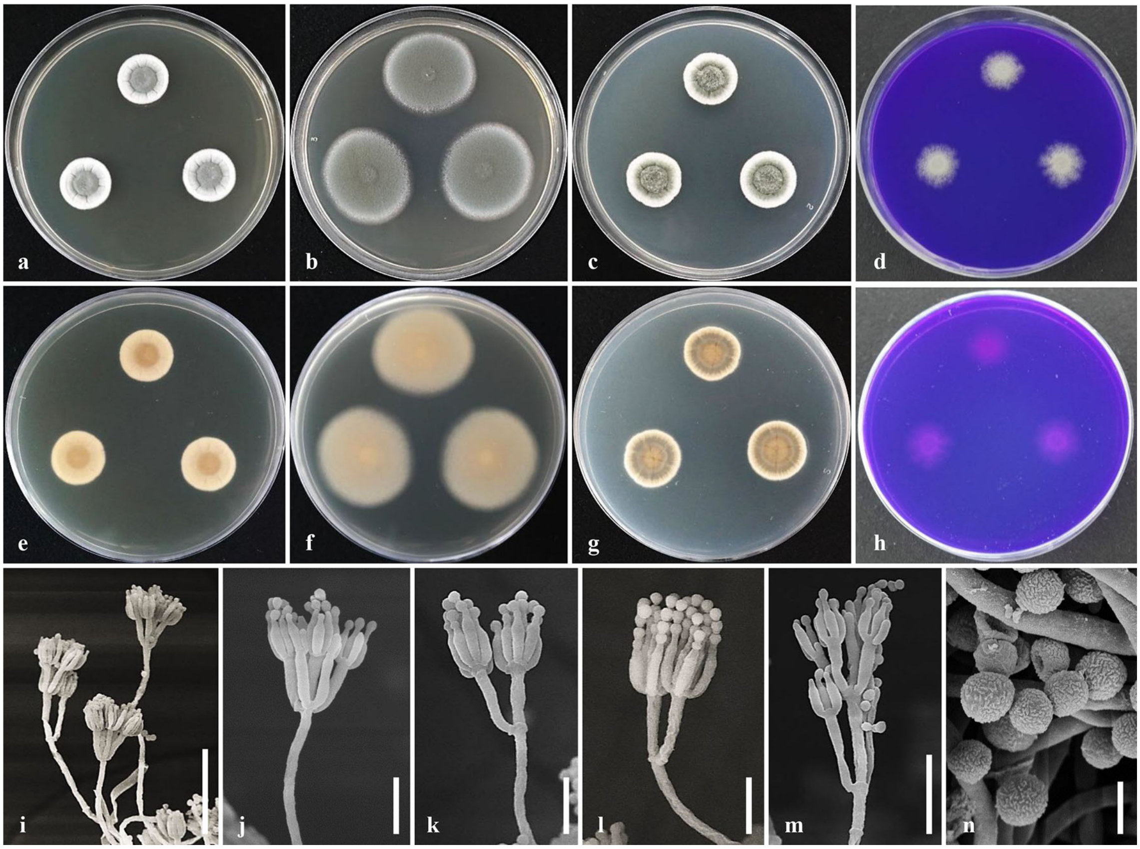


Fig. 64 ***Penicillium dokdoense*** (CNUFC-DDS11-1, **holotype**). **a, e** Colonies in yeast extract sucrose agar (YES). **b, f** Colonies in malt extract agar (MEA). **c, g** Colonies in Czapek yeast autolysate agar (CYA). **d, h** Colonies in creatine sucrose agar (CREA). (**a–d**: obverse view, **e–h**: reverse view). **i–m** Verticillate conidiophores and conidia on phialides. **n** Conidia. *Scale bars* **i** = 20 µm, **j–l** = 10 µm, **m** = 5 µm, **n** = 3 µm

the surface of hosts, circular, membranous, black, easy to detached, base poorly developed, with a central, irregular ostiole. *Upper walls* comprising an irregular, meandering arrangement of hyphae, from the central ostiole to the outside. *Peridium* 35–50 µm wide, composed of two strata, the outer stratum having bluish to black, occluded walls, inner stratum of greenish to hyaline, flattened cells. *Hamathecium* with evanescent pseudoparaphyses. *Asci* 50–68 × 11–16 µm ($\bar{x}$ = 60 × 14 µm, n = 10), 8-spored, bitunicate, broadly cylindrical to fusiform, with a short pedicel, apically rounded with ocular chamber. *Ascospores* 16–20 × 2–4 µm ($\bar{x}$ = 18 × 3 µm, n = 20), overlapping 2–3-seriate, hyaline, clavate, 3-septate, constricted at the septa, narrowly rounded at both ends, smooth-walled, surrounded by a mucilaginous sheath. **Asexual morph** Undetermined.

Material examined: THAILAND, Phetchaburi Province, Prachuap Khiri Khan, 77230 Bang Saphan, Ron Thong, on living leaves of an unidentified plant, 14 December 2015, M. Dayarathne, KLAP011 (MFLU 18-1408, **holotype**; HKAS102010, **isotype**).

GenBank numbers: LSU = MH656405, SSU = MH656406.

Notes: *Micropeltis phetchaburiensis* resembles *M. dendrophthoes* Hongsanan & K.D. Hyde and *M. zingiberacicola* H.X. Wu & K.D. Hyde in forming broadly cylindrical to fusiform asci and hyaline, clavate, septate ascospores (Wu et al. 2011; Hongsanan et al. 2015). *Micropeltis phetchaburiensis* can be distinguished from *M. dendrophthoes* and *M. zingiberacicola* in having 3-septate ascospores with the 4 cells being equal in length and width, while ascospores of the other two species are 4–5-septate and enlarged at the first cell and relatively longer lower end cells. In our phylogenetic analyses of a combined LSU and SSU sequence dataset, *M. phetchaburiensis* forms a basal lineage to *M. dendrophthoes* and *M. zingiberacicola* with moderate bootstrap support (97% ML and 93% MP; Fig. 65).

Class Leotiomycetes O.E. Erikss. & Winka

We follow the latest treatment and updated accounts of Leotiomycetes in Zhang and Wang (2015), Jaklitsch et al. (2016a) and Wijayawardene et al. (2018a) for the taxonomic outline of this class.

Helotiales Nannf. ex Korf & Lizoň

Lachnaceae Raitv.

Raitviir (2004) raised Nannfeldt's tribe Lachneae (fam. *Hyaloscyphaceae*; Nannfeldt 1932) to the family level and designated *Lachnum* Retz. as the type genus. Han et al. (2014) showed that *Lachneae* formed a monophyletic lineage within *Hyaloscyphaceae sensu lato*, justifying the existence of *Lachnaceae*. Jaklitsch et al. (2016a) and Wijayawardene et al. (2018a) recognize 16 genera in this family. Phylogenetic relationships of selected lachnoid taxa were studied previously by Cantrell and Hanlin (1997) and Hosoya et al. (2010). We introduce a new monospecific genus *Velebitea* in the family *Lachnaceae* based on microscopic and macroscopic features.

Velebitea I. Kušan, Matočec & Jadan, ***gen. nov.***

MycoBank number: MB827753; *Facesoffungi number*: FoF05713

Etymology: Named after the mountain, Velebit, on which it was collected.

Sexual morph *Ascomata* apothecial, comparatively robust and medium sized, superficial, stipitate, solitary or gregarious, deeply cupulate when young, becoming shallowly cupulate to ± plate-shaped. *Hymenium* creamy whitish, yellowish with age, margin upright, covered with long whitish hairs, as well as whole excipulum and stipe throughout the base, excipulum paler than hymenium, stipe centrally attached, tapering towards the base, base brownish. *Subhymenium* equally thick or thicker than medullary or ectal excipulum, composed of hyaline *textura epidermoidea-intricata*, in living state clearly discerned from the medulla. *Marginal texture* of hyaline *textura porrecta-prismatica*, often with abundant yellow resinous inclusions, beset with ± tidily organized cylindrical marginal hairs which are always clearly separated from excipular ones by a small hairless area just at the point of hymenial base level, individual hairs ± straight, multi-celled, markedly shorter than excipular flank hairs, apical cell cylindric-obtuse to subclavate, walls thin and hyaline, cells without refractive content when in living state, only basal 1–2 cells with firmly attached KOH resistant granules, not stainable in cotton blue, with additional abundant loosely attached KOH soluble pale yellowish resinous granules, no crystals. *Medullary excipulum* composed of hyaline densely woven *textura intricata*, producing small hyaline crystalloid particles with age, sometimes having abundant yellow resinous inclusions, intercellular spaces overall slightly gelified. *Ectal excipulum* composed of single layer of *textura prismatica* with cells running ± parallel to the surface, walls somewhat thickened, especially in some outermost cells, basal areas regularly with highly refractive golden yellow resinous accumulations; surface beset with very untidily intricately organized flexuous excipular hairs, multi-celled, longer than marginal hairs, walls thin, with apical localized thickenings in some hairs, only basal 1–2 cells with firmly attached KOH resistant granules, regularly supplemented by KOH soluble loosely attached pale yellowish granules, surface irregularly embedded in abundant gel plaques clearly stained lilac in brilliant cresyl blue, in cotton blue walls not cyanophilic, yellow resinous accumulations dissolved. *Overall texture and hairs* in Lugol's solution without any amyloid reactions, all yellow resinous accumulations in texture are rapidly soluble in KOH. *Paraphyses* cylindrical, apically obtuse, straight, not branching in the upper part, apical and often subapical cells contain hyaline non-refractive vacuoles. *Asci* 8-spored, elongated cylindrical-deltoid, apex conical obtuse, protruding above paraphyses at full maturity, arising from simple septate ascogenous cells, in Lugol's solution apical apparatus moderately euamyloid of *Calycina*-type. *Ascospores* elongated fusoid, ± straight to bent, bilaterally symmetrical, always 1-celled in full maturity, smooth, hyaline, poles tapered to sub-obtuse, eguttulate or with several minute guttules, uninucleate, the remaining sporoplasm regularly occupied by several conspicuous non-refractive vacuoles, when freshly ejected without sheath; in Lugol's solution cytoplasm without glycogen accumulations. **Asexual morph** Undetermined.

Type species: *Velebitea chrysotexta* I. Kušan, Matočec & Jadan

Notes: A data matrix for alignment was constructed to determine the phylogenetic position of *Velebitea chrysotexta* within *Lachnaceae* and also to test phylogenetic proximity to *Hyaloscyphaceae* (*Amicodisca virella* (P. Karst.) Huhtinen), and *Tetracladium* spp. Phylogenetic analysis (Fig. 67) included the ITS and LSU sequences generated from the holotype of *Velebitea chrysotexta* and other related sequence data, retrieved from GenBank as well as a newly sequenced collection of *Neodasyscypha cerina* (Pers.) Spooner (CNF 2/10442; ITS = MH886408, LSU = MH886412) which was collected from fallen decorticated branch of *Fagus sylvatica* L. in Croatia. Sequences of *Hymenoscyphus fructigenus* (Bull.) Gray were used as an outgroup taxon. Maximum likelihood analysis of the concatenated ITS and LSU alignment was performed by MEGA7 (Kumar et al. 2016), including 1361 total characters in the final dataset. The phylogeny based on concatenated analysis of ITS and LSU nests the genus *Velebitea* in the family *Lachnaceae* as a separate lineage having comparatively basal position not belonging to any of tested genera (Fig. 67).

Megablast search of NCBIs GenBank nucleotide database using the ITS sequence of *Velebitea chrysotexta* (CNF 2/10072, GenBank no. MH886407) shows that the closest hits belong to *Lachnellula* spp. with the similarities between 89% and 91% similarities. *Lachnellula* P. Karst. is a genus in *Lachnaceae*, strictly confined to coniferous hosts

(Dharne 1965). On the other hand, the closest hits using the LSU sequence (GenBank no. MH886411) are *Tetracladium furcatum* Descals (GenBank no. EU883428; similarity = 907/1009 (90%), gaps = 45/1009 (4%)) and *T. maxilliforme* (Rostr.) Ingold (GenBank no. EU883429 and EU883430; both with similarity = 903/1008 (90%), gaps = 43/1008 (4%)). *Tetracladium* De Wild. is an aquatic hyphomycete genus (Letourneau et al. 2010) classified as *Helotiales, incertae sedis* (Wijayawardene et al. 2017a, 2018a), but phylogenetic affinity is close to *Helotiaceae*, and *Hyaloscyphaceae* (Wang et al. 2015). Certain similarity exists between *Velebitea* and *Tetracladium* in their ecological preference to a colder climate; the sexual morph of *Velebitea* lives in subalpine forests with beech (*Fagus*) while some members of the genus *Tetracladium* were recorded in cold snow-covered soil in a glacier zone (Kuhnert et al. 2012).

Together with the genus *Dasyscyphella* Tranzschel, *Velebitea* is different from all other genera in the family *Lachnaceae* by partially granulated hyaline hairs. *Dasyscyphella* is clearly polyphyletic (Hosoya et al. 2010; this study) and therefore in need of taxonomic rearrangement. Since the type species of the genus *Dasyscyphella*, *D. cassandrae* Tranzschel is not present in public DNA sequence databases, we included all other available species from this genus in our phylogenetic analysis because species currently ascribed to *Dasyscyphella* display highest similarity to our material based on non-molecular data. The polyphyly of the genus *Dasyscyphella* could be in line with wide diversity of certain non-molecular features that may play important role in future species distinguishing at generic level, such as existence of hair crystals, resinous exudates and its microchemical properties, hair wall granulation degree, hamathecial features, details in ecology, apothecial development and anatomy, despite of high similarity among many of species in terms of "standard" microscopical characters (e.g. spore and ascus shape/measurements). Many of these characters already efficiently delimitate some monophyletic lachnacean genera, viz. *Capitotricha* (Raitv.) Baral, *Brunnipila* Baral and

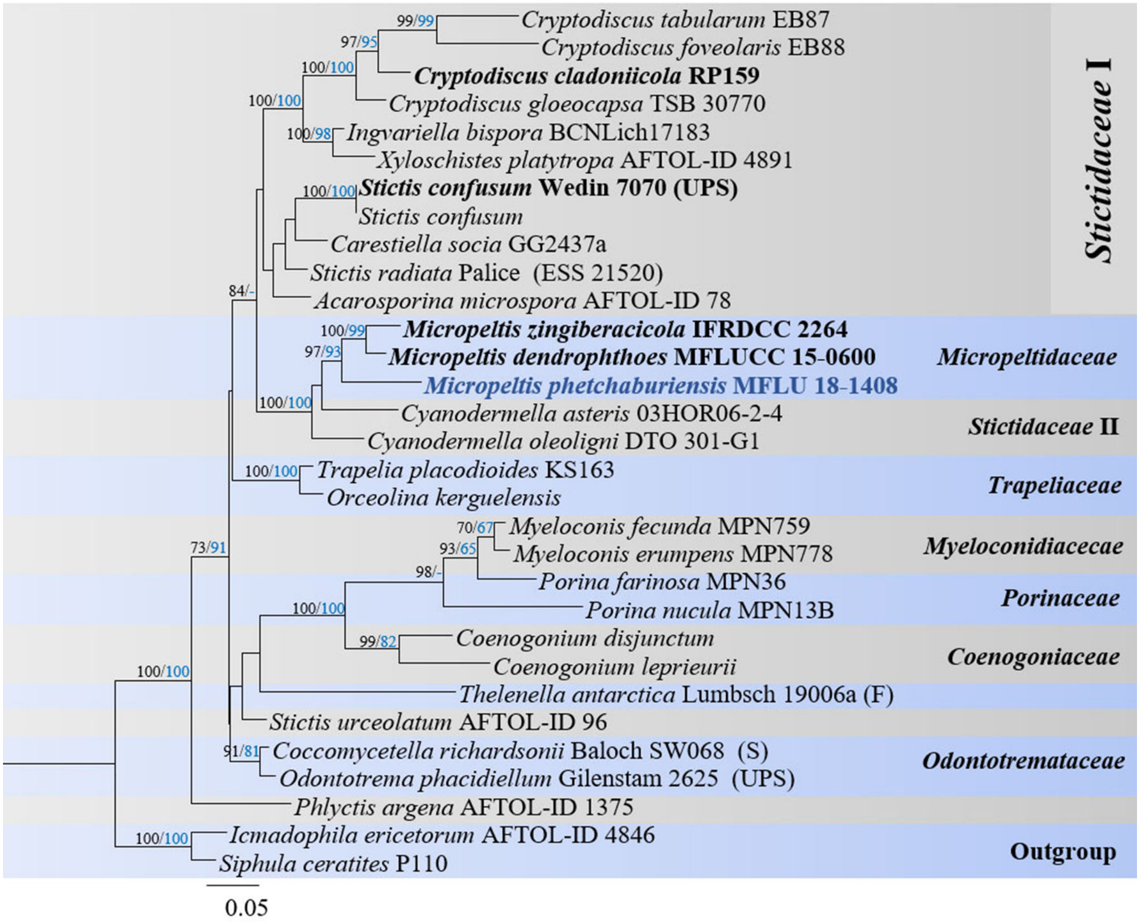


Fig. 65 Phylogram generated from maximum likelihood (RAxML) analysis based on combined LSU and SSU sequence dataset of representative families in Lecanoromycetes. Tree is rooted with *Icmadophila ericetorum* (AFTOL-ID 4846) and *Siphula ceratites* (P110). Maximum likelihood bootstrap (black) and maximum parsimony bootstrap (blue) values > 65% are given above the nodes. The scale bar indicates 0.05 changes. New isolate is in blue. Ex-type strains are indicated in bold

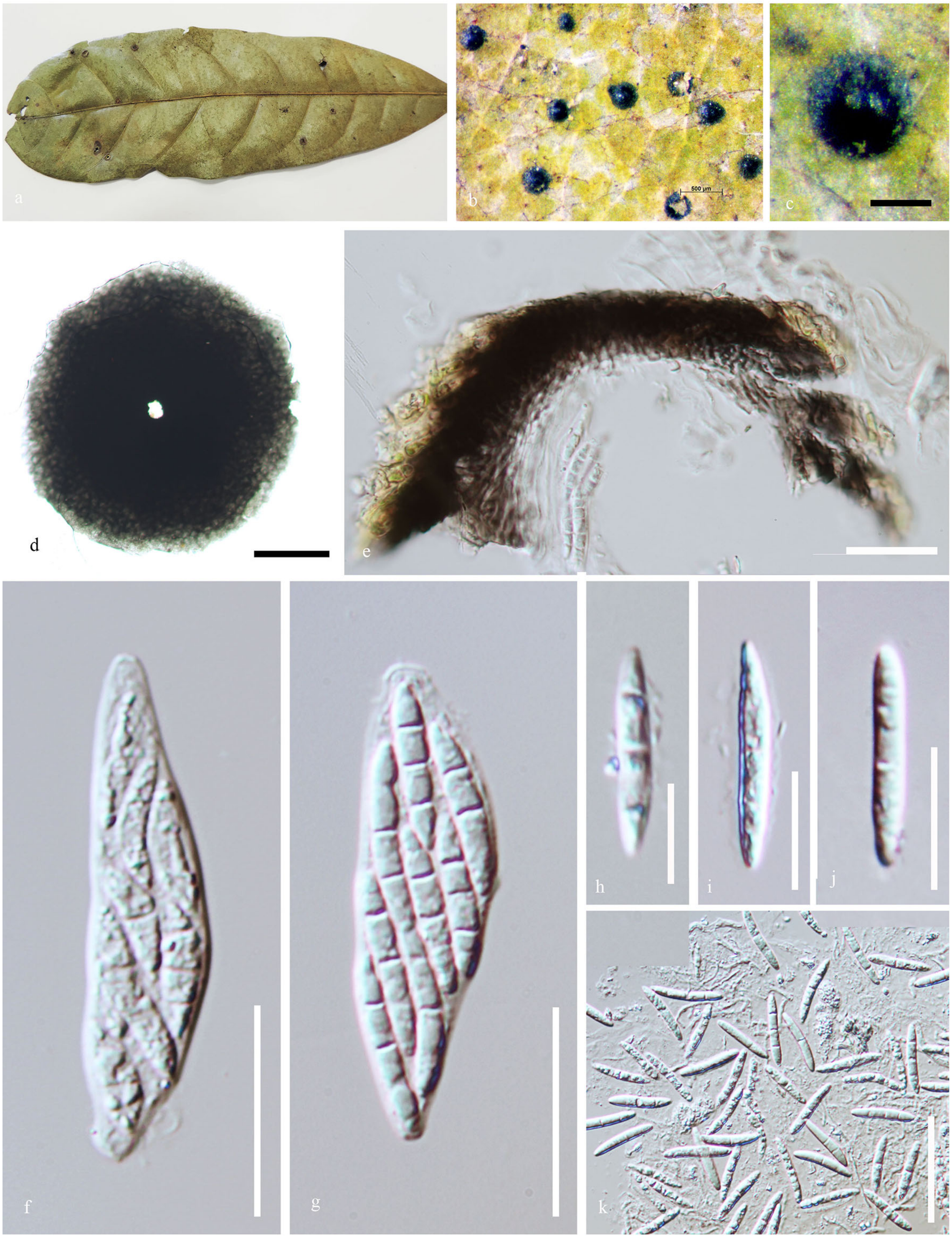


Fig. 66 ***Micropeltis phetchaburiensis*** (MFLU 18-1408, **holotype**). **a–c** Appearance of thyriothecia on host surface. **d** Thyriothecium viewed in squash mount. **e** Vertical section through thyriothecium. **f, g** Asci. **h–k** Ascospores. *Scale bars* **c** = 100 µm, **d, e** = 50 µm, **f, g, k** = 20 µm, **h–j** = 10 µm

Lachnellula. *Dasyscyphella cassandrae*, the type species of the genus, differs strikingly from *Velebitea chrysotexta* by very elongate flexuous-cylindric, septate ascospores, overall absence of KOH soluble resinous lumps and, together with all other known species currently ascribed to the genus *Dasyscyphella* in having only the apical (rarely also subapical) smooth hair cell. Whereas, hairs in *V. chrysotexta* are smooth except in basal 1–2 cells. Hairs in

D. cassandrae (as well as in many other species) are longer at the margin than on excipular flanks, quite opposite in *V. chrysotexta*. A number of species currently ascribed to a genus *Dasyscyphella* have hairs bearing conspicuous calcium oxalate crystals and/or crystal druses (such as *D. nivea* positioned well aside from *V. chrysotexta* in our phylogenetic analysis) that are completely lacking in *V. chrysotexta*. Nearly all species currently ascribed in the genus *Dasycyphella* have either lanceolate or cylindrical-pointed paraphyses (as in *D. cassandrae*). There are however some species of the genus *Dasyscyphella* that according to Raitviir (2002), also Dennis (1949), produce resinous pigments comparable to *Velebitea chrysotexta*: *Dasyscyphella claviculata* (Velen.) Baral & Svrček, *D. crystallina* (Fuckel) Raitv., *D. rubi* Raitv., *D. conicola* (Rehm) Raitv. & Arendh., *D. nivea* (R. Hedw.) Raitv., *D. tamajonica* (Raitv. & R. Galán) Raitv. (all producing calcium oxalate crystals, mostly having different ecology), *D. mughonicola* (Svrček) Raitv. & Arendh. (whose asci arising from croziers, coniferous substrate), *D. patuloides* Raitv. & R. Galán (producing hyaline resin, asci arising from croziers, having phyllophilous ecology) and *D. sulphuricolor* (Peck) J.H. Haines (producing brownish resin that reacts vinaceous with KOH). Much work is still to be done to uncover true phylogenetic affinities of a number of species currently accommodated in *Dasyscyphella* which might belong to severally phylogenetic lineages representing separate genera.

Velebitea chrysotexta I. Kušan, Matočec & Jadan, ***sp. nov.***

MycoBank number: MB827754; *Facesoffungi number*: FoF05714, Figs. 68, 69, 70

Etymology: Refers to its yellowish pigment inclusions in the apothecial texture

Holotype: CNF 2/10072

Sexual morph *Ascomata* apothecial, superficial, stipitate, solitary or gregarious, deeply cupulate when young, becoming shallowly cupulate to ± plate shaped, 2.5–3.2 mm high, 1.1–3 mm diam. *Hymenium* 80–105 µm thick, creamy whitish in primordial stage, becoming creamy to pale ochre yellow, yellowing with age, margin upright, covered with whitish hairs, as well as whole excipulum and stipe throughout the base, excipulum paler than hymenium, completely covered with whitish hairs, stipe 1.5–2.2 × 0.6–1 mm, centrally attached, tapering towards the base, hairy throughout, base brownish. *Subhymenium* 32–47 µm thick, composed of hyaline *textura epidermoidea-intricata*, cells 3.4–5.1 µm wide, while in living state clearly discerned from the medulla. *Marginal texture* forming very thin layer, composed of hyaline *textura porrecta-prismatica*, often containing abundant yellow resinous accumulations, beset with ± tidily organized marginal hairs which are always clearly separated from excipular ones by small hairless area just at the point of hymenial base level, individual hairs ± straight but bending slightly towards the hymenial rim, projecting towards the marginal surface perpendicularly, 5–7-celled, 66–109 µm long, 3.7–5.6 µm wide at the base, 2.2–3.8 µm in the middle and 2.3–3.7 µm in the apical part, apical cell cylindric-obtuse to subclavate, individual cells prismatic, containing low refractive globules, walls hyaline and refractive, 0.2–0.5 µm thick, may be slightly thickened in dead state, cells without refractive content when still alive, wall of the basal 1–2 cells firmly granulate, additionally beset with loosely attached pale yellowish granules, no crystals; in brilliant cresyl blue numerous non-refractive hyaline vacuoles stained deep lilac-violet to violet after longer exposure, cytoplasm in dead apical cells turquoise blue, basal wall granules grey cyan to violet grey, walls unstained; after adding 2.5% KOH hair granules persistent, subhyaline golden yellow accumulations instantly dissolved, for few moments giving localized yellow solution area; in cotton blue hair walls not cyanophilic, apical cells cytoplasm pale blue, wall granules pale cyan, yellow resinous accumulations dissolved. *Medullary excipulum* 30–44 µm thick, composed of hyaline densely woven *textura intricata* intertwining with ± vertical cells, cells thin-walled, 2.2–3.7 µm wide, running predominantly parallel to the excipulum surface, producing hyaline crystalloid particles with age, sometimes containing abundant yellow resinous accumulations; in brilliant cresyl blue intercellular space slightly rosy-lilac (gelified); in cotton blue walls not cyanophilic. *Ectal excipulum* 38–52 µm thick, composed of *textura prismatica*, cells 13.6–46.7 × 4.5–10.9 µm, running ± parallel to the surface, walls somewhat thickened, especially in some outermost cells, basal area with highly refractive golden yellow resinous accumulations; surface ornamented with flexuous excipular hairs which are very untidily intricately organized, 4–11-celled, 92–156 µm long, 2.5–4.1 µm wide at the base, 2.2–3.1 µm in the middle part and 2.4–3.7 µm at the apex, individual cells prismatic, walls highly refractive, sometimes with localized apical thickenings, in dead state more pronounced, 0.7–0.8 µm thick, basal 1–2 cells firmly granulate, with additional loosely attached pale yellowish granules, no crystals; in brilliant cresyl blue textural cells' cytoplasm lilac, thickest walls greenish cyan, slightly gelified, surface with revealed abundant, lilac irregular gel plaques; in cotton blue walls not cyanophilic, cytoplasm bluish, yellow resinous accumulations dissolved. *Stipe* excipulum of hyaline celled, wavy *textura prismatica*, cells 17.4–34.2 × 5.6–9.3 µm, walls thickened in the outermost cells, giving rise to hyaline hairs as those on ectal excipulum, 90–136 µm long, 3.8–4.4 µm wide at the base, 2.7–3.5 µm in the middle and 1.8–2.8 µm at the apical part, containing rich golden-yellow partly crystalloid accumulations. *Overall texture and hairs* in Lugol's solution without any amyloid reactions, while resinous matter is rapidly soluble by KOH. *Paraphyses* cylindrical, apically obtuse, straight, not branching in the upper part, apical cell 19.3–35.7 × 2.1–3.2 µm, apical and often subapical cells contain hyaline non-refractive vacuoles in a living state (not vacuolar bodies), dead cells with highly refractive lemon yellow content; in Lugol's solution, brilliant cresyl blue and cotton blue unstained. *Asci* 72.6–95.1 × 5.5–7.2 µm, elongated cylindrical deltoid, apex conical obtuse, protruding above paraphyses tips up to 12 µm at full maturity, *pars sporifera* 23.5–38.6 µm, 8-spored, arising from simple septate ascogenous cells, sometimes with lateral protuberance; in Lugol's solution apical apparatus moderately euamyloid, of *Calycina*-type. *Ascospores* (8.2–)8.4–10.8–14.2(–15.2) × (2.1–)2.2–2.6–2.8 µm, Q = (3.2–)3.3–5.4–5.7(–6) (n = 125), elongated fusoid, ± straight to slightly bent or sickle shaped, rarely subsigmoid, bilaterally symmetrical, poles tapered to subobtuse, 1-celled, smooth, hyaline, overmatured 1-septate, eguttulate or with several minute guttules, 0.2–0.6 µm diam., uninucleate, nucleus centrally positioned, 1.3–1.4 µm in diam., the remaining sporoplasm regularly occupied by several conspicuous non-refractive vacuoles; 3–4 ascospores at uppermost positions in living mature asci markedly shorter, mostly 2-seriate, when freshly ejected without sheath; in Lugol's solution cytoplasm partly yellowish, without glycogen accumulations, in brilliant cresyl blue wall unstained, no sheath revealed, after longer exposure internal small metachromatic corpuscles regularly formed. *Ascospores* in polysporic test cultures under axenic conditions obtained by shooting asci on PDA readily germinated nearly equally at both poles during 24 h at 24 °C. **Asexual morph** Undetermined.

Habitat and phenology: Saprobic on very rotten decorticated fragments and large branches of *Fagus sylvatica*

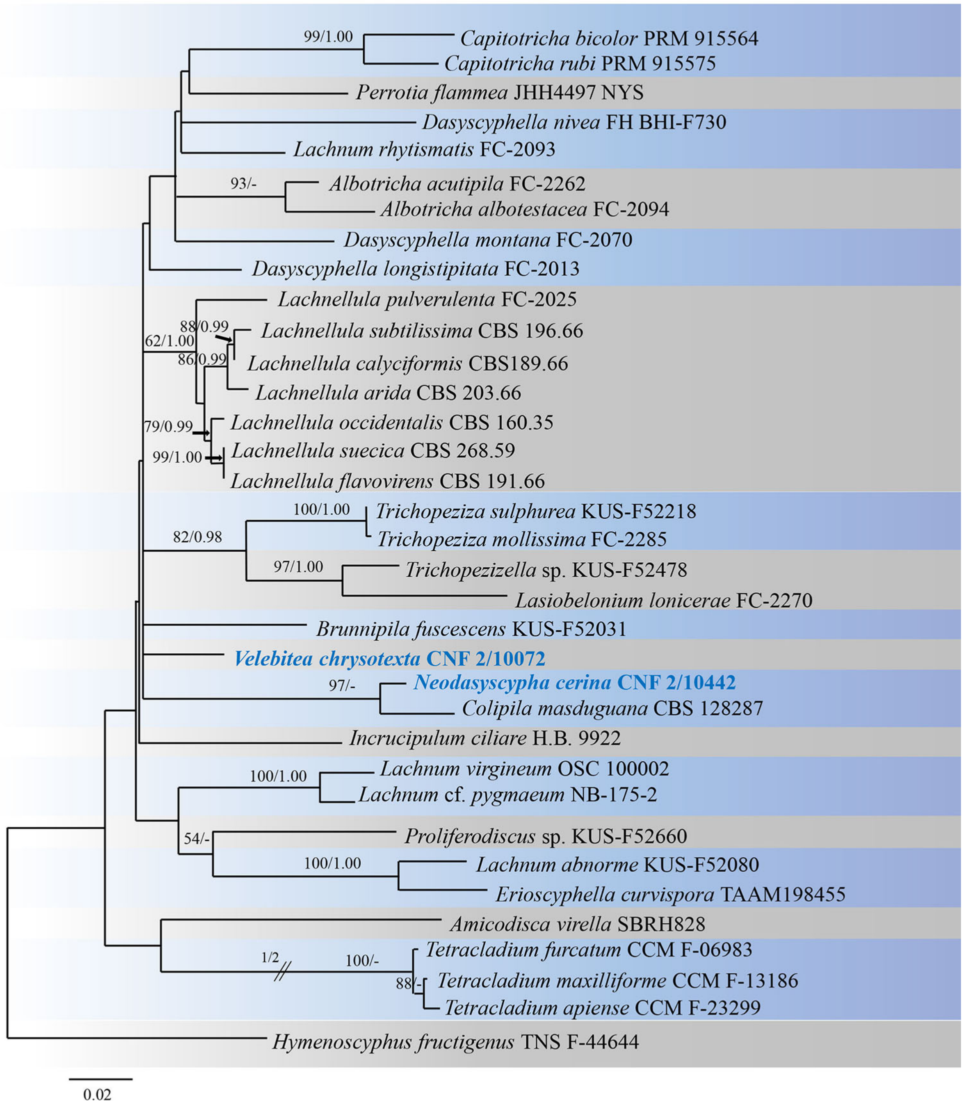


Fig. 67 Maximum likelihood phylogenetic tree based on a concatenated ITS and LSU sequence dataset. Sequences recovered during this study are shown in blue. The tree is rooted to *Hymenoscyphus fructigenus*. Maximum likelihood bootstrap support values greater than 50% and Bayesian posterior probabilities greater than 0.95 BYPP are shown at the nodes. The bar length indicates the number of nucleotide substitutions per site

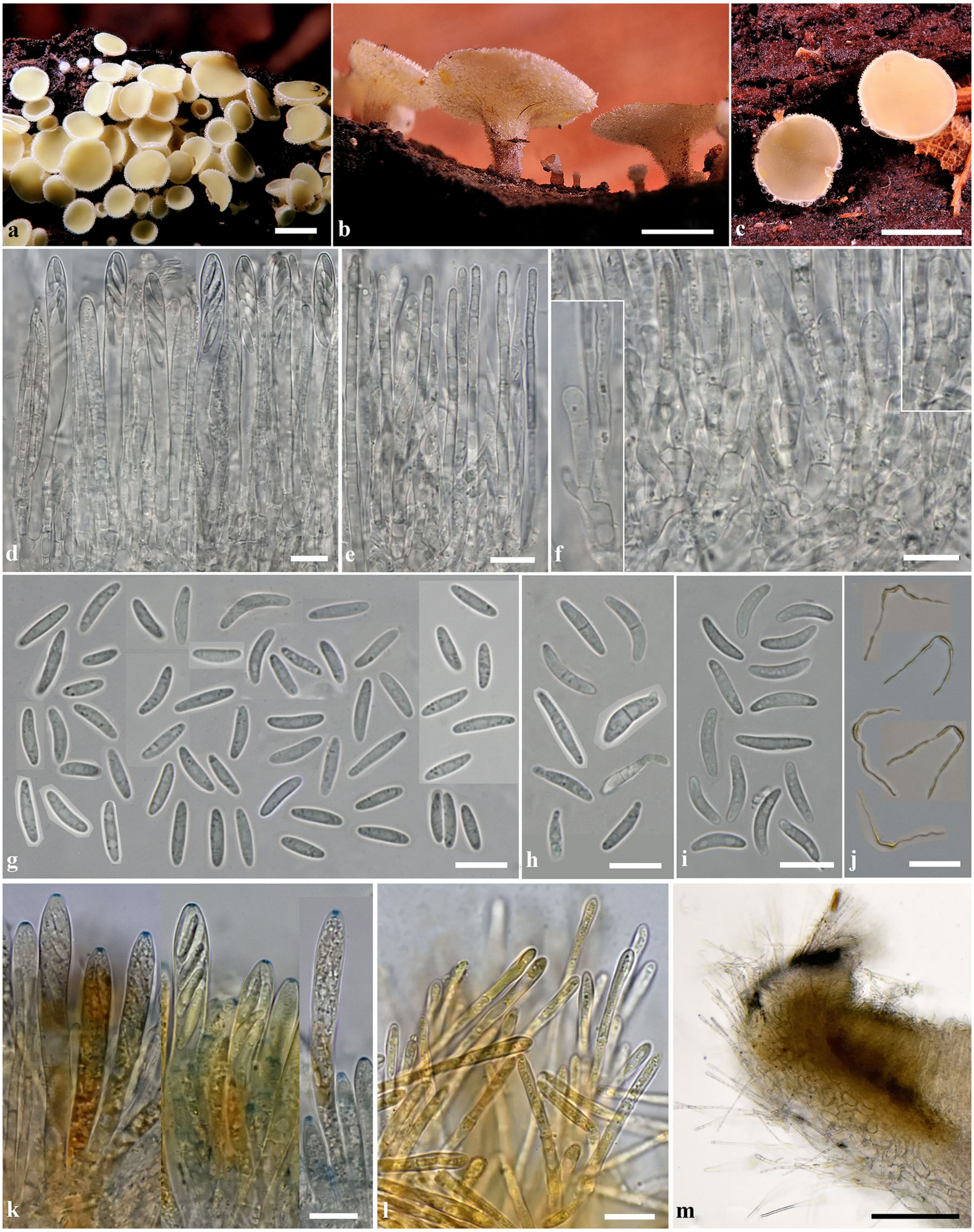


Fig. 68 ***Velebitea chrysotexta***. **a** Fructification growth in situ. **b** Apothecia, side view, resinous plaques visible. **c** Ascomata top view. **d** Living mature asci protruding above paraphyses tips. **e** Paraphyses. **f** Simple septate ascogenous cells. **g** Freshly ejected living mature ascospores. **h** Overmature ascospores. **i** Freshly ejected living mature ascospores. **j** Germinated ascospores on PDA after 24 h. **k** Amyloid reaction in asci. **l** Marginal hairs tips. **m** Marginal apothecial area largely beset by resinous matter. **d–i, m** in water mount, **k, l** in Lugol's solution, **j** on PDA. **c–h, l** CNF 2/10072 (**holotype**), **i, j, m** CNF 2/10661, **a, b, k** CNF 2/10736. Photo by N. Matočec and I. Kušan. *Scale bars* **a, c** = 2 mm, **b** = 1 mm, **d–i, k, l** = 10 µm, **j, m** = 50 µm

(*Fagaceae*) hidden in the litter, in subalpine forests, fruit bodies appear in May and June.

Known distribution: The species is known so far only from Mt. Velebit, Croatia.

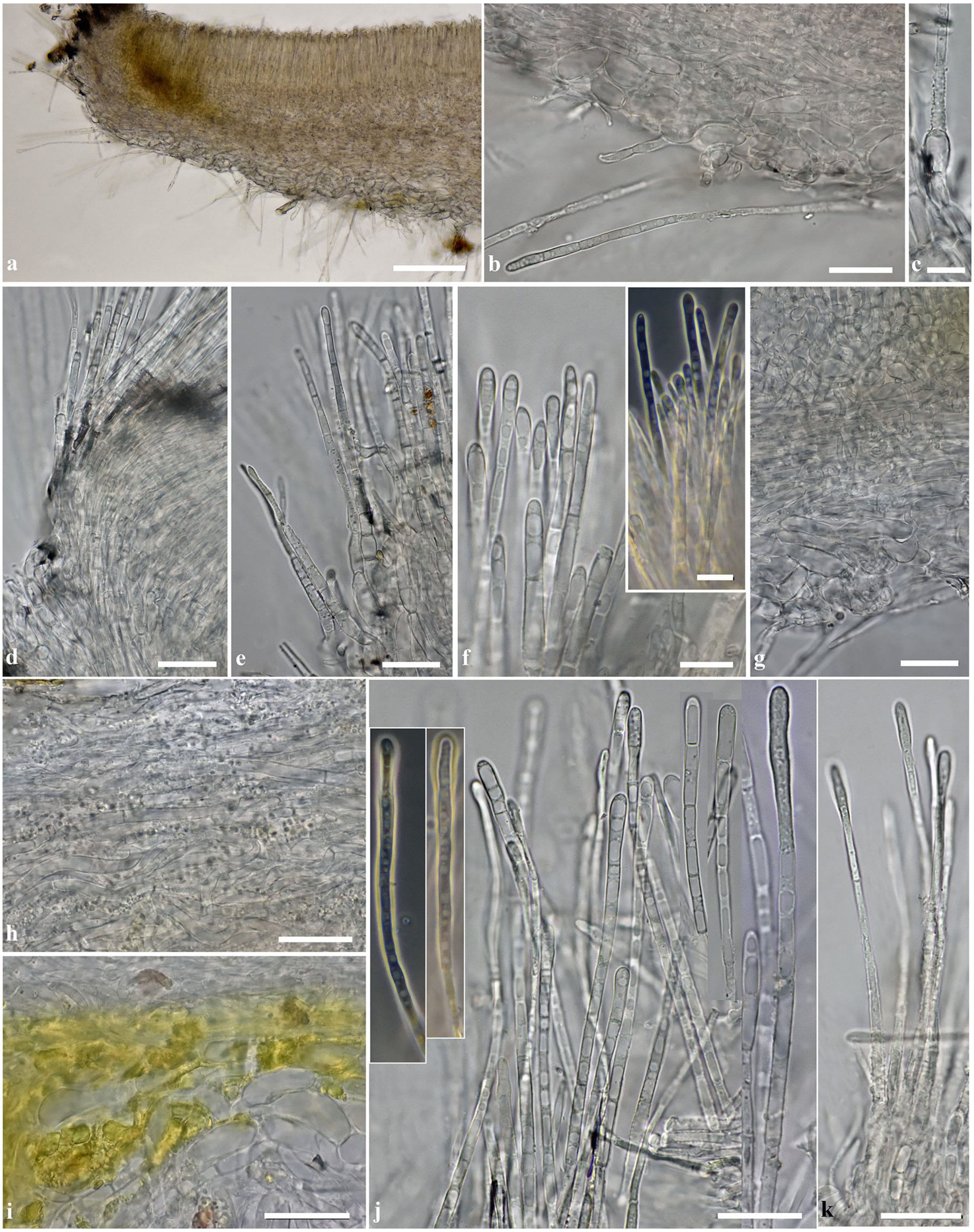


Fig. 69 ***Velebitea chrysotexta***. **a** Apothecial section beset with resinous matter. **b** Excipular flank with hairs. **c** Excipular hair base. **d** Marginal texture with hairless area. **e** Marginal hairs. **f** Marginal hair tips in bright field (left) and phase contrast (right). **g** Excipular texture with thick subhymenial layer. **h** Medulla with crystalloid particles. **i** Large resinous accumulations in ectal excipulum. **j** Excipular hairs, apical wall thickenings present in some hairs, phase contrast (left), bright field (right). **k** Excipular hairs in dead state. All in water mount. **b, d, f, j, k** CNF 2/10072 (**holotype**), **a, c, g, i** CNF 2/10661, **e, h** CNF 2/10736. Photo by N. Matočec and I. Kušan. *Scale bars* **a** = 50 µm, **b, d, e, g–k** = 20 µm, **c, f** = 10 µm

Material examined: CROATIA, Lika-Senj County, Sjeverni Velebit National Park, northern part of Mt. Velebit, Jurekovac area, 1050 m E-SE from Jurekovački kuk peak (1525 m), 44°45′16″N, 15°00′57″E, 1340 m a.s.l., forest of *Abies alba* Mill., *Fagus sylvatica* L. and *Picea abies* (L.) H. Karst., on decorticated rotten *Fagus*

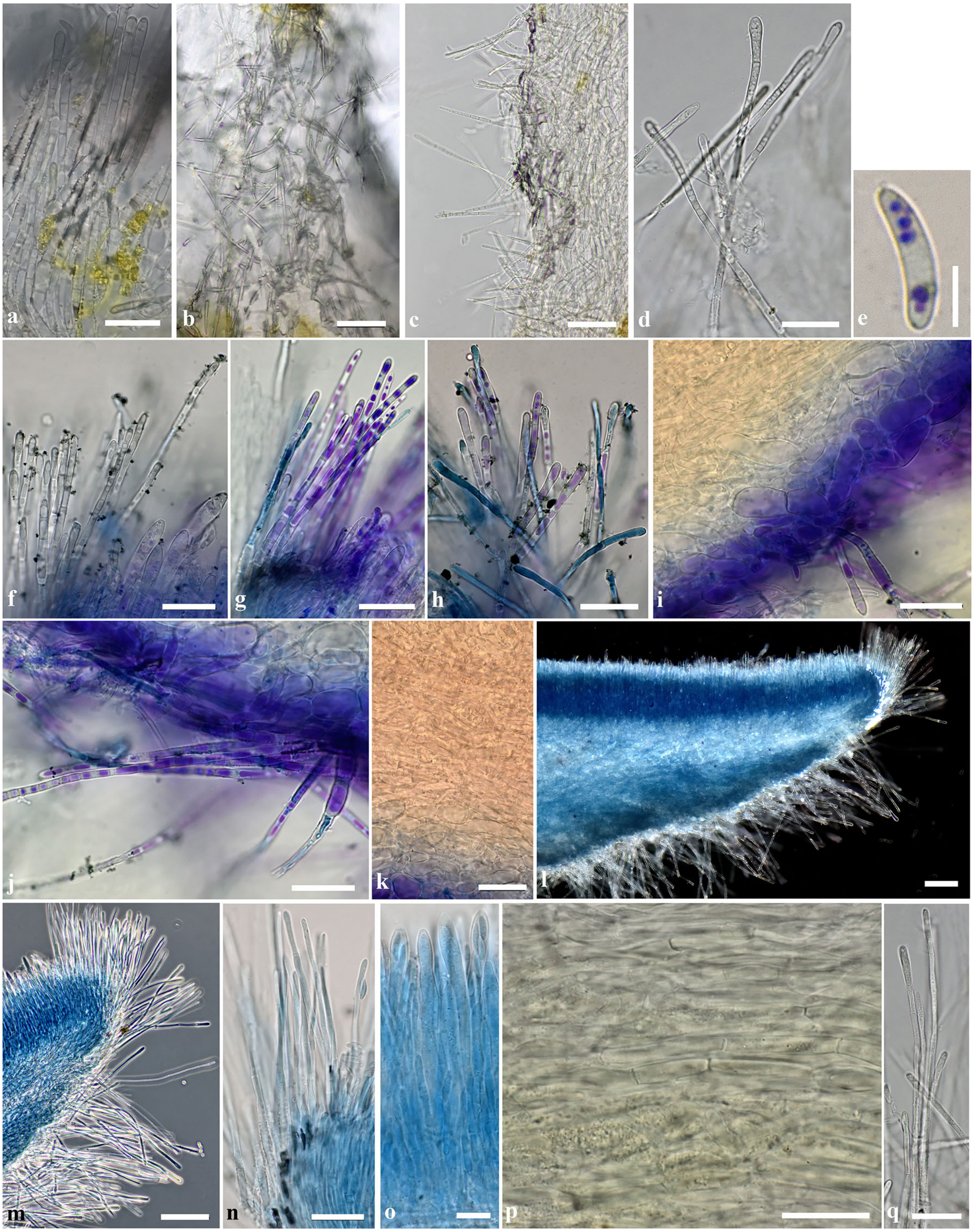


Fig. 70 ***Velebitea chrysotexta***. **a** Marginal hairs with resinous lumps. **b** Stipe vestiture, side view. **c** Stipe texture and vestiture in section. **d** Stipe hairs. **e** Living mature ascospore. **f** Marginal hairs with rapidly floculated surface matter. **g** Marginal hairs after longer exposure. **h** Excipular hairs in living and dead state. **i** Excipular tissue displaying gelified areas (lilac and rosy). **j** Living excipular hairs. **k** Medullary excipulum. **l** Apothecial section and vestiture, dark field. **m** Apothecial vestiture, phase contrast. **n** Marginal hairs. **o** Hymenial elements. **p** Excipular tissue, resinous lumps dissolved. **q** Excipular hairs. **a–d** in water mount, **e–k** in brilliant cresyl blue, **l–o** in cotton blue, **p, q** in KOH. **b–q** CNF 2/10072 (**holotype**), **a** CNF 2/10661. Photo by N. Matočec and I. Kušan. *Scale bars* **b**, **c**, **l**, **m** = 50 µm, **a, d, f–k, n, p, q** = 20 µm, **o** = 10 µm, **e** = 5 µm

sylvatica stump base together with *Chlorociboria aeruginosa* (Oeder) Seaver ex C.S. Ramamurthi et al. and *Hyaloscypha vitreola* (P. Karst.) Boud., 27 May 2017, I. Kušan and N. Matočec (CNF 2/10072, **holotype**); *ibid.* 2

June 2018 (CNF 2/10661); Lika-Senj County, Paklenica National Park, southern part of Mt. Velebit, Velika Ruja in Javornik area, 1160 m NE-E-NE from Badanj peak (1638 m), 44°22′60″N, 15°27′22″E, 1365 m a.s.l., forest of *Fagus sylvatica*, on fallen decorticated branch of *Fagus sylvatica*, 25 June 2018, N. Matočec and I. Kušan (CNF 2/10736).

GenBank numbers: ITS = MH886407, LSU = MH886411 (CNF 2/10072, holotype).

Class Pezizomycetes O.E. Erikss. & Winka

We follow the latest treatment and updated accounts of Pezizomycetes in Jaklitsch et al. (2016a), Ekanayaka et al. (2018) and Wijayawardene et al. (2018a).

Pezizales J. Schröt.

Pezizaceae Dumort.

The family *Pezizaceae* was introduced by Dumortier (1829) with *Peziza* Fr. as the type genus. A systematic overview of the family was recently given by Jaklitsch et al. (2016a) who recognized 32 genera in this family. Ekanayaka et al. (2018) reviewed the families in the class *Pezizomycetes* and outlined 45 genera names belonging to *Pezizaceae*, including also some taxa synonymized by other authors.

Sarcopeziza Loizides et al.

A new genus in the *Pezizaceae*, *Sarcopeziza* Loizides et al. was recently erected (Agnello et al. 2018) to accommodate a single species, *Peziza sicula* Inzenga (Inzenga 1869). This species was previously typified and treated by Agnello et al. (2013) and Agnello et al. (2015). Since the original description of Inzenga (1869) and the modern presentations by Agnello et al. (2013) and Agnello et al. (2018) are not fully adequate and accurate for further advancement in taxonomy of the group, a more detailed re-description of microscopical features of *Sarcopeziza sicula* is provided here, based on careful cyto- and histochemical analyses.

Sarcopeziza sicula (Inzenga) Agnello, Loizides & P. Alvarado, Ascomycete.org 10(4): 179 (2018)

MycoBank number: MB827574; *Facesoffungi number*: FoF05715, Figs. 71, 72

Basionym: Peziza sicula Inzenga, Funghi Siciliani, Centuria Seconda: 29 (1869)

= *Sarcosphaera sicula* (Inzenga) Pat., Bull. Soc. Hist. nat. Autun 17: 154 (1904)

Sexual morph *Ascomata* apothecial, hypogeous to semi-hypogeous at first, becoming epigeous during development, firstly globose with pre-defined narrowly circular apical opening, 2–5 cm in diam., expanding when ripe, cracked into lobes, becoming star-shaped, solitary or gregarious, reaching 4.5–10 cm in diam., base substipitate to stipitate deeply buried in the substrate, hymenial surface vinaceous-purplish to livid vinaceous, matte, margin tapered in section, entire in youth, smooth, excipulum concolorous or somewhat darker than hymenium, gibbous, ± smooth to finely pruinose; flesh of homogenous soft waxy consistence, on cut not exuding milk, 2.5–4.2 mm thick, of the same colour as external surface with more pinkish tinge, odourless and flavourless. *Hymenium* 360–400 µm thick, arranged as a regular palisade. *Subhymenium* reduced and faintly discerned from the upper medulla only by scattered ascogenous hyphae, other cells indistinct from those in upper medulla though slightly smaller, continuing upwards as moniliform lower paraphysal cells. *Upper medulla* 950–1200 µm thick, composed of *textura angularis* richly intertwined with elements of short-celled *textura intricata*, nearly ± isodiametric cells gradually more frequent and larger towards lower medulla, 13.5–55 µm diam., elongated cells 8.5–88 × 5.3–16.5 µm, walls hyaline, thin, many cells contain minute refractive crystalloid particles in water mount, but without globular content, highly refractive globules though present in cotton blue, 0.8–5.2 µm diam., but crystalloid matter absent; lower zone with many cells having thickened yellowish and highly refractive septal rings. *Lower medulla* 500–900 µm thick, generally as central *textura intricata*, but cell bundles in lower half mostly oriented ± vertically as *textura fasciculata*, while on the border with upper medulla or in central areas hyphae may be oriented predominantly ± horizontally, hyphae in upper 1/3 of the whole layer often without strict orientation, cells cylindrical-hyphoid, 6.2–14.8 µm wide, without any type of refractive contents, walls subhyaline, some ± cylindrical cells densely set with rich accumulations of golden-yellow and highly refractive minute granules that may consolidate to form irregular cytoplasmic patches of isabelline, extracellular crystalloid content very sparse. *Ectal excipulum* compact area 220–375 µm thick, composed of *textura angularis* to *textura prismatica*, cells 11.4–28.5 × 6.2–24.5 µm, some cells somewhat elongated, more elongated cells dominant in upper zone and then of ± vertical orientation, walls thickened, subhyaline to yellowish, 0.7–0.9 µm thick in cortical cells, inner cells with thin, hyaline walls, containing minute to medium sized refractive crystalloid particles in water mount, but without globular content, highly refractive globules though present in cotton blue, 0.8–6.5 µm diam., but crystalloid matter absent; surface with occasional low pustules, ornamented chiefly by individualized, mostly scattered, (1–)2–6-celled terminal outgrowths, 21.4–125 × 9.5–14.7 µm, individual cells sub-cuboid to cylindrical, 9.2–40 × 9.1–14.7 µm, walls subhyaline, thin-walled; cortical cells beset with yellowish to isabelline-ochre highly refractive minute to larger crystalloid matter, cytoplasm of some cortical cells pale isabelline. In KOH refractive cellular content in upper medulla coalesced, lower medullar/ectoexcipular cells without refractive content, crystals not dissolved. *Overall texture* in Melzer's reagent without dextrinoid reactions, refractive cellular granules coalesced to highly refractive large guttules; in congo red all cell walls ± stained; in cotton blue cell walls cyanophobic in entire excipulum, but some ectal excipular cells with bluish cytoplasm, medullar cell walls not cyanophilic. *Paraphyses* cylindrical, inconspicuous, apically obtuse to clavate, straight to apically bent, not branching in the upper part, apical cell 2.8–4.8 µm diam., middle and lower cells cylindric, moniliform cells exist near the margin, wall hyaline, thin; in Lugol's solution unstained. *Asci* 355–446 × 14–17.3 µm, cylindrical, apex subtruncate with comparatively weakly pronounced functional operculum, 8-spored, base pleurorhynchous, with two ± tightly set septa, arising from non-repetitive croziers at widely variable levels, operculum 5.2–5.8 µm in diam., 0.7–0.9 µm thick, strictly apical, flat-lenticular with only slight indentation ring best visible under oil immersion in cotton blue, periascal mucus very thin without thick apical accumulation, film-like, evenly thick throughout, lateral wall 3-layered, subhyaline to yellowish, 0.7–0.9 µm thick; in Lugol's solution periascal mucus in the broad upper area diffusely and moderately euamyloid, reaction gradually decreasing in intensity downwards, basally inamyloid, same in Melzer's reagent; in congo red periascal mucus weakly pronounced, very thin, outermost wall layer strongly grey-red, median layer less stained, innermost layer unstained, operculum differentially stained red while thin operculum ring area remained unstained. *Ascospores* (13.2–)13.4–15.1–16.1(–16.7) × (8.1–)8.3–8.9–10, Q = 1.48–1.57–1.76(–1.77) (n = 50, in cotton blue), hyaline, ellipsoid, sometimes broadly oblong, radially symmetrical, with rounded poles, 1-celled, seemingly smooth under immersion lens when in water mount, many spores (especially when outside of the asci) slightly roughened in cotton blue but markings are not cyanophilic, measuring below 0.2 µm high and up to 0.3 µm diam., mature spores initially with multiguttulate pattern, lipid bodies, when still not coalesced 0.3–1.5 µm diam., lipid bodies in dead spores coalesced in various degree up to maximal, uni-guttulate stage (visible only in water mount), uninucleate (visible in spores having lipids in multi-guttulate pattern), wall 3-layered, 0.7–0.8 µm thick; in Lugol's solution without glycogene accumulations; in KOH wall stable (not loosening); in cotton blue perispore weakly cyanophilic, wall not loosened, de Bary bubbles present in some mature spores, lipid bodies completely masked, sporoplasm unstained; in acetocarmine nucleus not differentially stained, only submature spores with weakly stained nucleus, perispore not loosened. **Asexual morph** Undetermined.

Material examined: ITALY, Province of Brindisi, San Pancrazio Salentino, San Antonio alla Macchia, 40°25′00″N, 17°50′00″E, 59 m a.s.l., on bare and mossy soil in a sunny *Pinus halepensis* Mill. forest with *Eryngium campestre* L. and *Poaceae*, 7 February 2008, A. Delle Donne and C. Agnello (MCVE 25877, **epitype**).

Habitat and phenology: On sandy or calcareous soils in frame of dry Mediterranean thickets (mostly dominated by *Cistus* spp.) and grasslands and parks, sometimes in vicinity of thermophilic *Pinus* spp., *Pyrus* spp. and *Olea europea* in thermo-Mediterranean bioclimatic belt, fruit bodies appear between January and April.

Known distribution: Cyprus, Greece, Israel, Italy, Spain and Tunisia.

GenBank numbers ITS = MH886405, LSU = MH886409 (MCVE 25877, epitype).

Notes: A data matrix for alignment was constructed to show a phylogenetic position of *Sarcopeziza sicula* within *Pezizaceae*, with a special emphasis on the genus *Peziza*. Phylogenetic analysis (Fig. 73) included the ITS and LSU sequences generated from the epitype collection of *Sarcopeziza sicula* and other related sequences retrieved from GenBank as well as a newly sequenced collection of *Adelphella babingtonii* (Berk. & Broome) Pfister, Matočec & I. Kušan (CNF 2/9430; ITS = MH886406, LSU = MH886410). *Ascobolus crenulatus* P. Karst. was used as an outgroup taxon. The maximum likelihood analysis of a combined ITS and LSU sequence dataset was conducted in MEGA 7 (Kumar et al. 2016) with a total of 1462 positions in the final dataset.

The phylogeny based on concatenate analysis of ITS and LSU nested the genus *Sarcopeziza* in the family *Pezizaceae*, in a species group along with *Eremiomyces* Trappe & Kagan-Zur, *Hapsidomyces venezuelensis* J.C. Krug & Jeng and *Peziza phyllogena* Cooke, next to the *Terfezia-Tirmania*, *P. depressa*, *P. saniosa* and *Peziza ostracoderma* clades (Fig. 73). *Eremiomyces echinulatus* (Trappe & Marasas) Trappe & Kagan-Zur and *E. magnisporus* G. Moreno et al. cluster with high support with *Sarcopeziza sicula* showing a high level of genetic similarity. *Sarcopeziza sicula* demonstrates a distant relationship to *Peziza vesiculosa* Bull. and *Sarcosphaera coronaria* (Jacq.) J. Schröt. which are type species of the genera where it was previously combined (Inzenga 1869; Patouillard 1904), suggesting taxonomic affinity outside of those genera.

Besides molecular evidence, *Sarcopeziza sicula* is different from *Peziza sensu stricto* [a core species group gathered around the type species, *P. vesiculosa*, cf. Hansen et al. (2001, 2002, 2005)], primarily by faintly visible, film-like periascal mucus that is revealed by moderately diffusely amyloid reaction in iodine mounts, gradually decreasing in strength downwards. Whereas, all species

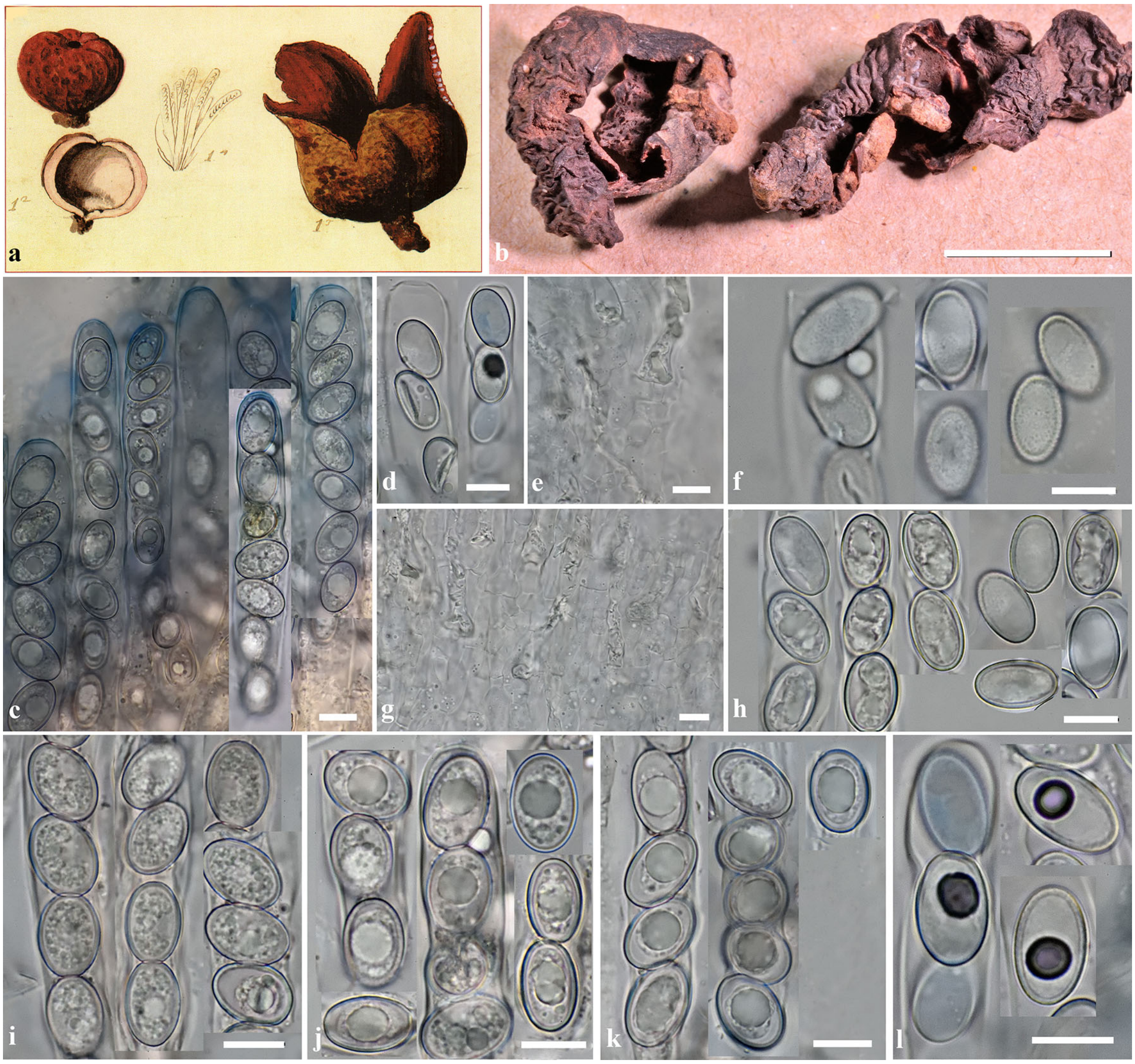


Fig. 71 ***Sarcopeziza sicula***. **a** Ascomata and part of hymenium after Inzenga (1869), scanned from Venturella (2005). **b** Dried ascomata. **c** Ascus amyloidity. **d** Opercular fine structure. **e** Ascus bases with ascogenous cells. **f** Ascospore ornamentation. **g** Ascus bases with ascogenous cells. **h** Ascospores. **i** Mature ascospores in multi-guttulate state displaying single nucleus. **j** Mature ascospores during coalescence of lipid bodies. **k** Completely coalesced lipid body matter. **l** Ascospores with de Bary bubble present in some spores. **c** in Lugol's solution, **e, g, i–k** in water mount, **d, f, h, l** in cotton blue. All from MCVE 25877 (epitype). Photo by N. Matočec and I. Kušan. *Scale bars* **b** = 1 cm, **c–l** = 10 µm

from *Peziza sensu stricto* have opercular (apical) thick accumulation of heavily amyloid mucus giving strong ring-like amyloid reaction confined to the ascal tops. Agnello et al. (2018) define asci as diffusely amyloid along the entire length of the asci and strongly amyloid at the apex (type I, cf. Hansen et al. 2001). Judging to both the authors' microphotograph and own observations, the type of amyloidity belongs to type III instead of type I. The fine structure of the ascus wall lacks strong apical indentation ring and lentiform operculum in *Sarcopeziza sicula*, characters that are constantly present in all studied species in *Peziza* core species group as well as in ascobolacean representatives and species of *Peziza succosa* and *P. succosella* clade (*pers. data*, cf. Samuelson 1978).

Moreover, *Sarcopeziza sicula* is also different by ontogenetically and cytochemically comparatively stable multi-guttulate lipid configuration in fully developed ascospores and violet-purplish in flesh. Contrary to Agnello et al. (2013, 2018), the spores in this study are recognized as multi-guttulate when fully mature and in living state whose lipids coalesce in dead state towards uni-guttulate or more rarely bi-guttulate pattern. The process of lipid body coalescence in dead spores is regularly observed throughout Ascomycota (Baral 1992). The microphotograph of ripe asci in Agnello et al. (2018, Fig. 2f), is clearly displaying multi-guttulate pattern of living and fully mature ascospores, while Fig. 2c, d in Agnello et al. (2013) resemble

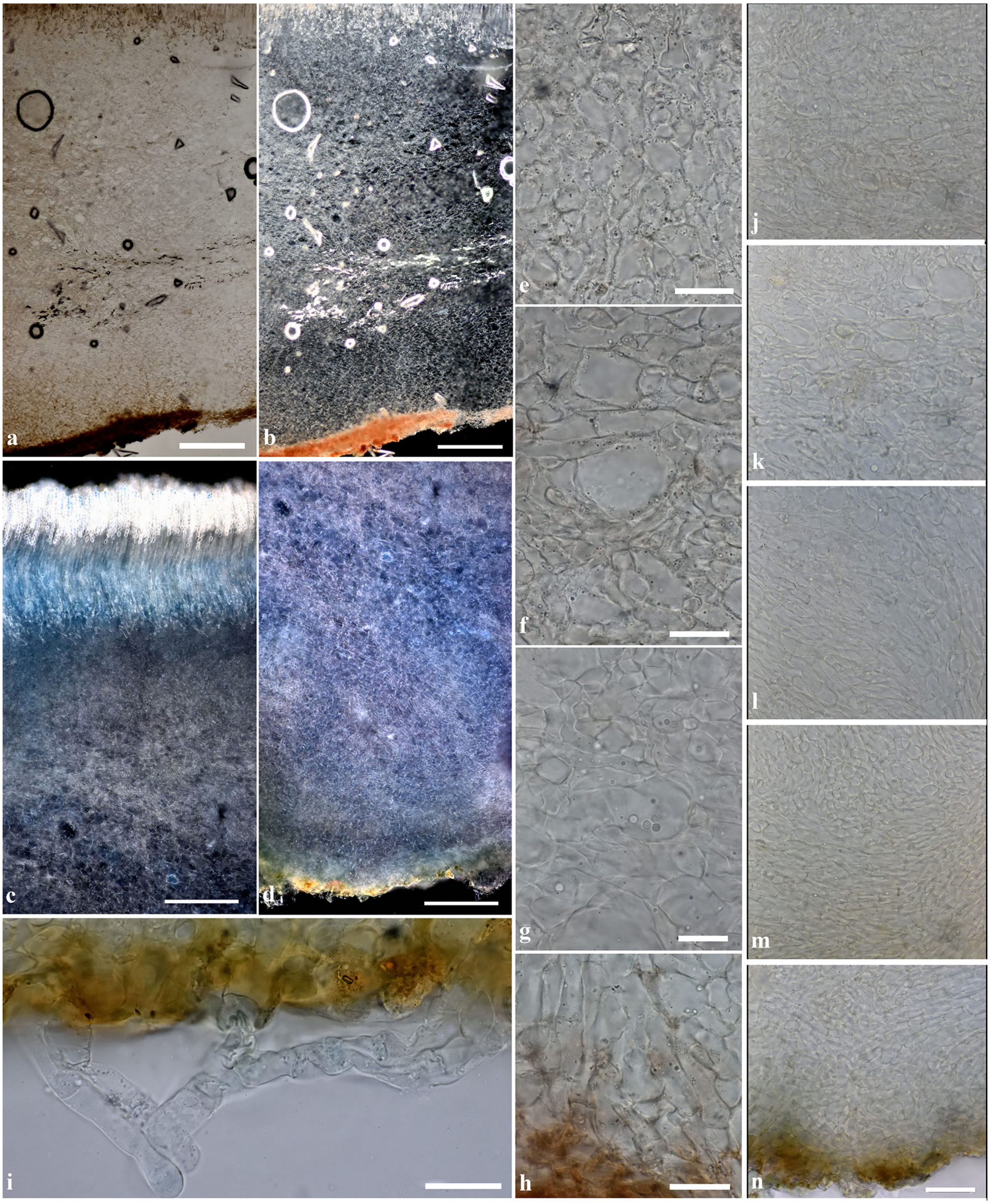


Fig. 72 ***Sarcopeziza sicula***. **a** Excipular structure (bright field). **b** Excipular structure (dark field). **c** Excipular structure, upper half with hymenium (dark field). **d** Excipular structure, lower half (dark field). **e** Subhymenium with minute crystalloid particles. **f** Upper medulla with minute crystalloid particles. **g** Upper medulla with lipid like globules. **h** Ectal excipulum with minute crystalloid particles. **i** Cortical cells with yellow cytoplasm and hyaline hyphoid outgrowths. **j** Subhymenium and upper medulla. **k** Upper medulla with largest cells. **l** Lower medulla. **m** Lower medulla with fasciculate texture. **n** Ectal excipulum. **a, b, e, f, h** in water mount, **c, d, g, i–n** in cotton blue. All from MCVE 25877 (epitype). Photo by N. Matočec and I. Kušan. *Scale bars* **a–d** = 200 µm, **e–i** = 20 µm, **j–n** = 50 µm

dead ascospores containing subsequently coalesced lipid bodies.

Furthermore, the authors presumed that ascospore ornamentation is not constant character in this species. It is quite possible that ornamentation in this species is normally formed after spore ejection and extraascal dormancy. Both available ascomata from the epitype produced large number of dormant ascospores whose fine ornamentation is clearly visible in lactic acid cotton blue under oil-immersion.

From the genus *Sarcosphaera* Auersw. (its type and the only species *S. coronaria*), *Sarcopeziza sicula* is different by the absence of paraphysal internal content, different original lipid body configuration in mature ascospores (multi-guttulate vs. bi-guttulate), intensively pigmented flesh and the excipular surface, substipitate to stipitate apothecia, and lack of discernable odour (*S. coronaria* has somewhat chlorine scent).

Agnello et al. (2018) describe the subhymenium as 150–180 µm thick layer but we detected it as very reduced and unclearly discerned tissue from the upper medulla using high contrasting techniques on a number of entire, thin sections (ranging from hymenium up to ectal excipular layer) from the epitype material.

The closest pezizacean relatives of *Sarcopeziza sicula* revealed in our phylogenetic analysis are species of the genus *Eremiomyces*, *Hapsidomyces venezuelensis* and *Peziza phyllogena* (a member of the genus *Peziza sensu lato*). All so far produced DNA based phylogenies (along with the present one), however, clearly showed polyphyly in the genus *Peziza*, where numerous species attributed to the other genera (especially of hypogeous representatives) build up monophyletic clades along with certain members ascribed to a genus *Peziza*. Therefore, all species putatively ascribed to a genus *Peziza* should be carefully restudied using integrative taxonomic approach. *Sarcopeziza sicula* is readily recognizable from all other currently known genera in the family *Pezizaceae* by specific combination of macroscopical features (semi-hypogeous sarcosphaeroid apothecia with unique pigmentation), ecology (subpsammophilic and/or xeric habitats in thermo-Mediterranean zone) and microscopy, principally cytochemistry and fine structure of the asci and multi-guttulate lipid body configuration of the ascospores, characters that were proved to be informative for differentiation in *Pezizaceae* in a previous study (Pfister et al. 2009).

There is a number of similarities in excipular structures of semi-hypogeous species *Sarcopeziza sicula* and peridial/glebal microscopic structures of the closest relative, hypogeous species *Eremiomyces magnisporus* (cf. Alvarado et al. 2011): (1) the same texture in peridia of *E. magnisporus* and cortical layer of ectal excipulum in *S. sicula*; (2) cytoplasmic pigments in peridial cells of *E. magnisporus* and cortical layer cells of *S. sicula*; (3) same texture in glebal sterile veins in *E. magnisporus* and medullary excipulum in *S. sicula*; and (4) lipid-like globules in glebal sterile vein cells in *E. magnisporus* and medullary excipular cells in *S. sicula*.

The other hypogeous species *Eremiomyces echinulatus* which is a type species of the genus *Eremiomyces*, and *E. innocentii* Ant. Rodr. & Bordallo as well as phylogenetically close *Kalaharituber pfeilii* (Hennings) Trappe & Kagan-Zur (cf. Ferdman et al. 2005 and Crous et al. 2017) also possess very similar structures in peridial and glebal cells and texture. Very similar excipular texture exists in *Peziza phyllogena* too (pers. data) and in wider apothecial marginal area of *Hapsidomyces venezuelensis* (cf. Krug and Jeng 1984), two epigeous phylogenetically closest relatives. Nearly the same fine opercular structure in cotton blue mount is found in both *Sarcopeziza sicula* and *Peziza phyllogena* (pers. data). On the other hand, genera *Eremiomyces* and *Kalaharituber* Trappe & Kagan-Zur differ from *Sarcopeziza sicula* by their entirely hypogeous living strategy developing permanently closed stereothecia with solid gleba and producing perfectly globose coarsely aculeate ascospores.

The closest apothecial representatives have different living strategy also viz. fimicolous in *Hapsidomyces venezuelensis* and phyllophilous in *Peziza phyllogena* versus terricolous-subpsammophilous in *Sarcopeziza sicula*. Ascal amyloidity is also different: thin but wider and moderately strong apical ring-like reactive zone exist in *Peziza phyllogena* extending downwards with abruptly weakened intensity (pers. data) while *Hapsidomyces venezuelensis* has weakly amyloid reaction over entire ascus length (Hansen et al. 2001). *Hapsidomyces venezuelensis* has ascospores very much resembling those of *Eremiomyces* (though spinulose-reticulate). While, *Peziza phyllogena* has ellipsoid ascospores (as in *Sarcopeziza sicula*), though rather coarsely sculptured by cyanophilic verrucae and higher tuberculae around the polar areas (pers. data).

Class Sordariomycetes O.E. Erikss. & Winka

The classification of the families in Sordariomycetes follow Maharachchikumbura et al. (2016), Hongsanan et al. (2017) and Wijayawardene et al. (2017a, 2018a).

Subclass Diaporthomycetidae Senan. et al.

Atractosporales H. Zhang et al.

Conlariaceae H. Zhang et al.

Conlariaceae was introduced by Zhang et al. (2017a) in the order *Atractosporales* to accommodate the freshwater genus *Conlarium*, with two species, *C. aquaticum* W. Dong et al. and *C. duplumascosporum* F. Liu & L. Cai. We follow the latest treatment in Zhang et al. (2017a) and the new species, *C. thailandense* is introduced based on morphological characteristics coupled with phylogenetic analysis of combined LSU, SSU and ITS sequence data (Fig. 74).

Conlarium F. Liu & L. Cai

Conlarium was introduced by Liu et al. (2012a) from a freshwater habitat in China to accommodate *C.*

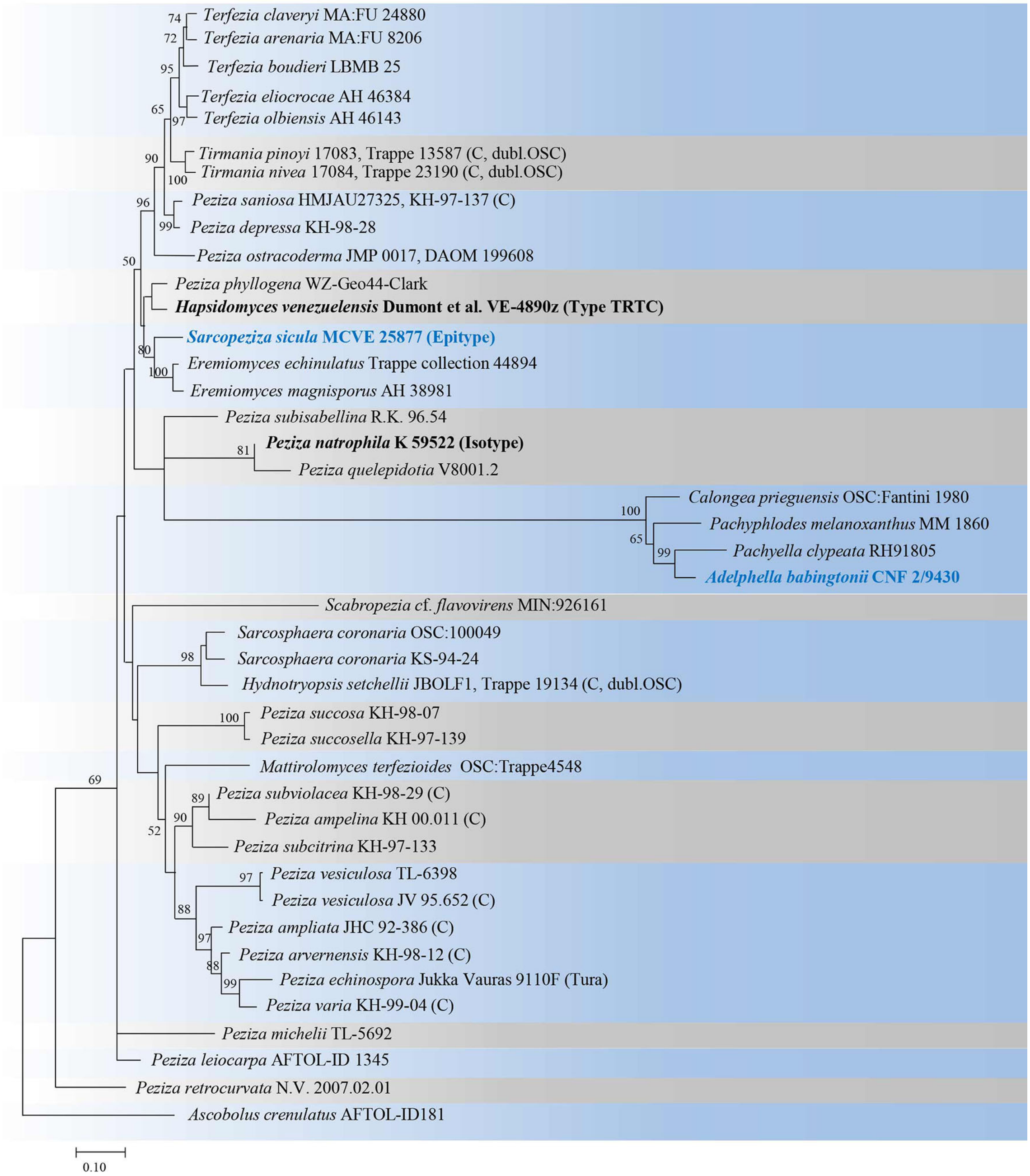


Fig. 73 Maximum likelihood phylogenetic tree based on a concatenated ITS and LSU sequence dataset. Sequences recovered during this study are shown in blue and ex-type strains are in bold. The tree is rooted to *Ascobolus crenulatus*. Bootstrap values greater than 50% are indicated at the nodes. The bar length indicates the number of nucleotide substitutions per site

duplumascosporum with sexual and asexual morphs (Liu et al. 2012a). Recently, Zhang et al. (2017a) introduced the second freshwater taxon *C. aquaticum* from Thailand.

Conlarium thailandense X.D. Yu, H. Zhang & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555288; *Facesoffungi number*: FoF04830, Fig. 75

Etymology: Named after the country where it was collected, Thailand

Holotype: MFLU 17-1711

Saprobic on dead wood in terrestrial habitat. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* sporodochial, broadly punctiform, gregarious, raised, dark brown to black. *Mycelium* mostly immersed on natural substratum, comprising branched, pale brown to hyaline, smooth and thin-walled hyphae. *Conidiophores* absent or reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, holoblastic, integrated, determinate, cylindrical, hyaline, smooth, up to 5.5 µm long. *Conidia* 25–45 × 17–33 µm ($\bar{x}$ = 35.9 × 26.9 µm, n = 20), acrogenous, solitary, dry, mostly irregular, subglobose to ellipsoidal, brown to dark brown, clathrate, muriform, 4–8-transversely septate, 4–6-longitudinally septate, slightly constricted at the septa, smooth and thin-walled, with a small, sub-rounded, dark brown ornamentation on the surface of each cell. *Conidial* secession schizolytic.

Culture characteristics: Colonies on PDA, irregular in shape, reaching 10–20 mm in 6 weeks at room temperature, black from above and below, umbonate, rough, dense, edge undulate.

Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, on dead wood, 17 July 2017, S. Boonmee, DP6 (MFLU 17-1711, **holotype**), ex-type living culture, MFLUCC 17-2349.

GenBank numbers: ITS = MH624129, LSU = MH624127, SSU = MH624128.

Notes: *Conlarium thailandense* is similar to the asexual morph of *C. duplumascosporum* and *C. aquaticum*. They all have monoblastic, holoblastic conidiogenous cells and mostly irregular, brown, clathrate, muriform conidia (Liu et al. 2012a). However, they can be easily distinguished by the number of septa (0–2-transversely septate, 0–1-longitudinally septate in *C. duplumascosporum*, 6–12-transversely septate, 4–10-longitudinally septate in *C. aquaticum* and 4–8-transversely septate, 4–6-longitudinally septate in *C. thailandense*) and conidial size (15.5–35 × 11–26.5 µm in *C. duplumascosporum*, 45–70 × 20–57 µm in *C. aquaticum* and 25–45 × 17–33 µm in *C. thailandense*) (Liu et al. 2012a; Zhang et al. 2017a). Apart from number of septa and conidial size, a number of air-bubbles were also observed on mature conidia of *C. thailandense*, which have not been reported in *C. aquaticum* and *C. duplumascosporum*. Phylogenetic analyses of a combined LSU, SSU and ITS sequence alignment based on maximum likelihood and Bayesian inference show that *C. thailandense* is sister to *C. aquaticum*. A comparison of ITS pairwise indicates that *C. thailandense* differs from *C. aquaticum* in 13 base positions and is therefore novel following the guidelines of Jeewon and Hyde (2016).

Diaporthales Nannf.

Cytosporaceae Fr.

The family *Cytosporaceae* was introduced by Fries (1825) and recognized a family in *Diaporthales*, which comprises phytopathogens and saprobes (Wehmeyer 1975; Barr 1978; Eriksson 2001; Castlebury et al. 2002). Maharachchikumbura et al. (2015, 2016) listed 13 genera under *Cytosporaceae*. Senanayake et al. (2017) accepted five genera, which belong to *Cytosporaceae* based on morphological characteristics viz. *Cytospora* Ehrenb., *Pachytrype* Berl. ex M.E. Barr et al., *Paravalsa* Ananthap., *Xenotypa* Petr. and *Waydora* B. Sutton. Wijayawardene et al. (2018a) listed only genera *Cytospora* and *Waydora* in *Cytosporaceae*.

Cytospora Ehrenb.

Cytospora was introduced by Ehrenberg (1818) as type genus of the family *Cytosporaceae* in *Diaporthales* (Wehmeyer 1975; Barr 1978; Eriksson 2001; Castlebury et al. 2002; Norphanphoun et al. 2017). The genus was introduced as important pathogens, which cause cankers and dieback disease on branches of a wide range of hosts worldwide (Adams et al. 2005, 2006; Hyde et al. 2017, 2018b; Norphanphoun et al. 2017, 2018). There are 630 epithets for *Cytospora* (Index Fungorum 2019) with an estimated 110 species in Kirk et al. (2008). Norphanphoun et al. (2017) provided a comprehensive account of the morphology and molecular background of the genus. Several new taxa have recently been introduced (Hyde et al. 2016, 2017, 2018b; Norphanphoun et al. 2017, 2018; Senanayake et al. 2017; Tibpromma et al. 2017; Zhu et al. 2018). In this study, a novel species of *Cytospora* is introduced from *Ulmus pumila* L. based on molecular data coupled with morphological characteristics (Fig. 76).

Cytospora ulmicola Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555487; *Facesoffungi number*: FoF05184, Fig. 77

Etymology: The specific epithet "*ulmicola*" refers to the host plant genus *Ulmus*, on which the fungus was first collected.

Holotype: MFLU 17-2080

Associated with twigs and branches of *Ulmus pumila* L. (*Ulmaceae*). **Sexual morph** Undetermined. **Asexual morph** *Conidiostromata* 1000–1700 × 500–800 µm diam., semi-immersed in host tissue, solitary, erumpent, scattered, discoid, circular to ovoid, with multi-loculate, pycnidial, embedded in stromatic tissue, with ostiole. *Ostioles* 200–500 µm long, with an ostiolar neck. *Conidiomata walls* comprising a few layers of pseudoparenchymatous cells of *textura angularis*, with inner layer thin, pale brown, outer layer brown to dark brown. *Conidiophores* unbranched or occasionally branched at the base, formed from the inner layer of the pycnidial wall. *Conidiogenous cells* (6–)9–14 × 1.3–1.8(–2.8) µm ($\bar{x}$ = 11 × 2 µm, n = 15), blastic, enteroblastic, flask-shaped, phialidic, hyaline, and smooth-walled. *Conidia* (7–)8–9.5 × 1.5–1.7(–1.9) µm ($\bar{x}$ = 8.5 × 1.6 µm, n = 30), unicellular, hyaline, oblong to allantoid, smooth-walled.

Culture characteristics: Conidia germinating on PDA within 12 h. Germ tubes produced from all sides. Colonies on PDA reaching 22–27 mm diam. after 2 weeks at room temperature, colonies irregular in shape, medium dense, flat to slightly raised, surface slightly rough, with small

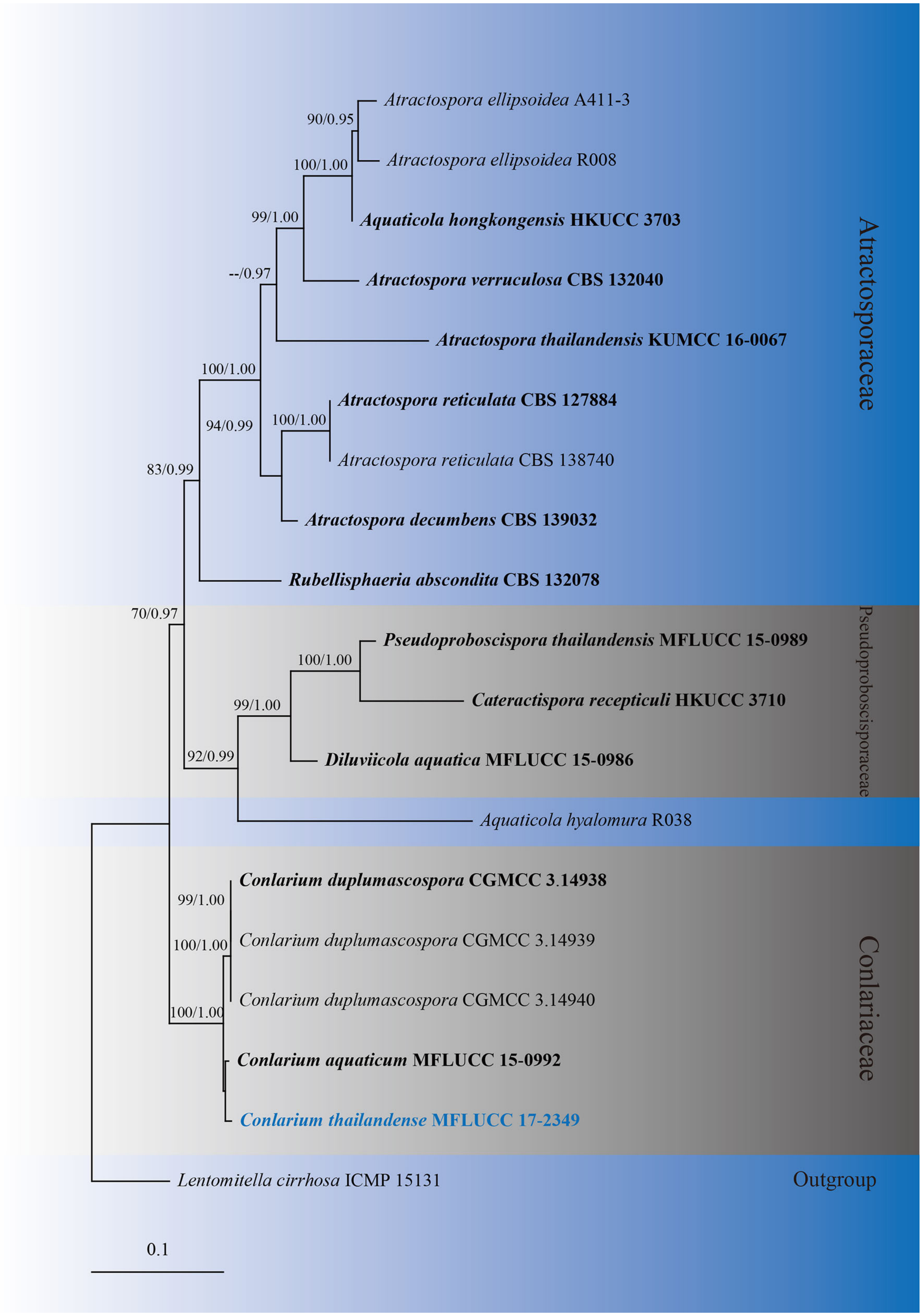


Fig. 74 Maximum likelihood (ML) majority rule consensus tree for the combined LSU, SSU and ITS sequence alignment for *Atractosporales*. The RAxML bootstrap support values (ML) greater than 70% and Bayesian posterior probabilities (BYPP) greater than 0.95 BYPP are given at the nodes (ML/BYPP). The ex-type strains are in bold and the new isolates are in blue. The tree is rooted to *Lentomitella cirrhosa* (ICMP 15131)

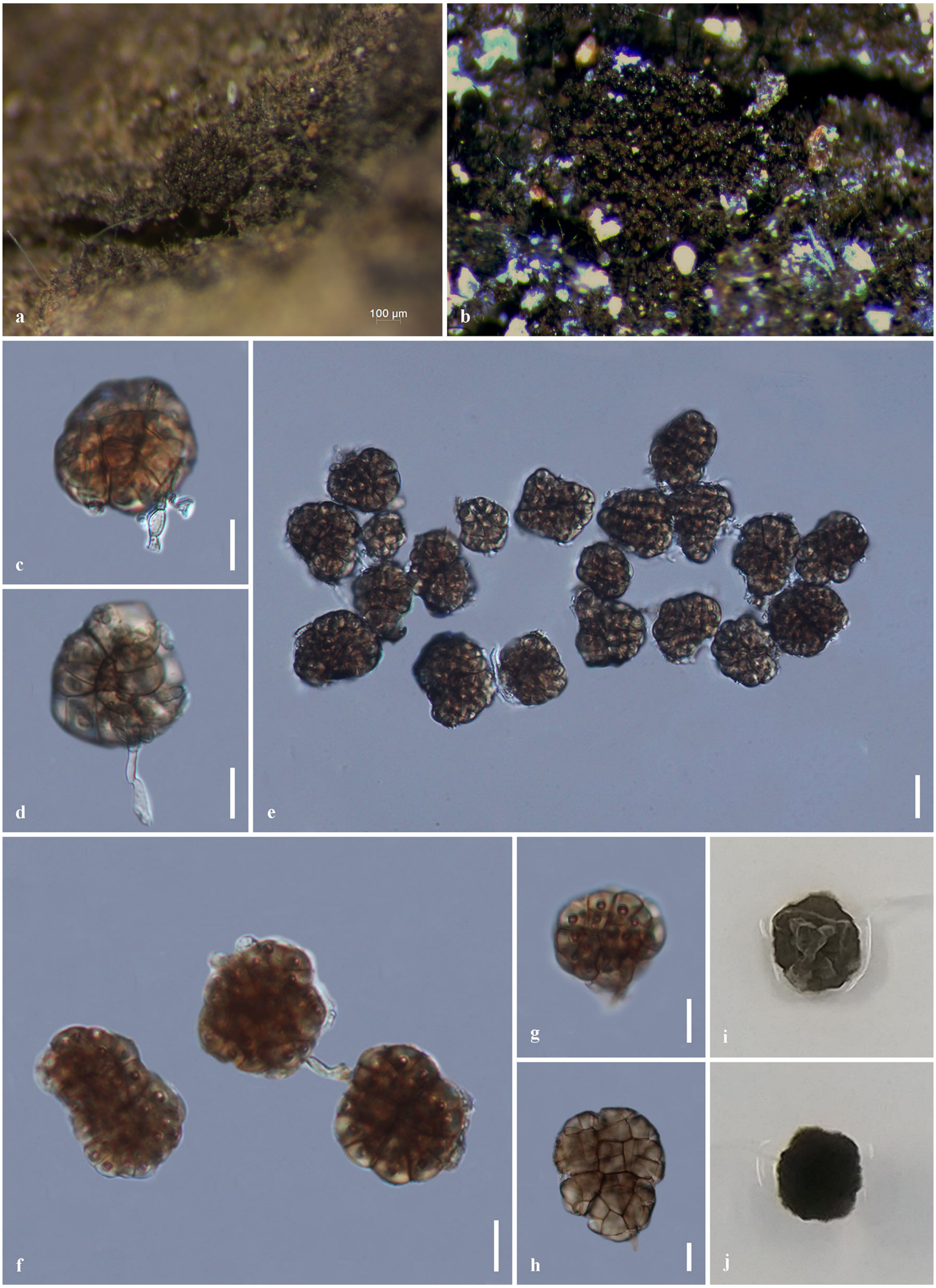


Fig. 75 ***Conlarium thailandense*** (MFLU 17-1711, **holotype**). **a, b** Colonies on the substratum. **c, d** Conidiogenous cells. **e, f** Conidia. **g** Conidia with the air-bubbles. **h** Fragile conidium. **i** Colonies on PDA (from front). **j** Colonies on PDA (from reverse). *Scale bars* **a** = 100 µm, **c, d, f–h** = 10 µm, **e** = 20 µm

granular, to velvety, edge undulate with well-defined margin, from above pale orange to light brown at the margin, amber near the margin, with, zonate, pale yellowish to dandelion and dark amber at the centre; from below pale yellowish at the margin, with dark amber at the centre; not producing pigmentation in agar.

Material examined: RUSSIA, Rostov region, Shakhty City, street trees, on dead branch of *Ulmus pumila* L. (*Ulmaceae*), 27 May 2017, T.S. Bulgakov, T-1778 (MFLU 17-2080, **holotype**; PDD, **isotype**), ex-type living culture, MFLUCC 18-1227.

GenBank numbers: ACT = MH940216, ITS = MH940220, LSU = MH940218, TUB2 = MH986792.

Notes: *Cytospora ulmicola* (MFLU 17-2080) was found on a dead branch (with signs of necrosis) of *Ulmus pumila* in European Russia. *Cytospora ulmicola* resembles *Cytospora* species in having an ostiolar neck with multi-loculate conidiostromata and unicellular, oblong to allantoid conidia. Phylogenetic analysis based on a combined ITS, LSU and ACT sequence dataset indicates that *C. ulmicola* clusters with *C. cotini* Norph. et al. (MFLUCC 14-1050), *C. ampulliformis* Norph. et al. (MFLUCC 16-0583), *C. gelida* Norph. et al. (MFLUCC 16-0634), and *C. ceratosperma* (Tode) G.C. Adams & Rossman (MFLUCC 16-0625) (Fig. 76). However, *C. ulmicola* can be distinguished from related species based on molecular data. A comparison of nucleotide polymorphisms of ITS and ACT shows that *C. ulmicola* differs from *C. cotini* with one polymorphism of ITS; from *C. ampulliformis* with one polymorphism of ITS and ten polymorphisms of ACT; from *C. gelida* with four polymorphisms of ITS and 13 polymorphisms of ACT; and from *C. ceratosperma* with five polymorphisms of ITS and eight polymorphisms of ACT. Therefore, following the guidelines of Jeewon and Hyde (2016) we introduce it as a new species.

Melanconiellaceae Senan. et al.

Melanconiellaceae was introduced by Senanayake et al. (2017) including phytopathogenic and saprobic species to accommodate *Greeneria* Scribn. & Viala, *Melanconiella* Sacc. and *Microascospora* Senan. & K.D. Hyde in the order *Diaporthales* (Senanayake et al. 2018; Braun et al. 2018). We introduce a new monotypic genus *Septomelanconiella* to the family *Melanconiellaceae* to accommodate a single species collected on rose apple in Thailand.

Septomelanconiella Samarak. & K.D. Hyde, ***gen. nov***.

Index Fungorum number: IF555301; *Facesoffungi number*: FoF04849

Etymology: The generic epithet "*Septomelanconiella*" reflects the septation of the conidia and parallel morphology to *Melanconiella*.

Saprobic on *Syzygium samarangense* in terrestrial habitats. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* pycnidial, immersed in the host, partially erumpent at maturity, mostly solitary or confluent, subglobose to irregular, to flattened and collabent, light brown. *Conidiomata walls* comprising 2–3 layers of hyaline cells, of *textura angularis* at the base, with light brown, thin outer layer. *Conidiophores* mostly reduced to conidiogenous cells, few with conidiophore and cylindrical conidiogenous cells. *Conidiogenous cells* enteroblastic, phialidic, integrated to discrete, cylindrical, determinate, hyaline, and finely roughened. *Conidia* cylindrical to clavate, one guttulate, becoming two guttules, hyaline, 1-septate when immature; mature conidia cylindrical to clavate, straight or slightly curved, brown, 1-euseptate, more often with 6 unequal lumina, guttulate, dark brown at the base.

Fig. 76 Phylogram generated from maximum likelihood analysis ▶ based on a combined ITS, LSU, and ACT sequence dataset. The tree is rooted to *Diaporthe eres* (AFTOL-ID 935). Maximum likelihood bootstrap values ≥ 50% are given at the nodes. Newly generated sequence is indicated in blue. Ex-type strains are indicated in bold

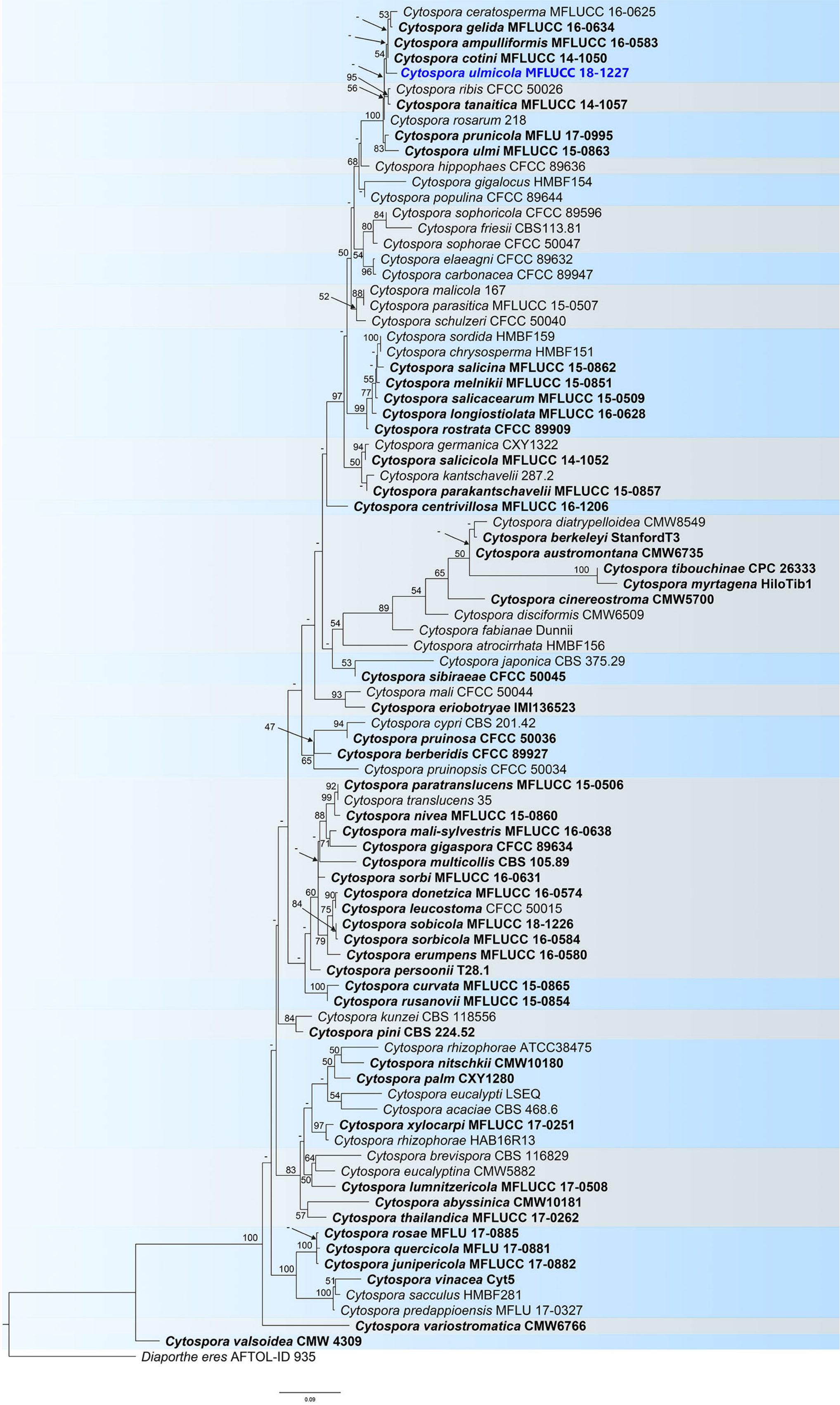
Type species: Septomelanconiella thailandica Samarak. & K.D. Hyde

Notes: *Septomelanconiella thailandica* constitutes an independent lineage basal to *Melanconiella syzygii* Crous & M.J. Wingf. Despite average phylogenetic support, *Septomelanconiella* is distinguished from other species as it is characterised by 1-euseptate and luminate conidia. *Septomelanconiella* is similar to *Melanconiella* in having finely verrucose, brown, mature conidia.

Septomelanconiella thailandica can be phylogenetically distingushed from the other genera in *Melanconiellaceae* as circumscribed by Senanayake et al. (2017). *Melanconiella syzygii* was isolated from a prominent leaf spot of *Syzygium* and is characterized by 2–3 layers of peridium, 1–2-septate conidiophores and hyaline to light brown aseptate conidia (Crous et al. 2016a). Multigene phylogenetic analyses also reveal that *Septomelanconiella thailandica* is separated from *Melanconiella syzygii*. Wijayawardene et al. (2016) described *Gloeocoryneum* and *Stegonosperiopsis* and referred them to Ascomycota, genera *incertae sedis.* They have similar brown, septate conidia as in *Septomelanconiella thailandica*. However, *Gloeocoryneum* differs in having 2–5 conidial septa, while *Stegonosperiopsis* is characterized by cylindrical conidiophores. Based on morphology and phylogeny in this study, *Septomelanconiella thailandica* is introduced as a new genus and species (Figs. 78, 79).

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

Index Fungorum number: IF555302; *Facesoffungi number*: FoF04850, Fig. 79


Cytospora ceratosperma MFLUCC 16-0625
Cytospora gelida MFLUCC 16-0634
Cytospora ampulliformis MFLUCC 16-0583
Cytospora cotini MFLUCC 14-1050
Cytospora ulmicola MFLUCC 18-1227
Cytospora ribis CFCC 50026
Cytospora tanaitica MFLUCC 14-1057
Cytospora rosarum 218
Cytospora prunicola MFLU 17-0995
Cytospora ulmi MFLUCC 15-0863
Cytospora hippophaes CFCC 89636
Cytospora gigalocus HMBF154
Cytospora populina CFCC 89644
Cytospora sophoricola CFCC 89596
Cytospora friesii CBS113.81
Cytospora sophorae CFCC 50047
Cytospora elaeagni CFCC 89632
Cytospora carbonacea CFCC 89947
Cytospora malicola 167
Cytospora parasitica MFLUCC 15-0507
Cytospora schulzeri CFCC 50040
Cytospora sordida HMBF159
Cytospora chrysosperma HMBF151
Cytospora salicina MFLUCC 15-0862
Cytospora melnikii MFLUCC 15-0851
Cytospora salicacearum MFLUCC 15-0509
Cytospora longiostiolata MFLUCC 16-0628
Cytospora rostrata CFCC 89909
Cytospora germanica CXY1322
Cytospora salicicola MFLUCC 14-1052
Cytospora kantschavelii 287.2
Cytospora parakantschavelii MFLUCC 15-0857
Cytospora centrivillosa MFLUCC 16-1206
Cytospora diatrypelloidea CMW8549
Cytospora berkeleyi StanfordT3
Cytospora austromontana CMW6735
Cytospora tibouchinae CPC 26333
Cytospora myrtagena HiloTib1
Cytospora cinereostroma CMW5700
Cytospora disciformis CMW6509
Cytospora fabianae Dunnii
Cytospora atrocirrhata HMBF156
Cytospora japonica CBS 375.29
Cytospora sibiraeae CFCC 50045
Cytospora mali CFCC 50044
Cytospora eriobotryae IMI136523
Cytospora cypri CBS 201.42
Cytospora pruinosa CFCC 50036
Cytospora berberidis CFCC 89927
Cytospora pruinopsis CFCC 50034
Cytospora paratranslucens MFLUCC 15-0506
Cytospora translucens 35
Cytospora nivea MFLUCC 15-0860
Cytospora mali-sylvestris MFLUCC 16-0638
Cytospora gigaspora CFCC 89634
Cytospora multicollis CBS 105.89
Cytospora sorbi MFLUCC 16-0631
Cytospora donetzica MFLUCC 16-0574
Cytospora leucostoma CFCC 50015
Cytospora sobicola MFLUCC 18-1226
Cytospora sorbicola MFLUCC 16-0584
Cytospora erumpens MFLUCC 16-0580
Cytospora persoonii T28.1
Cytospora curvata MFLUCC 15-0865
Cytospora rusanovii MFLUCC 15-0854
Cytospora kunzei CBS 118556
Cytospora pini CBS 224.52
Cytospora rhizophorae ATCC38475
Cytospora nitschkii CMW10180
Cytospora palm CXY1280
Cytospora eucalypti LSEQ
Cytospora acaciae CBS 468.6
Cytospora xylocarpi MFLUCC 17-0251
Cytospora rhizophorae HAB16R13
Cytospora brevispora CBS 116829
Cytospora eucalyptina CMW5882
Cytospora lumnitzericola MFLUCC 17-0508
Cytospora abyssinica CMW10181
Cytospora thailandica MFLUCC 17-0262
Cytospora rosae MFLU 17-0885
Cytospora quercicola MFLU 17-0881
Cytospora junipericola MFLUCC 17-0882
Cytospora vinacea Cyt5
Cytospora sacculus HMBF281
Cytospora predappioensis MFLU 17-0327
Cytospora variostromatica CMW6766
Cytospora valsoidea CMW 4309
Diaporthe eres AFTOL-ID 935
0.09

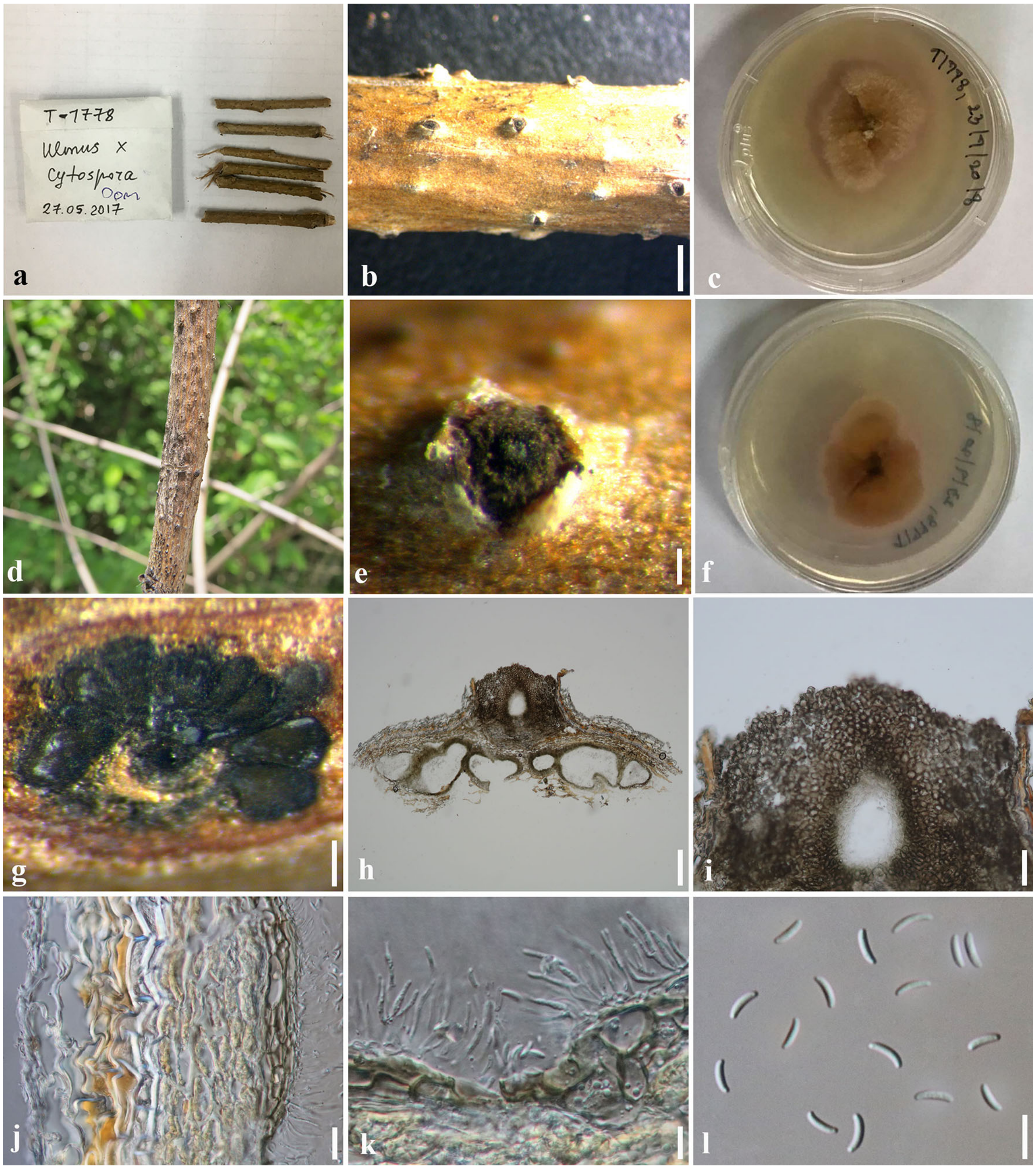


Fig. 77 ***Cytospora ulmicola*** (MFLU 17-2080, **holotype**). **a** Herbarium label and specimens. **b, d, e** Appearance of conidiostromata on branches of *Ulmus pumila*. **c, f** Colonies on PDA (**c** = from above, **f** = from below). **g** Transverse sections through conidiostroma to show an arrangement of the locules. **h** Longitudinal section through conidiostroma. **i** Ostiolar neck. **j** Conidiostroma wall. **k** Conidiogenous cells. **l** Conidia. *Scale bars* **b** = 1000 µm, **e** = 100 µm, **g, h** = 200 µm, **i** = 50 µm, **j** = 20 µm, **k, l** = 10 µm

Etymology: Name based on the country from which this species was collected, Thailand.

Holotype: MFLU 18-0793

Saprobic on recently dead twigs of *Syzygium samarangense*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 360–500 µm diam., 130–200 µm high, pycnidial, immersed, partially erumpent at maturity, solitary or confluent, subglobose to irregular, to flattened and collabent, light brown. *Conidiomata walls* 28–37.5 µm wide, comprising 2–3 layers of hyaline cells, of *textura angularis* at the base, with light brown, thin outer layer. *Conidiophores* mostly reduced to conidiogenous cells, few with conidiophore and cylindrical conidiogenous cells. *Conidiogenous cells* 10.3–15.9 × 4.4–7.3 µm ($\bar{x}$ = 13.2 × 5.9 µm, n = 20), enteroblastic, phialidic, integrated or discrete, cylindrical, determinate, hyaline, finely roughened. *Conidia* when immature, cylindrical to clavate, one guttulate, becoming two guttules, hyaline, one septate; mature conidia 37–52 × 15–23 µm ($\bar{x}$ = 43.8 × 19.1 µm, n = 40), cylindrical to clavate, straight or slightly curved, brown, 1-euseptate, with 6 unequal lumina, guttulate, dark brown at base with opening 1.8–3.6 µm diam. ($\bar{x}$ = 2.9 µm, n = 30).

Culture characteristics: Conidia germinating on PDA within 24 h, germ tubes produced from central part, often three hyphae. Colonies on PDA reaching 37 mm diam. in 2 weeks at 25 °C, hairy, white, superficial, rough surface, irregular edge, reverse yellowish brown.

Material examined: THAILAND, Chiang Rai Province, Muang District, Nang Lae, on dead twigs of *Syzygium samarangense* (Blume) Merr. & L.M. Perry (*Myrtaceae*), 25 January 2018, M.C. Samarakoon, SAMC091 (MFLU 18-0793, **holotype**; KUN-HKAS 102320, **isotype**), ex-type living culture, MFLUCC 18-0518, ICMP.

GenBank numbers: ITS = MH727706, LSU = MH727705, RPB2 = MH752072.

Pseudoplagiostomataceae Cheew. et al.

The monotypic family *Pseudoplagiostomataceae* was introduced by Cheewangkoon et al. (2010) to accommodate a cryptosporiopsis-like fungus isolated from *Eucalyptus*. *Pseudoplagiostomataceae* resembles *Gnomoniaceae* G. Winter based on morphological characters of its sexual morph, such as solitary, immersed, lacking stromatic ascomata with lateral beaks, asci with a distinct apical ring and 1-septate ascospores (Sogonov et al. 2008; Senanayake et al. 2017). Cheewangkoon et al. (2010) showed phylogenetically that *Pseudoplagiostomataceae* is closer to families with well-developed stromatic tissue such as *Diaporthaceae* Höhn. ex Wehm. and *Pseudovalsaceae* M.E. Barr, or families with stromatic and non-stromatic tissues such as *Valsaceae* Tul. & C. Tul. and *Sydowiellaceae* Lar.N. Vassiljeva. However, in our phylogenetic analyses it forms a fully-supported lineage, sister to *Apoharknessiaceae* Senan. et al. (Fig. 80).

Pseudoplagiostoma Cheew. et al.

We follow the latest treatment and updated accounts of *Pseudoplagiostoma* in Cheewangkoon et al. (2010), Suwannarach et al. (2016) and Du et al. (2017). Based on phylogenetic analyses of a combined ITS, LSU, TUB2 and TEF1-α dataset coupled with morphological characteristics, a novel species, *P. mangiferae* is introduced.

Pseudoplagiostoma mangiferae Dayarathne, Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555434; *Facesoffungi number*: FoF05111, Fig. 81

Etymology: The specific epithet "*mangiferae*" refers to the host genus *Mangifera*, of which the species was first collected.

Holotype: KUN-HKAS 102244

Associated with the leaf blight symptom on *Mangifera* sp. having amphigenous, subcircular to irregular, medium brown with blackish brown, reverse medium brown, surrounded by a purple-brown margin, which is dark brown in reverse. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 70–140 µm high, 90–150 µm diam. ($\bar{x}$ = 109 × 125 µm, n = 10), medium to dark brown, pycnidial with pale yellow drops of exuding conidia; subglobose, subcuticular to epidermal, with central rupture, breaking through plant tissue. *Conidiomata walls* 5–10 µm wide, thin-walled, composed of 2–4 layers of yellowish brown, pseudoparenchymatous cells, of *textura angularis*, intermixed with the host cells at the base and side. *Paraphyses* 0.8–2 µm wide, branched, septate, hyaline. *Conidiophores* absent. *Conidiogenous cells* 5–11 × 3.2–12.6 µm ($\bar{x}$ = 9 × 6 µm, n = 30), proliferating enteroblastic, appearing as phialides with periclinal thickening and collarette, or with percurrent proliferation in the apical part; discrete, arising from the inner cell layer, hyaline, smooth, cylindrical to ampulliform, wider at the base, straight. *Conidia* 18–24 × 11–14 µm ($\bar{x}$ = 22 × 13 µm, n = 50), hyaline, ellipsoidal, guttulate, smooth, thick-walled, aseptate, straight or slightly curved, frequently slightly narrow at the middle, with obtuse apex; base tapering to flat protruding scar.

Culture characteristics: Colonies on PDA reaching 80–85 mm diam. after 4 weeks at 20–25 °C, sparse to medium sparse, circular, flat, surface slightly rough with tufts of hyphae, edge entire, woolly to cottony, radiating with sparse mycelia in the middle part; from above, pink-white to cream, from below, pale yellowish; not producing pigmentation in agar.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Jinghong, Nabanhe, associated with leaf blight symtom on living leaf of *Mangifera* sp. (*Anacardiaceae*), 21 November 2015, R. Phookamsak, XB010 (KUN-HKAS 102244, **holotype**), ex-type living culture, KUMCC 18-0179.

GenBank numbers: ITS = MK084824, LSU = MK084825, TEF1-α = MK084822, TUB2 = MK084823.

Notes: Morphological characteristics clearly distinguish *Pseudoplagiostoma mangiferae* from other *Pseudoplagiostoma* species. The conidiogenous cells of *P. mangiferae* (5–11 × 3.2–12.6 µm) are wider than those of *P. eucalypti* (6–15 × 2–6 µm) (Cheewangkoon et al. 2010). *Pseudoplagiostoma variabile* is distinguished from *P. mangiferae* by its subglobose to bean-shaped, variable conidia shape (Cheewangkoon et al. 2010). The conidia of *P. corymbiae* (14–19 × 7–10 µm), *P. eucalypti* (14–22 × 6–11 µm), *P. oldie* (11–20 × 6–11 µm) and *P. variabile* (6.5–19 × 6.5–10.5 µm) are shorter than those of *P. mangiferae* (18.8–24 × 11.3–14.2 µm) while *P. dipterocarpi* (14–36 × 7–11 µm) has longer conidia

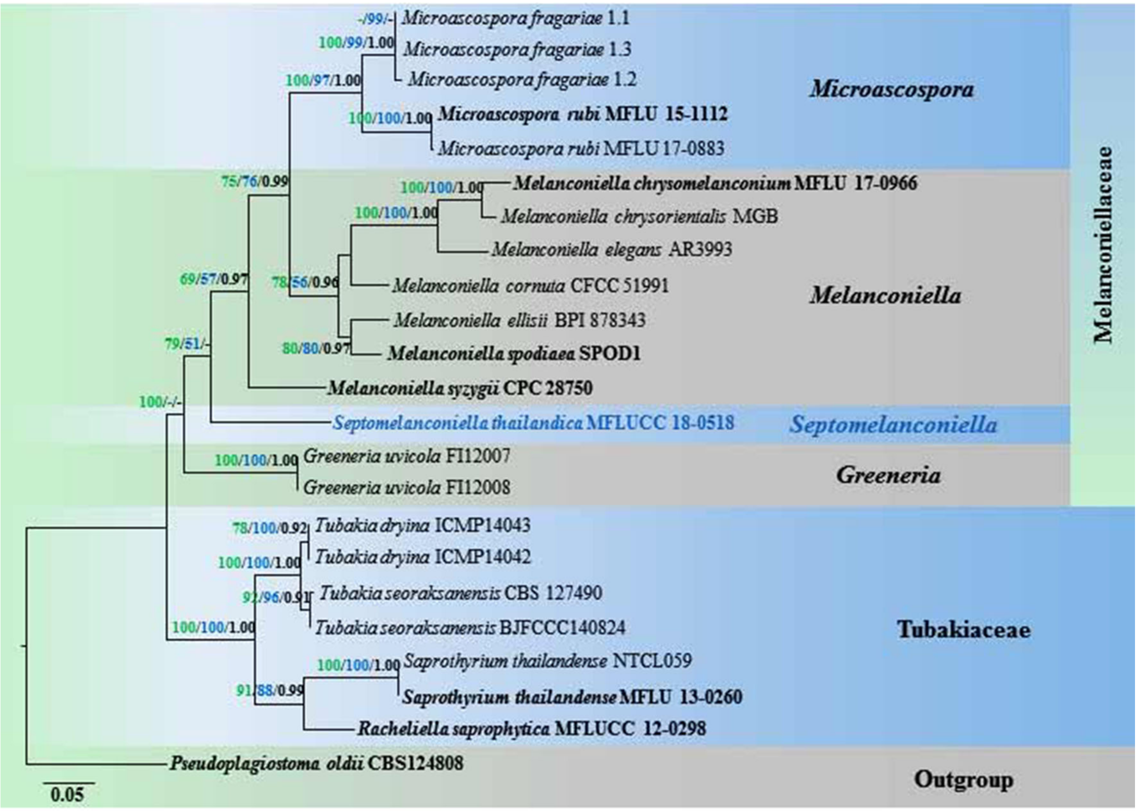


Fig. 78 Phylogram generated from maximum likelihood (RAxML) based on ITS, LSU and RPB2 partial sequence data analyses of 23 taxa and *Pseudoplagiostoma oldii* (CBS 124808) as an outgroup taxon. Bootstrap values for maximum parsimony (green) and maximum likelihood (blue) $\geq 50\%$ and Bayesian posterior probabilities (black) ≥ 0.90 are given at the nodes. The newly generated sequence is in blue. The ex-type strains are in bold. The scale bar represents the expected number of nucleotide substitutions per site

(Cheewangkoon et al. 2010; Crous et al. 2012; Suwannarach et al. 2016). Furthermore, *P. oldie* is distinguished from *P. dipterocarpi* by its conidia turning brown when mature (Cheewangkoon et al. 2010). According to our multigene analyses, *P. mangiferae* shows a close phylogenetic relationship with *P. dipterocarpi* (Fig. 80). However, they form well-separated lineages with high support (94% ML, 98% MP and 0.97 BYPP). A comparison of ITS nucleotide bases shows that *P. mangiferae* differs from *P. dipterocarpi* in 67/512 bp (13.1%). We therefore, introduce *P. mangiferae* as a new species following the guidelines of Jeewon and Hyde (2016).

Schizoparmaceae Rossman

Schizoparmaceae was introduced by Rossman et al. (2007) and is typified by *Schizoparme* Shear. The family also includes *Pilidiella* Petr. & Syd., the asexual morph of *Schizoparme* and the closely related *Coniella* Höhn (Rossman et al. 2007). In a recent revision, these three genera were synonymized under the old name, *Coniella* (Alvarez et al. 2016).

Coniella Höhn.

The genus *Coniella* was introduced by von Höhnel (1918) and is typified by *Coniella pulchella* Höhn. (= *C. fragariae* (Oudem.) B. Sutton). This genus comprises endophytes, saprobes and plant pathogens (Van Niekerk et al. 2004; Alvarez et al. 2016; Chethana et al. 2017). A new host record collected on *Prunus armeniaca* L. from Russia is reported for *C. vitis*, which has been previously reported as a plant pathogen from *Vitis vinifera* L. (*Vitaceae*; Chethana et al. 2017) (Fig. 82).

Coniella vitis Chethana, J.Y. Yan, X.H. Li & K.D. Hyde, Pl. Dis. 101: 2129 (2017).

Facesoffungi number: FoF02722, Fig. 83

Holotype: CHINA, Yanqing, Beijing, on white rot-infected berries of *Vitis vinifera* (*Vitaceae*), 13 May 2015, X–H Li, JZB3700001 (MFLU 16-2677), ex-type living culture, MFLUCC 16-1399.

Saprobic or *pathogenic* on branches and twigs of *Prunus armeniaca* L. (*Rosaceae*). **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 200–370 µm diam. ($\bar{x}$ = 304.2 µm, n = 20), pycnidial, solitary, submerged in PDA, globose to slightly depressed globose, with verruculose wall, initially hyaline becoming dark brown to black at maturity, with a central ostiole.

Fig. 79 ***Septomelanconiella thailandica*** (MFLU 18-0793, **holotype**). **a** Host. **b** Conidiomata on the substrate. **c** Vertical section of conidioma. **d–h** Conidiophores, conidiogenous cells and developing conidia. **i–l** Conidia. **m** Germinated conidium. **n** Culture on PDA from above after 16 days. **o** Culture on PDA from below after 16 days. *Scale bars* **b** = 1000 µm, **c** = 100 µm, **m** = 50 µm, **d–l** = 20 µm

Conidiophores 5–9 × 2–4 µm ($\bar{x}$ = 7.8 × 3.3 µm, n = 10), formed on a dense, cushion-like aggregation of hyaline cells, subcylindrical, hyaline, smooth, simple or branched below, mostly reduced to conidiogenous cells.

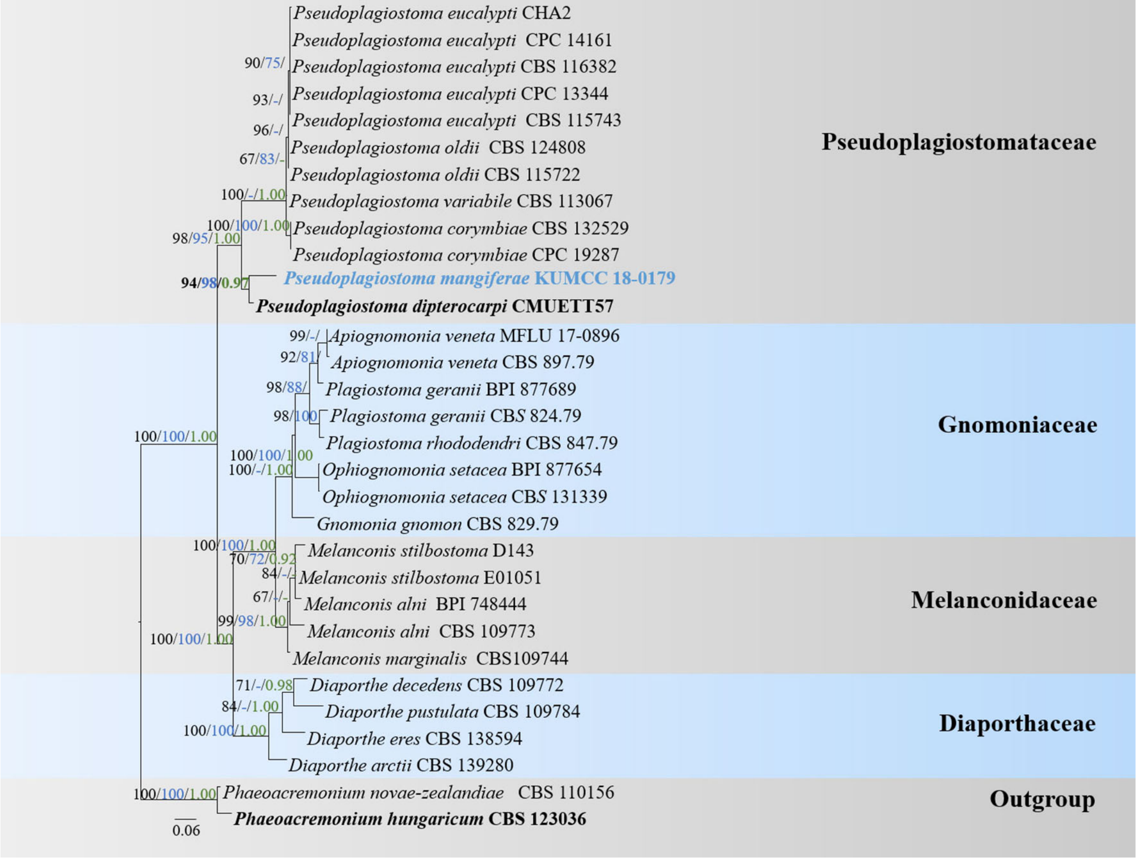


Fig. 80 Phylogenetic tree generated by maximum likelihood analysis of a combined ITS, LSU, TUB2 and TEF1-α sequence dataset of *Pseudoplagiostomataceae* and related families. Related sequences were obtained from GenBank. Thirty one strains are included in the analyses and the tree is rooted with *Phaeoacremonium novae-zealandiae* (CBS 110156) and *P. hungaricum* (CBS 123036). Tree topology of the ML analysis was similar to the MP and BI. The best scoring RAxML tree with a final likelihood value of -15510.220382 is presented. The matrix had 1138 distinct alignment patterns, with 50.26% of undetermined characters or gaps. Estimated base frequencies were as follows: **A** = 0.226739, **C** = 0.283205, G = 0.257579, T = 0.232477; substitution rates **AC** = 1.368247, AG = 2.869863, AT = 1.349096, CG = 0.967468, CT = 5.138587, GT = 1.000000; gamma distribution shape parameter α = 0.391573. RAxML (black) and maximum parsimony (blue) bootstrap support values ≥ 60% are shown respectively above the nodes. Bayesian posterior probabilities ≥ 0.95 BYPP indicated in green. The scale bar indicates 0.06 changes. The ex-type strains are in bold and new isolates in blue bold

Conidiogenous cells 9.5–16 × 2.5–4 µm ($\bar{x}$ = 13.2 × 3.3 µm, n = 10), phialidic, percurrently proliferating, hyaline, simple, slender, smooth with a prominent periclinal thickening. *Conidia* 8.5–12 × 3.5–6.5 µm ($\bar{x}$ = 10.2 × 4.9 µm, n = 40), l:w ratio 2, inequilateral, hyaline when immature becoming pale brown, aseptate, straight to slightly curved, narrowly ellipsoidal, often somewhat flattened on one side, both sides gradually tapering towards the subobtusely rounded apex, subtruncate base, smooth-walled, and multi-guttulate with one or two prominent guttules.

Culture characteristics: Colonies on PDA, reaching 8 cm diam. after 5 days at 28 °C, effuse, flat, mostly immersed mycelium, aerial mycelium mostly sparse, crenulated edges with concentric rings, white on surface and buff in reverse. Conidia in mass, hyaline.

Material examined: RUSSIA, Rostov Region, Shakhty City, on dead twigs (with signs of necrosis) of *Prunus armeniaca* L. (*Rosaceae*), 1 March 2016, T.S. Bulgakov, T1243 (MFLU 16-1537), living culture, MFLUCC 18-0093.

GenBank numbers: ITS = MH569466, LSU = MH569461, HIS3 = MH645901, TEF1-α = MH645902.

Known hosts and distribution: *Vitis vinifera* (China) and *Prunus armeniaca* (Russia) (Chethana et al. 2017; Farr and Rossman 2018).

Notes: *Coniella vitis* has been reported from *Vitis vinifera* as causing grape white rot in China (Chethana et al. 2017; Jayawardena et al. 2018). Based on our phylogenetic analysis of a combined ITS, LSU, HIS3 and TEF1-α sequence dataset of *Coniella* species (Fig. 82), our strain MFLUCC 18-0093 clusters together with the ex-type strain of *Coniella vitis* (MFLUCC 16-1399) with high bootstrap and Bayesian probabilities (100% MP and 1.00 BYPP). When comparing our strain with the type specimen of *C. vitis* (MFLUCC 16-1399), they are similar in morphology. However, our strain has slightly larger conidiomata, and

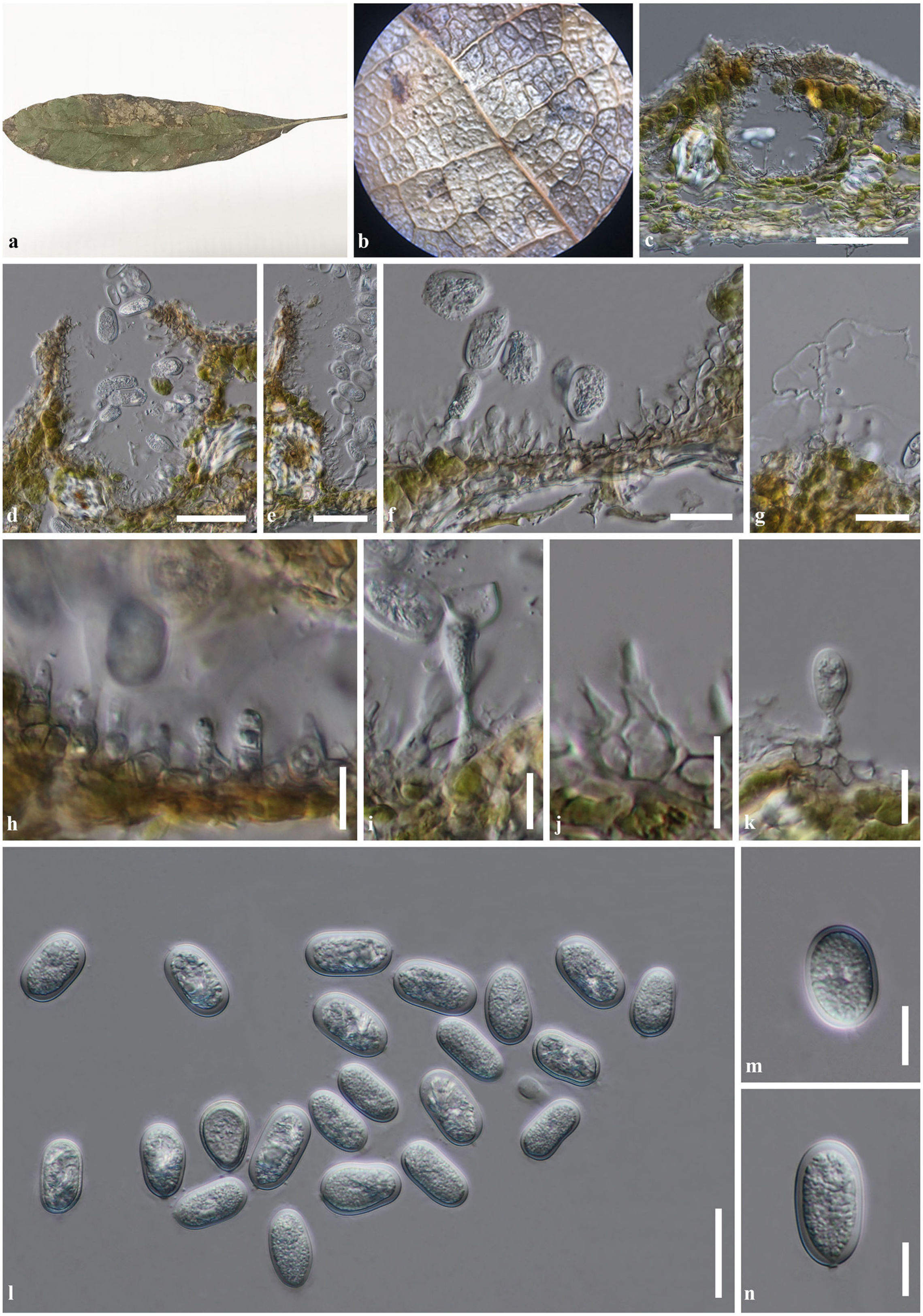


Fig. 81 ***Pseudoplagiostoma mangiferae*** (KUN-HKAS 102244, **holotype**). **a** Leaf blight symptom on living leaf of *Mangifera* sp. **b** Conidiomata on host surface. **c, d** Section through conidiomata. **e, f** Conidiomata walls at the side and the base respectively. **g** Paraphyses. **h–k** Conidiogenous cells. **l–n** Conidia. *Scale bars* **c–e** = 50 µm, **f, g, l** = 20 µm, **h–k, m, n** = 10 µm

larger conidiogenous cells compared to the type strain (Chethana et al. 2017).

Diaporthomycetidae, families *incertae sedis*

Distoseptisporaceae K.D. Hyde & McKenzie

Distoseptisporaceae was introduced by Su et al. (2016) and classified in Diaporthomycetidae, families *incertae sedis* by Wijayawardene et al. (2018a). The family consists of one hyphomycetous genus, *Distoseptispora* which is typified by *D. fluminicola* McKenzie et al. Seventeen *Distoseptispora* species have been introduced through previous studies, out of which eleven species are from freshwater, and five species are from terrestrial habitats (Hyde et al. 2016; Su et al. 2016; Xia et al. 2017; Luo et al. 2018; Tibpromma et al. 2018; Yang et al. 2018c) (Fig. 84).

Distoseptispora thysanolaenae Goonas., Dayarathne, Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555408; *Facesoffungi number*: FoF05011, Fig. 85

Etymology: Refers to the host from which the species was isolated

Holotype: KUN-HKAS 102247

Saprobic on dead culms of *Thysanolaena maxima*. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* effuse, brown to dark brown, hairy or fluffy, arising from subiculum, with tufts. *Mycelium* partly superficial, composed of branched, septate, smooth, brown hyphae. *Conidiophores* 30–80 × 3.5–5.5 µm ($\bar{x}$ = 52 × 4.5 µm, n = 30), macronematous, mononematous, light to dark brown, 2–8-septate, smooth, usually flexuous or sometimes straight, unbranched, cylindrical, rounded at the apex. *Conidiogenous cells* monoblastic, integrated, terminal, determinate, hyaline to light brown, cylindrical. *Conidia* 21.5–80 × 6.5–12.8 µm ($\bar{x}$ = 53 × 9.5 µm, n = 30), acrogenous, solitary, narrow and elongated obclavate, slightly curved, 8–14-distoseptate, thick-walled, light to dark brown, paler at the apex, tapering towards a rounded, flat apex, truncate with flat base, with conspicuous spore attachment loci, guttulate, smooth-walled.

Culture characteristics: Colonies on PDA reaching 43–45 mm diam. after 4 weeks at 20–25 °C, colonies dense, circular, flat, surface slightly rough, rugose with edge entire, floccose to velvety; colony from above, greenish grey at the margin, brown-grey at the centre, from below dark grey at the margin, black at the centre; not producing pigmentation in PDA. Sporulation on PDA after two months. *Conidiophores* 10–30(–47) × 3–5 µm ($\bar{x}$ = 21.4 × 4.6 µm, n = 25), macronematous, micronematous, mononematous, light to dark brown, 1–3-septate, smooth, usually flexuous or sometimes straight, unbranched, cylindrical, rounded at the apex. *Conidiogenous cells* monoblastic, integrated, terminal, determinate, hyaline to light brown, cylindrical. *Conidia* (20–)30–70(–243) × 5–8(–11) µm ($\bar{x}$ = 53 × 8.4 µm, n = 30), acrogenous, varied in shape, elongate cylindrical to obclavate, lanceolate, rostrate, 6–22(–50)-distoseptate, light brown to dark brown, tapering towards a rounded, sometimes bulbous apex, truncate at the base, with conspicuous spore attachment loci, smooth-walled.

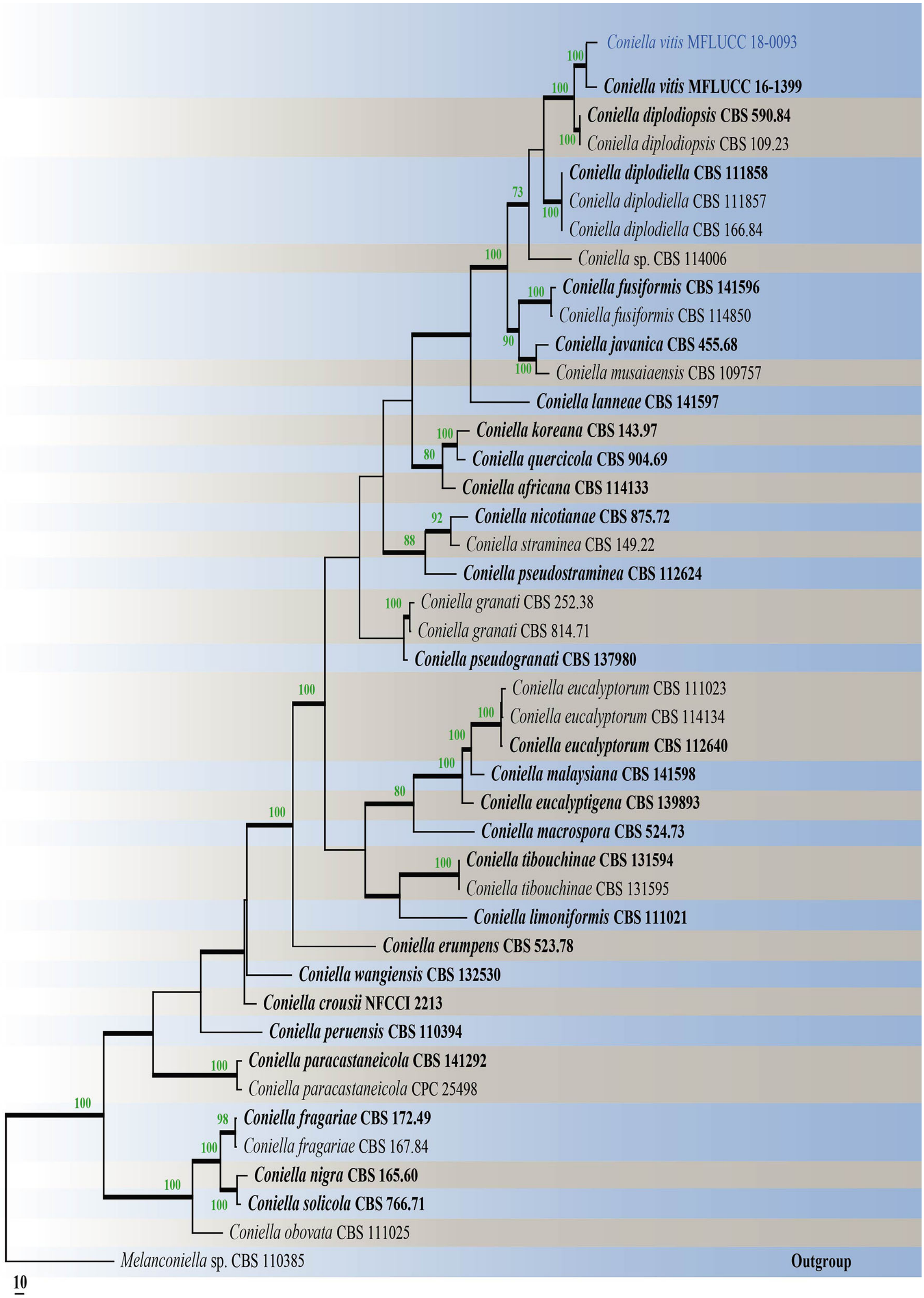
Material examined: CHINA, Yunnan Province, Xishuangbanna, Mengla County, Xishuangbanna Tropical Botanical Garden (XTBG), on dead culms of *Thysanolaena maxima* (Roxb.) Kuntze (*Poaceae*), 22 April 2017, R. Phookamsak, IS004 (KUN-HKAS 102247, **holotype**), ex-type living culture, KUMCC 18-0182 (IS004A), KUMCC 18-0183 (IS004B).

GenBank numbers: ITS = MK045851, LSU = MK064091, TEF1-α = MK086031.

Notes: *Distoseptispora thysanolaenae* is the sixth species in this genus to be introduced from a terrestrial habitat. The previously introduced species are *D. martini* (J.L. Crane & Dumont) J.W. Xia & X.G. Zhang, *D. tectonae* Doilom & K.D. Hyde, *D. tectonigena* Doilom & K.D. Hyde, *D. thailandica* Tibpromma & K.D. Hyde and *D. xishuangbannaensis* Tibpromma & K.D. Hyde (Hyde et al. 2016; Xia et al. 2017; Luo et al. 2018; Tibpromma et al. 2018). *Distoseptispora thysanolaenae* can be distinguished from these species by its 2–8-septate conidiophore that are 30–80 × 3.5–5.5 µm and narrow elongated, obclavate, light to dark brown conidia that are 21.5–80 × 6.5–12.8 µm, 8–14-distoseptate and smooth-walled. *Distoseptispora martini* has longer conidiophores (50–110 × 3.5–4.5 µm), shorter and wider conidia (15–20 × 11–16 µm) that are ellipsoid, oblate or subglobose (Xia et al. 2017).

Distoseptispora tectonae and *D. tectonigena* differ in their conidiophore dimensions (up to 40 × 4–6 µm, and up to 110 × 5–11 µm, respectively) and conidial dimensions

Fig. 82 Phylogenetic tree generated by maximum parsimony analysis ▶ of combined ITS, LSU, HIS3 and TEF1-α sequence dataset of *Coniella* species. Related sequences were obtained from GenBank. Forty four strains are included in the analyses, which comprise 2881 characters including gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. The tree is rooted with *Melanconiella* sp. (CBS 110385). The maximum parsimonious dataset consisted of 2109 constant, 558 parsimony-informative and 214 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of two equally most parsimonious trees with a length of 2551 steps (CI = 0.509, RI = 0.708, RC = 0.360, HI = 0.491) in the first tree. Maximum parsimony bootstrap support values ≥ 70% are shown near the nodes. Bayesian posterior probabilities ≥ 0.95 BYPP indicated as thickened black branches. The scale bar indicates 10 changes. The ex-type strains are in bold


Coniella vitis MFLUCC 18-0093
100
Coniella vitis MFLUCC 16-1399
100
Coniella diplodiopsis CBS 590.84
100
Coniella diplodiopsis CBS 109.23
Coniella diplodiella CBS 111858
73
Coniella diplodiella CBS 111857
100
Coniella diplodiella CBS 166.84
Coniella sp. CBS 114006
100
Coniella fusiformis CBS 141596
100
Coniella fusiformis CBS 114850
90
Coniella javanica CBS 455.68
100
Coniella musaiaensis CBS 109757
Coniella lanneae CBS 141597
100
Coniella koreana CBS 143.97
80
Coniella quercicola CBS 904.69
Coniella africana CBS 114133
92
Coniella nicotianae CBS 875.72
88
Coniella straminea CBS 149.22
Coniella pseudostraminea CBS 112624
100
Coniella granati CBS 252.38
Coniella granati CBS 814.71
Coniella pseudogranati CBS 137980
100
Coniella eucalyptorum CBS 111023
100
Coniella eucalyptorum CBS 114134
100
Coniella eucalyptorum CBS 112640
100
Coniella malaysiana CBS 141598
80
Coniella eucalyptigena CBS 139893
100
Coniella macrospora CBS 524.73
100
Coniella tibouchinae CBS 131594
Coniella tibouchinae CBS 131595
Coniella limoniformis CBS 111021
Coniella erumpens CBS 523.78
Coniella wangiensis CBS 132530
Coniella crousii NFCCI 2213
Coniella peruensis CBS 110394
100
Coniella paracastaneicola CBS 141292
Coniella paracastaneicola CPC 25498
100
98
Coniella fragariae CBS 172.49
100
Coniella fragariae CBS 167.84
Coniella nigra CBS 165.60
100
100
Coniella solicola CBS 766.71
Coniella obovata CBS 111025
Melanconiella sp. CBS 110385
Outgroup
10

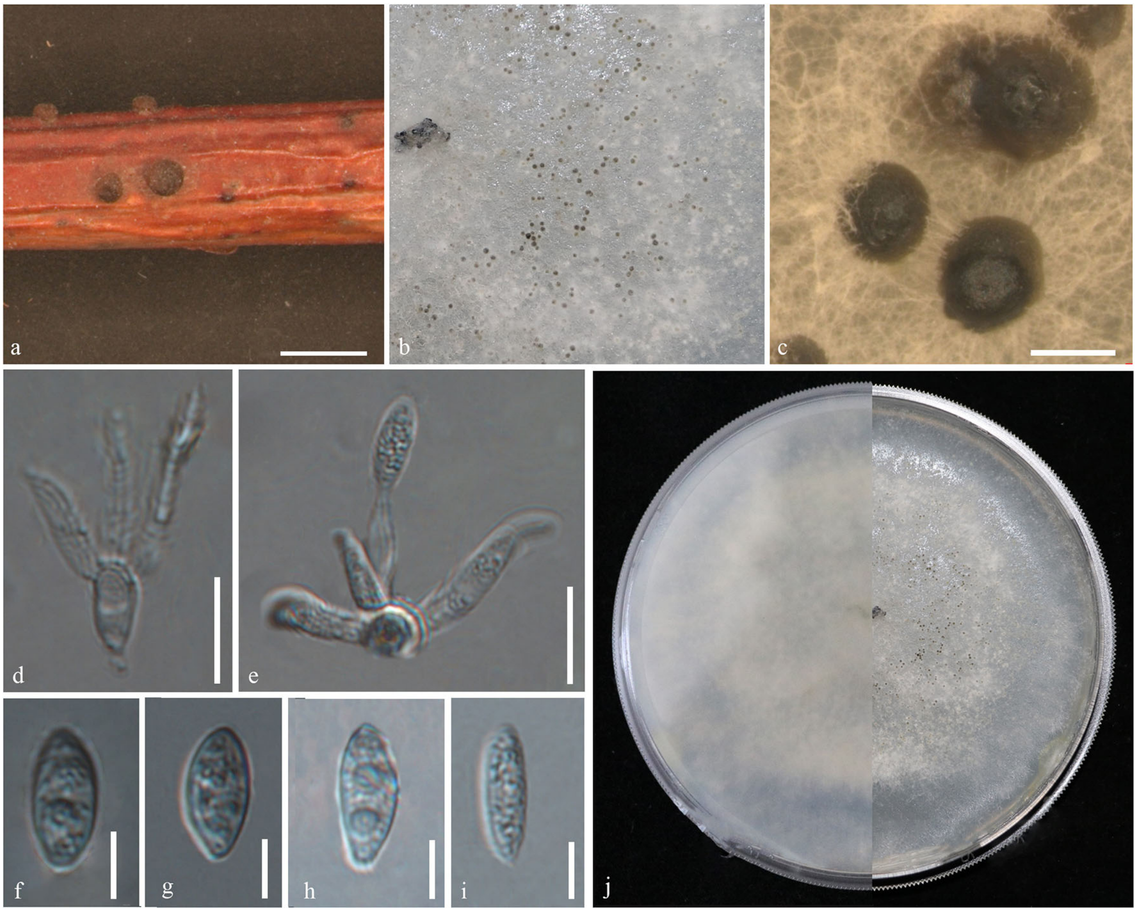


Fig. 83 ***Coniella vitis*** (MFLUCC 18-0093). **a** Host surface from which the saprobe was isolated. **b** Immature white pycnidia on PDA. **c** Mature black pycnidia with hyaline spore mass on PDA. **d** Conidiogenous cells. **e** Periclinal thickening at the apex of the conidiogenous cells. **f–i** Different shapes of conidia. **j** Upper-view (right) and the reverse view (left) of the colony on PDA. *Scale bars* **a** = 2 mm, **c** = 500 µm, **d, e** = 10 µm, **f–i** = 5 µm

((90–)130–140(–170) × 13–14 µm, and 148–225(–360) × 11–12 µm, respectively) and number of septa. *Distoseptispora thailandica* and *D. xishuangbannaensis* have larger conidia (130–230 × 13.5–17 µm and 160–305 × 8–15 µm, respectively) and more septa (35–52-distoseptate, and up to 40-distoseptate, respectively) (Tibpromma et al. 2018).

Phylogenetic analyses based on a combined ITS, LSU and TEF1-α sequence dataset show that our taxon clusters with other *Distoseptispora* species (Fig. 84). The species is sister to *D. guttulata* J. Yang & K.D. Hyde (MFLUCC 16-0183). A comparison of ITS and TEF1-α nucleotide bases shows that *D. thysanolaenae* differs from *D. guttulata* with 59 nucleotide bases of ITS and 64 nucleotide bases of TEF1-α. *Distoseptispora thysanolaenae* shares similar morphological features with *D. guttulata* but can be distinguished from the latter in having shorter conidia (21.5–80 µm versus 75–130 µm; Yang et al. 2018c). Therefore, following the guidelines of Jeewon and Hyde (2016) we introduce it as a new species.

Diaporthomycetidae, genera *incertae sedis*

Proliferophorum G.N. Wang, H. Zhang, K.D. Hyde & Senan., ***gen. nov.***

Index Fungorum number: IF555401; *Facesoffungi number*: FoF04847

Etymology: The generic epithet "*Proliferophorum*" refers to the proliferation of conidiophores.

Saprobic on decaying, submerged wood in freshwater habitat. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* irregular, hairy, black, gregarious. *Mycelium* mostly immersed in substratum, consisting of branched, septate, subhyaline to pale brown, smooth hyphae. *Conidiophores* macronematous, mononematous, caespitose, cylindrical, unbranched, erect, straight and curved at the upper part, dark brown, light brown at the apex, 8–10-septate, not constricted at the septa, smooth, sometimes percurrently proliferating 1–2 times at broken ends, with few upper cells, guttulate. *Conidiogenous cells* holoblastic, polyblastic, terminal, sympodial, pale brown or subhyaline, with minute, truncate conidiogenous loci.

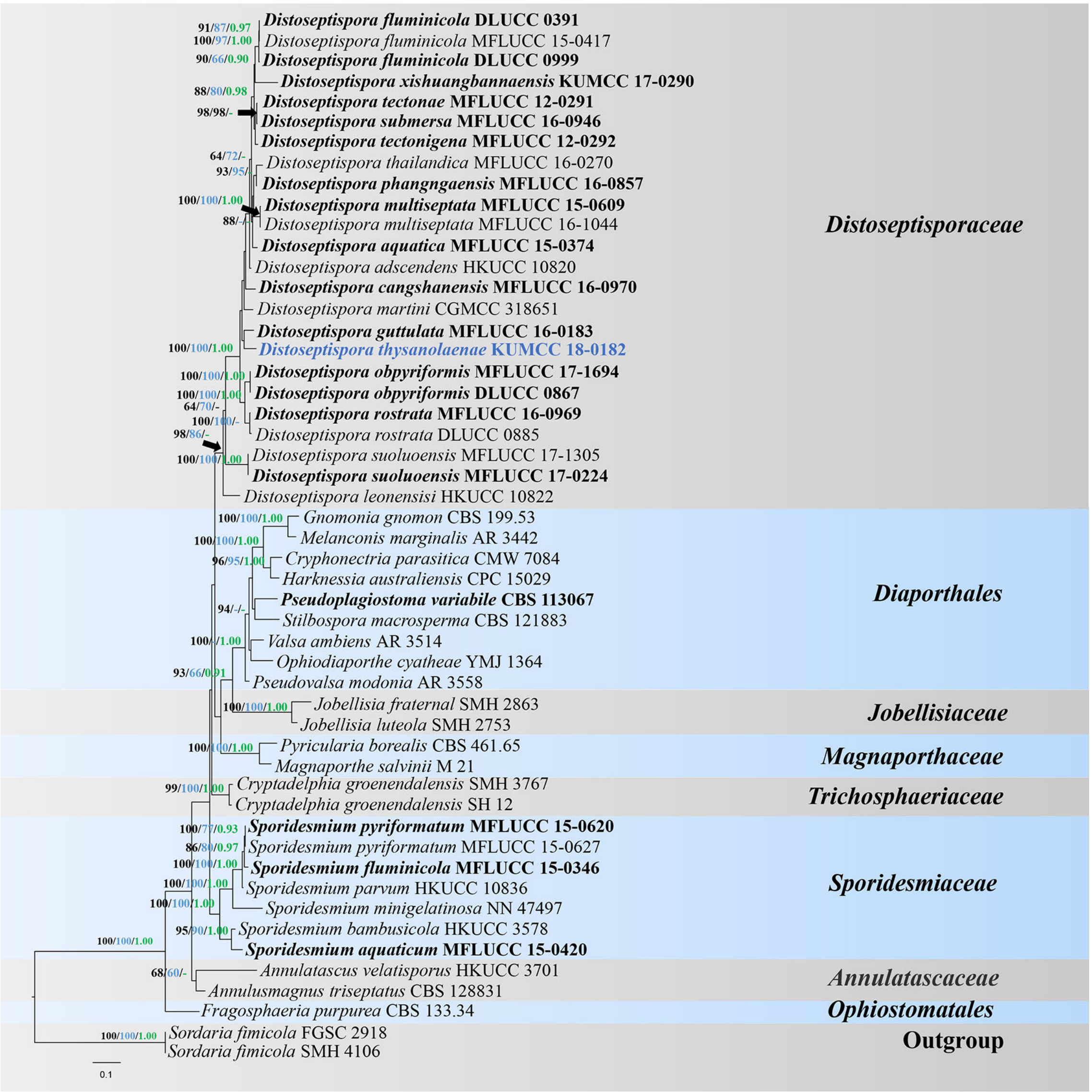


Fig. 84 Phylogenetic tree generated by maximum likelihood analysis of a combined ITS, LSU and TEF1-α sequence dataset of *Distoseptisporaceae* and other related families in Diaporthomycetidae. Related sequences were obtained from GenBank. Fifty one strains are included in the analyses, which comprised 2409 characters including gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. The tree is rooted with *Sordaria fimicola* (SMH 4106, FGSC 2918). Tree topology of the ML analysis was similar to the MP and BI. The best scoring RAxML tree with a final likelihood value of -17019.410141 is presented. The matrix had 1186 distinct alignment patterns, with 38.62% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.237054, C = 0.262859, G = 0.290202, T = 0.209884; substitution rates AC = 1.172995, AG = 2.180726, AT = 1.594744, CG = 1.095103, CT = 6.416481, GT = 1.000000; gamma distribution shape parameter α = 0.352856. The maximum parsimonious dataset consisted of 1183 constant characters, 751 parsimony-informative and 475 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of two equally most parsimonious trees with a length of 2985 steps (CI = 0.590, RI = 0.726, RC = 0.428, HI = 0.410) in the first tree. RAxML (black) and maximum parsimony (blue) bootstrap support values ≥ 60% are shown respectively above the nodes. Bayesian posterior probabilities ≥ 0.95 BYPP indicated in green. The scale bar indicates 0.1 changes. The ex-type strains are in bold and a new isolate is in blue

Conidia fusiform to cylindrical, aseptate when young, 2–3-septate when mature, rarely up to 4-septate, slightly constricted at the septa, dark brown at central cells, pale brown at end cells, guttulate at some stage, dry, smooth.

Type species: *Proliferophorum thailandicum* G.N. Wang, H. Zhang, K.D. Hyde & Senan.

Notes: *Proliferophorum* is introduced as a monotypic genus in the subclass Diaporthomycetidae to accommodate a hyphomycetous species forming mononematous, caespitose conidiophores, sometimes percurrently proliferating 1–2 times at broken ends of conidiogenous cells and fusiform to cylindrical conidia. The genus was found on wood,


a
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r
s

◀**Fig. 85** ***Distoseptispora thysanolaenae*** (KUN-HKAS 102247, **holotype**). On host substrate: **a** Appearance of colonies on host surface. **b, d, e** Conidiophores. **c, f** Conidiophores with attached conidia. **g–i** Variable shapes of conidia. In vitro: **j** Sporulation of conidia on PDA after 4 weeks. **k–m** Conidiophores with attached conidia. **n–s** Variable shapes of conidia. *Scale bars* **a** = 500 µm, **b–i, k–r** = 20 µm, **s** = 50 µm

similar to the genus *Minimelanolocus* R.F. Castañeda & Heredia, which has conidiophores that are generally conspicuous, mononematous, solitary or fasciculate, septate, erect, straight or flexuous, smooth or verrucose, and brown to dark brown with a melanised base (Castañeda-Ruiz et al. 2003). The conidia of *Minimelanolocus* are generally, cylindrical, naviculate, clavate, obclavate and pale brown to dark brown (Liu et al. 2015b). However, *Proliferophorum* differs from *Minimelanolocus* in its conidiophores that have a few upper guttulate cells and conidia having obvious droplets. In addition, LSU sequence data analysis shows the genus does not group with species in *Chaetothyriales*. Phylogenetic analyses (Fig. 86) of taxa within Diaporthomycetidae indicate that *Proliferophorum* forms a single lineage, between *Phomatosporales* Senan. et al. and *Amplistromatales* M.J. D'souza et al. The sporothrix-like asexual morph of *Phomatosporales* was reported from culture by Rappaz (1992).

Amplistromatales comprises the families *Amplistromataceae* Huhndorf et al. and *Catabotrydaceae* Petr. ex M.E. Barr and their asexual morphs have been reported as acrodontium-like for *Amplistroma* Huhndorf et al. (Maharachchikumbura et al. 2015). *Proliferophorum* and acrodontium-like asexual morphs are distinct.

Proliferophorum thailandicum G.N. Wang, H. Zhang, K.D. Hyde & Senan., ***sp. nov.***

Index Fungorum number: IF555400; *Facesoffungi number*: FoF04848, Fig. 87

Etymology: In reference to Thailand, where the species was collected.

Holotype: MFLU 17-1054

Saprobic on decaying, submerged wood in freshwater habitat. **Sexual morph** Undetermined. **Asexual morph** *Colonies* irregular, hairy, black, gregarious. *Mycelium* mostly immersed in substratum, consisting of branched, septate, subhyaline to pale brown, smooth hyphae. *Conidiophores* macronematous, mononematous, caespitose, cylindrical, unbranched, erect, straight and curved at the upper part, dark brown, light brown at the apex, 8–10-septate, not constricted at the septa, 50–100 × 4–7 µm ($\bar{x}$ = 82 × 5.5 µm, n = 10), smooth, sometimes percurrently proliferating 1–2 times at broken ends, with few upper cells guttulate. *Conidiogenous cells* holoblastic, polyblastic, terminal, sympodial, pale brown or subhyaline, up to 20–30 µm long, with minute, truncate conidiogenous loci. *Conidia* fusiform to cylindrical, aseptate when young, 2–3-septate when mature, rarely up to 4-septate, slightly constricted at the septa, dark brown at central cells, pale brown at end cells, guttulate at some stage, dry, smooth, 15–25 × 3–7 µm ($\bar{x}$ = 23 × 5 µm, n = 20).

Culture characteristics: Colonies on PDA reaching 10 mm diam. within 15 days at 25 °C, colony circular, medium dense slightly raised to umbonate, surface slightly rough with edge entire, floccose to velvety, colony from above and below black; not producing pigmentation in agar.

Material examined: THAILAND, Chiang Rai Province, Longkhot Subdistrict, saprobic on decaying submerged wood in a stream, 1 September 2017, G.N Wang, 4.14.1 (MFLU 17-1054, **holotype**), ex-type living culture, MFLUCC 17-0293.

GenBank numbers: ITS = MK028344, LSU = MK028343, SSU = MK028345.

Subclass Hypocreomycetidae O.E. Erikss. & Winka

Glomerellales Chadef. ex Réblová et al.

Plectosphaerellaceae W. Gams et al.

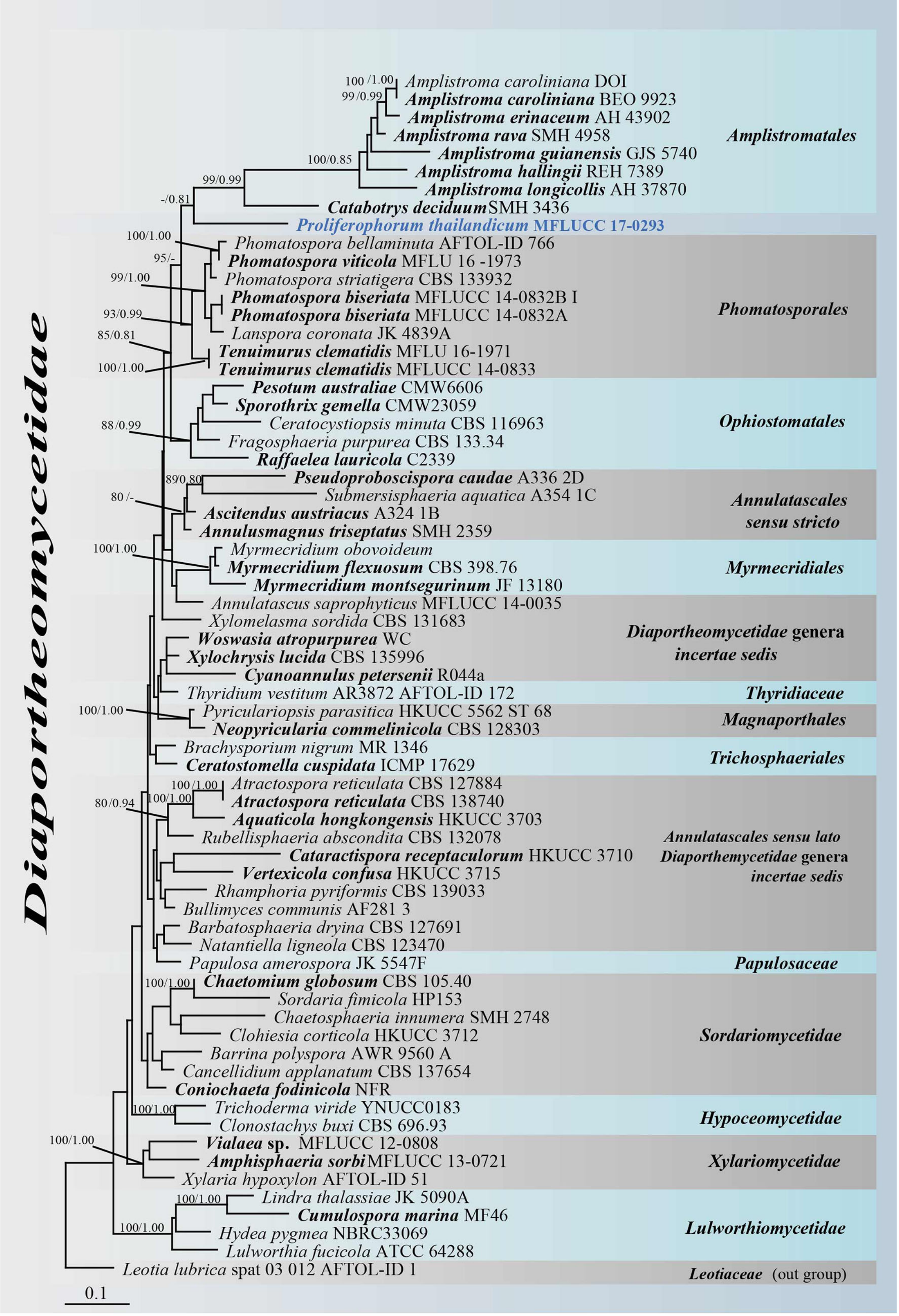
Plectosphaerellaceae was introduced by Zare et al. (2007) to accommodate the genera *Acrostalagmus* Corda, *Gibellulopsis* Bat. & Maia, *Musicillium* Zare & W. Gams, *Plectosphaerella* and *Verticillium* Nees, with *Plectosphaerella* as the type genus and *P. cucumeris* Kleb. being the type species. Eleven genera are accepted in this family viz. *Acrostalagmus*, *Brunneomyces* A. Giraldo et al., *Chordomyces* Bilanenko et al., *Gibellulopsis*, *Lectera* P.F. Cannon, *Longitudinalis* Tibpromma & K.D. Hyde, *Musicillium*, *Plectosphaerella*, *Sodiomyces* A.A. Grum-Grzhim. et al., *Stachylidium* Link and *Verticillium* (Wijayawardene et al. 2018a).

Plectosphaerella Kleb.

We follow the latest treatment and updated accounts of *Plectosphaerella* in Zare et al. (2007), Carlucci et al. (2012), Hyde et al. (2017) and Su et al. (2017), with the updated phylogenetic analyses based on a combined ITS, LSU and TEF1-α which were retrieved from Hyde et al. (2017) and Su et al. (2017). A novel species, *Plectosphaerella kunmingensis* is introduced based on its holomorphic characteristics and phylogenetic affinities in *Plectosphaerellaceae* (Fig. 88)

Plectosphaerella kunmingensis Phookamsak, J.F. Li & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556180; *Facesoffungi number*: FoF05716, Fig. 89


Diaportheomycetidae
100 /1.00
Amplistroma caroliniana DOI
99 /0.99
Amplistroma caroliniana BEO 9923
Amplistroma erinaceum AH 43902
Amplistroma rava SMH 4958
Amplistroma guianensis GJS 5740
Amplistroma hallingii REH 7389
Amplistroma longicollis AH 37870
100/0.85
99/0.99
-/0.81
Catabotrys deciduum SMH 3436
Amplistromatales
Proliferophorum thailandicum MFLUCC 17-0293
100/1.00
Phomatospora bellaminuta AFTOL-ID 766
95/-
Phomatospora viticola MFLU 16 -1973
99/1.00
Phomatospora striatigera CBS 133932
Phomatospora biseriata MFLUCC 14-0832B I
93/0.99
Phomatospora biseriata MFLUCC 14-0832A
85/0.81
Lanspora coronata JK 4839A
Tenuimurus clematidis MFLU 16-1971
100/1.00
Tenuimurus clematidis MFLUCC 14-0833
Phomatosporales
Pesotum australiae CMW6606
Sporothrix gemella CMW23059
Ceratocystiopsis minuta CBS 116963
88/0.99
Fragosphaeria purpurea CBS 133.34
Raffaelea lauricola C2339
Ophiostomatales
89/0.80
Pseudoproboscispora caudae A336 2D
Submersisphaeria aquatica A354 1C
80 /-
Ascitendus austriacus A324 1B
Annulusmagnus triseptatus SMH 2359
Annulatascales sensu stricto
100/1.00
Myrmecridium obovoideum
Myrmecridium flexuosum CBS 398.76
Myrmecridium montsegurinum JF 13180
Myrmecridiales
Annulatascus saprophyticus MFLUCC 14-0035
Xylomelasma sordida CBS 131683
Woswasia atropurpurea WC
Xylochrysis lucida CBS 135996
Cyanoannulus petersenii R044a
Diaportheomycetidae genera incertae sedis
Thyridium vestitum AR3872 AFTOL-ID 172
Thyridiaceae
100/1.00
Pyriculariopsis parasitica HKUCC 5562 ST 68
Neopyricularia commelinicola CBS 128303
Magnaporthales
Brachysporium nigrum MR 1346
Ceratostomella cuspidata ICMP 17629
Trichosphaeriales
100/1.00
Atractospora reticulata CBS 127884
100/1.00
80/0.94
Atractospora reticulata CBS 138740
Aquaticola hongkongensis HKUCC 3703
Rubellisphaeria abscondita CBS 132078
Cataractispora receptaculorum HKUCC 3710
Vertexicola confusa HKUCC 3715
Rhamphoria pyriformis CBS 139033
Bullimyces communis AF281 3
Barbatosphaeria dryina CBS 127691
Natantiella ligneola CBS 123470
Annulatascales sensu lato Diaporthemycetidae genera incertae sedis
Papulosa amerospora JK 5547F
Papulosaceae
100/1.00
Chaetomium globosum CBS 105.40
Sordaria fimicola HP153
Chaetosphaeria innumera SMH 2748
Clohiesia corticola HKUCC 3712
Barrina polyspora AWR 9560 A
Cancellidium applanatum CBS 137654
Coniochaeta fodinicola NFR
Sordariomycetidae
100/1.00
Trichoderma viride YNUCC0183
Clonostachys buxi CBS 696.93
Hypoceomycetidae
100/1.00
Vialaea sp. MFLUCC 12-0808
Amphisphaeria sorbi MFLUCC 13-0721
Xylaria hypoxylon AFTOL-ID 51
Xylariomycetidae
100/1.00
Lindra thalassiae JK 5090A
Cumulospora marina MF46
100/1.00
Hydea pygmea NBRC33069
Lulworthia fucicola ATCC 64288
Lulworthiomycetidae
Leotia lubrica spat 03 012 AFTOL-ID 1
Leotiaceae (out group)
0.1

◀**Fig. 86** Phylogram inferred from maximum likelihood analysis of a combined LSU, SSU and ITS sequence dataset using a GTRGAMMA model of evolution. Maximum likelihood bootstrap support greater than 80% and Bayesian posterior probability greater than 0.80 BYPP are indicated at the nodes. Newly introduced strain is in blue bold and type strains are in bold. The tree is rooted to *Leotia lubrica* (AFTOL-ID 1 = OSC 100001). The combined LSU, SSU and ITS sequence dataset comprised 67 strains (including the new strain and outgroup taxon) and manually adjusted dataset totally comprised 2228 characters including gaps. The best scoring RAxML tree was selected to represent the relationships among taxa, in which a final likelihood value of − 22073.200898

Etymology: The specific epithet "*kunmingensis*" refers to Kunming City, Yunnan, China where the species was first collected.

Holotype: KUN-HKAS 102246

Colonies forming on PDA. *Mycelium* composed of 1–3 µm wide, septate, branched, smooth and thin-walled, hyaline hyphae, partly immersed on PDA. **Sexual morph** forming black, obpyriform ascomata after 8 weeks at 20–25 °C. *Ascomata* 100–185 µm high, 80–110 µm diam., perithecial, superficial or immersed in culture colonies, scattered, solitary to gregarious, subglobose to ovoid, or obpyriform, uni-loculate, glabrous, ostiole at centre, with a minute papilla. *Peridium* 7–18 µm wide, thin-walled, of equal thickness, composed of 1–3 layers, of dark brown pseudoparenchymatous cells, arranged in a *textura angularis*. *Asci* (42–)45–55(–62) × 10–13 µm ($\bar{x}$ = 51.9 × 11.6 µm, n = 15), 8-spored, unitunicate, cylindric-obclavate to obpyriform, subsessile, thick-walled at apex, with J-, subapical ring. *Ascospores* (8–)10–13(–15) × 3–5 µm ($\bar{x}$ = 11.9 × 4.3 µm, n = 50), overlapping 1–2-seriate, hyaline, ellipsoidal to subfusoid, with round ends, 1-septate, smooth-walled with small guttules, becoming finely echinulate when stained by Melzer's reagent. **Asexual morph** Hyphomycetous, *Conidiophores* 15–50(–58) × (1.5–)3–5 µm ($\bar{x}$ = 38.5 × 4.2 µm, n = 20), macronematous or micronematous, produced from prostrate hyphae, lacking hyphal coils, sometimes branched, hyaline, yellowish brown at the base, thick-walled, smooth, septate, branched, straight or flexuous. *Conidiogenous cells* phialidic, determinate, integrated to discrete, hyaline, subcylindrical to ampulliform, smooth-walled, with periclinal wall thickening, with minute collarette. *Conidia* 7–10 × 4–7 µm ($\bar{x}$ = 8.7 × 5.4 µm, n = 50), pleurogenous or acropleurogenous, formed in slimy heads at the apex of the phialides, hyaline, subglobose to ellipsoidal, aseptate, smooth, thin-walled, with granular contents. *Chlamydospores* not produced.

Culture characteristics: Colonies on PDA reaching 40–48 mm diam. after 3 weeks at 20–25 °C, dense, irregular in shape, flat to slightly raised, slightly rough at surface, with mycelia radiating outwards, sometimes forming sectors of different folds, fimbriate at edge, mucoid to floccose; from above, white yellowish to cream; from below, pale yellowish; not producing pigmentation in agar medium.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, colonies forming on WA as a contaminated fungus, 5 July 2017, R. Phookamsak, KIB042 (dried culture herbarium: KUN-HKAS 102246, **holotype**), ex-type living culture, KUMCC 18-0181.

GenBank numbers: ITS = MH254296, LSU = MH254298, RPB2 = MH254297, TEF1-α = MH254295.

Notes: Phylogenetic analyses of a combined ITS, LSU and TEF1-α sequence dataset (Fig. 88) show the new species, *Plectosphaerella kunmingensis* forming a distinct lineage at the basal clade of *Plectosphaerella* in *Plectosphaerellaceae* with moderate support (76% ML and 0.96 BYPP). *Plectosphaerella kunmingensis* can be distinguished from other *Plectosphaerella* species in the lack of hyphal coils, as well as having partly coloured conidiophores. The sexual morph of *P. kunmingensis* differs from *P. cucumerina* in having smaller asci (*P. kunmingensis*, (42–)45–55(–62) × 10–13 µm versus 50–80 × 6–9 µm, *P. cucumerina*; Carlucci et al. 2012) and wider ascospores (*P. kunmingensis*, (8–)10–13(–15) × 3–5 µm versus (9–)10.5–14(–15) × 2.5–3(–4) µm, *P. cucumerina*; Carlucci et al. 2012) (Fig. 90).

Another species, *Plectosphaerella sinensis* was also found from China isolated from a healthy stem of *Cucumis melo* L. (*Cucurbitaceae*) (Su et al. 2017). Whereas, our isolate was found as a contaminated fungus on WA. *Plectosphaerella kunmingensis* has subglobose to ellipsoidal, aseptate conidia and lacks chlamydospores, while *P. sinensis* has ellipsoidal, 0–1-septate conidia with a slightly apiculate base, and forming intercalary or terminal, irregular, thick-walled chlamydospores (Su et al. 2017). In the BLASTn search on NCBI GenBank, the closest matches of ITS sequence of *P. kunmingensis* are *P. nepalense* (CBS 971.72) and *P. cucumerina* (XSD-75) with 95% similarities for both strains. In addition, a comparison of ITS nucleotide bases between *P. kunmingensis* and *P. niemeijerarum* (CBS 143233) shows that they differ in 42 base positions (8.08%/520 bp). Based on a molecular analyses coupled with morphological characteristics, we therefore, propose *P. kunmingensis* as a new species.

Hypocreales Lindau

Cordycipitaceae Kreisel ex G.H. Sung et al.

Cordycipitaceae was validated by Sung et al. (2007) to accommodate the type of *Cordyceps* Fr., *C. militaris* (L.) Fr. and most of *Cordyceps* species forming brightly coloured, fleshy stromata. Species of *Cordycipitaceae* have

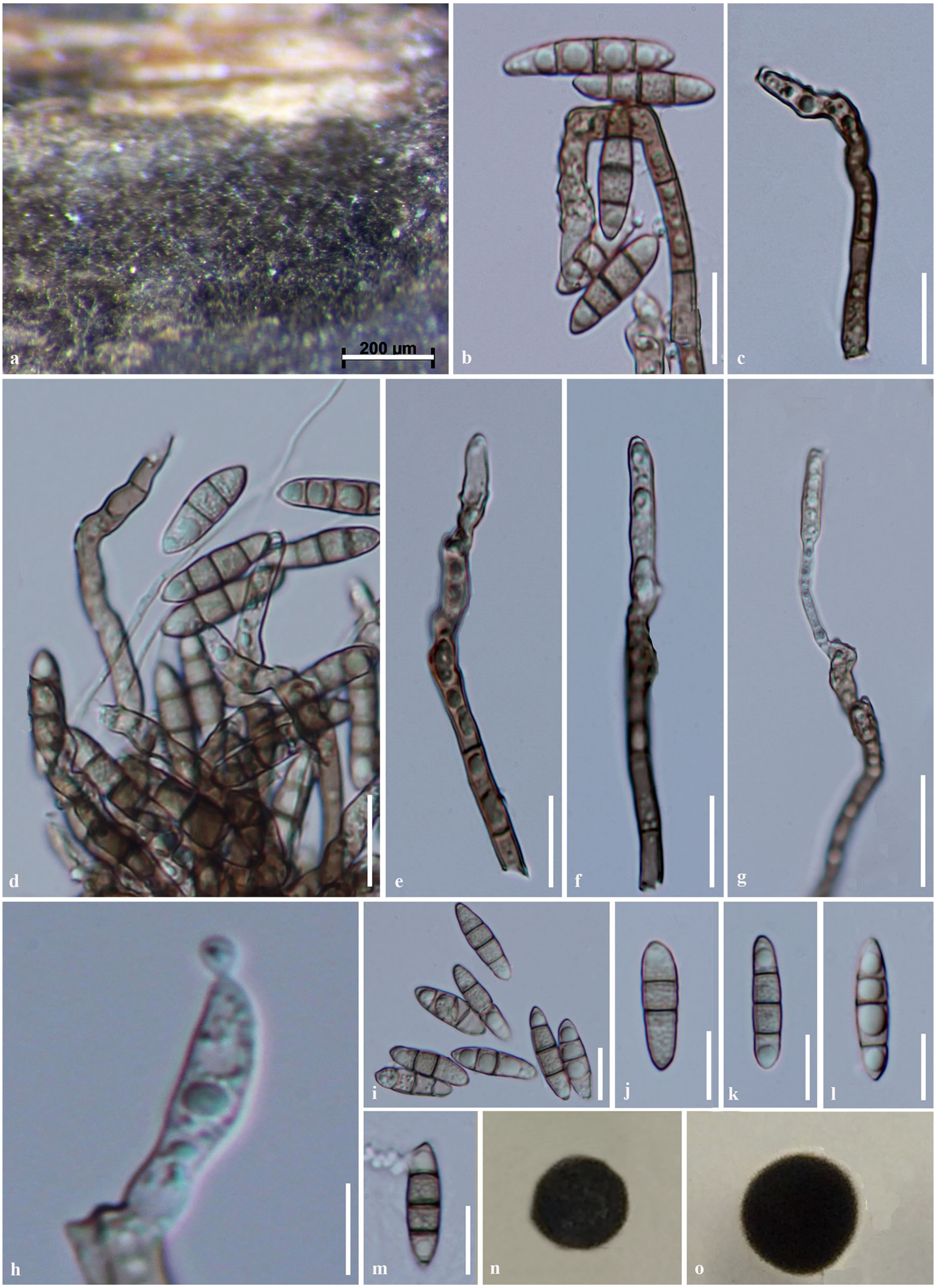


Fig. 87 ***Proliferophorum thailandicum*** (MFLU 17-1054, **holotype**). **a** Colonies on submerged wood. **b–h** Conidiophores. **i–l** Conidia. **m** Germinated conidium. **n** Colony on PDA (from above). **o** Colony on PDA (from below). *Scale bars* **a** = 200 µm, **b–g** = 20 µm, **h** = 10 µm, **i–l** = 10 µm

been reported as obligate saprotrophs, parasites and symbionts with insects and fungi or grasses, rushes or sedges (Sung et al. 2007; Schardl et al. 2013; Kepler et al. 2013, 2017; Li et al. 2016; Tibpromma et al. 2017; Huang et al. 2018). Eighteen genera are listed in this family (Wijayawardene et al. 2018a). We follow the latest treatment and updated accounts of *Cordycipitaceae* in Kepler et al. (2017).

Leptobacillium Zare & W. Gams

The genus *Leptobacillium* was introduced by Zare and Gams (2016) to accommodate saprotrophic and fungicolous phialidic hyphomycetes and *Leptobacillium leptobactrum* (W. Gams) Zare & W. Gams is the type species. We follow the latest treatment in Zare and Gams (2016). *Leptobacillium leptobactrum* var. *calidius* is reported for the first time in India.

Leptobacillium leptobactrum* var. *calidius Zare & W. Gams, Mycol Progr 15: 1003 (2016)

Facesoffungi number: FoF04832, Fig. 91

Holotype: GHANA, Atewa. CBS H-22406, a dried culture of CBS 748.73 (= IHEM 3708), from living lepidopteran larva collected by H.C. Evans.

Colour codes follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978)

Saprobic on phylloplane. **Sexual morph** Undetermined. **Asexual morph** *Conidiophores* 36–173.5 × 1.2–2.8 µm ($\bar{x}$ = 97 × 1.5 µm, n = 30), cylindrical, mainly solitary or in groups (2–3), simple to branched, smooth-walled, hyaline. *Conidiogenous cells* 3.5–66.5 × 0.8–2 µm ($\bar{x}$ = 29.5 × 1.4 µm, n = 30), phialidic, cylindrical, septate, slightly tapering towards apex, 1–3 arising from single node of condiophores. *Conidia* 2.5–6.2 × 0.8–1.8 µm ($\bar{x}$ = 4 × 1.2 µm, n = 30), produced in long chains (about 20 in a chain) and in gloeosporic masses, cylindrical, bacilliform, fusiform, smooth-walled, aseptate, hyaline. *Chlamydospores* absent.

Culture characteristics: Colonies on PDA reaching 15–28 mm diam. in 10 days, at 25 °C, white (4A1), margin smooth, entire, flat to slightly raised, puffy, sometimes produces exudates. Reverse yellowish white (4A2) to crème (4A3), wrinkled.

Known hosts and distribution: *Hemileia vastatrix* Berk. & Broome on Coffee (Brazil), technical equipment (France, Netherlands), living lepidopteran larva (Ghana), decaying wood (Poland), cyst of *Heterodera glycines* Ichinohe (USA) (Zare and Gams 2016).

Material examined: INDIA, Maharashtra, Pune, on phylloplane of *Colocasia esculenta* (L.) Schott (*Araceae*), 10 November 2017, S.K. Singh, living culture, NFCCI 4235, voucher specimen, AMH 10000.

GenBank numbers: ITS = MG786580, LSU = MG786581.

Notes: Phylogenetic analysis based on a combined ITS and LSU sequence dataset of 24 taxa shows that the Indian taxon (NFCCI 4235) clusters with type of *Leptobacillium leptobactrum* var. *calidius* Zare & W. Gams (CBS 748.73) (Fig. 90). Mega blast search of ITS sequence shows 99% similarity (505/508) with *L. leptobactrum* var. *calidius* (CBS 748.73) and same similarity (99% similarity, 592/594) for LSU analysis. In this isolate conidia are produced in long chains and in gloeosporic masses. Though slight variations in conidial length and width were observed, our isolate is similar to *L. leptobactrum* var. *calidius* (CBS 748.73) in overall morphological characteristics. In addition, our isolate optimally grows at 25–26 °C, the same as reported for *L. leptobactrum* var. *calidius* (CBS 748.73) with negligible growth at 30 °C. Optimum temperature for growth of *L. leptobactrum* var. *leptobactrum* is 18–21 °C (Zare and Gams 2016). *Leptobacillium leptobactrum* var. *calidius* and *L. leptobactrum* var. *leptobactrum* were treated as a synonym of *L. leptobactrum* (Index Fungorum 2019). However, *L. leptobactrum* var. *calidius* (CBS 748.73) forms a distinct lineage with the type strain of *L. leptobactrum* (CBS 771.69). Hence, based on similarity in morphological characteristics, temperature requirements, and phylogenetic analysis this Indian isolate is identified as *L. leptobactrum* var. *calidius* (Zare and Gams 2016). To our knowledge, this is the first report of this genus, species and variety isolated from phylloplane of a different host, *Colocasia esculenta* from India.

Hypocreaceae De Not.

Hypocreaceae was introduced by De Notaris (1844) and is typified by *Hypocrea* Fr. Species of *Hypocreaceae* are characterized by their brightly coloured, fleshy perithecial stromata (Rogerson 1970). The family comprises 18 genera and more than 450 species (Kirk et al. 2008; Wijayawardene et al. 2018a).

Trichoderma Pers.

Trichoderma is frequently isolated from various habitats including soil, decaying wood, and vegetable matter (Samuels 2006) and is known to play an important ecological role as biocontrol agents of plant diseases, producers of bioactive compounds, and pathogens of animals and mushrooms (Schuster and Schmoll 2010). Based on molecular data, more than 250 species are currently accepted in this genus (Bissett et al. 2015). Three novel species are introduced based upon their phylogenetic affinities clarified by maximum likelihood and Bayesian inference analyses of a combined TEF1-α and RPB2 sequence dataset (Fig. 92).

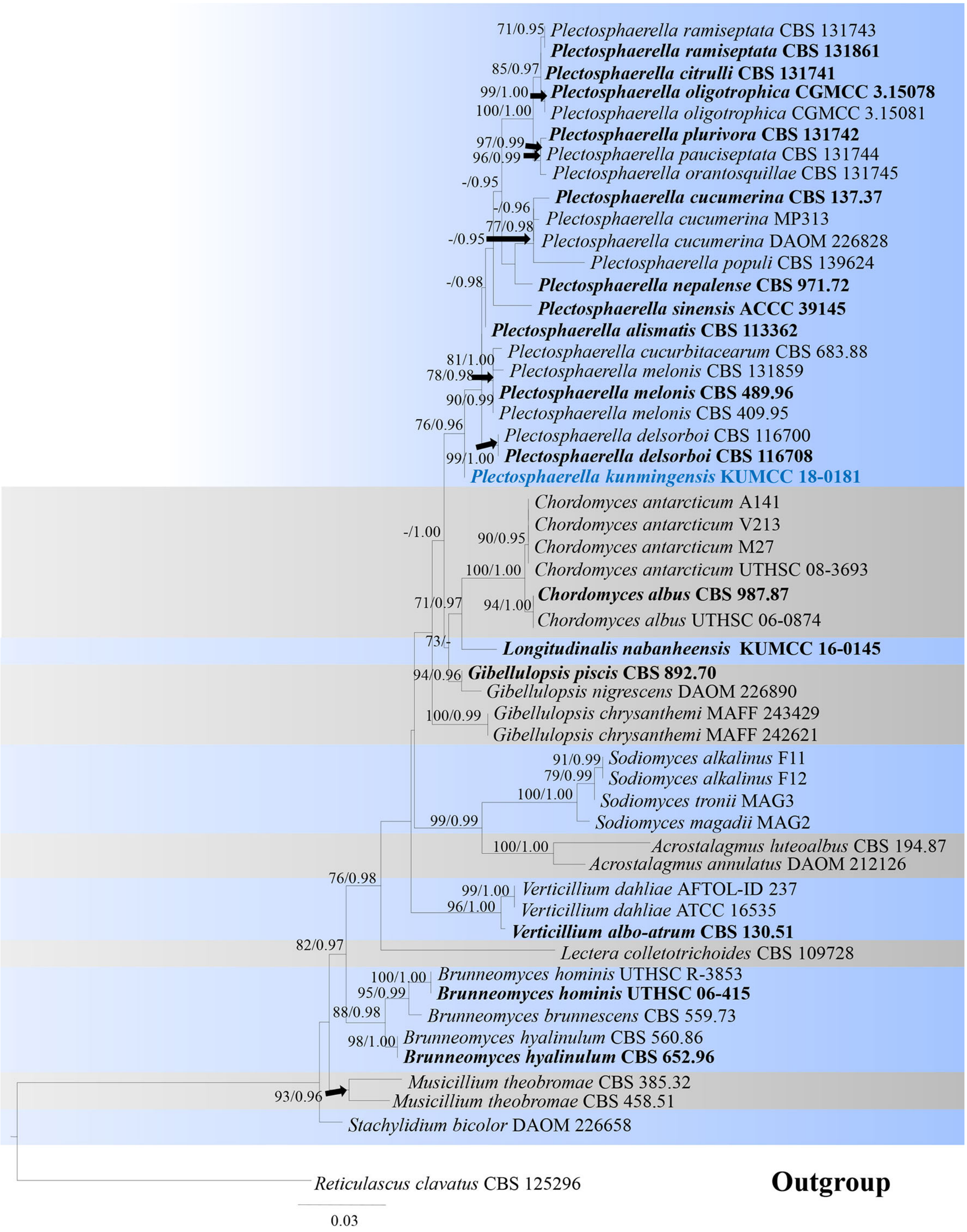


Fig. 88 Phylogenetic tree generated from maximum likelihood analysis based on a combined LSU, ITS and TEF1-α sequence dataset of the genera in *Plectosphaerellaceae*. Bootstrap support value of maximum likelihood (left) equal to or greater than 70% and Bayesian posterior probability equal to or greater than 0.95 BYPP are indicated above or below the nodes. Type strains are in black bold. The new species are in blue bold. The tree is rooted with *Reticulascus clavatus* (CBS 125296)

Trichoderma koreanum S-Y. Oh, M.S. Park & Y.W. Lim, ***sp. nov.***

MycoBank number: MB824661; *Facesoffungi number*: FoF04459, Fig. 93

Etymology: The specific epithet "*koreanum*" refers to the type locality.

Holotype: SFC20131005-S066.

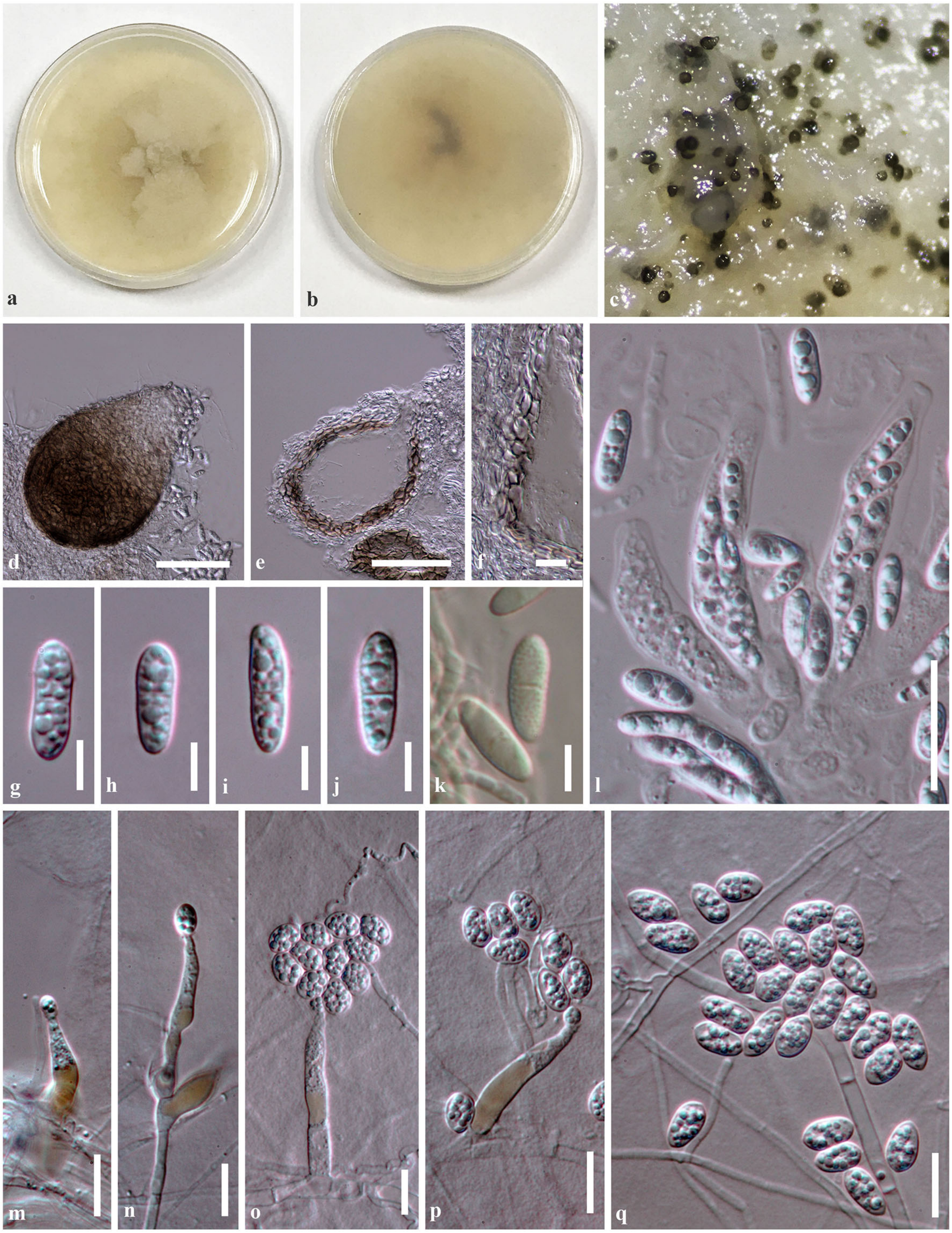


Fig. 89 ***Plectosphaerella kunmingensis*** (KUN-HKAS 102246, **holotype**). **a, b** Culture characteristics on PDA (**a** = from above, **b** = from below). **c** Ascomata forming on PDA after 2 months. **d** Squash mount of the ascoma. **e** Section through ascoma. **e, f** Section through peridium. **g–j** Ascospores. **k** Ascospores stained in Melzer's reagent. **l** Asci. **m–p** Conidiophores attached with conidia. **q** Conidia. *Scale bars* **d, e** = 50 µm, **l** = 20 µm, **f, m–p, q** = 10 µm, **g–k** = 5 µm

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1963).

Sexual morph Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* branched at an acute or right angle to the main axis, mostly unpaired. *Phialides*

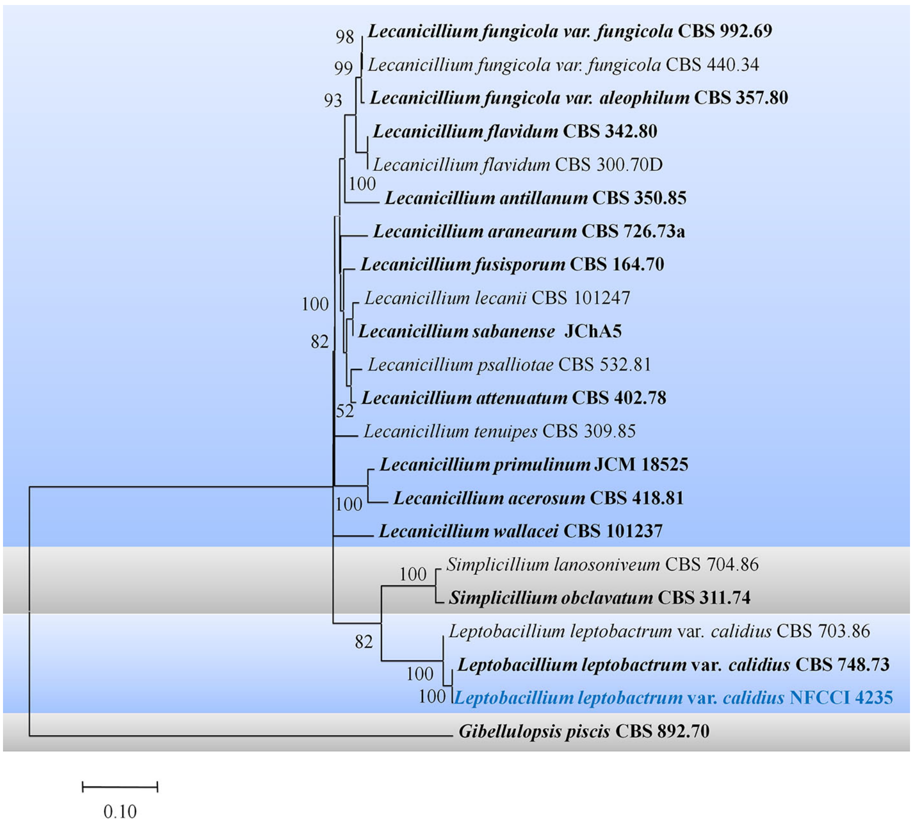


Fig. 90 Phylogram generated from maximum parsimony based on a combined ITS and LSU sequence dataset of the genus *Leptobacillium* and related genera in *Cordycipitaceae*. Bootstrap support value of maximum likelihood (left) and maximum parsimony (right) equal to or greater than 70% are indicated above the nodes. Type strains are in bold. The new strain is in blue bold. The tree is rooted with *Gibellulopsis piscis* (CBS 892.70)

8.6–13.4 × 2.4–3.7 µm, l/w 2.5–4.9, 1.7–2.6 µm wide at the base (n = 30), typically formed in whorls of 3–5, subulate or lageniform. *Conidia* smooth, subglobose to ellipsoid, 3.1–4.4 × 2.6–3.3 µm, l/w 1.1–1.4(−1.5) (n = 30).

Culture characteristics: On CMD after 72 h colony radius 17–22 mm at 15 °C, 29–35 mm at 20 °C, 44–49 mm at 25 °C, 20–29 mm at 30 °C; colonies on CMD fill a 90 mm diam. Petri dish within 5 days at 25 °C. Colony hyaline, radial, indistinctly zonate, aerial hyphae spreading uniformly throughout the colony. Conidiation starting after 4 days, light green (M. 28A5) or deep green (M. 27E8) conidia forming in pustules, appearing around the margin of the colony. No chlamydospores observed. No distinct odour. Agar not pigmented. On PDA after 72 h colony radius 12–17 mm at 15 °C, 21–30 mm at 20 °C, 35–44 mm at 25 °C, 21–24 mm at 30 °C; colonies on PDA fill a 90 mm diam. Petri dish within 5–6 days at 25 °C. Colony radial, mycelium dense, not finely zonate, aerial hyphae abundant, more abundant in distance from the inoculum. Conidiation starting after 3 days, greyish yellow (M. 2C5) or greyish green (M. 29C5) conidia formed abundant on aerial hyphae. On SNA after 72 h colony radius 11–14 mm at 15 °C, 17–24 mm at 20 °C, 33–36 mm at 25 °C, 14–22 mm at 30 °C; colonies on SNA fill a 90 mm diam. Petri dish within 6 days at 25 °C. Colony hyaline, radial, mycelium loose, indistinctly zonate, aerial hyphae more abundant in distance from the inoculum. Conidiation starting after 3 days, greyish yellow (M. 2B4) or greyish green (M. 29C5) conidia formed abundant on aerial hyphae.

Material examined: REPUBLIC OF KOREA, Gyeongsangbuk Province, Uljin, Jinjosan Mountain, elev. 170 m, isolated from root of *Pinus densiflora* Siebold & Zucc. (*Pinaceae*) under a fairy ring of *Tricholoma matsutake* (S. Ito & S. Imai) Singer, October 2013, S.Y. Oh, PF066 (SFC20131005-S066, **holotype**), ex-type living culture KACC 48487; *ibid*., Gangwon Province, Hongcheon, Gongjaksan Mountain, elev. 300 m, isolated from root of *P. densiflora* under a fairy ring of *T. matsutake*, September 2013, S-Y. Oh, SFC20130926-S004.

GenBank numbers: ITS = MH050352, RPB2 = MH025988, TEF1-α = MH025979.

Notes: Morphologically and phylogenetically (Figs. 92, 93), *Trichoderma koreanum* is closely related to *T. tomentosum* Bissett, *T. ceraceum* P. Chaverri & Samuels, and *T. linzhiense* K. Chen & W.Y. Zhuang. However, *T. tomentosum* has shorter phialides (4.5–5 × 3–3.2 µm) and narrower conidia (3.2–3.5 × 2.2–2.5 µm). *Trichoderma linzhiense* grows faster at 25 °C (51–60 mm on CMD, 62–63 mm on PDA, and 50–51 mm on SNA after 3 days). *Trichoderma ceraceum* grows slower at 20 °C (15–17 mm

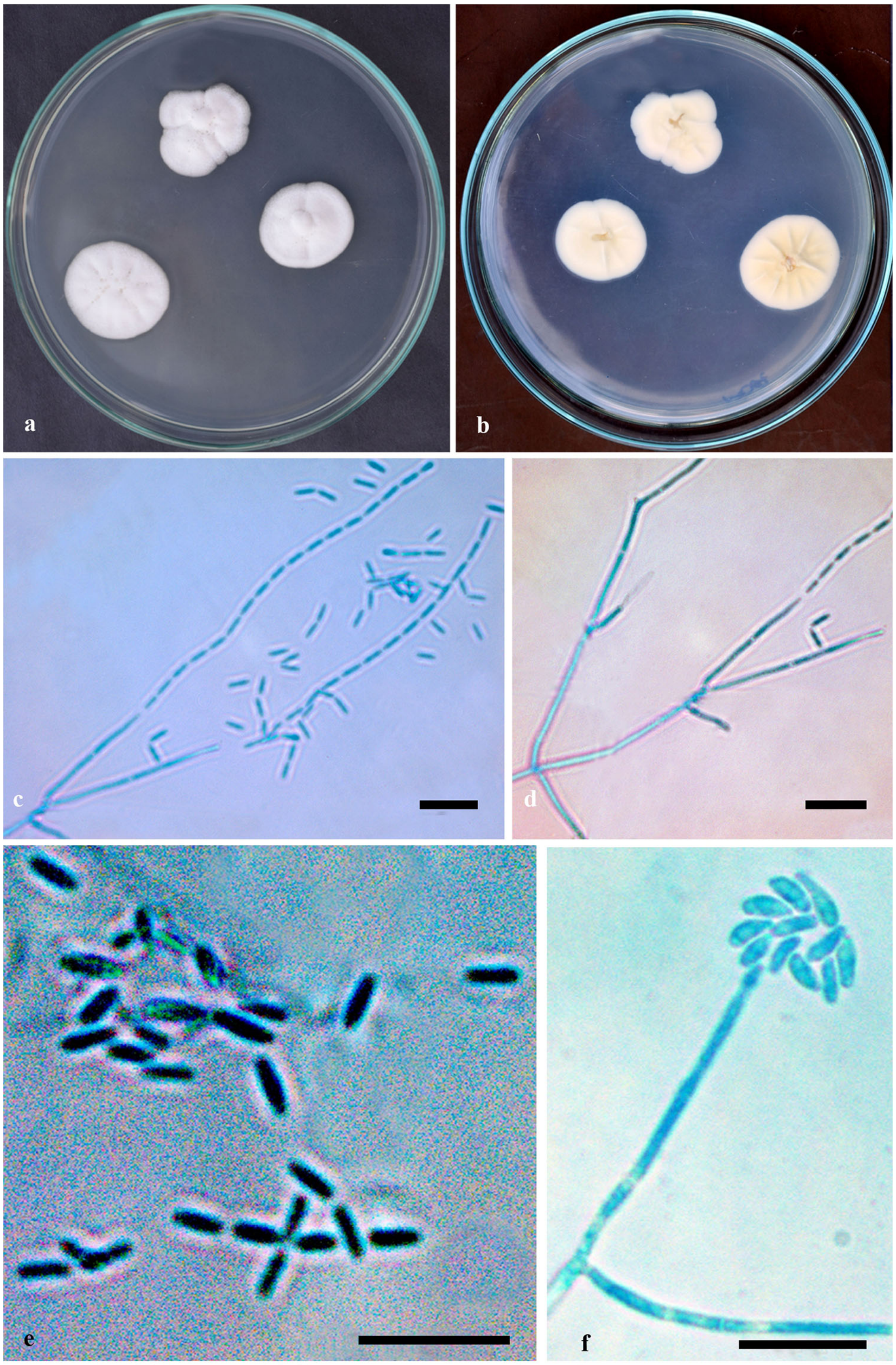


Fig. 91 ***Leptobacillium leptobactrum* var. *calidius*** (NFCCI 4235). **a** Colony morphology on PDA (front view). **b** Colony morphology on PDA (reverse view). **c** Conidia produced in long chains from phialides. **d** Conidiophores bearing phialides producing conidia in chain. **e** Enlarged view of conidia. **f** Conidia produced in gloeosporic mass at the tip of phialides. *Scale bars* 10 µm

on PDA and 6–14 mm on SNA) and has shorter phialides (6.5–7.7 × 3–3.5 µm).

Trichoderma pinicola S-Y. Oh, M.S. Park & Y.W. Lim, ***sp. nov.***

MycoBank number: MB824662; *Facesoffungi number*: FoF04460, Fig. 94

Etymology: The specific epithet "*pinicola*" refers to the genus name of *Pinus densiflora*, the source of type strain

Holotype: SFC20130926-S233.

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1963).

Sexual morph Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* branched at an acute to

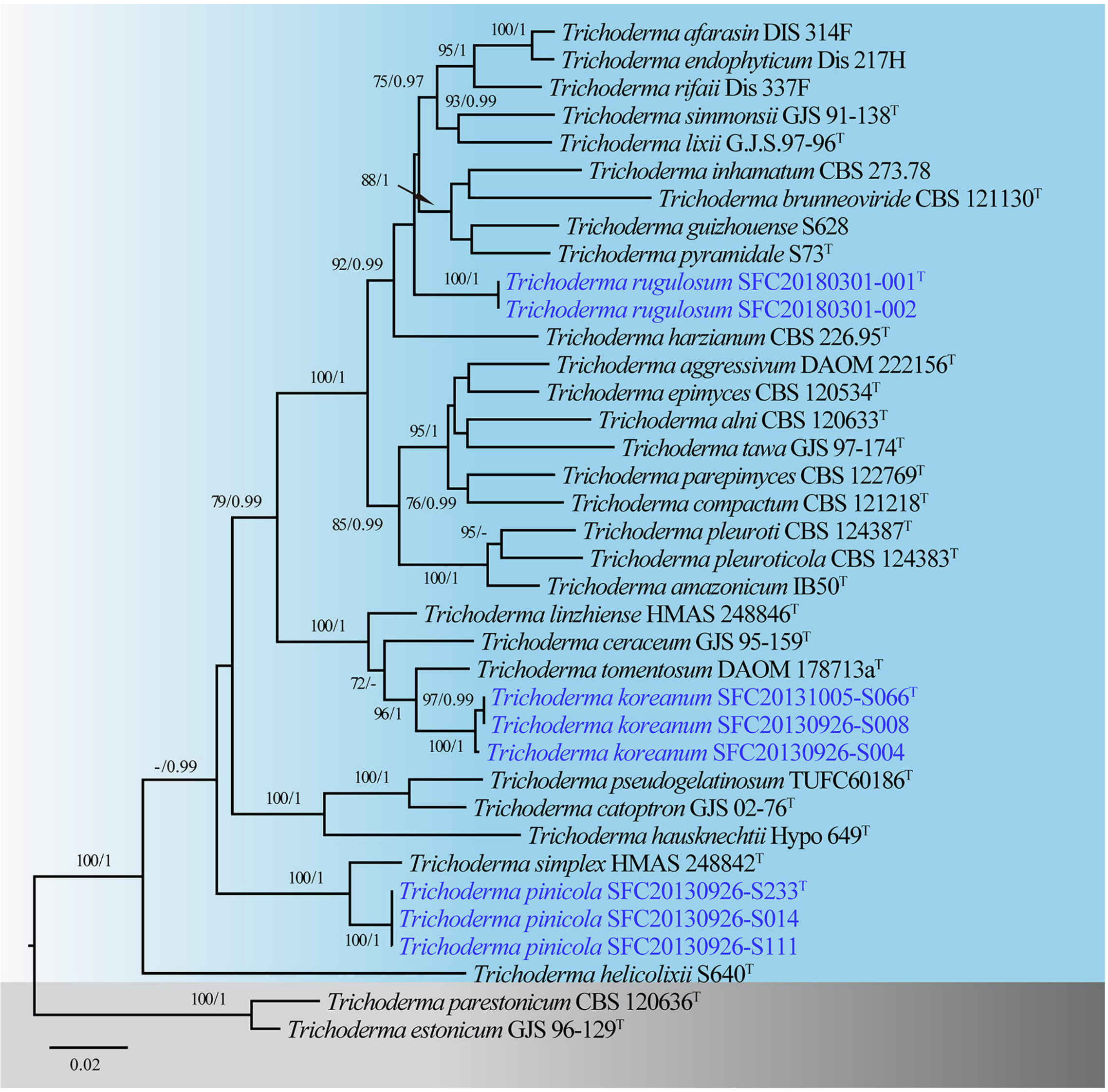


Fig. 92 Phylogenetic tree for *Trichoderma* from a maximum likelihood analysis based on the combined TEF1-α and RPB2 alignments. Branch support values are given as ML bootstrap values (≥ 70% ML) and Bayesian posterior probabilities (≥ 0.95 BYPP). The scale bar indicates the number of nucleotide substitutions per site. New species names are in blue. The letter "T" indicates ex-type strains

the main axis, mostly paired. *Phialides* 7.8–13.3 × (2.5 –)2.6–4.1(−4.5) µm, l/w 1.9–4.4(−4.5), 1.8–3.3 µm wide at the base (n = 30), typically formed in whorls of 3 or rarely solitary, subulate or lageniform. *Conidia* 3.5–4.9(−5) × 2.8–3.5(−3.6) µm, l/w 1.1–1.6 (n = 30), smooth, subglobose to ellipsoid. *Chlamydospores* rare, globose, 5.2–10(−10.1) × 5.2–10 µm, l/w 1–1.02 (n = 10). No distinct odour. Agar not pigmented.

Culture characteristics: On CMD after 72 h colony radius 14–18 mm at 15 °C, 23–34 mm at 20 °C, 39–50 mm at 25 °C, 34–45 mm at 30 °C; colonies on CMD fill a 90 mm diam. Petri dish at 4 days at 25 °C. Colony hyaline, radial, not zonate, mycelium common, aerial hyphae inconspicuous. Conidiation starting after 4 days, greyish green (M. 28B5) or deep green (M. 28E8) conidia formed scarcely on aerial hyphae around the margin of the colony. On PDA after 72 h colony radius 12–15 mm at 15 °C, 18–28 mm at 20 °C, 30–38 mm at 25 °C, 21–36 mm at 30 °C; colonies on PDA fill a 90 mm diam. Petri dish within 6 days at 25 °C. Colony hyaline, radial, with wavy margin, mycelium common, aerial hyphae more abundant in colony centre. Conidiation starting after 9 days, greyish green (M. 27C6) or pastel green (M. 29A4) conidia formed on aerial hyphae, more abundant around the margin of the colony. On SNA after 72 h colony radius 9–12 mm at 15 °C, 19–24 mm at 20 °C, 30–43 mm at 25 °C, 19–33 mm at 30 °C; colonies on SNA fill a 90 mm diam. Petri dish within 5–6 days at 25 °C. Colony hyaline, radial, mycelium loose, spreading uniformly throughout the colony. Conidiation starting after

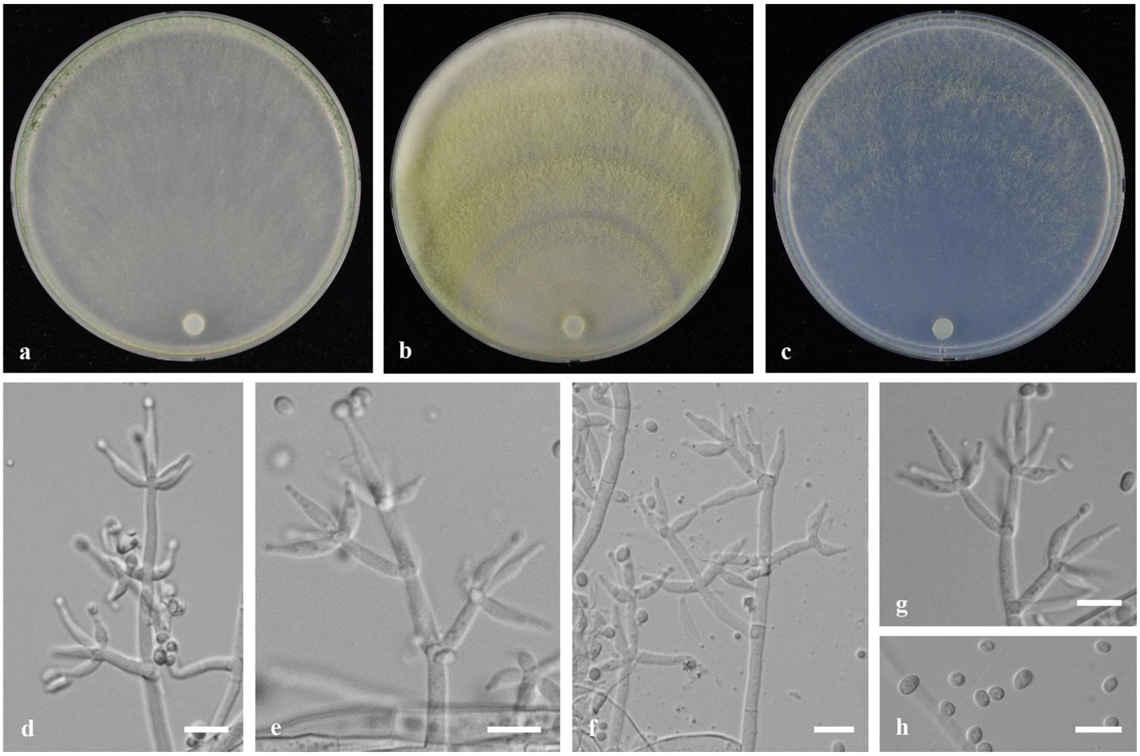


Fig. 93 ***Trichoderma koreanum*** (SFC20131005-S066, **holotype**). **a** Colony on CMD after 72 h. **b** Colony on PDA after 72 h. **c** Colony on SNA after 72 h. **d–g** Conidiophores. **h** Conidia. *Scale bars* **d–h** = 20 µm

3–4 days, greyish green (M. 29C5) or deep green (M. 27E8) conidia formed abundant on aerial hyphae.

Material examined: REPUBLIC OF KOREA, Gangwon Province, Hongcheon, Gongjaksan Mountain, elev. 300 m, isolated from root of *Pinus densiflora* under a fairy ring of *Tricholoma matsutake*, September 2013, S-Y. Oh, PF233 (SFC20130926-S233, **holotype**), ex-type living culture KACC 48486; *ibid.*, Hongcheon, Gongjaksan Mountain, elev. 300 m, isolated from root of *P. densiflora* under a fairy ring of *T. matsutake*, September 2013, S-Y. Oh, SFC20130926-S111.

GenBank numbers: ITS = MH050354, RPB2 = MH025993, TEF1-α = MH025981.

Notes: *Trichoderma pinicola* is morphologically similar to *T. hirsutum* K. Chen & W.Y. Zhuang, the latter has longer phialides (11.4–18.3 × 2.5–3.1 µm) and lacks chlamydospores in CMD. Phylogenetically (Fig. 92), *T. pinicola* is closely related to *T. simplex* K. Chen & W.Y. Zhuang. However, *T. simplex* has more abundant aerial hyphae and conidia formation, and faster growth at 25 °C (49–56 mm on CMD and 52–56 mm on PDA after 3 days). In addition, *T. pinicola* showed wavy margin on PDA.

Trichoderma rugulosum M.S. Park, S-Y. Oh & Y.W. Lim, ***sp. nov.***

MycoBank number: MB824663; *Facesoffungi number*: FoF04461, Fig. 95

Etymology: The specific epithet refers to the wrinkle in colony reverse on PDA.

Holotype: SFC20180301-001

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1963).

Sexual morph Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* symmetry, branches mostly paired. *Phialides* typically formed in whorls of 3–4, ampulliform to lageniform, 5.9–10.3(−10.5) × 2.1–3.6(−3.9) µm, l/w 1.9–3.7(−3.8), (1.2 −)1.3–1.9 µm wide at the base (n = 30). *Conidia* green, smooth, globose, subglobose or broadly ellipsoidal, (2.5–)2.6–3.2 × (2.3–)2.3–2.9 µm, l/w 1–1.2(−1.3) (n = 30).

Culture characteristics: On CMD after 72 h colony radius 10–14 mm at 15 °C, 24–29 mm at 20 °C, 62–69 mm at 25 °C, 69–75 mm at 30 °C; colonies on CMD fill a 90 mm diam. Petri dish within 4 days at 25 °C. Colony hyaline, radial, mycelium loose, indistinctly zonate, aerial hyphae more abundant in distance from the inoculum. Conidiation starting after 3 days, deep green (M. 27E8) or greyish green (M. 27c4) conidia forming in pustules. No chlamydospores observed. No distinct odour. Agar not pigmented. On PDA after 72 h colony radius 9–11 mm at 15 °C, 13–21 mm at 20 °C, 38–43 mm at 25 °C, 22–42 mm at 30 °C, colonies on PDA fill a 90 mm diam. Petri dish within 6 days at 25 °C. Colony radial,

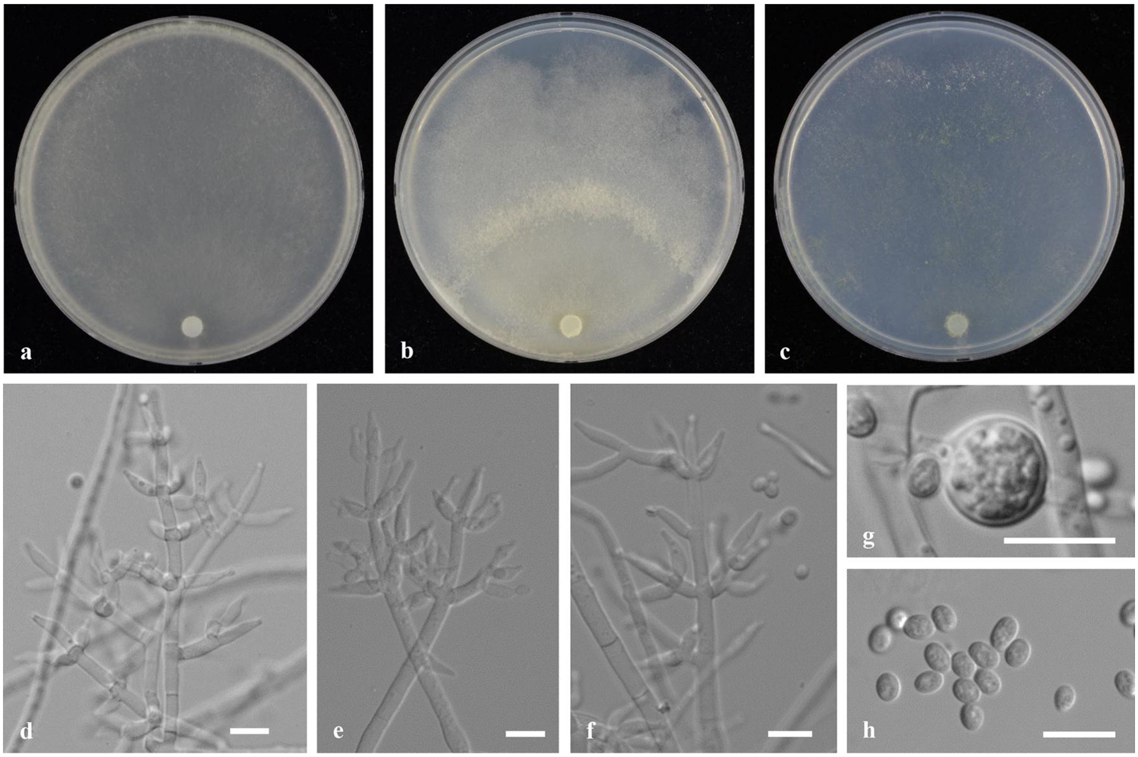


Fig. 94 ***Trichoderma pinicola*** (SFC20130926-S233, **holotype**). **a** Colony on CMD after 72 h. **b** Colony on PDA after 72 h. **c** Colony on SNA after 72 h. **d–f** Conidiophores. **g** Chlamydospores. **h** Conidia. *Scale bars* **d–h** = 20 µm

mycelium dense, zonate, aerial hyphae abundant, spreading uniformly throughout the colony, forming wrinkle in distance from the inoculum in reverse colony, at 30 °C colony radial, mycelium dense, with wavy margin. Conidiation starting after 3 days, effuse in aerial hyphae or in densely disposed granules, more abundant in 4–5 concentric rings, yellowish green (M. 30B8). No chlamydospores observed. No distinct odour. Olive yellow (M. 3C8) pigment diffusing into the agar. On SNA after 72 h colony radius 3–6 mm at 15 °C, 7–11 mm at 20 °C, 14–29 mm at 25 °C, 10–21 mm at 30 °C; colonies on SNA a 90 mm diam. the Petri dish within 8–9 days at 25 °C. Colony hyaline, radial, mycelium loose, not finely zonate, aerial hyphae common. Conidiation starting after 3 days, deep green (M. 27E8) or yellowish green (M. 30B8) conidia forming in pustules, pustules forming in 2–3 concentric rings.

Material examined: REPUBLIC OF KOREA, Jeju Province, Chuja-do Island, isolated from *Chondria crassicaulis* Harvey, September 2017. M.S. Park, F181 (SFC20180301-001, **holotype**), ex-type living culture KACC 48485; *ibid*., Chuja-do, isolated from *Sargassum thunbergii* (Mertens ex Roth) Kuntze, September 2017, M.S. Park, SFC20180301-002.

GenBank numbers: ITS = MH050353, RPB2 = MH025986, TEF1-α = MH025984.

Notes: *Trichoderma rugulosum* is isolated from *Chondria crassicaulis* and *Sargassum thunbergii* (seaweeds) in South Korea. Morphologically and phylogenetically, *T. rugulosum* is closely related to species in the *T. harzianum* complex. However, these species have faster growth at 30 °C on SNA (32–70 mm on SNA after 3 days). *T. rugulosum* shows a wrinkle in colony reverse on PDA at 25 °C and wavy margin on PDA at 30 °C, features not seen in members of the *T. harzianum* complex.

Hypocreales, genera *incertae sedis*

Emericellopsis Beyma

Emericellopsis Beyma (1940) was introduced with *E. terricola* Beyma as the type species. *Emericellopsis* species have been mostly isolated as saprobes from marine environments, soda lakes, and terrestrial habitats (Grum-Grzhimaylo et al. 2013). We describe a novel species from Korea based on phylogenetic analysis of a combined ITS and TUB2 sequence dataset (Fig. 96).

Emericellopsis koreana Hyang B. Lee, S.J. Jeon & T.T.T. Nguyen, ***sp. nov.***

Index Fungorum number: IF554458; *Facesoffungi number*: FoF05732, Fig. 97

Etymology: Named after the country where it was collected, Korea.

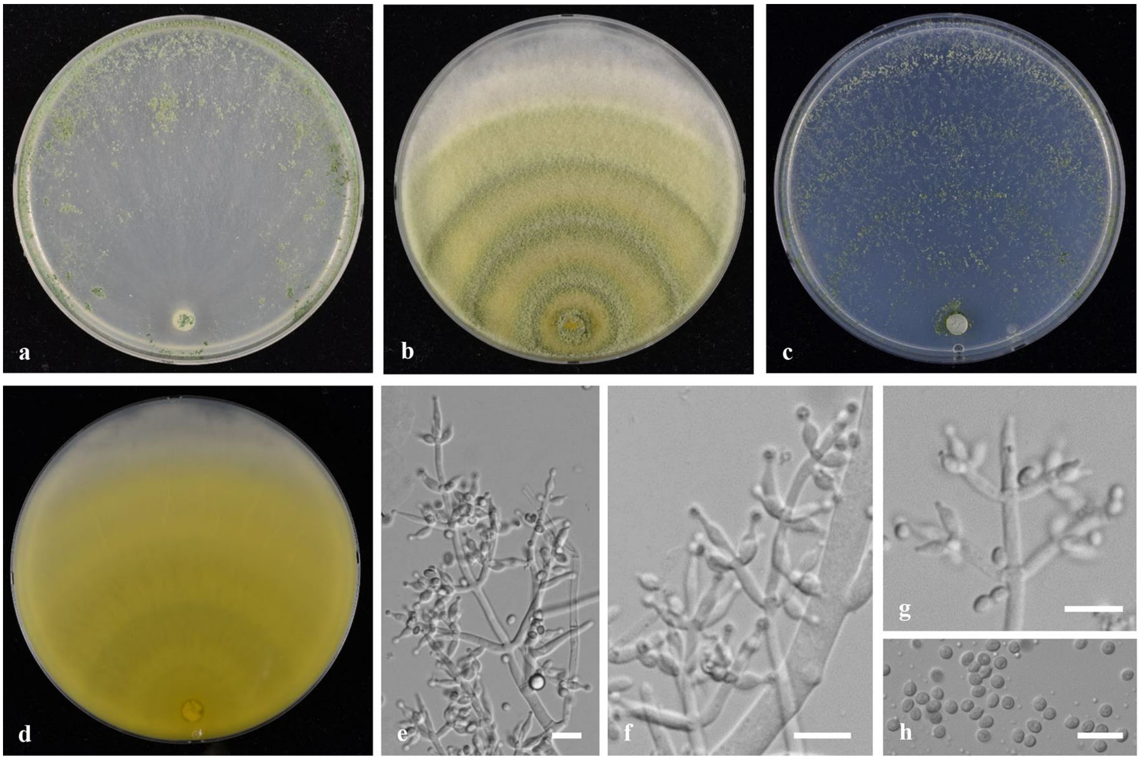


Fig. 95 ***Trichoderma rugulosum*** (SFC20180301-001, **holotype**). **a** Colony on CMD after 72 h. **b** Colony on PDA after 72 h. **c** Colony on SNA after 72 h. **d** Colony on PDA after 72 h from reverse. **e–g** Conidiophores. **h** Conidia. *Scale bars* **e–h** = 20 µm

Holotype: CNUFC-MOG1-1

Sexual morph Undetermined. **Asexual morph** Hyphomycetous observed from MEA, acremonium-like. *Mycelia* consisting of hyaline, smooth-walled, septate hyphae, single or in bundles. *Conidiophores* mostly simple and orthotropic. *Conidiogenous cells* (15.5–)31.5–40(–59) µm long, tapering from 2(–2.5) µm at the base to 0.5 µm at the apex. *Conidia* ellipsoid or oblong-ellipsoid, smooth-surfaced, 3–4(–5) × 1.5–2(–2.5) µm (n = 50), hyaline, adhering in slimy heads. No chlamydospores observed.

Culture characteristics: The isolate grows over a wide range of temperatures with varying growth rates. The average growth rates of CNUFC-MOG1-1 on MEA, CYA, and PDA medium at 25 °C were 27.5, 17, and 15.5 mm after 7 days, respectively. Optimal growth was observed around 25 °C, slow growth was observed below 10 °C, and no growth at 40 °C.

Material examined: REPUBLIC OF KOREA, Jeonnam Province, garden of the Chonnam National University located in Gwangju (35°10’20.2”N 126°53′57.2″E), from gut of a mosquito larva, 15 September 2016, H.B. Lee, CNUFC-MOG1-1 (**holotype**), ex-type living culture, JMRC:SF:013604.

GenBank numbers: ITS = MH173304, TUB2 = MH243035 (CNUFC-MOG1-1); ITS = MH173305, TUB2 = MH243036 (CNUFC-MOG1-2).

Notes: Emericellopsis koreana, which forms a subclade with *E. donezkii* Beliakova, *E. humicola* (Cain) Cain ex Grosklags & Swift, *E. persica* Papizadeh et al. and *Emericellopsis* sp., differs by having smaller conidia. In the phylogenetic tree based on a combined ITS and TUB2 sequence dataset (Fig. 96), the strains CNUFC-MOG1-1 and CNUFC-MOG1-2 form a separate branch from other related species of *Emericellopsis* and is considered to be a new species.

Subclass Savoryellomycetidae Hongsanan et al.

Savoryellales Boonyuen et al.

Savoryellaceae Jaklitsch & Réblová

Savoryellaceae was introduced by Jaklitsch (2015) and is typified by *Savoryella* E.B.G. Jones & R.A. Eaton. The family is characterized by immersed to superficial, globose to pyriform, coriaceous, papillate ascomata, clavate to cylindrical, unitunicate asci, with an inamyloid apical ring, paraphyses, ellipsoidal to fusiform, versicolorous, septate ascospores, with or without polar mucilaginous pads or appendages and dematiaceous, hyphomycetous asexual morphs (Jaklitsch 2015). Most species of *Savoryellaceae* are aquatic occurring on submerged wood in freshwater, marine and brackish habitats worldwide (Jaklitsch 2015; Xia et al. 2017). The generic type, *Savoryella* was re-circumscribed by Maharachchikumbura et al. (2016) and the higher level classification of the families in Savoryellomycetidae was revised by Hongsanan et al. (2017) based on phylogenetic and molecular clock evidence. Six genera are accepted in this family (Wijayawardene et al. 2017a, 2018a).

Canalisporium Nawawi & Kuthub.

The genus *Canalisporium* was introduced by Nawawi and Kuthubutheen (1989) to accommodate muriform asexual morph species, with conidia that are flattened dorsiventrally, comprising a single layer of regularly arranged cells, which are supported by a small, thin-walled, cuneiform, pale basal cell. There are 12 species in this genus (Zhao et al. 2013). Five species lack molecular data, viz. *C. kenyense* Goh et al., *C. microsporum* G.Z. Zhao, *C. nigrum* G.Z. Zhao, *C. panamense* A. Ferrer & Shearer and *C. variabile* Goh & K.D. Hyde (Goh et al. 1998; Sri-Indrasutdhi et al. 2010; Zhao et al. 2013). In this study, *Canalisporium kenyense* was collected from submerged decaying wood in a freshwater stream in Thailand. The taxon is re-circumscribed and illustrated as the reference specimen (Figs. 98, 99).

Canalisporium kenyense Goh, W.H. Ho & K.D. Hyde, Can J Bot 76: 148 (1998)

Facesoffungi number: FoF04845, Fig. 99

Holotype: KENYA, Mt. Kenya, Castle Forest, on rotten wood, 25 Jan. 1984, P.M. Kirk, 1593a, IMI 285428a.

Saprobic on decaying wood submerged in a freshwater stream. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous, dictyosporous. *Conidiophores* macronematous, mononematous, unbranched, septate, up to 25 × 3–6 µm, hyaline to pale brown, smooth-walled. *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, determinate, hyaline to pale brown, smooth-walled. *Conidia* acrogenous, solitary, subglobose, flattened, muriform, smooth, pale brown to dark brown, 40–50 × 25–30 × 13–20 µm with 2 straight columns of vertical septa and 4–6 rows of transverse septa, slightly constricted at the septa, apical rows of cells darker than the basal rows, dark and thickly banded at the septa, canals in the septa obscured by dark pigmentation, apex comprising a single cell, the number of cells per conidium varies from 13 to 20, base comprising a single cell, cuneiform, sometimes swollen, thin-walled, pale brown, or comprising three thin-walled, pale brown, small cells in a row.

Material examined: THAILAND, Chiang Rai Province, Muang District, Nang Lae Nai Village, on submerged decaying wood in a freshwater stream, 31 December 2016, Y.Z. Lu, CR01 (MFLU 17-1086, **reference specimen designated here**); *ibid.*, KUN-HKAS 97477.

GenBank numbers: ITS = MH701998, LSU = MH701999, TEF1-α = MH708885.

Known hosts and distribution: On decaying wood (Kenya), submerged wood (Hong Kong), decorticated branches of dead tree (China), decaying branches of unidentified plant (China) (Goh et al. 1998; Zhuang 2001; Zhao et al. 2013; Farr and Rossman 2018).

Notes: Our new collection resembles *Canalisporium kenyense* in morphological characters of the conidiophores, conidiogenous cells and conidia, and their measurements align with those of the holotype (IMI 285428a) (Goh et al. 1998) and other specimens of *C. kenyense* (Zhao et al. 2013). Therefore, we identify our new collection as *C. kenyense* which is the first report from Thailand. Phylogenetically, *C. kenyense* forms a distinct lineage within the genus *Canalisporium* with strong support (96% ML and 1.00 BYPP; Fig. 98). Based on morphological characters and phylogenetic support, we designate our collection MFLU 17-1086 as a reference specimen.

Subclass Sordariomycetidae O.E. Erikss. & Winka

Chaetosphaeriales Huhndorf et al.

Chaetosphaeriaceae Réblová et al.

Chaetosphaeriaceae is a widespread, species-rich family, which was invalidly introduced by Locquin (1984) to accommodate *Chaetosphaeria* Tul. & C. Tul., *Loramyces* W. Weston, *Niesslia* Auersw., *Rhagadostoma* Körb. and *Zignoëlla* Sacc., (Réblová et al. 1999; Hyde et al. 2017). Réblová et al. (1999) re-described and validated *Chaetosphaeriaceae* and accepted *Ascocodinaea* Samuels et al., *Chaetosphaeria*, *Melanochaeta* E. Müll. et al., *Melanopsammella* Höhn., *Porosphaerella* E. Müll. & Samuels, *Porosphaerellopsis* Samuels & E. Müll. and *Striatosphaeria* Samuels & E. Müll. Currently, 38 genera are accepted in *Chaetosphaeriaceae* (Hyde et al. 2017; Tibpromma et al. 2018; Wijayawardene et al. 2018a). We introduce *Thozetella lithocarpi* sp. nov. from *Lithocarpus* sp. and record *Macaranga tanarius* as a new host record for *Chaetosphaeria panamensis* based on both morphological and phylogenetic analyses (Fig. 100).

Chaetosphaeria Tul. & C. Tul.

The saprobic genus, *Chaetosphaeria* was introduced by Tulasne and Tulasne (1863) based on the type species, *C. innumera* Berk. & Broome ex Tul. & C. Tul., and currently comprise 165 epithets (Index Fungorum 2019). *Chaetosphaeria* is placed in *Chaetosphaeriaceae* (*Chaetosphaeriales*) based on molecular data (Réblová et al. 1999; Huhndorf et al. 2004; Maharachchikumbura et al. 2015), although it was previously placed in *Lasiosphaeriaceae* by Barr (1990). *Chaetosphaeria* species have a diverse distribution having been recorded from both temperate and tropical countries (i.e. Canada, China, Europe, Hong Kong, New Zealand, Thailand) (Hyde et al. 1999, 2017; Réblová 2000; Perera et al. 2016; Wijayawardene et al. 2017a). Host-

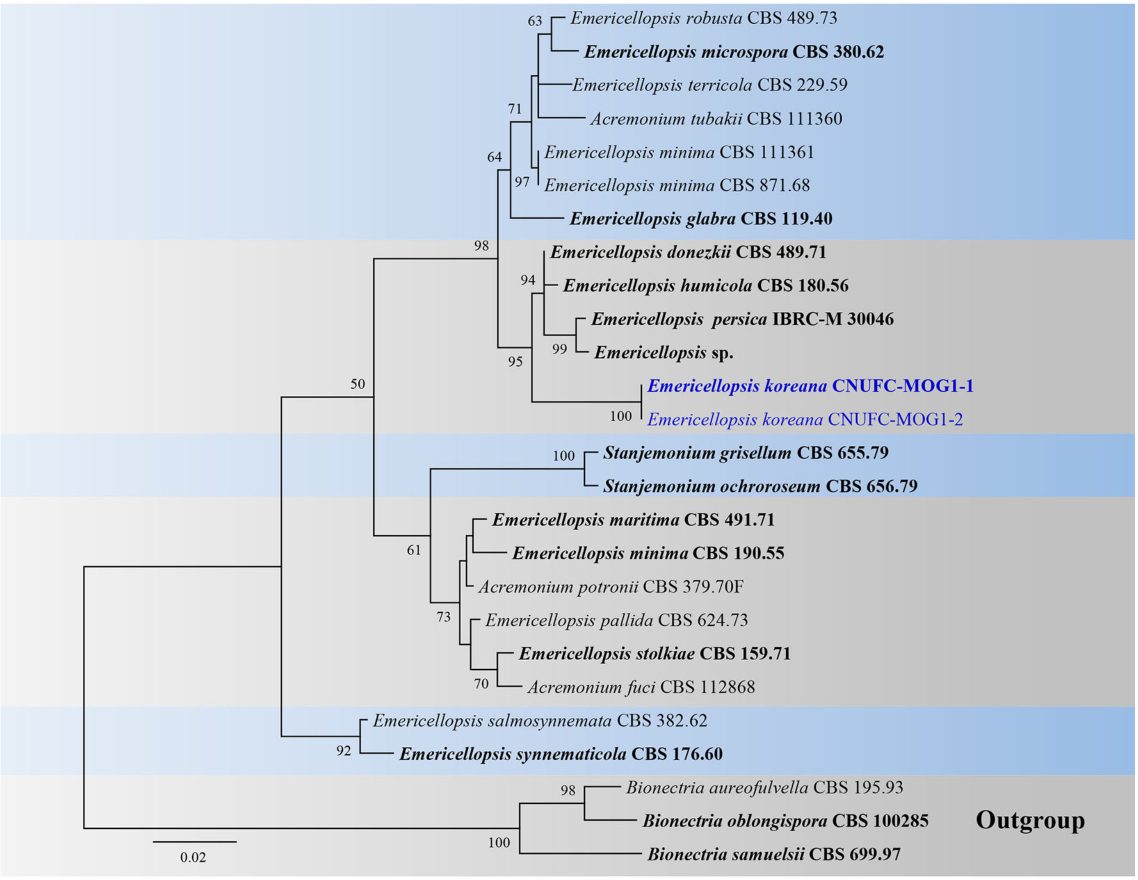


Fig. 96 Phylogenetic tree of *Emericellopsis koreana* (CNUFC-MOG1-1 and CNUFC-MOG1-2) and related species based on maximum likelihood analysis of a combined ITS and TUB2 sequence dataset. Sequences of *Bionectria* spp. were used as outgroup taxa. Bootstrap values (≥ 50%) from 1000 replications are indicated at the nodes. New taxa are shown in blue and ex-type strains in bold

specificity of the taxa in this group has not yet been proven given that they have been recorded from various plant families (i.e. *Arecaceae*, *Euphorbiaceae*, *Pinaceae*) (Hyde et al. 1999; Perera et al. 2016; Farr and Rossman 2018).

Chaetosphaeria panamensis Huhndorf & F.A. Fernández, Fungal divers 19:33 (2005)

Facesoffungi number: FoF02657, Fig. 101

Holotype: PANAMA, Barro Colorado Island National Monument, Shannon trail, 50 to 150 m, [9.1667, -79.8333], on decorticated wood, 23 August 1997, SMH, FAF, SMH3596 (in F).

Saprobic on decaying wood of *Macaranga tanarius*. **Sexual morph** *Ascomata* 200–250 µm diam., 180–230 µm high, black, scattered, solitary, sparse, semi-immersed in the host at the base of ascomata, becoming superficial, globose, coriaceous, setose, ostiolate, papillate. *Setae* scattered over entire ascomata, dark brown, stiff, pointed, 50–60 µm long. *Papilla* central, short, brown, with periphyses. *Peridium* 25–35 µm thick, composed of two cell layers, outer layer comprising 4–5 layers of thick, dark brown cells, arranged in *textura angularis* to *textura globosa*, inner layer comprising several layers of flattened, brown pseudoparenchymatous cells, arranged in *textura prismatica*. *Paraphyses* 3–4 µm wide at the base, tapering towards the apex, numerous, septate, arising from the basal cavity, embedded in a hyaline gelatinous matrix. *Asci* 125–150 × 9–12 µm ($\bar{x}$ = 137.5 × 11.2 µm, n = 10), 8-spored, unitunicate, arising from the basal hymenium, cylindrical, rounded at the apex, with a J-, apical ring. *Ascospores* 50–60 × 3–4 µm ($\bar{x}$ = 56.4 × 3.5 µm, n = 20), fasciculate, hyaline, filiform, straight to gently curved, with rounded ends, slightly tapering to base, 7-septate, smooth-walled, lacking a gelatinous sheath. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 8 mm diam. after 2 weeks at 25–30 °C, colonies medium dense, circular, surface slightly rough with edge fimbriate, effuse, velvety, margin, slightly irregular; from above, light brown to yellowish at the margin, light brown to grey at the centre, from below white to yellowish at the middle, light brown at the margin, grey to whitish at the centre, white to light purple at the middle; mycelium cream to whitish with tufting; not producing pigmentation in PDA.

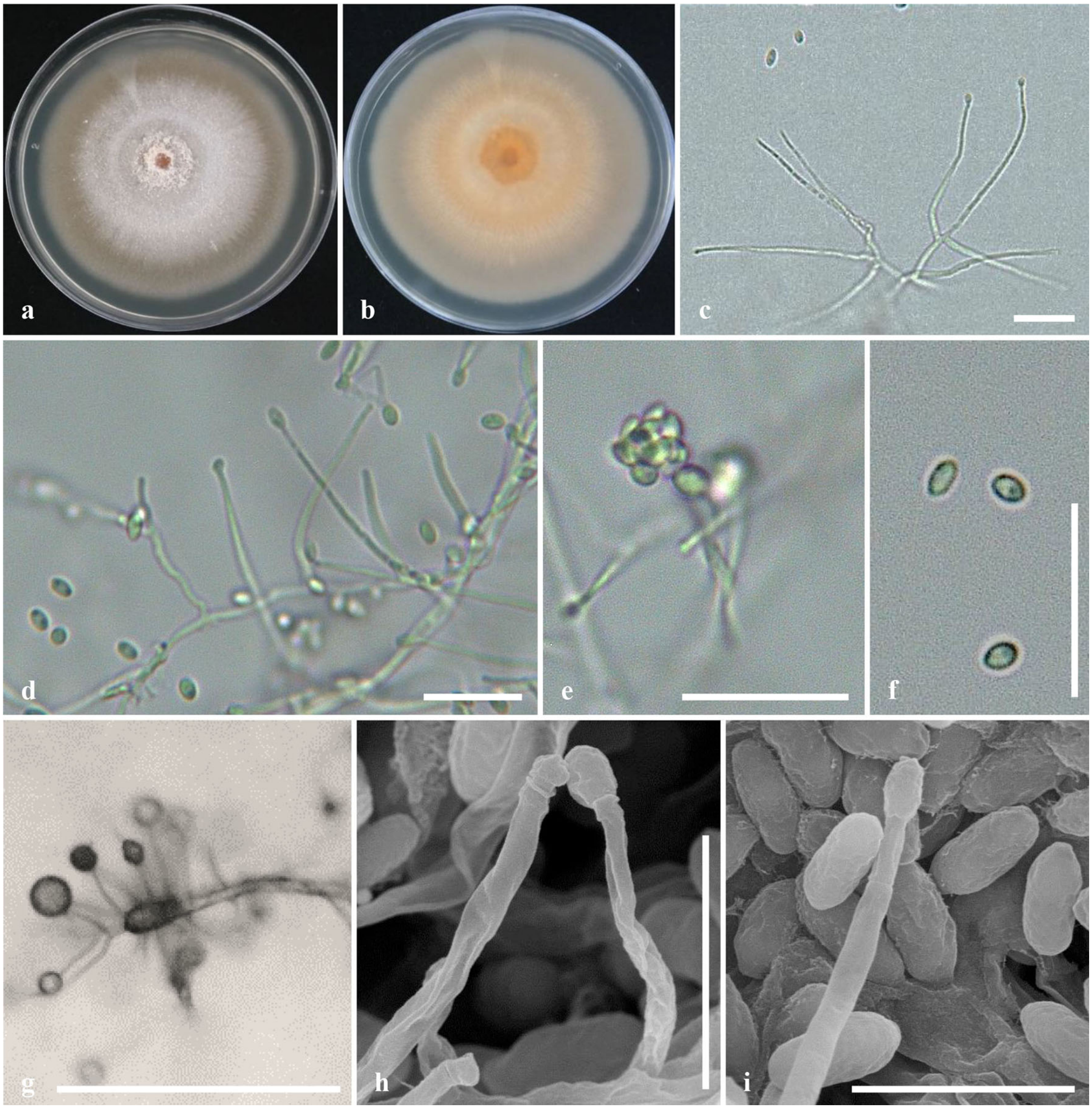


Fig. 97 ***Emericellopsis koreana*** (CNUFC-MOG1-1, **holotype**). **a, b** Colonies on malt extract agar (MEA) (a: obverse view, b: reverse view). **c** Conidiophores with branched form in the basal region (LM). **d, g** Unbranched conidiophores, conidial heads (LM). **e, f** Conidia on slimy head and single conidia (LM). **g–i** Curved or straight conidiophore and ellipsoid or oblong-ellipsoid conidia (SEM). *Scale bars* **c–g** = 20 µm, **h** = 4 µm, **i** = 5 µm

Material examined: TAIWAN, Chiayi, Shihnong Forest Area, decaying wood of *Macaranga tanarius* (L.) Müll.Arg (*Euphorbiaceae*), 25 June 2017, D.S. Tennakoon, DTW027 (MFLU18-0087), living culture, FU30910.

Known hosts and distribution: Decorticated wood (Panama), *Pinus* sp. (Thailand), *Macaranga tanarius* (Taiwan) (Huhndorf and Fernández 2005; Perera et al. 2016).

GenBank numbers: ITS = MH974685, LSU = MH974686.

Notes: *Chaetosphaeria panamensis* was introduced by Huhndorf and Fernández (2005), and was collected from decorticated wood in Panama. In this study, *C. panamensis* is reported on another host, *Macaranga tanarius* from Taiwan. Phylogenetic analyses based on a combined LSU, ITS and TUB2 sequence dataset show that our strain (FU30910) clusters with the ex-type strain of *C. panamensis* (SMH 3596) and another representative strain (MFLUCC 15-1011) with high support (100% ML and 1.00 BYPP; Fig. 100). Based on morphological characters (superficial, globose ascomata with setae, cylindrical asci and filiform, slightly curved, 7-septate, hyaline ascospores) and molecular data of ITS region, our isolate is identical to the type (SMH 3596; Huhndorf and Fernández 2005) and hence, the new isolate is identified as *C. panamensis*. This

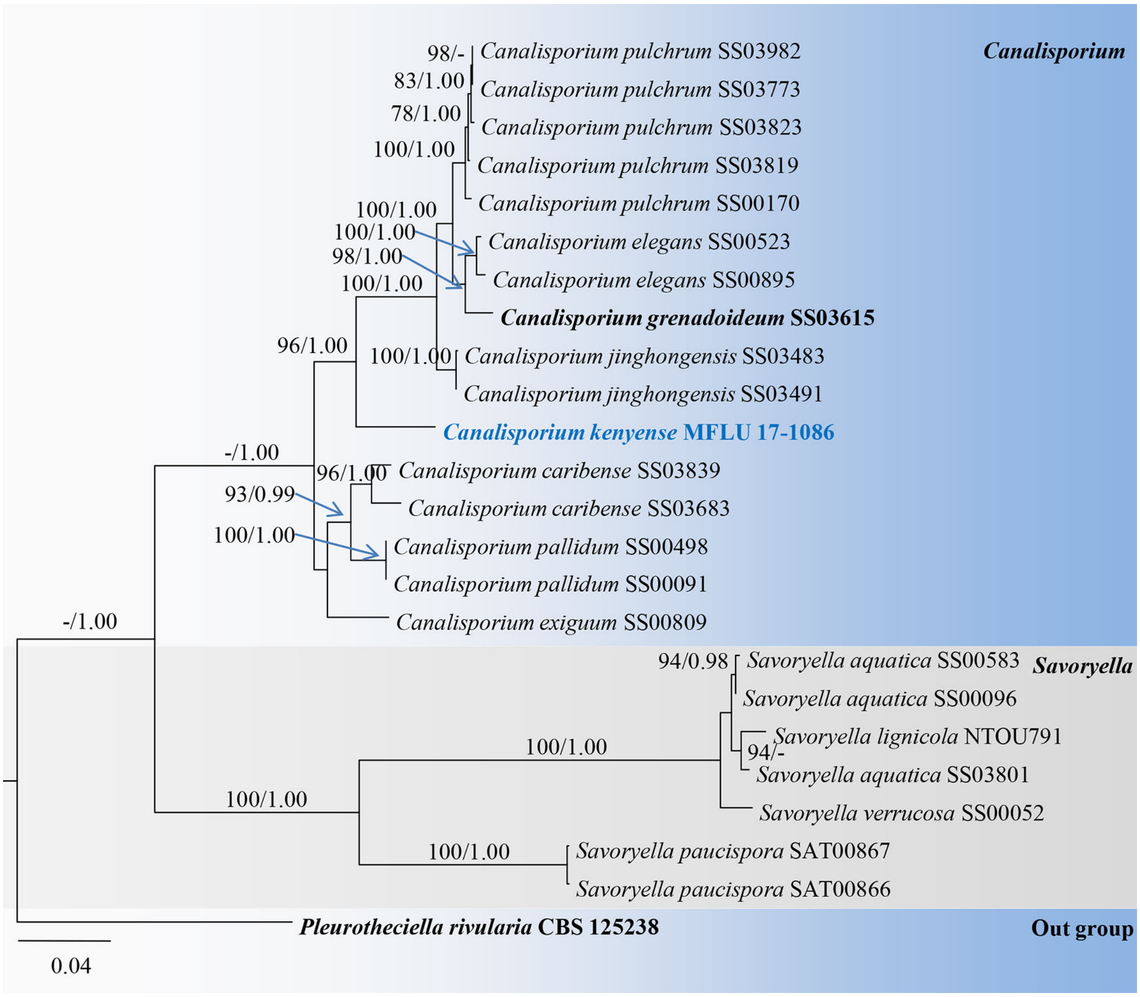


Fig. 98 Phylogram generated from maximum likelihood analysis of a combined LSU and ITS sequence dataset of species in *Canalisporium* Nawawi & Kuthub. and *Savoryella* E.B.G. Jones & R.A. Eaton (*Savoryellaceae*). Twenty-three strains are included in the combined sequence dataset, consisting of 1768 total characters with gaps (655 characters for ITS and 1113 for LSU). *Pleurotheciella rivularia* Réblová et al. (CBS 125238) is the outgroup taxon. The best scoring RAxML tree with a final likelihood value of -7016.458694 is presented. RAxML bootstrap support values equal to or greater than 75% and Bayesian posterior probabilities equal to or higher than 0.95 BYPP are given above the nodes (ML/BYPP). Hyphen ("–") indicates a value lower than 75% for RAxML and a posterior probabilities lower than 0.95 for Bayesian inference analysis. Newly generated sequences are in blue. Ex-type strains are in bold

is the first record of *C. panamensis* on decaying wood of *Macaranga tanarius* from Taiwan.

Thozetella Kuntze

We follow the latest treatment and updated accounts of *Thozetella* in Tibpromma et al. (2018).

Thozetella lithocarpi R.H. Perera & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555300; *Facesoffungi number*: FoF04923, Fig. 102

Etymology: Referring to the host genus, *Lithocarpus*.

Holotype: MFLU 16-1068

Saprobic on *Lithocarpus* fruits. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* effuse, superficial, sessile sporodochial, greenish white. *Sporodochia* subulate, scattered, sessile, of greenish white mass, with a white spore mass at the apex. *Microawns* 24–54 µm long, 3–3.5 µm wide, visible as small hairs on the sporodochial mass, aseptate, variously-shaped, sigmoid or sickle-shaped, apex straight, hyaline, smooth-walled, thick-walled. *Conidiophores* 21–30 × 1.5–3.5 µm, macronematous, packed in a bundle, usually ramose. *Conidia* 20–35 × 2–3 µm ($\bar{x}$ = 26 × 2.7 µm, n = 25), falcate, inequilateral, truncate at both ends, hyaline, smooth-walled, with a single filiform setula at each end, 6.9–8.7 µm long.

Culture characteristics: Colonies on MEA reaching 35 mm diam. after 3 weeks, margins effuse, grey to dark brown, flat, lacking aerial mycelium, reverse dark brown to black.

Material examined: THAILAND, Chiang Mai Province, on a dried seed of *Lithocarpus* sp. (*Fagaceae*; 19 species of

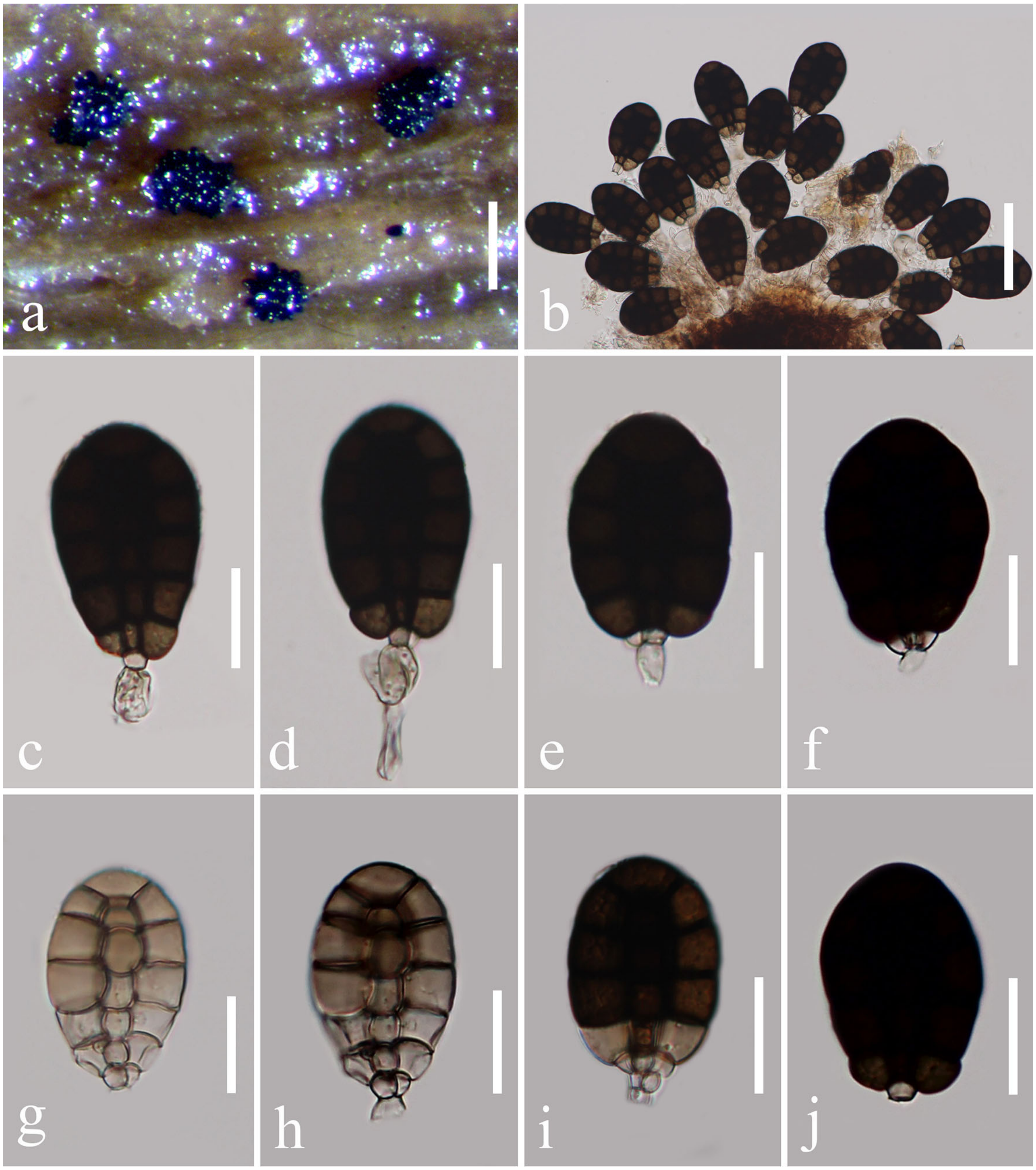


Fig. 99 ***Canalisporium kenyense*** (MFLU 17-1086, **reference specimen**). **a** Colony on substrate. **b–e** Conidia with attached conidiogenous cells. **f–j** Conidia. *Scale bars* **a** = 200 µm, **b** = 50 µm, **c–j** = 20 µm

Lithocarpus have been reported from Chiang Mai Province, according to BGO plant database), 22 December 2015, R.H. Perera, S-7 (MFLU 16-1068, **holotype**), ex-type living culture, MFLUCC 16-0194.

GenBank numbers: ITS = MH810433, LSU = MH810432.

Notes: *Thozetella lithocarpi* (MFLUCC 16-0194) shows a close relationship with *T. pandanicola* Tibpromma & K.D. Hyde, *T. pinicola* S.Y. Yeung et al. and *T. nivea* (Berk.) Kuntze (Fig. 100). However, *T. lithocarpi* can be distinguished from *T. pandanicola* and *T. pinicola* in having larger conidia and presence of microawns (Jeewon et al. 2009; Tibpromma et al. 2018). *Thozetella lithocarpi* produces microawns with a straight apex, while they are undulating to geniculate in *T. nivea* (Barbosa et al. 2011). A comparison of nucleotides in ITS gene region shows that *T. lithocarpi* differs from *T. pandanicola* and *T. pinicola* by 9 nucleotides (1.9%) and *T. nivea* by 18 nucleotides (3.9%). Our new species is also compared with *Thozetella* species that lack molecular data. *Thozetella lithocarpi*

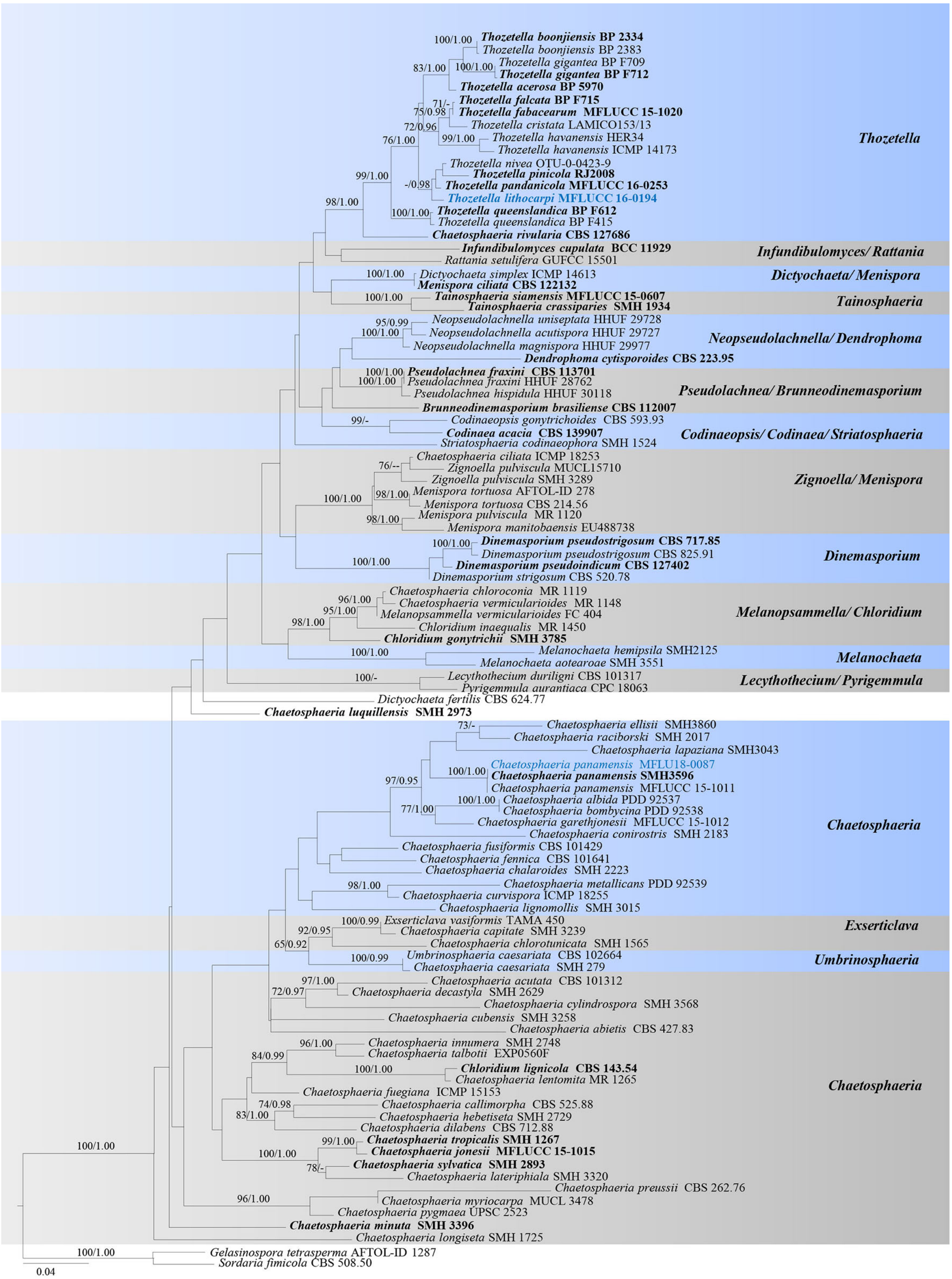


Fig. 100 Phylogram generated from maximum likelihood analysis of a combined LSU, ITS and TUB2 sequence dataset of *Chaetosphaeriaceae*. Maximum likelihood bootstrap support values greater than 70% and Bayesian posterior probabilities (BYPP) above 0.95 are shown above the nodes. The new isolates are in blue and ex-type strains in bold. The tree is rooted with *Gelasinospora tetrasperma* (AFTOL-ID 1287) and *Sordaria fimicola* (CBS 508.50)

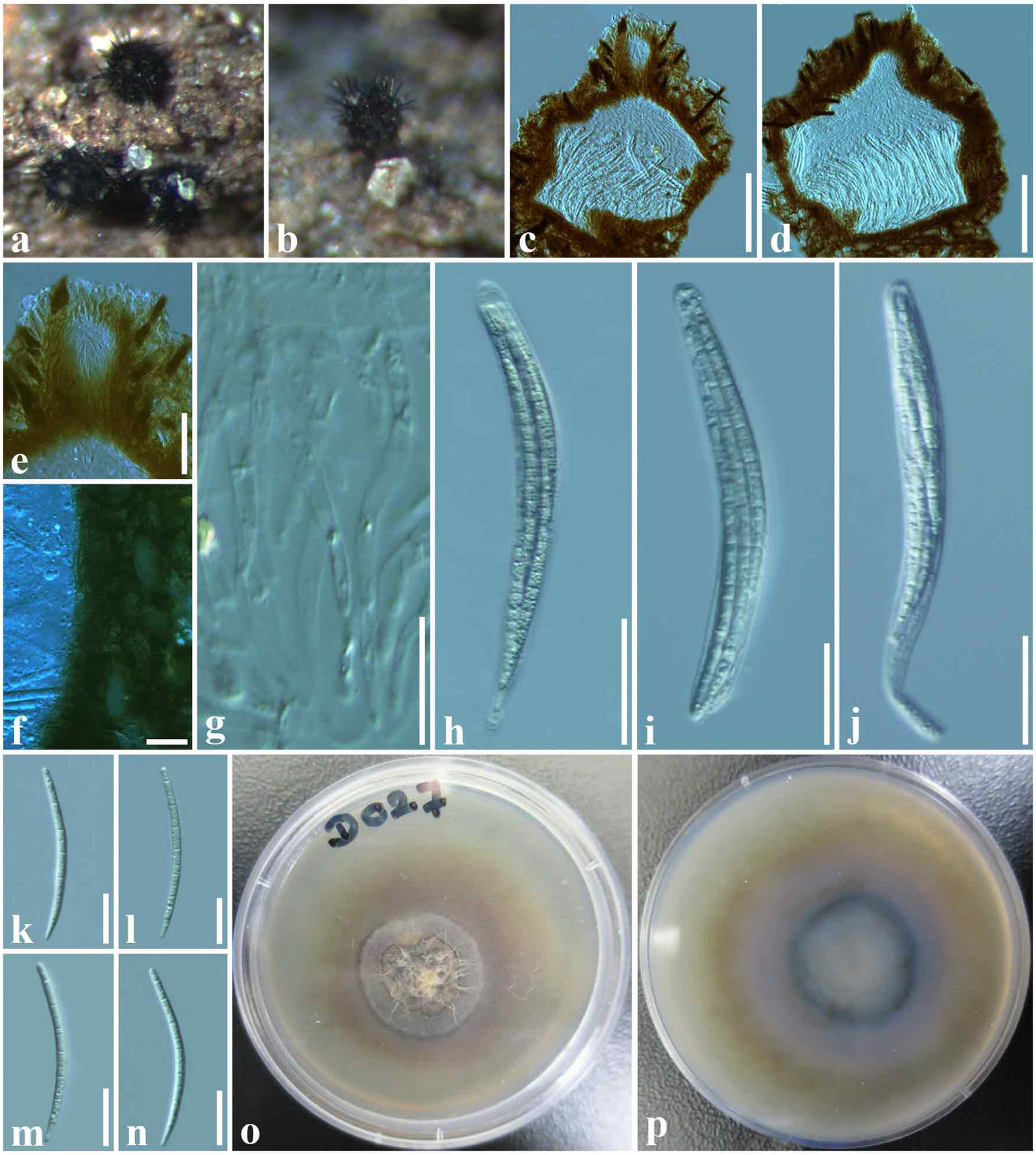


Fig. 101 ***Chaetosphaeria panamensis*** (MFLU 18-0087). **a** Appearance of ascomata on host. **b** Close-up of the ascoma. **c, d** Section of ascoma. **e** Section through ostiole. **f** Section of peridium. **g** Paraphyses. **h–j** Asci. **k–n** Ascospores. **o** Colony from above. **p** Colony from below. *Scale bars* **c, d** = 100 μm, **e** = 50 μm, **f** = 30 μm, **g–j** = 60 μm, **k–n** = 20 μm

produces comparatively larger conidia (20–35 × 2–3 μm versus 11–17 × 2–2.5 μm) and smaller microawns (24–54 μm long, 3–3.5 μm wide versus 40–100 μm long, 2.5–4 μm wide) than *T. cubensis* R.F. Castañeda & G.R.W. Arnold (Castañeda-Ruiz and Arnold 1985). *Thozetella canadensis* Nag Raj produces verrucose microawns, while *T. lithocarpi* produces smooth-walled microawns (Nag Raj 1976). *Thozetella aculeata* Prisc. Silva & Grandi, *T. buxifolia* Allegr. et al., *T. effusa* B. Sutton & G.T. Cole, *T. radicata* (E.F. Morris) Piroz. & Hodges, *T. serrata* Whitton et al., *T. submersa* F.R. Barbosa & Gusmão and *T. tocklaiensis* (Agnihothr.) Piroz. & Hodges also produces smaller conidia than those of *T. lithocarpi*. *Thozetella ypsiloidea* J.S. Monteiro et al. differs from *T. lithocarpi* by its Y-shaped microawns. Microawns of *T. serrata* have a serrated edge, while microawns have a straight apex in *T. lithocarpi* (Monteiro et al. 2016).

Coniochaetales Huhndorf et al.

Coniochaetaceae Malloch & Cain

Coniochaetaceae was established to accommodate two genera *Coniochaeta* (Sacc.) Cooke and *Coniochaetidium* Malloch & Cain by Malloch and Cain (1971). Species of *Coniochaetaceae* can be distinguished from other families in having ascospores with elongated germ slits. Cultures are frequently pink or orange and have a yeast-like appearance. They usually grow better at low temperatures. Conidia are produced in abundance as phialospores or rarely as aleuriospores (Malloch and Cain 1971; Huhndorf et al. 2004; Wanasinghe et al. 2018). We followed the latest phylogenetic analyses and the updated accounts of *Coniochaeta* in Nasr et al. (2018), Samarakoon et al. (2018) and Wanasinghe et al. (2018). A new species is introduced based on its morphological distinctiveness coupled with strong phylogenetic support (Fig. 103).

Coniochaeta **(Sacc.) Cooke**

We follow the latest treatment and updated accounts of *Coniochaeta* in Samarakoon et al. (2018) and Wanasinghe et al. (2018).

Coniochaeta simbalensis S. Rana & S.K. Singh, ***sp. nov.***

MycoBank number: MB824288; *Facesoffungi number*: FoF04831, Fig. 104

Etymology: The specific epithet "*simbalensis*" refers to the place of collection.

Holotype: AMH-9941

Colour codes follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978).

Saprobic on mushroom rhizospheric soil. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Hyphae* thin- to thick-walled, simple to branched, smooth-walled, constricted near the septa, wall thickened, guttulate, anastomosis observed. *Conidiophores* 1.2–6.3 µm wide, starting in 2–3 days from slender, thin hyaline to thick, smooth-walled hyphae, mostly reduced to conidiogenous cells. *Phialides* 1.8–60 × 1–3.7 µm ($\bar{x}$ = 14.3 × 2.2 µm, n = 30), variable, produced laterally from superficial hyphae, solitary or in groups (1–3), ventricose, base narrow, and middle swollen with elongated narrow tip (collar) tapered collula, variable in length, all curved, reduced in size to dentate structure like adelophialides to elongated branched. *Conidia* 2.2–8.8 × 1.3–3.3 µm ($\bar{x}$ = 4.5 × 2 µm, n = 30), 1-celled, oval to cylindrical to subglobose, produced sarcinately in gleosporic mass, rarely found in zipper-like arrangement, yeast-like cells observed frequently, monopolar budding seen in conidia, sporulation abundant, variable in size. *Chlamydospores* 5–8.6 × 3.4–6.7 µm ($\bar{x}$ = 6.8 × 4.9 µm, n = 30), light to dark olivaceous brown, observed frequently, terminal to intercalary, solitary or in branched chains, wall thickened and darkened, constricted near the septa, variable in shape, globose, cylindrical to pyriform, sometimes produced laterally from short and long stalk of ~ 16–28 µm. *Stalks* septate, simple to branched, light to olivaceous brown, smooth-walled.

Culture characteristics: Colonies on PDA reaching 39–45 mm diam. after 2 weeks at 25 °C; from above brownish grey (9D2) with margins fading to dull red (9B3), flat, sulcate, entire with smooth margin; from below, brownish grey (9E2) with outer margins fading to pale orange (6A3), sulcate. Colonies on MEA reaching to 15–20 mm diam. after 2 weeks at 25 °C; from above brownish grey (6F2), slightly raised, sulcate, and irregular; from below grey (6E1). Colonies on PCA reaching 29–34 mm diam. after 2 weeks at 25 °C; from above smoke brown (4F3); from below, silver grey (4E2) with a margin of nearly 5 mm yellowish white (4A2) in flat, glazy, margin entire and irregular.

Material examined: INDIA, Himachal Pradesh, Kangra Dist, Simbal (31.9754 N" 76.6507 E"), Mushroom rhizospheric soil, 8 July 2017, S. Rana, (AMH 9941, **holotype**), ex-type living culture, NFCCI 4236.

GenBank numbers: ITS = MG825743, LSU = MG917738.

Notes: *Coniochaeta simbalensis* differs from other *Coniochaeta* species based on the sequence analysis. On megablast analysis, ITS sequence of *C. simbalensis* shows 94.92% (468/493) similarity and 25 gaps (5%) with *C. cateniformis* (Perdomo et al.) Gené & Guarro (UTHSC 01-1644, type), 92.23% (487/528) similarity and 29 gaps (5%) with *C. canina* (Deanna A. Sutton et al.) Deanna A. Sutton et al. (UTHSC 11-2460, type), 93.37% (366/392) similarity and 5 gaps (1%) with *C. hoffmannii* (J.F.H. Beyma) Z.U. Khan et al. (CBS 245.38, type) and 87.36% (491/562) similarity and 42 gaps (7%) with *C. acaciae* Samarakoon et al. (MFLUCC 17-2298). Interestingly, the sources of isolation of these species are quite distinct. *Coniochaeta cateniformis* (UTHSC 01-1644) was isolated from canine bone marrow, *C. canina* (UTHSC 11-2460) from bone aspirate, canine breed German Shepard, *C. hoffmannii* (CBS 245.38) from butter (Khan et al. 2013) and *C. acaciae* (MFLUCC 17-2298) from dead trunk and branches of *Acacia* sp. (Samarakoon et al. 2018), whereas, *C. simbalensis* was isolated from rhizospheric soil of unidentified mushroom growing in soil.

Coniochaeta simbalensis produces brownish grey (9D2) colonies with margins fading to dull red (9B3) and sulcate on PDA, whereas *C. cateniformis* and *C. canina* produces orange white and non-sulcate colonies. Similarly, *C. simbalensis* produces brownish grey (6F2), colonies on MEA as against orange red to yellowish red colonies produced by *C. acaciae*. Phialides of highly variable length were frequently observed in vitro by *C. simbalensis.* Conidia are highly variable in shape and size in *C. simbalensis*, ranging from oval to cylindrical to subglobose, non-truncate, and straight; whereas conidia are ovoidal to ellipsoidal, truncate and smaller in *C. cateniformis*, and ellipsoidal, straight

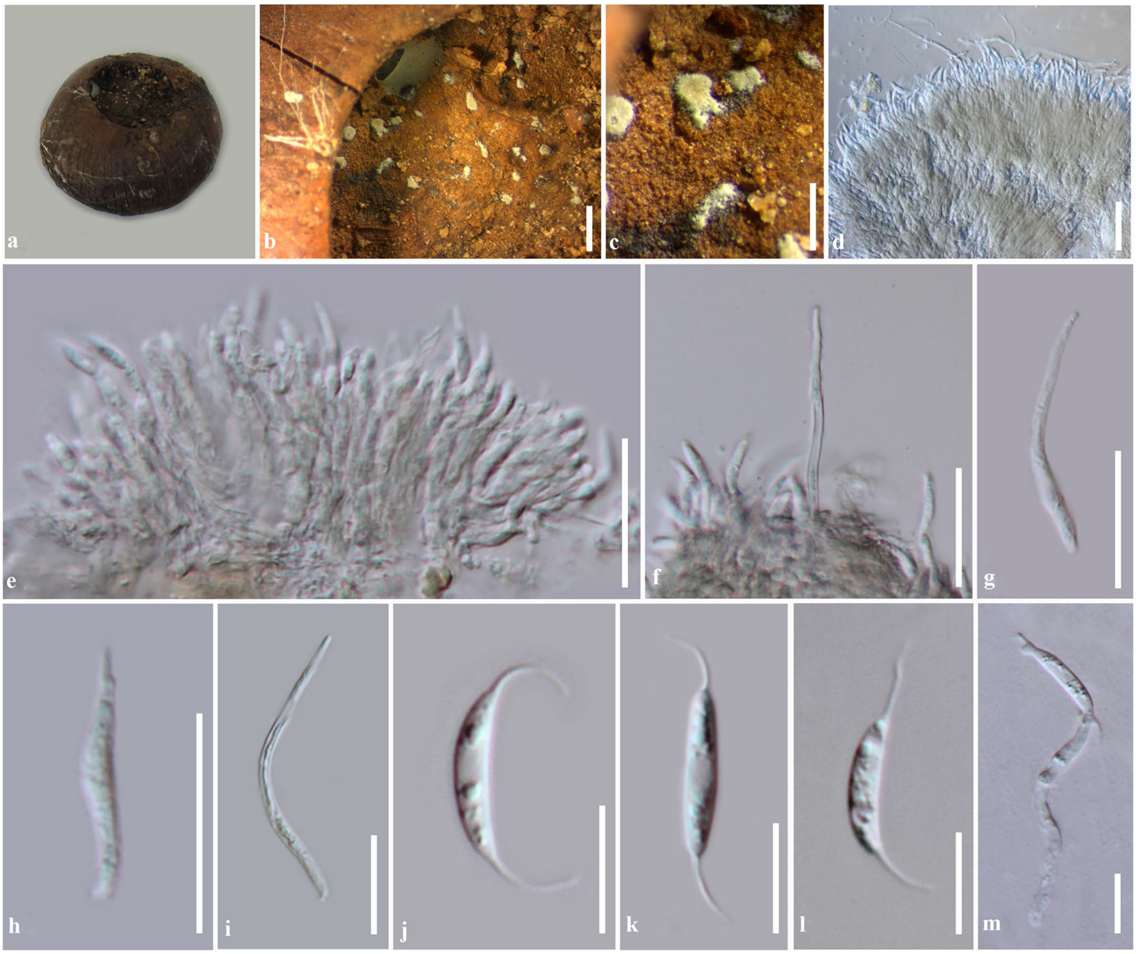


Fig. 102 ***Thozetella lithocarpi*** (MFLU 16-1068, **holotype**). **a** Dried seed of *Lithocarpus* sp. **b, c** Appearance of conidiomata on host substrate. **d–f** Conidiophores with conidia. **g–i** Microawns. **j–l** Conidia. **m** Germinating conidium. *Scale bars* **b** = 1 mm, **c** = 500 µm, **d–i** = 20 µm, **j–m** = 10 µm

to slightly curved in *C. canina* (Perdomo et al. 2013; Troy et al. 2013) and ellipsoidal in *C. acaciae* (Samarakoon et al. 2018). *Coniochaeta simbalensis* also readily produces chlamydospores in culture, a feature absent in *C. acaciae* and *C. prunicola* Damm & Crous (Damm et al. 2010). Therefore, based on phylogenetic inference (Fig. 103), morphological and cultural distinctness *C. simbalensis* is proposed as a new species.

Phyllachorales M.E. Barr

Phyllachoraceae Theiss. & H. Syd.

We follow the latest treatment and updated accounts of *Phyllachoraceae* in Dayarathne et al. (2017) and Mardones et al. (2017, 2018). Updated phylogenetic analysis (Fig. 105) was retrieved from Dayarathne et al. (2017).

Tamsiniella S.W. Wong et al.

Tamsiniella was introduced as a monotypic genus by Wong et al. (1998) to accommodate the freshwater fungus, *T. labiosa* S.W. Wong et al., which was collected from submerged wood in a small stream in Australia and Hong Kong (Wong et al. 1998). The genus is characterized by dark brown, immersed to semi-immersed, subglobose ascomata, with periphyses, papillate, thin-walled, pale brown peridium, paraphyses, 8-spored, unitunicate, cylindrical asci, with an unusual J-, lip-like, refractive apical ring, and hyaline, ellipsoidal-fusiform, aseptate ascospores, with narrow, roughed mucilaginous sheath (Wong et al. 1998). The asexual morph of this genus is unknown (Wijayawardene et al. 2017b). Based on the general morphology of the ascus apical ring observed with light microscopy and scanning, transmission electron microscopy, a new genus was established (Wong et al. 1998). Wong et al. (1998) suggested to place the genus in its own family due to a unique character of its apical ring. Wijayawardene et al. (2018a) treated the genus in Sordariomycetes, genera *incertae sedis*. We collected a

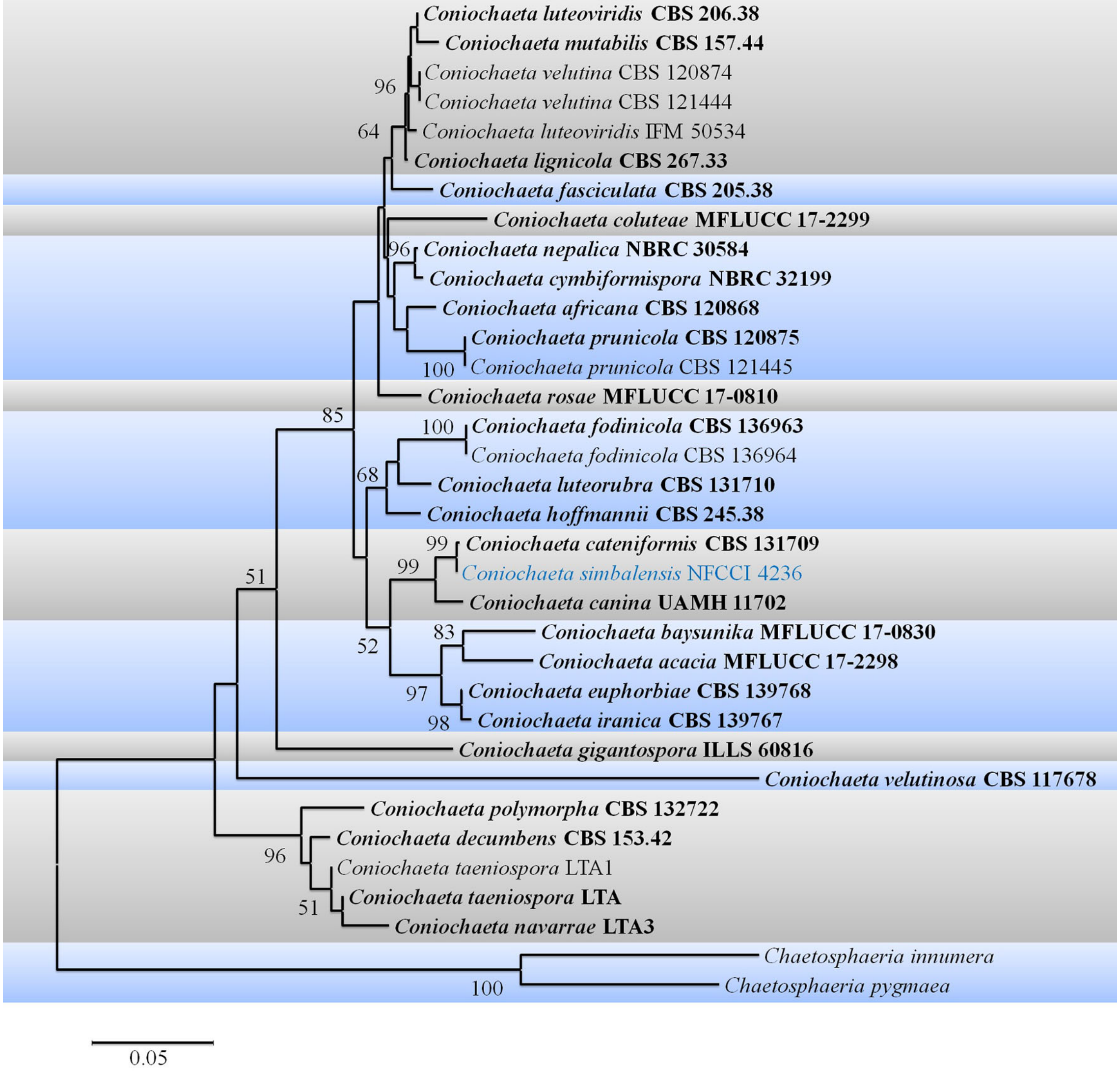


Fig. 103 Phylogram generated from maximum likelihood analysis for *Coniochaeta simbalensis* using a combined LSU and ITS sequence dataset based on the Tamura–Nei model (Tamura and Nei 1993). Phylogenetics analyses were conducted in MEGA7 (Kumar et al. 2016). *Chaetosphaeria innumera* and *C. pygmaea* were used as outgroup taxa. Type strains are indicated in bold. Newly generated sequence is indicated in blue

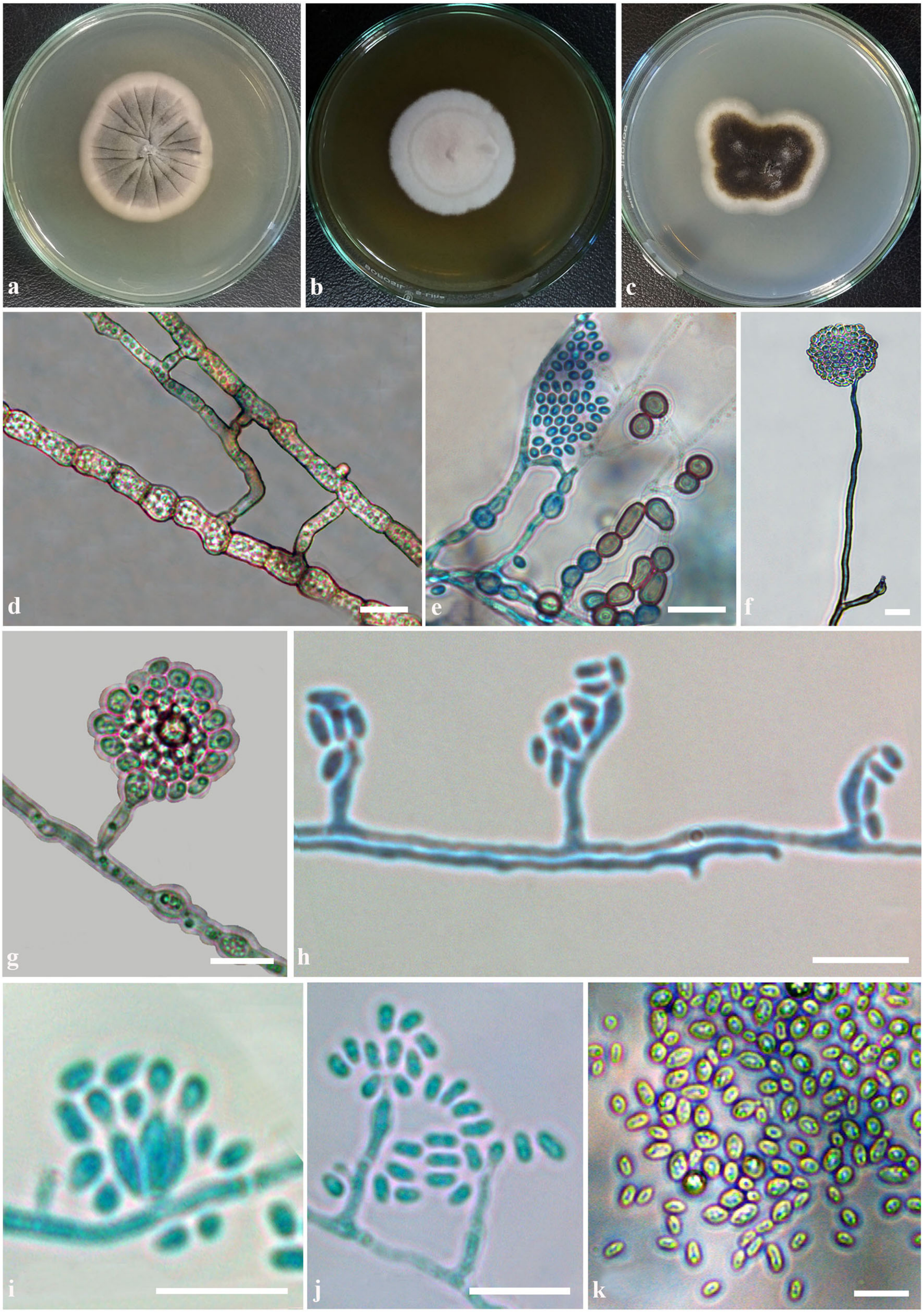
specimen from a small river in Yunnan, China. Based on morphological comparison, our collection is typical of the type of *Tamsiniella*. We therefore, designate our collection as an reference specimen based on morphological characteristics and geographical distribution (Fig. 105).

Tamsiniella labiosa S.W. Wong, K.D. Hyde, W.H. Ho & S.J. Stanley, Can J Bot 76(2): 334 (1998)

Facesoffungi number: FoF05052, Fig. 106

Holotype: AUSTRALIA, North Queensland, Mount Lewis, on submerged wood in a small stream, July 1993, T.M. and K.D. Hyde, ML9 (HKU (M) 2276; IFRD199-014).

Saprobic on decaying wood submerged in freshwater. **Sexual morph** *Ascomata* 100–120 µm high, 130–150 µm diam. [type: 130–225 µm high, 180–250 µm diam.], black, gregarious or scattered, superficial, subglobose to ellipsoidal, uni-loculate, thin-walled, laterally ostiolate, with a mass of spores oozing when old. *Peridium* 6–9 µm wide [type: 5–11 µm wide], comprising 3–4 layers of dark brown, thick-walled, compressed cells of *textura angularis*. *Hamathecium* comprising numerous, ca 6 µm wide at the base, 2 µm diam. at the apex [type: 4–5 µm wide], cylindrical, unbranched, hyaline, septate, paraphyses, slightly constricted at the septa, tapering towards the apex. *Asci* 80–110 × 7.5–9 µm ($\bar{x}$ = 93 × 8.5 µm, n = 15) [type: 80–102 × 8–10.5 µm], 8-spored, unitunicate, cylindrical to cylindric-clavate with a short, twisted pedicel, apically obtuse and inwardly concave, slightly wider than subapical apparatus, with J-, a refractive, lip-like apical ring, 1.9–2 × 2.9–3.1 µm. *Ascospores*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◀**Fig. 104** ***Coniochaeta simbalensis*** (AMH 9941, **holotype**). **a** Colony morphology on PDA (front view). **b** Colony morphology on SDA (front view). **c** Colony morphology on PCA (front view). **d** Hyphal wall septate, thickened, guttulate, and showing anastomoses. **e** Terminal to intercalary chlamydospores. **f** Phialides with gleosporic mass of conidia. **g** Adelophialide with gleosporic mass of conidia (magnified view). **h** Discrete phialides and adelophialides. **i** Ventricose phialides in group with conidia. **j** Discrete phialides and dispersed conidia. **k** Mass of conidia. *Scale bars* = 10 µm

17–20 × 3.5–5 µm ($\bar{x}$ = 19 × 4.5 µm, n = 15) [type: (12–)15–21 × 3.8–4.5(–5) µm], overlapping 1-seriate, hyaline, aseptate, fusiform to ellipsoidal, straight or curved, guttulate, thin-walled, with a thin, hyaline, mucilaginous sheath, 1–2 µm wide. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 20 mm in 12 days at 25 °C, circular, white to yellow–brown from above, white to light yellow from below, surface smooth with sparse mycelium, dry, edge entire.

Material examined: CHINA, Yunnan Province, Pingbian, on submerged wood in a small river, 20 September 2017, W. Dong, WF-33A (MFLU 18-1191, **a reference specimen is designated here**; *ibid*., KUN-HKAS 101711), living culture, MFLUCC 18-1018 = KUMCC 18-0060.

Known hosts and distribution: On submerged woods or twigs in Australia, Brazil, China, Hong Kong (Wong et al. 1998; Barbosa et al. 2013; this study).

GenBank numbers: ITS = MK034865, LSU = MK034866, SSU = MK034867.

Notes: Our isolate shares the size range of asci, ascospores, peridium and paraphyses with the type of *Tamsiniella labiosa* (see description). However, it has a slightly smaller ascomata compared to the type. Our isolate was collected from submerged wood in Yunnan, China, whereas the type specimen was collected from submerged wood in North Queensland, Australia. Based on morphological comparison and geographical distribution, we hence, designate our collection as a reference specimen of *T. labiosa*.

In phylogenetic tree, *Tamsiniella labiosa* forms a distinct lineage in the order *Phyllachorales* M.E. Barr with moderate support (77% ML and 0.99 BYPP, Fig. 105). *Phyllachorales* species are distinctive as they are biotrophic on various hosts (Pearce and Hyde 1994; Dayarathne et al. 2017; Mardones et al. 2017, 2018). *Phyllachorales* species are characterized by deep black stromata of various shapes; pseudostroma inside the host tissue and usually beneath an epidermal clypeus; perithecia usually strongly melanized; cylindrical to clavate asci with an inconspicuous apical ring; and globose to filiform, mostly hyaline, 1-celled, rarely brown or septate ascospores (Parbery 1967; Cannon 1991; Dayarathne et al. 2017; Mardones et al. 2017, 2018). However, our collection was isolated from decaying wood submerged in freshwater, which was the same habitat as another freshwater ascomycete genus *Ascovaginospora* Fallah et al. in *Phyllachoraceae* (Wijayawardene et al. 2018a). Therefore, *Tamsiniella* is accommodated in *Phyllachoraceae* based on phylogenetic analyses.

Sordariales Chadef. ex D. Hawksw. & O.E. Erikss

Lasiosphaeriaceae Nannf.

Lasiosphaeriaceae was established by Nannfeldt (1932), circumscribed by species with black ascomata and cylindrical asci, brown to hyaline ascospores, and typified by *Lasiosphaeria* Ces. & De Not. The family was re-circumscribed by Maharachchikumbura et al. (2015, 2016) and 35 genera were accepted in the family. Based on phylogeny, *Lasiosphaeriaceae* is sister to *Chaetomiaceae* with high support and this family has been shown to be paraphyletic, with many genera polyphyletic (Chang et al. 2010; Kruys et al. 2015; Maharachchikumbura et al. 2015, 2016). Wijayawardene et al. (2018a) listed 32 genera in *Lasiosphaeriaceae*.

Zopfiella G. Winter

Zopfiella was established by Winter (1884) to introduce *Z. tabulata* (Zopf) G. Winter and *Z. curvata* (Fuckel) G. Winter. Phylogenetic studies reported that the genera *Zopfiella*, *Triangularia* Boedijn, *Cercophora* Fuckel and *Podospora* Ces. are polyphyletic (Miller and Huhndorf 2005; Cai et al. 2005, 2006a, b; Chang et al. 2010; Kruys et al. 2015; Maharachchikumbura et al. 2015, 2016). A new species *Z. indica*, is introduced within *Lasiosphaeriaceae* based on evidence from morphology and DNA sequence data (Fig. 107).

Zopfiella indica Devadatha, Jeewon & V.V. Sarma, ***sp. nov.***

Index Fungorum number: IF554286; *Facesoffungi number*: FoF04269, Fig. 108

Etymology: Refers to country of its origin

Holotype: AMH-9907

Saprobic on the bark of intertidal mangrove wood. **Sexual morph** *Ascomata* 320–555 µm high, 220–405 µm diam. ($\bar{x}$ = 455.4 × 317 µm, n = 10), perithecial, lacking stromatic tissues, superficial, pyriform, solitary to gregarious, coriaceous, dark brown to black, enclosed with copious, flexuous, septate, light brown to dark brown, short to long hyphae, prevalent at the base, about 75–200 µm long, 1–2.5 µm thick, ostiolate. *Ostiole* 50–130 µm long, 40–125 µm diam. ($\bar{x}$ = 105 × 104 µm, n = 10), black, short papillate, straight to curved, darker than remaining part of the perithecium, filled with brown cells. *Periphyses* 1–2 µm wide ($\bar{x}$ = 1.7 µm, n = 20). *Peridium* 5–25 µm wide ($\bar{x}$ = 13.2 µm, n = 10), membranous to coriaceous, pale brown to dark brown, comprising two layers, inner stratum

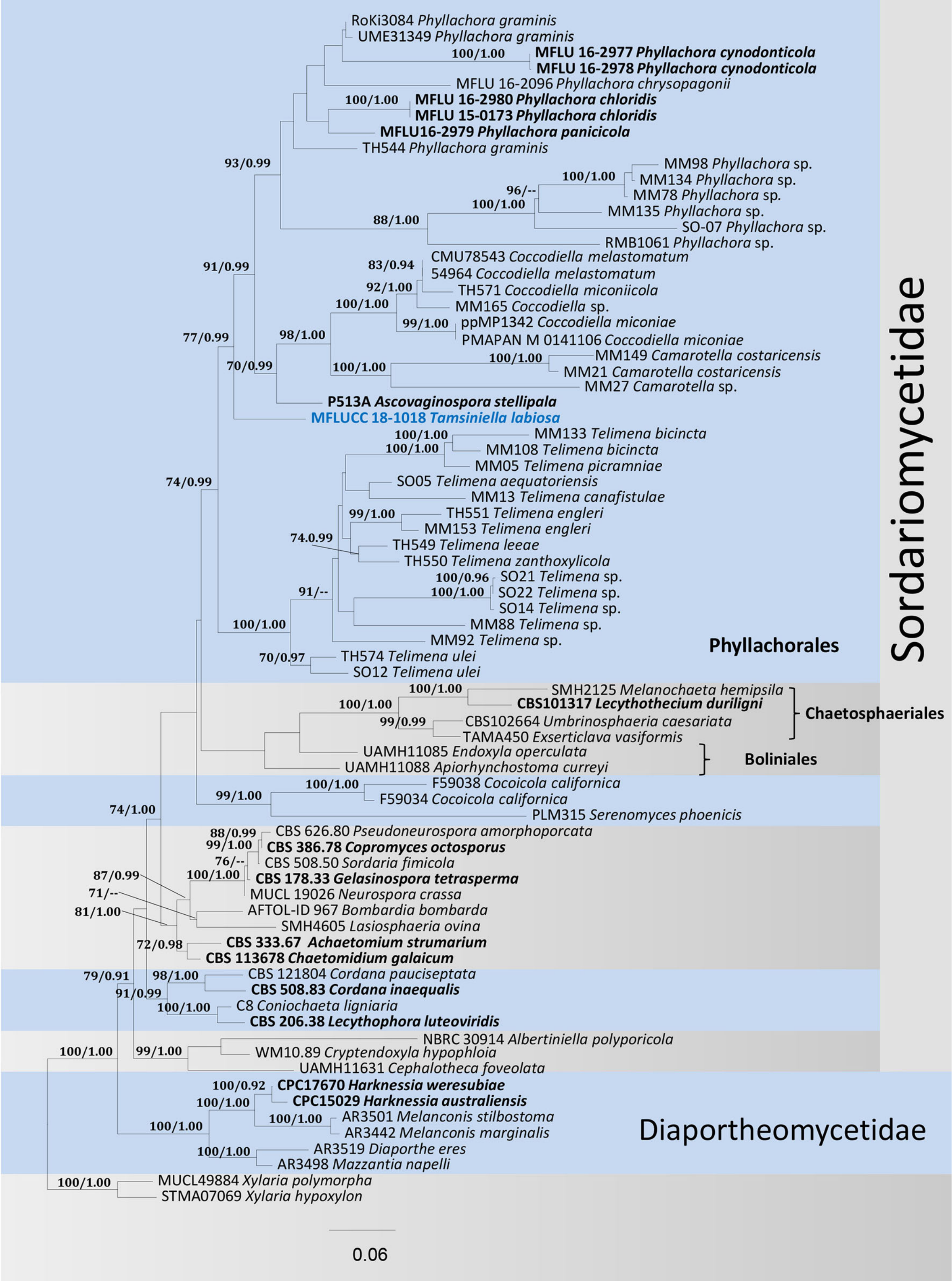


Fig. 105 Phylogram generated from maximum likelihood analysis based on a combined LSU, SSU and ITS sequence dataset of taxa in *Phyllachorales* and related orders. Bootstrap support values for maximum likelihood (left) equal to or greater than 70% and the values of Bayesian posterior probabilities (right) equal to or greater than 0.90 are given above the nodes. The new isolate is in blue. The tree is rooted with *Xylaria polymorpha* (MUCL49884) and *X. hypoxylon* (STMA07069). Ex-type strains are indicated in bold

Fig. 106 ***Tamsiniella labiosa*** (MFLU 18-1191, **reference specimen**). **a–c** Appearance of black ascomata superficial on host. **d** Vertical section of ascoma. **e** Structure of peridium. **f** Paraphyses. **g–j** Unitunicate asci. **k–m** Ascospores. **n** Germinated ascospore **o** Colony on PDA (from above). **p** Colony on PDA (from below). *Scale bars* **d** = 50 µm, **e, j–n** = 10 µm, **f–i, o** = 20 µm

flattened with several layers of hyaline to pale brown cells of *textura prismatica*, outer stratum comprising 2–3 layers of *textura angularis*. *Paraphyses* 1–2.5 µm wide ($\bar{x}$ = 1.9 µm, n = 20), hyaline, filiform. *Asci* 115–200 × 15–45 µm ($\bar{x}$ = 147.1 × 26.5 µm, n = 40), 8-spored, unitunicate, cylindrical to clavate, evanescent, short pedicellate, 20–75 µm × 2.5–7.5 µm ($\bar{x}$ = 46 × 5 µm, n = 40), apical ring indistinct. *Ascospores* 23–35 × 10–20 µm ($\bar{x}$ = 29.9 × 15.7 µm, n = 50), partially overlapping 1–2-seriate, hyaline at first turning golden yellow and olivaceous brown to dark brown at maturity, apical cell ovoid to ellipsoidal, rugose, apical cauda, single, lash-like, attached to the apical part of the terminal cell, 8–55 × 3–8 µm ($\bar{x}$ = 20 × 5 µm, n = 20), smooth-walled, collapsing, primary appendage attached to the base of the pedicel and similar to apical cauda, 15–25 × 3–8 µm ($\bar{x}$ = 20 × 5 µm, n = 20), mostly collapsing. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinated on SWA within 24 h, germ tubes arise from ends of the ascospore. Colonies on MEA reaching 70–85 mm diam. after 25 days of incubation at room temperature, initially deep olive grey, becoming dark olive grey at maturity, surface umbonate, margin entire, velvety, circular, reverse dark olive grey.

Material examined: INDIA, Tamil Nadu, Tiruvarur District, Muthupet mangroves (10.4°N 79.5°E), on the bark of intertidal mangrove wood, 28 November 2015, B. Devadatha, AMH-9907 (**holotype**), ex-type living culture, NFCCI-4217.

GenBank numbers: ITS = KY863506, LSU = KY863507, SSU = MF168941, RPB2 = MF182396, TEF1-α = MF182400, TUB2 = MF406208.

Notes: Multigene phylogenetic analyses indicate that *Zopfiella indica* shares a sister relation with *Z. karachiensis* (S.I. Ahmed & Asad) Guarro and *Triangularia tanzaniensis* R.S. Khan & J.C. Krug in a strongly supported monophyletic clade (Fig. 107). *Zopfiella indica* is clearly distinguished from *Z. karachiensis* and *Triangularia tanzaniensis* based on its ascospores having ovoid to ellipsoidal, rugose head cell, apical cauda attached to apical part of the terminal cell and primary appendage attached to the basal pedicel.

Species belonging to *Podospora* are predominantly coprophilous whereas those belonging to *Zopfiella* predominantly thrive in soil or on plant substrata and less on dung. Given the existing taxonomic confusion vis-a-vis the genera *Zopfiella* and *Podospora*, we prefer to place *Z. indica* in the genus *Zopfiella* based on its occurrence on decaying wood, and presence of a septum in the dark cell.

Recent phylogenetic analysis showed that *Zopfiella* is polyphyletic, interspersed with species belonging to other genera and hence is in need of revision along with other closely related genera such as *Podospora* and *Triangularia*, both at the morphological and molecular level, by including a larger representation of the species belonging to these genera. Phylogenetic analyses carried out by Cai et al. (2006b) also indicated that *Zopfiella* does not constitute a monophyletic group. They felt that the characters of non-ostiolate ascomata, and the absence of gelatinous appendages in ascospores that are considered important in delineating *Zopfiella* from *Podospora* (Guarro et al. 1991) are not reliable in understanding phylogenetic relationships (Cai et al. 2006b). This is because they found non-ostiolate *Zopfiella* species interspersed in different clades in the trees suggesting multiple origins of this morphological character. Also they found that the presence or absence of gelatinous appendages are phylogenetically less informative as different *Zopfiella* species grouped in different clades that also include many species possessing elaborate gelatinous appendages. Cai et al. (2006b) suggested that *Zopfiella* should be restricted to species with a septum in the dark cell.

There are two strains under the name *Zopfiella karachiensis* (IFO32902 and CBS 657.74) in GenBank, which were included in our phylogenetic analysis. However, these two strains formed a separated lineage in our phylogenetic tree (Fig. 107). *Zopfiella karachiensis* (IFO32902) is sister to *Z. lundqvistii* (NBRC30585); whereas, *Z. karachiensis* (CBS 657.74) clustered with *Triangularia tanzaniensis* and *Z. indica* (our present strain). Taxonomic revision of genera in this family is needed based on multigene phylogenetic analyses.

Subclass Xylariomycetidae O.E. Erikss. & Winka

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

Amphisphaeriaceae G. Winter

The family *Amphisphaeriaceae* was introduced by Winter (1887) to accommodate *Amphisphaeria* and allied taxa. *Amphisphaeriaceae* is mainly characterized by perithecial, semi-immersed to erumpent ascomata, dark peridium, unitunicate, cylindrical asci, with J + or J-, apical rings, pale to dark brown, septate ascospores and forming coelomycetous asexual morphs (Senanayake et al. 2015; Maharachchikumbura et al. 2016). Three genera are accepted in this family, *Amphisphaeria* Ces & De Not., *Griphosphaerioma* Höhn., and *Lepteutypa* Petr. (Wijayawardene et al. 2018a). An updated evolutionary relationship of the family in Xylariomycetidae was presented by Samarakoon et al. (2016) and Hongsanan et al. (2017).

Amphisphaeria Ces. & De Not.

Amphisphaeria was established by Cesati and De Notaris (1863) without assigning a generic type. Petrak (1923) proposed *A. umbrina* (Fr.) De Not. as the lectotype of *Amphisphaeria*. Hyde et al. (1996) epitypified and described *A. umbrina*. Senanayake et al. (2015) re-

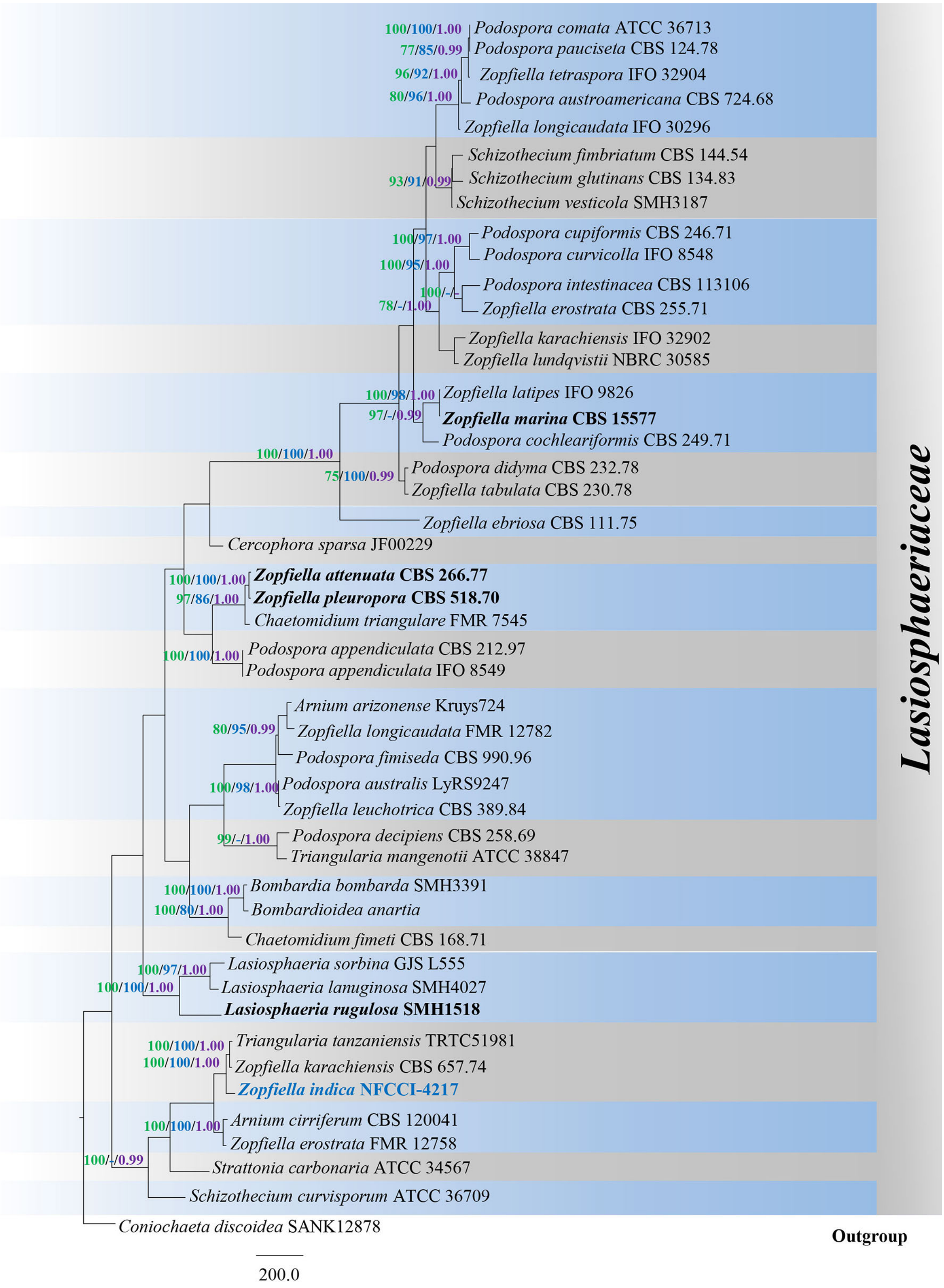
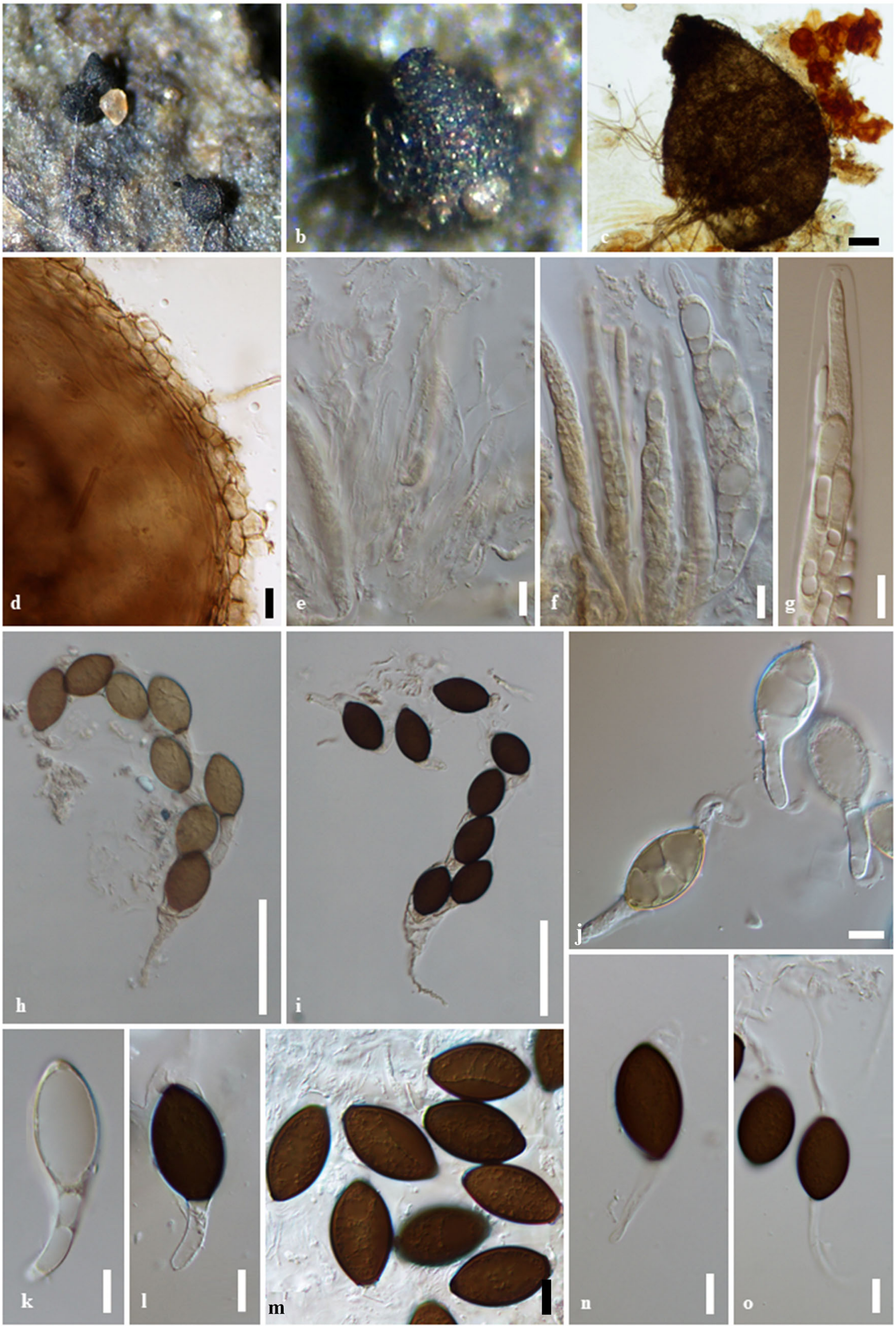


Fig. 107 Phylogram generated from maximum parsimony analysis based on a combined LSU, TUB2, ITS and RPB2 gene regions of *Zopfiella* and related taxa in *Lasiosphaeriaceae*. Bootstrap support values for maximum likelihood (green), maximum parsimony (blue) equal to or greater than 75% and the values of Bayesian posterior probabilities (purple) equal to or greater than 0.95 BYPP are given above each branch respectively. The new isolate is in blue. Ex-type strains are indicated in bold. The tree is rooted with *Coniochaeta discoidea* (Udagawa & Furuya) Dania García et al. (SANK12878)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◀**Fig. 108** ***Zopfiella indica*** (AMH-9907, **holotype**). **a, b** Ascomata superficial on the bark of intertidal mangrove wood. **c** Squash mount of ascoma. **d** Section through peridium. **e** Hyaline filiform paraphyses. **f–i** Immature and mature asci. **j–o** Ascospores with apical and basal cauda. *Scale bars* **c** = 100 μm, **h–i** = 50 μm. **d–g, j–o** = 10 μm

circumscribed *Amphisphaeria* and introduced *A. sorbi* Senan. & K.D. Hyde with the link between the sexual and asexual morphs. We follow the latest treatment and updated accounts of *Amphisphaeriaceae* in Senanayake et al. (2015) and Maharachchikumbura et al. (2016). Based on phylogenetic analyses of a combined LSU, SSU and ITS sequence dataset (Fig. 109) coupled with morphological characteristics, we therefore, introduce a new species from intertidal branches and twigs of *Suaeda monoica* Lam. (*Amaranthaceae*) in India.

Amphisphaeria mangrovei Devadatha & V.V. Sarma, ***sp. nov.***

Index Fungorum number: IF554279; *Facesoffungi number*: FoF04273, Fig. 110

Etymology: Named after the fungal habitat from marine environment, where the fungus found.

Holotype: AMH-9948

Saprobic on intertidal branches and twigs of *Suaeda monoica*. **Sexual morph** *Ascomata* 150–280 μm high, 140–250 μm diam. ($\bar{x}$ = 192 × 211 μm, n = 10), immersed to erumpent, globose to subglobose, gregarious to solitary, coriaceous, brown, short papillate, ostiolate. *Ostioles* 45–60 μm long, 35–45 μm diam. ($\bar{x}$ = 50 × 40 μm, n = 10), short, periphysate, brown, 0.5–2 μm ($\bar{x}$ = 1.5 μm, n = 20). *Peridium* equal in thickness, 10–20 μm wide ($\bar{x}$ = 13 μm, n = 10), both at the base and sides, comprising two layers, inner stratum with 3–4 layers of hyaline to light brown cells of *textura angularis* and outer stratum with 2–3 layers of light brown to brown cells of *textura angularis*, fusing with the host tissue. *Paraphyses* 1–2 μm wide ($\bar{x}$ = 1.7 μm, n = 20), filamentous, septate, longer than asci, embedded in a gelatinous matrix. *Asci* 80–130 × 5–10 μm ($\bar{x}$ = 100 × 8 μm, n = 30), 8-spored, unitunicate, cylindrical to obclavate, apically rounded with a J-, apical ring, short pedicellate. *Ascospores* 12–15 × 4–6 μm ($\bar{x}$ = 13 × 5 μm, n = 50), partly overlapping 1-seriate, light brown, one median septate, ellipsoidal, smooth-walled, lacking a mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on SWA within 24 h, germ tubes arising from both ends of the ascospore. Colonies on MEA reaching 80–90 mm diam. after 7 days of incubation at room temperature, cream to white from above, yellow and white at margin from below, granular and cottony, undulate, umbonate, irregular.

Material examined: INDIA, Tamil Nadu, Tiruvarur, Muthupet mangroves (10.4°N 79.5°E), on intertidal branches and twigs of *Suaeda monoica*, 29 October 2016, B. Devadatha, AMH-9948 (**holotype**), ex-type living culture, NFCCI-4247.

GenBank numbers: ITS = MG844283, LSU = MG767311, SSU = MG844279.

Notes: *Amphisphaeria mangrovei* differs from other *Amphisphaeria* species in having smaller ascomata, asci and ascospore dimensions and the marine habitat. *Amphisphaeria mangrovei* has similar morphological characters to *A. sorbi* such as clypeate ascomata, asci with J-, apical ring and single, median septate, ellipsoidal ascospores (Senanayake et al. 2015). However, *A. sorbi* has larger ascomata, asci and ascospores, and slightly constricted ascospores with a thick mucilaginous sheath. *Amphisphaeria umbrina* and *A. vibratilis* (Fuckel) E. Müll. have clypeate ascomata, asci with J + , discoid subapical rings and larger ascospores. Phylogenetic analyses of a combined LSU, SSU and ITS regions reveal that *A. mangrovei* is sister to *A. sorbi* and *A. umbrina* with significant support (96% ML, 90% MP and 1.00 BYPP; Fig. 109). Based on morphological characters and molecular phylogenetic analyses, a new species *A. mangrovei* is introduced.

Sporocadaceae Corda.

Jaklitsch et al. (2016b) proposed the family *Sporocadaceae* based on morphological observations and phylogenetic analyses of a concatenated ITS-LSU sequence dataset with asexual morph genera that are acervular coelomycetes having hyaline, pale or dark brown, septate conidia. The type genus is *Seimatosporium* Corda (Jaklitsch et al. 2016b). The family *Sporocadaceae* hitherto includes 22 genera (Jaklitsch et al. 2016b; Wijayawardene et al. 2017a, 2018a). We follow the latest treatment and updated accounts of *Sporocadaceae* in Jaklitsch et al. (2016b), Maharachchikumbura et al. (2017) and Wanasinghe et al. (2018). The updated phylogenetic analyses are derived from Maharachchikumbura et al. (2017) and Wanasinghe et al. (2018).

Bartalinia Tassi

We follow the latest treatment and updated accounts of *Bartalinia* in Jaklitsch et al. (2016b) and Wanasinghe et al. (2018). In this study, *Bartalinia kunmingensis* is introduced from *Zea mays* (*Poaceae*) in Yunnan, China based on morphological characteristic and phylogenetic analyses of ITS and LSU sequence data (Fig. 111).

Bartalinia kunmingensis Thiyag., Wanas., Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556209; *Facesoffungi number*: FoF05717, Fig. 112

Etymology: The specific epithet "*kunmingensis*" refers to Kunming City, Yunnan, China, where the holotype was collected.

Holotype: KUN-HKAS 102242

Saprobic on dead leaves of *Zea mays*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 80–110 µm high, 110–140 µm diam. ($\bar{x}$ = 126.2 × 99 µm, n = 10), pycnidial, dark brown to black, immersed, slightly raised, solitary to gregarious, uniloculate, globose to subglobose, glabrous, ostiolate, with a minute papilla. *Conidiomata walls* 8–20 µm wide, slightly thick-walled, of equal thickness, comprising several cell layers of brown, pseudoparenchymatous cells of *textura angularis*, paler towards the inner layers. *Conidiophores* arising from the inner cavity, reduced to conidiogenous cells. *Conidiogenous cells* (3.6–)4–7.5 × 2–5 µm ($\bar{x}$ = 5.4 × 2.8 µm, n = 30), holoblastic, phialidic, rarely with 1–2 percurrent proliferations, discrete, hyaline, ampulliform to subcylindrical, or obclavate, aseptate, smooth-walled. *Conidia* (17.5–)20–25 × 3–4 µm ($\bar{x}$ = 22.1 × 3.9 µm, n = 30), cylindrical to subcylindrical, straight to slightly curved, 4-septate, not constricted at the septa, with longest cell at the second from base, bearing appendages; basal cell 2.5–4 µm long ($\bar{x}$ = 3.2 µm), obconic, truncate at base, hyaline, thin and smooth-walled, second cell from the base 6.5–8 µm long ($\bar{x}$ = 7.4 µm), pale yellowish, third cell 4–5.5 µm long ($\bar{x}$ = 4.8 µm), pale yellowish, fourth cell 4–5.5(–6) µm long ($\bar{x}$ = 5 µm), pale yellowish, apical cell 2–3(–3.7) µm long ($\bar{x}$ = 2.9 µm), conical, hyaline and smooth-walled, forming three-branched tubular, flexuous, 10–20 µm long apical appendages; basal appendages 5–6 µm long, single, absent at immature state, tubular, unbranched, centric.

Culture characteristics: Colonies on PDA reaching 38–40 mm diam. after one week at room temperature. Colony dense, irregular in shape, flat, slightly raised, surface smooth, with edge undulate, floccose to fluffy, entire margin, forming black stromatic after 2 months; from above, white yellowish to cream at the margin, grey yellowish to dark yellowish, slightly radiated outwards colony, from below, black; not producing pigmentation on agar medium.

Material examined: CHINA, Yunnan Province, Kumming, Kunming Institute of Botany, on dead leaves of *Zea mays* L. (*Poaceae*), 5 November 2015, D.S. Tennakoon, COE002 (KUN-HKAS 102242, **holotype**), ex-type living culture, KUMCC 18-0178.

GenBank numbers: ITS = MK353083, LSU = MK353085, SSU = MK353148, RPB2 = MK492668, TEF1-α = MK492656.

Notes: Phylogenetic analyses of a combined ITS and LSU sequence dataset (Fig. 111) show that *Bartalinia kunmingensis* (KUMCC 18-0178) clusters with *Bartalinia* species and is sister to *B. robillardoides* Tassi (CBS 122705, ex-epitype strain). A comparison of ITS region shows that *B. kunmingensis* is not significant different from *B. robillardoides* (only two differentiated nucleotide bases); however, *B. kunmingensis* is different from *B. robillardoides* in 207/890 bp (23.2%) in RPB2 region. We therefore, identify our isolate as a new species which was found from corn (*Zea mays*) in China. *Bartalinia kunmingensis* differs from *B. robillardoides* (CBS H-21728) in having smaller conidiomata and paler yellowish conidia. (Crous et al. 2014a).

Robillarda Sacc.

The genus *Robillarda* was introduced by Saccardo (1880a) and is typified by *R. sessile* Sacc. This genus contains about 38 species (Crous et al. 2015a). The asexual morph has been reported with its unique characteristics such as solitary or gregarious, separate, subglobose, unicellular, immersed, ostiolate, glabrous pycnidia, holoblastic, ampulliform, hyaline, conidiogenous cells, originating on the inner wall of the pycnidium and ellipsoidal, 1-septate, smooth-walled, hyaline conidia with single branched, apical appendage (Crous et al. 2015a; Borse et al. 2016; Wijayawardene et al. 2016). In this study, the new species, *Robillarda mangiferae* is introduced from leaf blight on mango in Yunnan, China.

Robillarda mangiferae Thiyag., Wanas., Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556210; *Facesoffungi number*: FoF05718, Fig. 113

Etymology: The specific epithet "*mangiferae*" is based on the host genus *Mangifera*, from which the taxon was isolated.

Holotype: KUN-HKAS 102245

Associated with a leaf blight symptom on *Mangifera*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 250–310 µm high, 300–340 µm diam., black, pycnidial, semi-immersed to erumpent, solitary, scattered, irregular in shape, uni-loculate, glabrous, minutely ostiolate, with beak-like papilla. *Conidiomata walls* 8–27 µm wide, thin-walled, of unequal thickness, slightly thick at the sides, composed of two types of cell layers, inner layers comprising hyaline, flattened, pseudoparenchymatous cells of *textura angularis* to *textura prismatica*; outer layers comprising dark brown to black, thick-walled, coriaceous cells, of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–10 × 3–7 µm ($\bar{x}$ = 6.9 × 4.8 µm, n = 30), holoblastic, proliferating percurrently 1–3 times, discrete, subcylindrical to ampulliform, hyaline, aseptate, smooth-walled, arising from the inner cavity. *Conidia* (7.5–)10–11(–12) × (2.5–)3–4(–4.5) µm ($\bar{x}$ = 10.9 × 3.5 µm, n = 50), hyaline, oblong to ellipsoidal, or subfusoid, narrower towards the basal cell, straight, (0–)1-septate, thin and smooth-walled, apical cell developed into a branched appendage; appendages 25–35 × 1–2.5 µm ($\bar{x}$ = 29.3 × 1.7 µm, n = 50), dividing into 2–3 branches, straight, non-

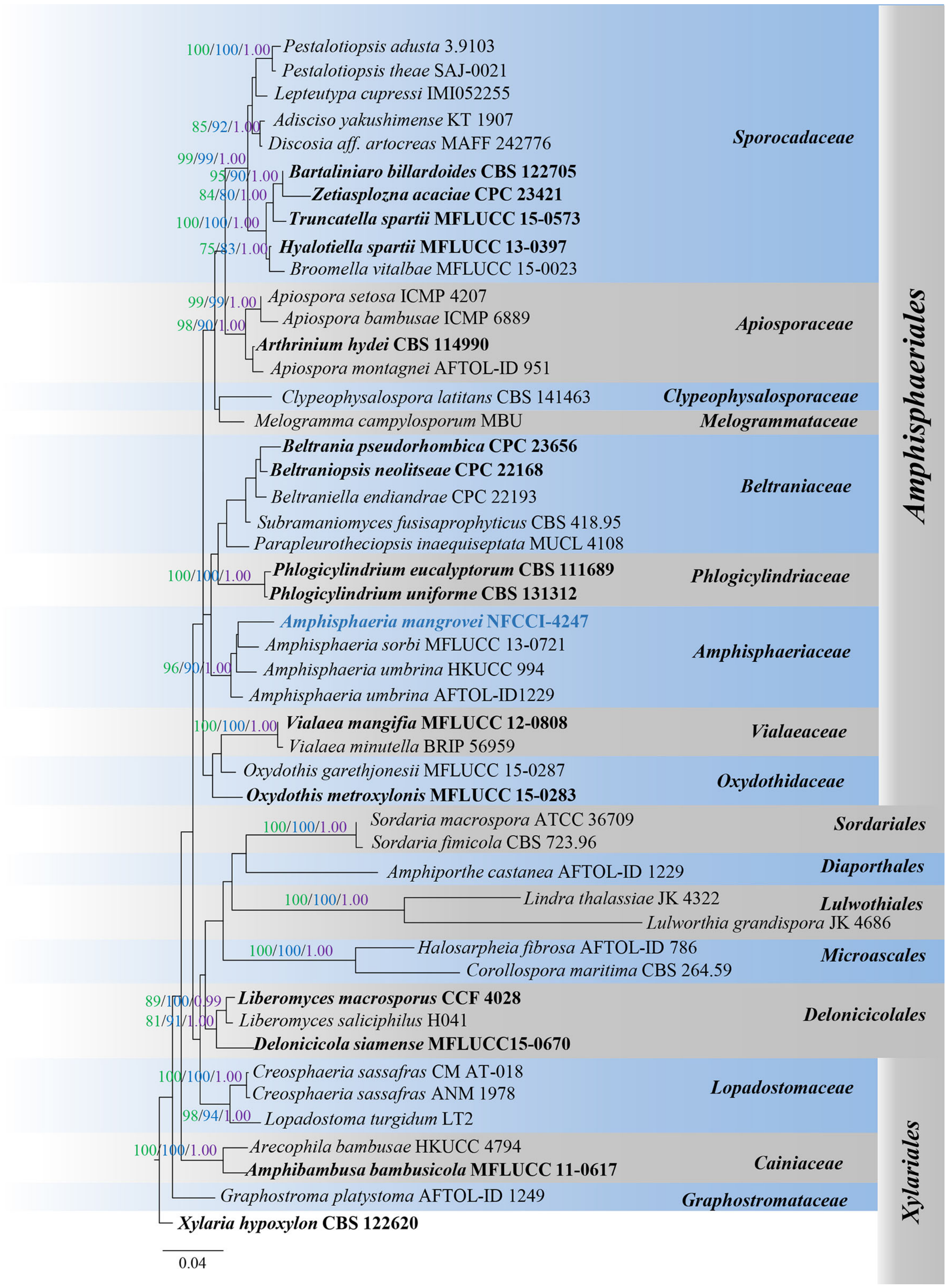


Fig. 109 Phylogram generated from maximum likelihood analysis based on a combined LSU, SSU and ITS gene regions of *Amphisphaeriaceae* and other related taxa. Bootstrap support values for maximum likelihood (green), maximum parsimony (blue) equal to or greater than 75% and the values of Bayesian posterior probabilities (purple) equal to or greater than 0.95 BYPP are given above each branch respectively. The new isolate is in blue. Ex-type strains are in bold. The tree is rooted with *Xylaria hypoxylon* (CBS 122620)

Fig. 110 ***Amphisphaeria mangrovei*** (AMH-9948, **holotype**). **a** Ascomata immersed in intertidal branches and twigs of *Suaeda monoica*. **b, c** Vertical sections of ascomata. **d** Peridium. **e** Paraphyses. **f–i** Immature and mature asci. **j–n** Ascospores. *Scale bars* **b, c** = 50 µm, **d–n** = 10 µm

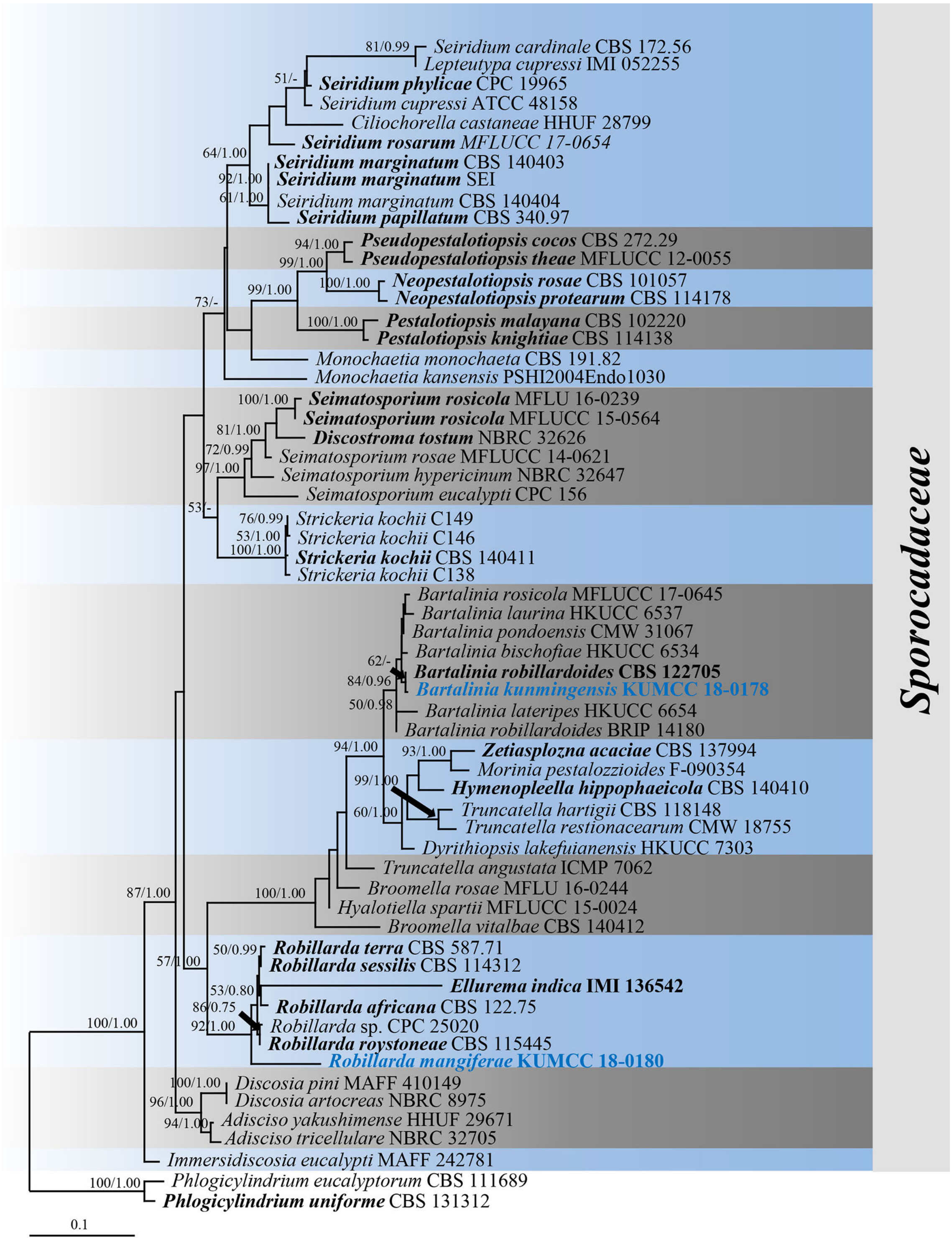


Fig. 111 Phylogram generated from maximum likelihood analysis based on ITS and LSU sequence dataset of the representative species in *Sporocadaceae*. The updated sequence dataset was derived from Wanasinghe et al. (2018). Sixty strains are included in the sequence analyses. *Phlogicylindrium eucalyptorum* (CBS 111689) and *Phlogicylindrium uniforme* (CBS 131312) are used as outgroup taxa. Bootstrap support values for ML equal to or greater than 50% are given above the nodes. Newly generated sequences are in blue. Ex-type strains are indicated in bold

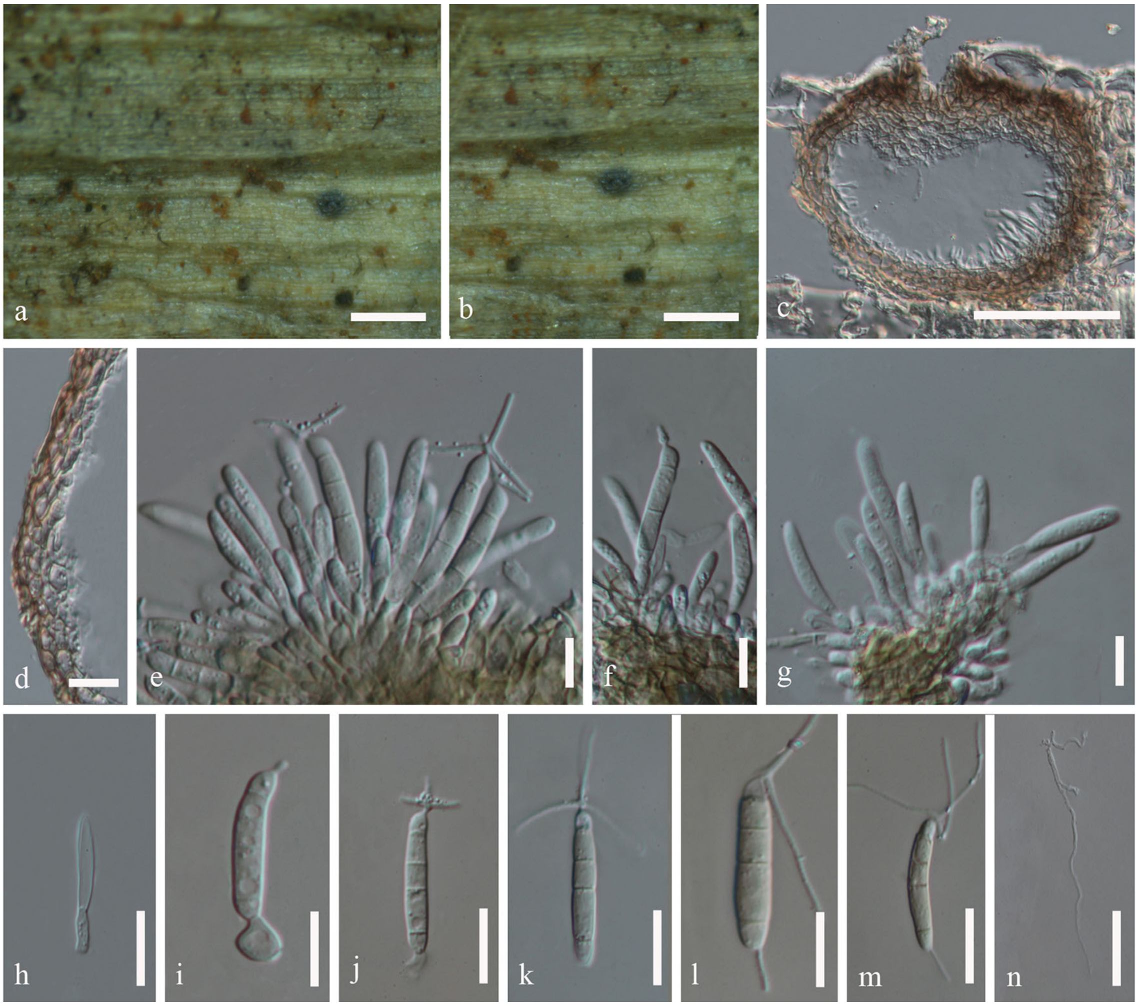


Fig. 112 ***Bartalinia kunmingensis*** (KUN-HKAS 102242, **holotype**). **a, b** Conidiomata on host substrate. **c** Vertical section of conidioma. **d** Conidioma wall. **e–i** Conidiogenous cells with conidia. **j–m** Conidia. **n** Germinating conidium. *Scale bars* **a, b** = 200 µm, **c** = 50 µm, **d–m** = 10 µm, **n** = 20 µm

flexuous, broadly tubular, narrower towards apex, inconspicuously septate at the apex.

Culture characteristics: Colonies on PDA reaching 80–85 mm diam. after 1 week at 20–25 °C, sparse to medium sparse, circular, flat, surface slightly rough with white tufts hyphae, or small granular, edge entire, floccose, forming small, black pycnidia on colony and embedded in media agar after 3 weeks; from above, white-grey to greenish grey, from below, white to cream at the margin, radiated with pale brown to black concentric ring at the middle, white-grey at the centre; not producing pigmentation in agar.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Jinghong, Nabanhe, associated with leaf blight symptom on living leaf of *Mangifera* sp., 21 November 2015, R. Phookamsak, XB011 (KUN-HKAS 102245, **holotype**), ex-type living culture, KUMCC 18-0180.

GenBank numbers: ITS = MK353084, LSU = MK353086, SSU = MK353149.

Notes: *Robillarda mangiferae* resembles *Robillarda* species in having oblong to subfusoid, septate conidia, with an apical cell modified into a branched appendage. However, *R. mangiferae* can be distinguished from other *Robillarda* species by its appendage being straight, non-flexuous, broad tubular and narrower towards the apex, with inconspicuous septa at the apex, as well as its conidiogenous cells being holoblastic and proliferating percurrently. *Robillarda* species have flexuous, narrow tubular, aseptate appendages and holoblastic conidiogenous cells, proliferating sympodially or percurrently near the apex (Crous et al. 2015a; Wijayawardene et al. 2016). Phylogenetic analyses of a combined ITS and LSU sequence dataset show that *R. mangiferae* clusters with other *Robillarda* species and *Ellurema indica* Nag Raj & W.B. Kendr. [current name = *Hyalotiopsis* Punith., proposed by Réblová et al. (2016), and Wijayawardene et al. (2016)] in *Sporocadaceae*, but the species forms a distinct lineage at the base of this clade with moderate support (92% ML and 1.00 BYPP; Fig. 111). *Robillarda mangiferae* differs from *Ellurema indica* in having oblong to ellipsoidal, or subfusoid, (0–)1-septate conidia, with straight, non-flexuous, broadly tubular apical appendages. The asexual morph of *Ellurema indica* (= *Hyalotiopsis*) has cylindrical to fusiform or obclavate conidia, with more than 1-septate and 2–3 apical bi- or tri-furcate, filiform, flexuous appendages (Wijayawardene et al. 2016, 2017a). Based on morphological characteristics and phylogenetic analyses of a combined ITS and LSU sequence dataset (Fig. 111), we hence, introduce a new species, *R. mangiferae* in this study.

Xylariales Nannf.

Diatrypaceae Nitschke

We follow the latest treatment and updated accounts of *Diatrypaceae* in de Almeida et al. (2016), Shang et al. (2017, 2018) and Senwanna et al. (2017). A higher level classification with divergence time estimates for *Diatrypaceae* was provided by Hongsanan et al. (2017) and placed the family in order *Xylariales* (Xylariomycetidae, Sordariomycetes) and a similar scheme is followed in Wijayawardene et al. (2018a). A novel species, *Peroneutypa mangrovei* is introduced in *Diatrypaceae* based on analysis of a combined ITS and TUB2 sequence dataset (Fig. 114), coupled with morphological characteristics. In addition, the new genus *Neoeutypella* is introduced as a monotypic genus to accommodate *N. baoshanensis*. The new genus was collected from dead wood in Baoshan, China. The sexual and asexual morphs are described and illustrated.

Neoeutypella M. Raza, Q.J. Shang, Phookamsak & L. Cai, ***gen. nov.***

Index Fungorum number: IF555373; *Facesoffungi number*: FoF04927

Etymology: The generic epithet "*Neoeutypella*" refers to the taxon resembling *Eutypella*.

Saprobic on dead wood of *Pinus armandii*. **Sexual morph** *Ascostromata* entostromatic, carbonaceous, visible as black, solitary to gregarious, globose to long irregular in shape on host surface, erumpent through host epidermis, producing yellow pigments surrounding ascostroma. *Ascomata* perithecial, black, immersed to semi-immersed in stromatic tissues, aggregated, globose or subglobose, ostiolate, papillate, slightly conspicuous, with periphyses. *Peridium* thickened unequally, two-layered, outer layer comprising 5–7 layers of thick-walled, hyaline to dark brown cells of *textura angularis*, inner layer comprising 3–5 layers of thin-walled, hyaline to brown cells of *textura prismatica*. *Hamathecium* comprising aseptate, filamentous paraphyses, tapering toward the apex, embedded in hyaline gelatinous matrix. *Asci* 8-spored, unitunicate, spindle-shaped, long pedicellate, apically rounded with refractive cytoplasmic strands, amyloid, with a J + , subapical ring. *Ascospores* overlapping 1–3-seriate, allantoid, slightly or moderately curved, initially hyaline, becoming pale brown at maturity, aseptate, mostly with small 1–2 guttules. **Asexual morph** *Hyphae* branched, smooth, hyaline, septate. *Conidiophores* long, branched, with phialides, mononematous, macronematous, hyaline. *Conidiogenous cells* smooth-walled, hyaline, holoblastic, discrete, phialidic, doliiform, ampulliform or irregular in shape. *Conidia* filiform, solitary, aseptate, smooth-walled, unbranched, hyaline to pale yellow.

Type species: *Neoeutypella baoshanensis* M. Raza, Q.J. Shang, Phookamsak & L. Cai

Notes: *Neoeutypella* resembles *Eutypella* (Nitschke) Sacc. in forming large entostroma, 8-spored, spindle-shaped asci and allantoid ascospores, with a libertella-like asexual morph. Phylogenetic analyses of maximum likelihood, maximum parsimony and Bayesian inference based on the combined ITS and TUB2 sequence dataset (Fig. 114) show that *Neoeutypella baoshanensis* groups with *Eutypella caricae* (De Not.) Berl. (strains EL51C and GL08362). Sequences of these two strains are available in GenBank, but no morphological description is available for comparative studies. The two *Eutypella caricae* strains and *Neoeutypella* form a distinct lineage from *Eutypella sensu stricto*. Acero et al. (2004) mentioned that these two strains might have been misidentified and a taxonomic revision of these species is needed. *Eutypella caricae* and *Neoeutypella* are phylogenetically closely related to *Diatrypella banksiae* Crous which produced an asexual morph (Crous et al. 2016a). Nevertheless, *Neoeutypella* can be differentiated from *D. banksiae* in shape and size of conidia. *Neoeutypella baoshanensis* (see below) has filiform conidia [(16.5–)25–37(–40) × 1.2–1.9 μm], whereas *Diatrypella banksiae* has spindle-shaped conidia [(25–)27–30(–35) × 1.5(–2) μm] (Crous et al. 2016a).

Based on morphological comparison of our new taxon and *Eutypella caricae* described by Saccardo (1882) and Berlese (1902), *Neoeutypella baoshanensis* (99% similarity in ITS, 90% similarity in TUB2) differs from *Eutypella caricae* in having larger asci (*N. baoshanensis*, (45–)52–110(–125) × (19–)26–37(–40) versus 35–45 × 6–7, *E. caricae*) and ascospores (*N. baoshanensis*, (30–)35–43(–50) × (8–)9–11(–12) versus 9–11 × 2.5–3, *E. caricae*) (Saccardo 1882; Berlese 1902). *Neoeutypella baoshanensis* has spindle-shaped asci and pale yellowish to pale brown ascospores, whereas *E. caricae* has clavate asci and hyaline ascospores (Saccardo 1882; Berlese 1902). Based on phylogenetic support coupled with morphological differences,

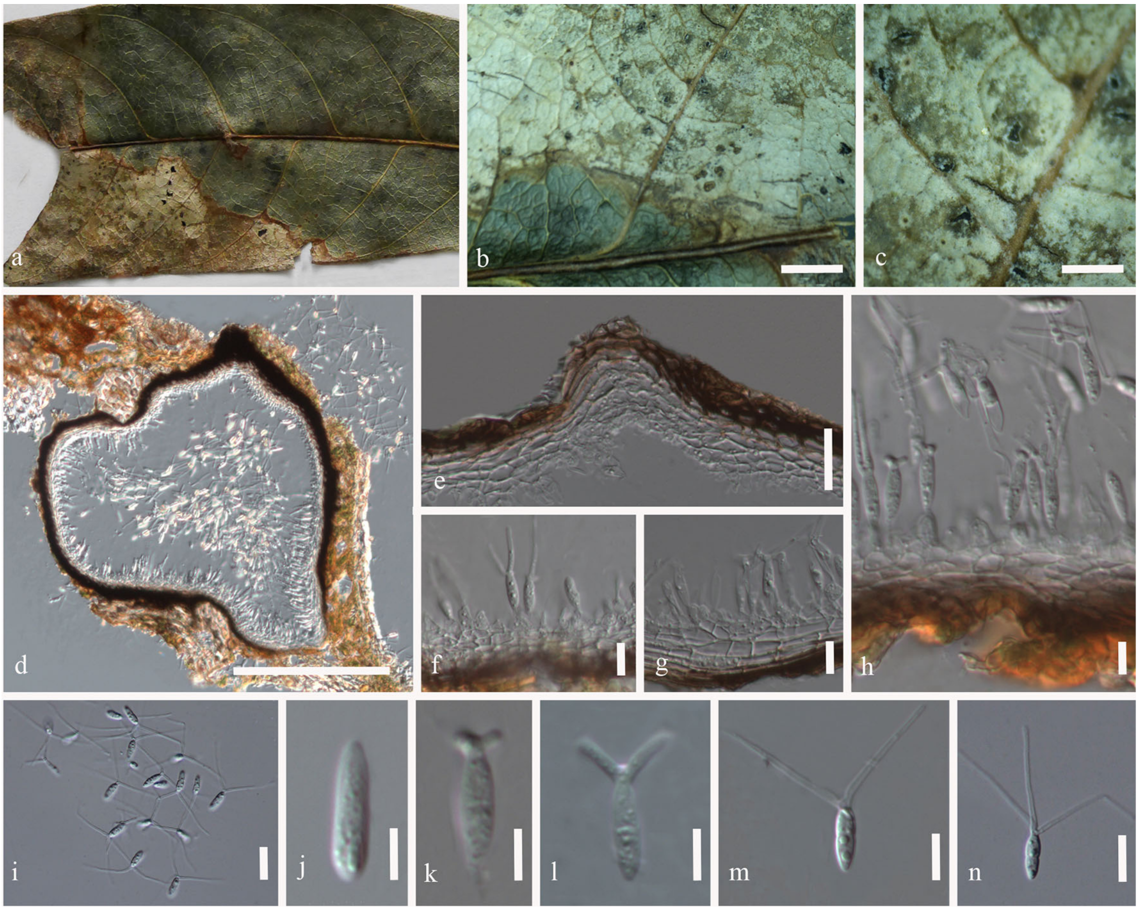


Fig. 113 ***Robillarda mangiferae*** (KUN-HKAS 102245, **holotype**). **a** Substrate showing disease symptoms. **b, c** Conidiomata on substrate. **d** Section through conidioma. **e** Conidioma wall. **f–h** Conidiogenous cells attached to conidia. **i–n** Conidia. *Scale bars* **b–d** = 100 μm, **e–h, i, m, n** = 10 μm, **j–l** = 5 μm

we therefore introduce our isolate as a new species in the new genus *Neoeutypella*.

Neoeutypella baoshanensis M. Raza, Q.J. Shang, Phookamsak & L. Cai, ***sp. nov.***

Index Fungorum number: IF555372; *Facesoffungi number*: FoF04928, Fig. 115

Etymology: The specific epithet "*baoshanensis*" refers to the locality Baoshan (Yunnan, China), where the holotype was collected.

Holotype: HMAS 255436

Saprobic on dead wood of *Pinus armandii*. **Sexual morph** *Ascostromata* 650–1100 μm diam., entostromatic, carbonaceous, black, solitary to gregarious, globose to long irregular in shape on host surface, erumpent through host epidermis, producing yellow pigments surrounding ascostroma. *Ascomata* perithecial, 500–770 high, 450–530 diam., black, immersed to semi-immersed in stromatic tissues, aggregated, globose or subglobose, ostiolate, papillate, slightly conspicuous, with periphyses. *Peridium* 145–250 wide, thickened unequally, two-layered, outer layer comprising 5–7 layers of thick-walled, hyaline to dark brown cells of *textura angularis*, inner layer comprising 3–5 layers of thin-walled, hyaline to brown cells of *textura prismatica*. *Hamathecium* 3–7 μm wide ($\bar{x}$ = 4.7 μm, n = 20), comprising aseptate, filamentous paraphyses, tapering towards the apex, embedded in hyaline gelatinous matrix. *Asci* (60–)75–85(–90) × (5.5–)6.5–7.5(–8) μm ($\bar{x}$ = 77.5 × 8 μm, n = 25), 8-spored, unitunicate, spindle-shaped, long pedicellate, apically rounded with refractive cytoplasmic strands, amyloid, with a J +, subapical ring. *Ascospores* (8.5–)10–11.5(–13) × (2–)2.3–2.5(–3) μm ($\bar{x}$ = 10.8 × 2.4 μm, n = 50), overlapping 1–3-seriate, initially hyaline, becoming pale brown at maturity, allantoid, slightly or moderately curved, aseptate, mostly with 1–2 small guttules. **Asexual morph** *Hyphae* branched, smooth, hyaline, septate, 1.5–3.5 μm diam. *Conidiophores* long, branched, with phialides, mononematous, macronematous, hyaline. *Conidiogenous cells* (12–)14–35.5(–40) × 4–13(–15) μm ($\bar{x}$ = 25 × 8.5 μm, n = 20), smooth-walled, hyaline, holoblastic, discrete, phialidic, doliiform, ampulliform or irregular in shape. *Conidia* (16.5–)25–37(–40) × 1.2–1.9 μm ($\bar{x}$ = 29 × 1.5 μm, n = 50), filiform, solitary, aseptate, smooth-walled, unbranched, hyaline to pale yellow.

Culture characteristics: Colonies on PDA reaching 6.5–7 mm diam. after 1 week at 25 ± 2 °C, circular, flat, slightly raised, surface dull with edge undulate, filamentous at the margin; from above, white with cotton consistency; from below, pale yellow and not producing pigment in PDA medium. Asexual morph produced on PDA after 3 weeks and colony becomes black from below.

Material examined: CHINA, Yunnan Province, Baoshan City, Longling County, on dead wood of *Pinus armandii* Franch. (*Pinaceae*), October 2015, M. Raza, HMAS 255436 (**holotype**), ex-type living culture, LC 12111.

GenBank numbers: ITS = MH822887, TUB2 = MH822888.

Peroneutypa Berl.

We follow the latest treatment and updated accounts of *Peroneutypa* in Senwanna et al. (2017) and Shang et al. (2018).

Peroneutypa mangrovei Devadatha & V.V. Sarma, ***sp. nov.***

Index Fungorum number: IF554285; *Facesoffungi number*: FoF04271, Fig. 116

Etymology: Specific epithet in reference to the habitat.

Holotype: AMH-9944

Saprobic on decaying wood of *Avicennia marina*. **Sexual morph** *Ascostromata* absent or poorly developed between perithecial necks, perithecia solitary to gregarious, up to four in groups, dark brown to black, immersed becoming raised to erumpent through the host tissue with median necks. *Ascomata* 250–525 µm high, 100–330 µm diam. ($\bar{x}$ = 375 × 202 µm, n = 10), erumpent to immersed, globose to subglobose, gregarious to solitary, ostiolate, with short beaks, periphysate, brown to black. *Ostiolar canals* 50–85 µm wide ($\bar{x}$ = 67 µm, n = 5), with moderate neck length 100–350 µm ($\bar{x}$ = 231 µm, n = 5), cylindrical, straight, dark brown to black. *Periphyses* filamentous, short, 0.5–2 µm wide ($\bar{x}$ = 1.5 µm, n = 10). *Peridium* 15–35 µm wide ($\bar{x}$ = 22 µm, n = 10), comprising two layers, inner stratum with many layers of hyaline cells of *textura angularis* and outer stratum with 2–3 layers of light brown to black cells of *textura angularis*. *Hamathecium* composed of numerous, 1–2 µm ($\bar{x}$ = 1 µm, n = 20) wide, filamentous, septate paraphyses, longer than asci, embedded in a gelatinous matrix. *Asci* 14–20 × 3–4 µm ($\bar{x}$ = 17 × 3.5 µm, n = 20), 8-spored, unitunicate, cylindrical to clavate, short pedicellate, apically rounded to truncate, with a J-, apical ring. *Ascospores* 3–5 × 1–1.5 µm ($\bar{x}$ = 4 × 1 µm, n = 30), overlapping 1–3-seriate, hyaline to pale yellow, straight to allantoid, aseptate, smooth-walled, lacking guttules, light brown in mass. **Asexual morph** Undetermined.

Culture characteristics: Colonies on MEA reaching 50–80 mm diam. after 15 days of incubation at room temperature, initially white, becoming light grey at maturity, reverse light yellow, cottony, punctiform, flat, circular, entire.

Material examined: INDIA, Puducherry, Thengaithittu mangroves (11.5°N 79.5°E), on decaying wood of *Avicennia marina* (Forssk.) Vierh. (*Acanthaceae*), 12 March 2016, B. Devadatha (AMH-9944, **holotype**), ex-type living culture, NFCCI-4246.

GenBank numbers: ITS = MG844286, LSU = MG844278, SSU = MG844282, TUB2 = MG844282.

Notes: Peroneutypa mangrovei shares similar morphological characters such as J-, apical ring asci, overlapping ascospores dimensions with *P. diminutispora* D.A.C. Almeida et al. (de Almeida et al. 2016). However, it differs in having perithecia single or in groups of up to four, shorter ascomata and ostiole, longer asci (14–20 × 3–4 µm) and its exclusive occurrence in marine habitat. *Peroneutypa diminutispora* has perithecia arranged in a single layer, occurring singly or in groups of up to seven, shorter asci (8–14 × 3.5–5 µm) that are urn-shaped (de Almeida et al. 2016). *Peroneutypa cosmosa* (Speg.) Carmarán & A.I. Romero has larger asci (18–25 × 5–7 µm) with J+, apical rings and longer ascospores (6–8 µm) (Carmarán et al. 2006). *Peroneutypa longiasca* Senwanna et al. and *P. mackenziei* Q.J. Shang et al. have longer ascospores (5–7 µm) (Senwanna et al. 2017; Shang et al. 2017). This is the first report of *Peroneutypa* species from a marine habitat (Jones et al. 2015). ITS and TUB2 gene phylogeny also supports *P. mangrovei* as distinct forming an independent lineage, sister to *Eutypa microasca* E. Grassi & Carmarán, and cluster with *Peroneutypa diminutispora* and *P. cosmosa* (Fig. 114). A comparison of ITS nucleotides between *P. mangrovei* and *P. dimunitispora* (GenBank no. KM396647) results in 7.4% (47 nucleotides) and 5.5% (26 nucleotides) along with *P. cosmosa* (GenBank no. KF964568).

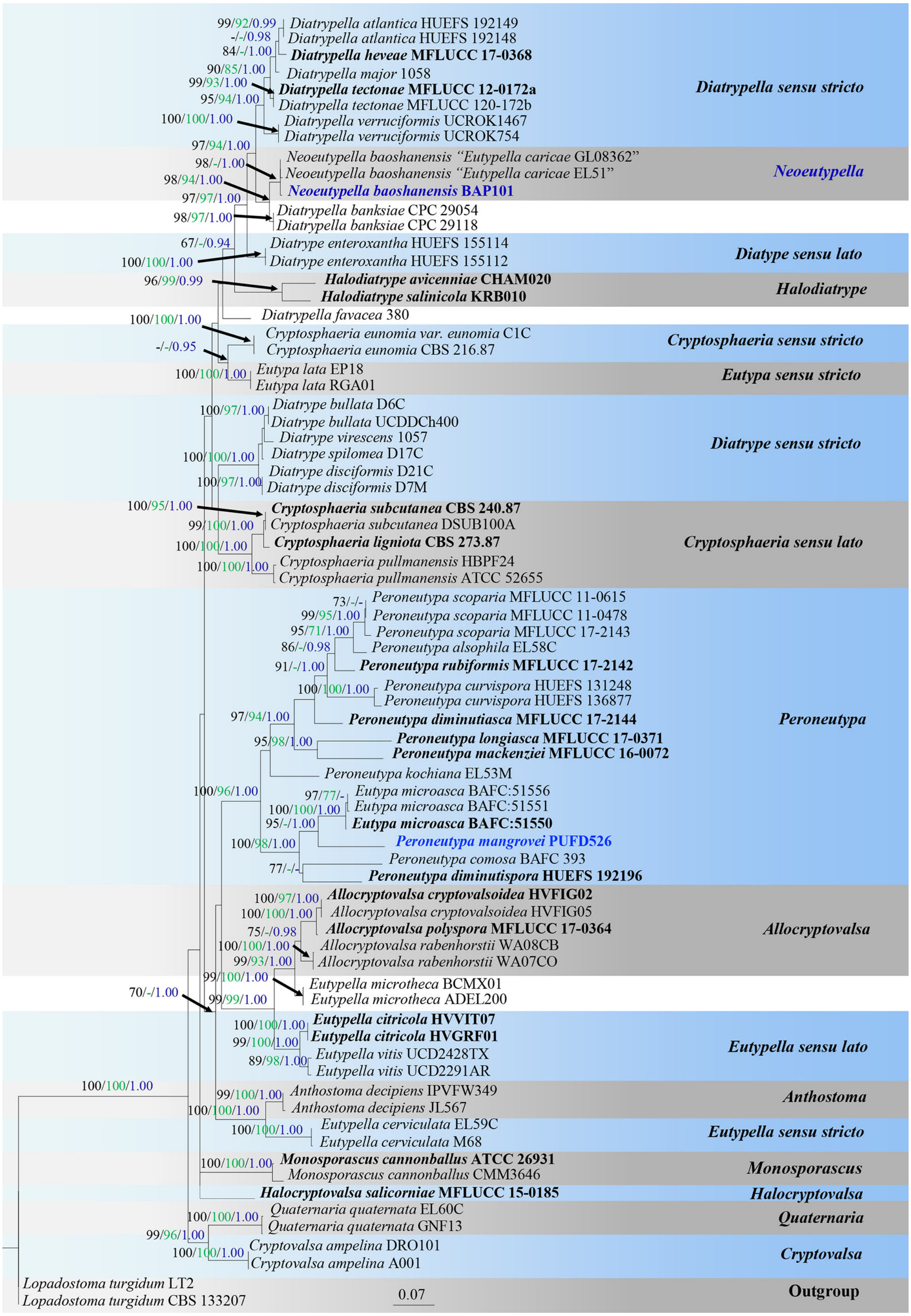
Hypoxylaceae DC.

We follow the latest treatment and updated accounts of *Hypoxylaceae* in Daranagama et al. (2018) and Wendt et al. (2018).

Hypoxylon Bull.

Hypoxylon is the largest genus in *Hypoxylaceae* with over 140 accepted species classified on the basis of morphology, phylogeny and chemotaxonomy (Kuhnert et al. 2014; Wijayawardene et al. 2017a). More than 1000 epithets are listed in Index Fungorum (2019). We introduce a new species *Hypoxylon teeravasati* based on morphology and multigene analysis (Fig. 117).

Hypoxylon teeravasati Devadatha, V.V Sarma & E.B.G Jones, ***sp. nov.***


Diatrypella atlantica HUEFS 192149
Diatrypella atlantica HUEFS 192148
Diatrypella heveae MFLUCC 17-0368
Diatrypella major 1058
Diatrypella tectonae MFLUCC 12-0172a
Diatrypella tectonae MFLUCC 120-172b
Diatrypella verruciformis UCROK1467
Diatrypella verruciformis UCROK754
Diatrypella sensu stricto
Neoeutypella baoshanensis "Eutypella caricae GL08362"
Neoeutypella baoshanensis "Eutypella caricae EL51"
Neoeutypella baoshanensis BAP101
Neoeutypella
Diatrypella banksiae CPC 29054
Diatrypella banksiae CPC 29118
Diatrype enteroxantha HUEFS 155114
Diatrype enteroxantha HUEFS 155112
Diatype sensu lato
Halodiatrype avicenniae CHAM020
Halodiatrype salinicola KRB010
Halodiatrype
Diatrypella favacea 380
Cryptosphaeria eunomia var. eunomia C1C
Cryptosphaeria eunomia CBS 216.87
Cryptosphaeria sensu stricto
Eutypa lata EP18
Eutypa lata RGA01
Eutypa sensu stricto
Diatrype bullata D6C
Diatrype bullata UCDDCh400
Diatrype virescens 1057
Diatrype spilomea D17C
Diatrype disciformis D21C
Diatrype disciformis D7M
Diatrype sensu stricto
Cryptosphaeria subcutanea CBS 240.87
Cryptosphaeria subcutanea DSUB100A
Cryptosphaeria ligniota CBS 273.87
Cryptosphaeria pullmanensis HBPF24
Cryptosphaeria pullmanensis ATCC 52655
Cryptosphaeria sensu lato
Peroneutypa scoparia MFLUCC 11-0615
Peroneutypa scoparia MFLUCC 11-0478
Peroneutypa scoparia MFLUCC 17-2143
Peroneutypa alsophila EL58C
Peroneutypa rubiformis MFLUCC 17-2142
Peroneutypa curvispora HUEFS 131248
Peroneutypa curvispora HUEFS 136877
Peroneutypa diminutiasca MFLUCC 17-2144
Peroneutypa longiasca MFLUCC 17-0371
Peroneutypa mackenziei MFLUCC 16-0072
Peroneutypa kochiana EL53M
Eutypa microasca BAFC:51556
Eutypa microasca BAFC:51551
Eutypa microasca BAFC:51550
Peroneutypa mangrovei PUFD526
Peroneutypa comosa BAFC 393
Peroneutypa diminutispora HUEFS 192196
Peroneutypa
Allocryptovalsa cryptovalsoidea HVFIG02
Allocryptovalsa cryptovalsoidea HVFIG05
Allocryptovalsa polyspora MFLUCC 17-0364
Allocryptovalsa rabenhorstii WA08CB
Allocryptovalsa rabenhorstii WA07CO
Allocryptovalsa
Eutypella microtheca BCMX01
Eutypella microtheca ADEL200
Eutypella citricola HVVIT07
Eutypella citricola HVGRF01
Eutypella vitis UCD2428TX
Eutypella vitis UCD2291AR
Eutypella sensu lato
Anthostoma decipiens IPVFW349
Anthostoma decipiens JL567
Anthostoma
Eutypella cerviculata EL59C
Eutypella cerviculata M68
Eutypella sensu stricto
Monosporascus cannonballus ATCC 26931
Monosporascus cannonballus CMM3646
Monosporascus
Halocryptovalsa salicorniae MFLUCC 15-0185
Halocryptovalsa
Quaternaria quaternata EL60C
Quaternaria quaternata GNF13
Quaternaria
Cryptovalsa ampelina DRO101
Cryptovalsa ampelina A001
Cryptovalsa
Lopadostoma turgidum LT2
Lopadostoma turgidum CBS 133207
0.07
Outgroup

◀**Fig. 114** Phylogram generated from maximum likelihood, maximum parsimony and Bayesian inference analyses based on a combined ITS and TUB2 sequence dataset of diatrypaceous species. Bootstrap support values for maximum likelihood (black) and maximum parsimony (green) equal to or greater than 60% and Bayesian posterior probabilities (blue) equal to or greater than 0.95 BYPP are shown above the nodes. The new isolates are in blue and ex-type strains are in bold. The tree is rooted to *Lopadostoma turgidum* (LT2 and CBS 133207)

Index Fungorum number: IF554278; *Facesoffungi number*: FoF04272, Fig. 118

Etymology: The specific epithet "*teeravasati*" in Sanskrit, refers to the coastal environment where the fungus thrives

Holotype: AMH-9906

Colour codes follow: A mycological colour chart (Rayner 1970).

Saprobic on decaying wood of mangrove trees. **Sexual morph** *Ascostromata* 310–770 × 400–655 µm diam. ($\bar{x}$ = 533 × 498 µm, n = 10), glomerate to hemispherical, effuse-pulvinate, connected to each other by thick stromatal tissue at the base, with very conspicuous perithecial mounds, surface burnt sienna (plate 7, D8), with KOH extractable pigments eye brown (plate 7, F6), the tissue below the perithecial layer inconspicuous. *Perithecia* 300–650 µm diam. ($\bar{x}$ = 442 µm, n = 10), immersed, sphaerical. *Ostioles* papillate, without apparent disk formation. *Peridium* 45–100 µm ($\bar{x}$ = 68 µm, n = 10), comprising several layers of *textura angularis* and outer layer of pseudoparenchyma. *Hamathecium* composed of 1–3 µm

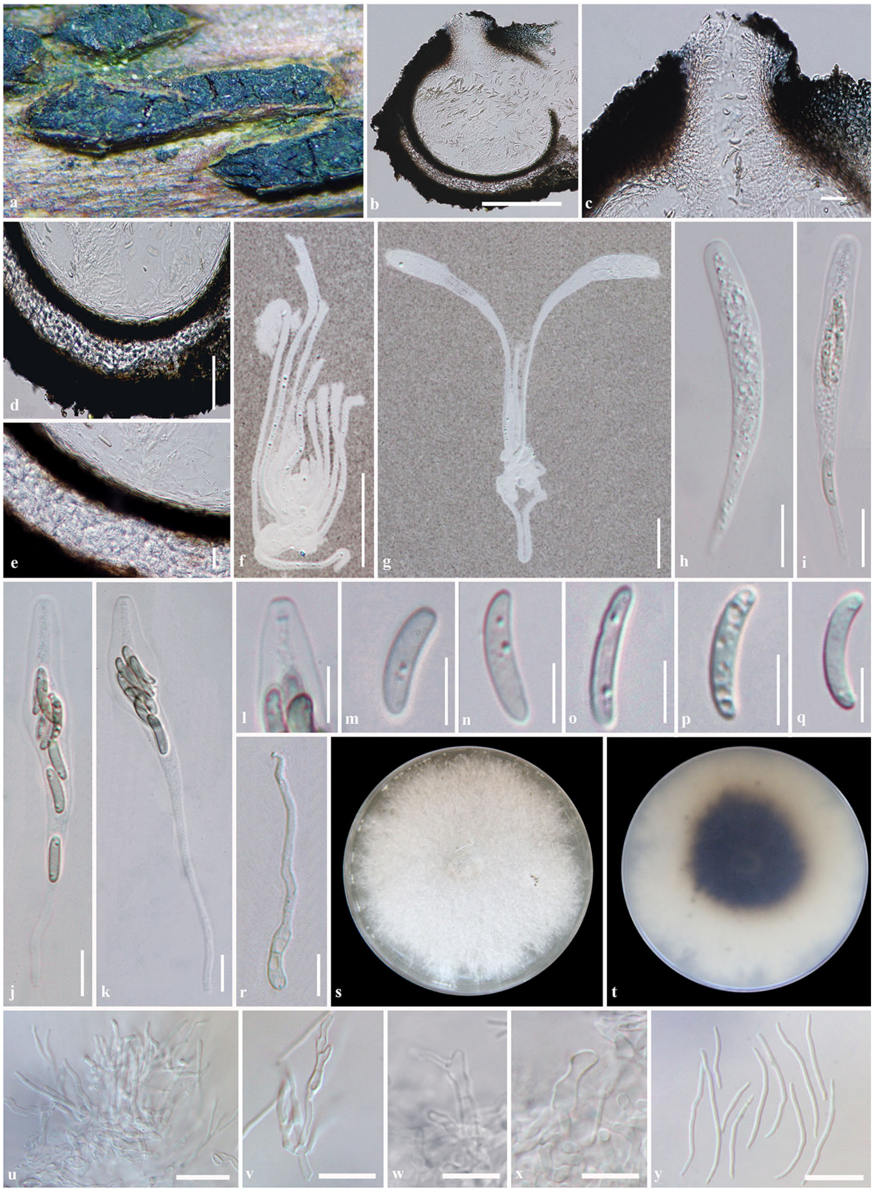


Fig. 115 ***Neoeutypella baoshanensis*** (HMAS 255436, **holotype**). **a** Blackish ascostromata surrounded by yellow pigments on *Pinus armandii*. **b** Vertical section of ascostroma. **c** Ostiole. **d, e** Peridial structure. **f** Paraphyses stained with Indian ink. **g** Asci attached with paraphyses stained with Indian ink. **h** Immature ascus. **i–k** Mature asci. **l** J+, apical ring stained with Melzer's reagent. **m–q** Ascospores. **r** Germinated ascospore. **s, t** Culture characteristics on PDA (**s** = from above, **t** = from below). **u** Conidiogenous cells with conidia. **v** Phialides with young developing conidia. **w, x** Conidiogenous cells. **y** Conidia. *Scale bars* **b** = 1000 µm, **c, d** = 50 µm, **e–g** = 20 µm, **h–k, r, u, y** = 10 µm, **l–q** = 5 µm

diam., hyaline, aseptate and filiform paraphyses, longer than asci. *Asci* 65–160 × 7–13 µm ($\bar{x}$ = 105 × 8.2 µm, n = 20), 8-spored, unitunicate, cylindrical, pedicellate, with apical ring bluing in Lugol's solution, discoid, 1–2.5 × 2–3.5 µm ($\bar{x}$ = 1.9 × 3.1 µm, n = 20). *Ascospores* 9–15 × 4–7 µm ($\bar{x}$ = 11.7 × 7.6 µm, n = 30), 1-seriate, unicellular, ellipsoid-inequilateral, with narrowly rounded ends, brown to dark brown, with a straight germ slit more or less running the entire spore-length, perispore dehiscent in 10% KOH, epispore smooth. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on SWA within 24 h, germ tubes arising from terminal ends of the ascospore. Colonies on MEA at room temperature reaching 45–60 mm diam. within 25 days, honey yellow at centre and olive buff at margin, reverse clove brown with yellow exudates and dawn grey at margin, honey yellow diffusible pigments, filiform, umbonate, circular and velvety.

Material examined: INDIA, Tamil Nadu, Tiruvarur, Muthupet mangroves (10.4°N 79.5°E), on decaying wood of *Avicennia marina* (*Acanthaceae*), 28 November 2015, B. Devadatha, AMH-9906 (**holotype**), ex-type living culture, NFCCI-4216; *ibid.* on decaying branches and twigs of *Suaeda monoica* Forssk. ex J.F. Gmel, PUFD4 (**paratype** at Pondicherry University, Puducherry).

GenBank numbers: ITS = KY863509, LSU = MF385274, SSU = MF385273, RPB2 = MG986895, TEF1-α = MF182401, TUB2 = MG986894.

Notes: Multigene analysis shows that *Hypoxylon teeravasati* shares a strongly supported sister relationship with *H. jaklitschii* Sir & Kuhnert and *H. lenormandii* Berk. & M.A. Curtis as a basal taxon. All three taxa constitute a single monophyletic clade with high support (Fig. 117), but their relationships with other *Hypoxylon* species are not well-resolved. We found distinct nucleotide base pair differences between *H. teeravasati* and *H. jaklitschii* across ITS and TUB2 genes [36 within ITS and 23 within TUB2] which is in agreement with guidelines by Jeewon and Hyde (2016) to establish new species. *Hypoxylon teeravasati*, *H. lenormandii*, *H. jaklitschii* and *H. croceum* J.H. Mill. share similar stromatal characters and overlapping asci dimensions. However, *H. teeravasati* can be easily distinguished from *H. lenormandii*, *H. jaklitschii* and *H. croceum* in having a burnt sienna surface, with KOH extractable pigments eye brown and larger perithecia. *Hypoxylon lenormandii* has surface greyish sepia, fuscous, or brown vinaceous, dull orange brown to dark brown granules beneath and between perithecia, with KOH extractable pigments hazel, fulvous, umber or ochreous (Kuhnert et al. 2015; Liu et al. 2015a). *Hypoxylon jaklitschii* has a sepia to dark brick surface, pruinose, with orange brown or dark brown granules immediately beneath the surface and between perithecia, with KOH extractable pigment umber or dark brick and smaller ascospores (9.5–12 × 4–5.5 versus 9–15 × 4–7) (Kuhnert et al. 2015). *Hypoxylon croceum* is distinguished from *H. teeravasati* in having an initially sepia or fuscous surface, becoming dark brown at maturity and abelline or hazel KOH extractable pigments (Miller 1933). *Hypoxylon croceum* is the only report of *Hypoxylon* species from a marine habitat (Jones et al. 2015). *Hypoxylon teeravasati* is saprobic on decaying branches and twigs of *Avicennia marina* and *Suaeda monoica*, exclusively from marine environments. *Hypoxylon lenormandii* and *H. jaklitschii* have been reported from terrestrial habitats.

Phylum Basidiomycota R.T. Moore

We follow the latest treatment of Basidiomycota in Zhao et al. (2017).

Class Agaricomycetes Doweld

The classifications of the families in Agaricomycetes herein follow Hibbett et al. (2014) and Zhao et al. (2017). The subclasses, orders and families of Agaricomycetes are listed in alphabetical order.

Subclass Agaricomycetidae Parmasto

Agaricales Underw.

Agaricaceae Chevall.

We follow the latest treatments and updated accounts of *Agaricaceae* in Zhao et al. (2016), Zhou et al. (2016) and Hyde et al. (2017). Three specimens were collected and preliminary BLAST using ITS sequence data indicated that two taxa belong to *Agaricus* sect. *Xanthodermatei* and the third to *Coprinus*. Based on distinctive morphological characteristics and phylogenetic support, two novel species of *Agaricus* sect. *Xanthodermatei* as well as *Coprinus trigonosporus* sp. nov. are introduced in this study. An updated phylogenetic tree based on maximum likelihood and Bayesian inference analyses also confirms their placement (Fig. 119).

Agaricus L.: Fr.

We follow the latest treatment and updated accounts of *Agaricus* in Thongklang et al. (2014), Karunarathna et al. (2016), Zhao et al. (2016) and Zhou et al. (2016). Detailed taxonomic revision of taxa in *Agaricus* sect. *Xanthodermatei* was discussed by Chen et al. (2016), Kerrigan (2016), Mahdizadeh et al. (2016), Zhao et al. (2016) and Parra et al. (2018).

Agaricus memnonius M.Q. He & R.L. Zhao, ***sp. nov.***

Fungal names: FN570535; *Faceoffungi number*: FoF03940, Fig. 120

Etymology: The Latin epithet "*memnonius*" meaning "brown-black" refers to the colour of the pileus surface.

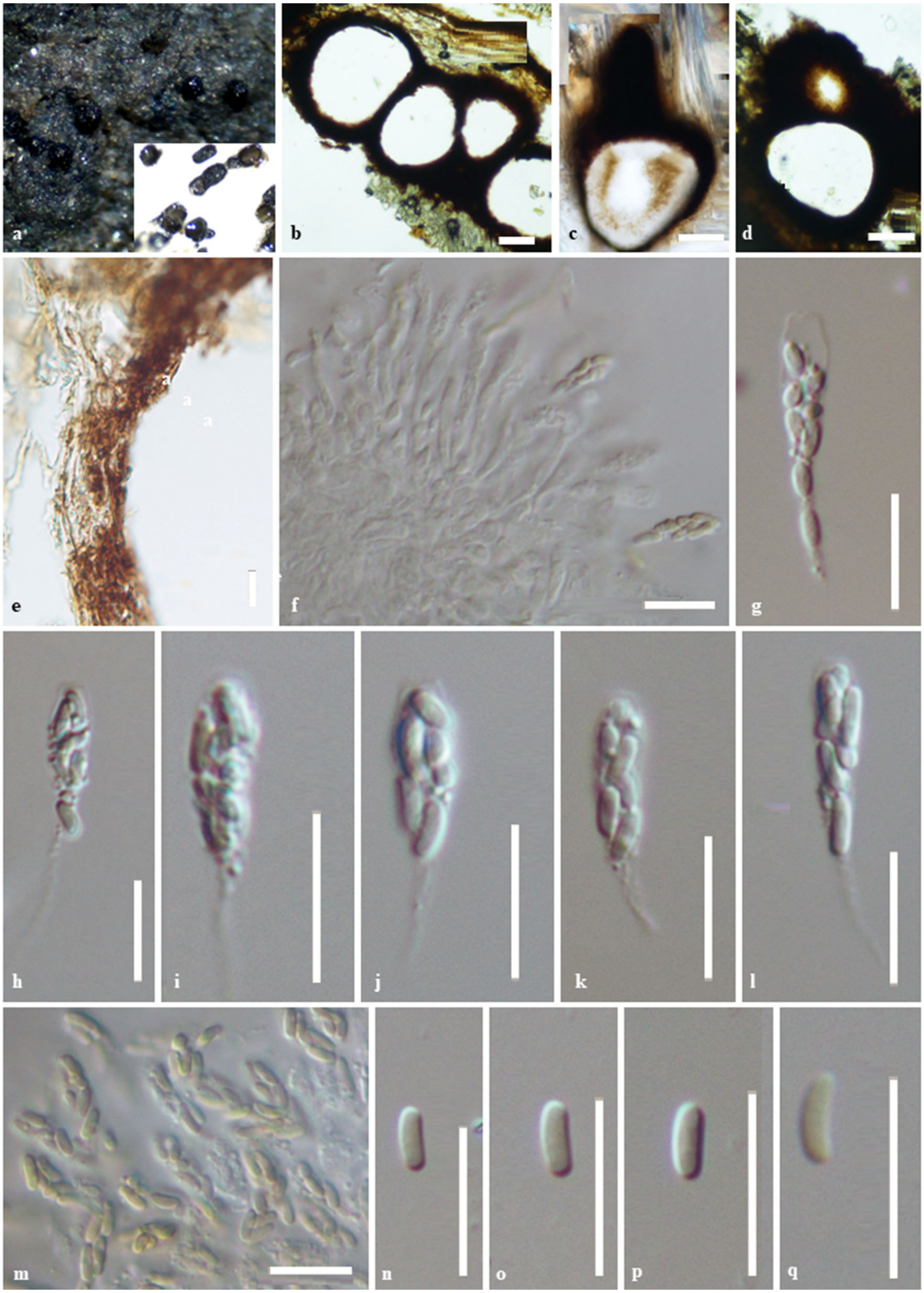


Fig. 116 ***Peroneutypa mangrovei*** (AMH-9944, **holotype**). **a** Ascomata semi-immersed in the decaying wood of *Avicennia marina*. **b–d** Longitudinal sections of ascoma. **e** Section through peridium. **f** Paraphyses interspersed with asci. **g–l** Immature and mature asci. **m–q** Ascospores. *Scale bars* **b–d** = 100 µm, **e–q** = 10 µm

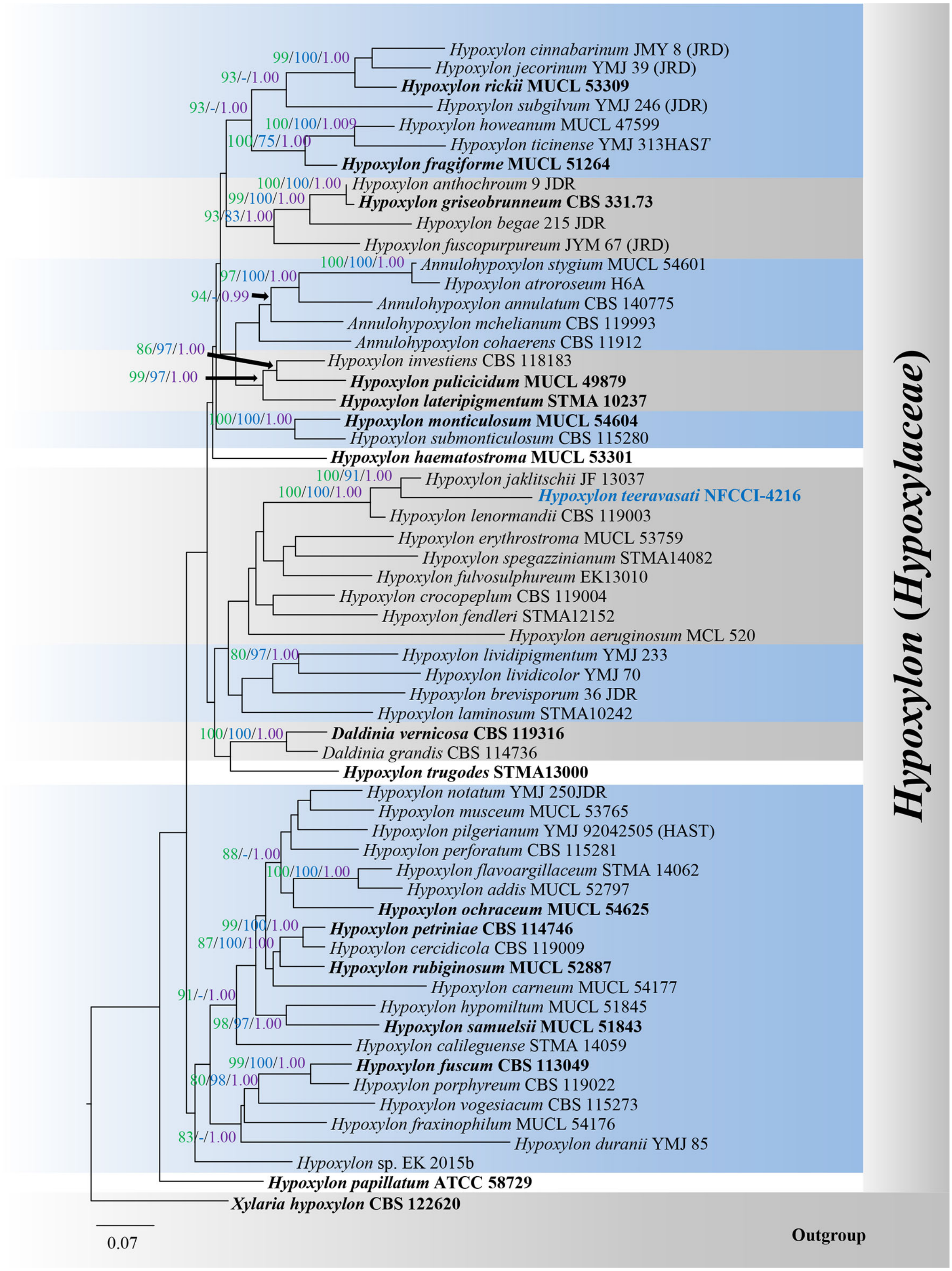
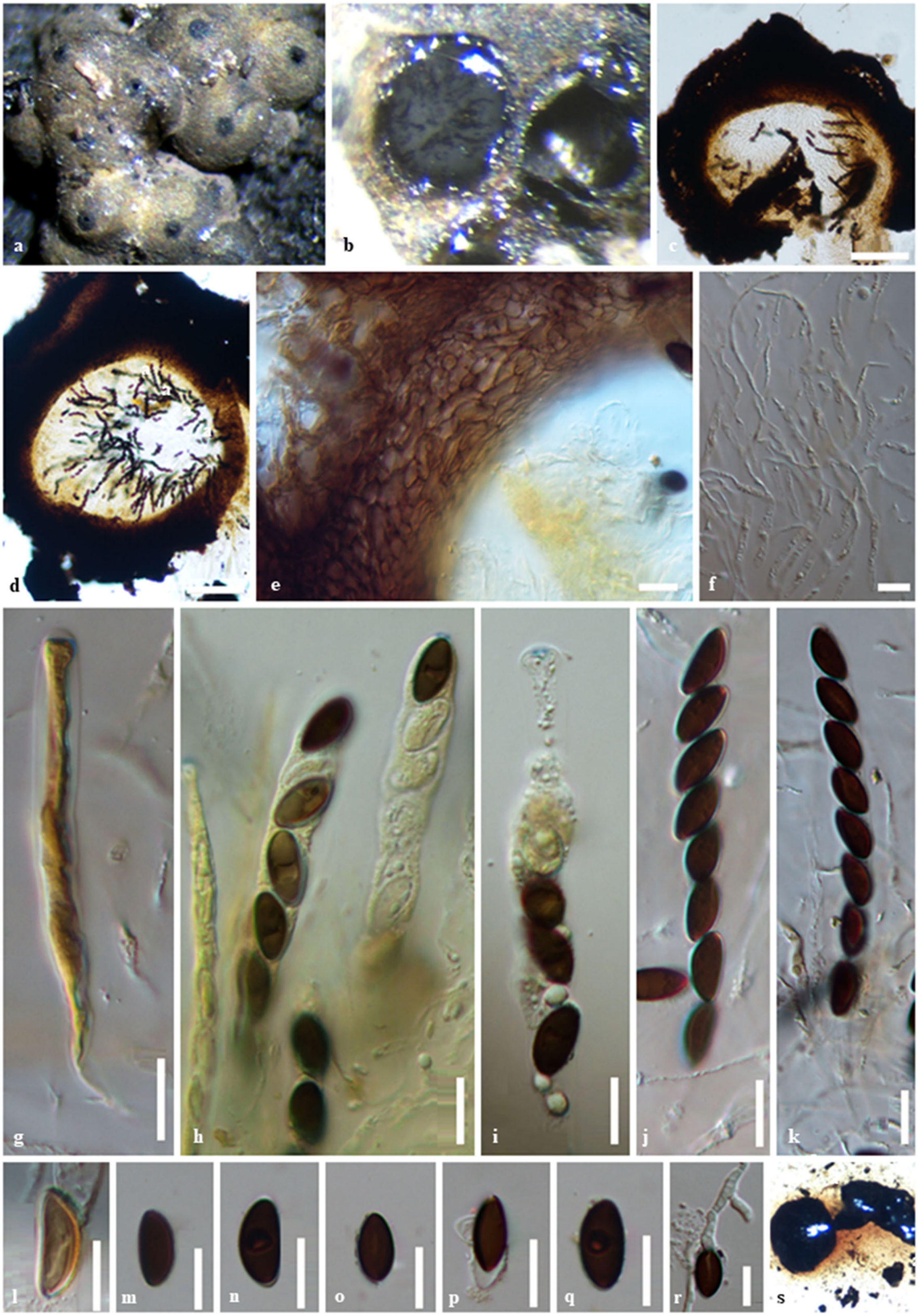


Fig. 117 Phylogram generated from maximum likelihood analysis based on ITS, LSU, RPB2 and TUB2 gene regions of *Hypoxylaceae* and related taxa in *Xylariales*. Bootstrap support values for maximum likelihood (green), maximum parsimony (blue) equal to or greater than 75% and the values of Bayesian posterior probabilities (purple) equal to or greater than 0.95 are given above each branch respectively. The new isolate is in blue. Ex-type strains are indicated in bold. The tree is rooted with *Xylaria hypoxylon* (CBS122620)


a
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◀ **Fig. 118** ***Hypoxylon teeravasati*** (AMH-9906, **holotype**). **a** Ascostromata on the decaying wood of *Avicennia marina.* **b** Cross section of ascostroma. **c, d** Longitudinal sections of ascostroma. **e** Peridium. **f** Filamentous paraphyses. **g–k** Immature and mature asci (g–i = Asci showing apical bluing in Lugol's solution). **l** Immature ascospore. **m–o, q** Mature ascospores. **p** Mature ascospore with dehiscent perispore in KOH. **r** Germinating ascospore. **s** KOH extractable pigments. *Scale bars* **c**, **d** = 100 µm, **e–r** = 10 µm

Holotype: HMAS 0278359

Pileus 50 mm diam., plane or plano-concave, disc black or black-brown, slightly depressed, margin straight, exceeding lamellae; surface dry, with black-brown fibrillose scales against white background, scales triangular, appressed, extremely denser at disc, scattered towards the margin. *Lamellae* up to 3 mm broad, free, crowded, pink, edge even, intercalated with lamellulae. *Annulus* superous, double, membranous, white, pendant, upper side smooth, lower side cogwheel, white, edge light brown. *Stipe* 57 × 5 mm (8 mm at base), white, hollow, cylindrical with slightly bulbous base, surface dry, smooth, silky, with rhizomorphs. *Context* fleshy, white. *Odour* unknown. *KOH reaction*: positive yellow. *Schäffer's reaction*: negative. *Basidia* 15–19.5 × 6.5–9.3 µm, clavate, hyaline, 4-spored, smooth. *Basidiospores* 4.5–5.3 × 3.3–4.1 µm, ($\bar{x}$ = 5 ± 0.2 × 3.6 ± 0.2, Q = 1.2–1.5, Q_m = 1.4 ± 0.1, n = 20), ellipsoid, smooth, thick-walled, brown. *Pleurocystidia* absent. *Cheilocystidia* not very conspicuous, can be single and multiseptate (generally no more than three elements), the terminal element clavate, cylindrical, 12.1–24.8 × 6.9–13.7 µm. *Pileipellis* a cutis composed of hyphae of 4.6–14.4 µm diam., smooth, cylindrical, slightly constricted at septa, pigment intracellular, light brown or brown.

Material examined: CHINA, Sichuan Province, Miyi County, 13 September 2015, ZRL20151118 (HMAS 0278359, **holotype**).

Host and habitat: Solitary on soil in forest with bamboo around.

Distribution: Sichuan Province (China).

GenBank numbers: ITS = MG763128, LSU = MG765263, TEF1-α = MG765265.

Notes: The phylogenetic trees generated by maximum likelihood and Bayesian inference analyses (Fig. 119) show that *Agaricus memnonius* forms a distinct lineage within *Agaricus* sect. *Xanthodermatei* in the clade Xan II and the tree topology is similar with previous studies (Zhao et al 2016; Zhou et al. 2016; Parra et al. 2018).

Agaricus memnonius has relatively small and slender basidiomes, which are similar to the European species *A. laskibarii* L.A. Parra & Arrillaga, *A. xanthodermulus* Callac & Guinb. and *A. parvitigrinus* Guinb. & Callac (Parra 2013). However, *A. memnonius* has black-brown and triangular scales on the pileus, while the other three species have greyish brown and not triangular scales. Some species described from China also have small and slender basidiomes, such as *A. gregariomyces* J.L. Zhou & R.L. Zhao and *A. karstomyces* R.L. Zhao. However, *A. gregariomyces* has larger and elongate basidiospores (5.6–6.3 × 3.5–4.0 µm, Q = 1.6–1.9; Zhou et al. 2016). *Agaricus karstomyces* has dot-like scales on the pileus, while *A. memnonius* has triangular scales. Based on phylogenetic and morphological studies, *A. memnonius* is introduced as a new species and is characterized by its distinct phylogenetic position in section *Xanthodermatei*, small and slender basidiome, black-brown and triangular scales on the pileus, and the single and multiseptate cheilocystidia.

Agaricus langensis M.Q. He & R.L. Zhao, ***sp. nov.***

Fungal names: FN570534; *Facesoffungi number*: FoF03941, Fig. 121

Etymology: The Latin epithet "*langensis*" meaning "originating from Lang" refers to the Lang County where the holotype was collected.

Holotype: HMAS 0278317

Basidiomes flavescent when rubbed. *Pileus* 26–49 mm diam., parabolic when young, then convex, disc slightly subumbonate, margin straight, sometimes with appendiculate remains of veil; surface dry, with grayish brown fibrillose scales against white background, scales appressed, covering the whole pileus, denser at disc, scattered towards the margin. *Lamellae* up to 5 mm broad, free, crowded, pink, edge even, intercalated with lamellulae. *Annulus* up to 6 mm in diam., superous, double, membranous, white when fresh, yellowish when dry, pendant, upper side smooth, lower side cogwheel, white, edge light brown. *Stipe* 59–76 × 6–7 mm (7–10 mm at base), white, hollow, cylindrical, surface dry, smooth or slightly fibrillose, with rhizomorphs. *Context* fleshy, white. *Odour* unknown. *KOH reaction*: positive yellow. *Schäffer's reaction*: negative. *Basidia* 18.5–25.3 × 6.7–8.9 µm, clavate, hyaline, 4-spored, smooth. *Basidiospores* 6.3–8.3(–8.5) × 3.7–5.1 µm, ($\bar{x}$ = 7.2 ± 0.6 × 4.4 ± 0.3, Q = 1.4–1.9, Q_m = 1.6 ± 0.1, n = 20), ellipsoid, elongate, smooth, thick-walled, brown. *Pleurocystidia* absent. *Cheilocystidia* absent. *Pileipellis* a cutis composed of hyphae of 4.8–12.1 µm diam., smooth, cylindrical, slightly constricted at septa, hyaline, light brown or brown.

Material examined: CHINA, Tibet, Lang County, Gongga Village, Alt. 3384 m, 29°16′ N, 93°11′ E, S-Y. Su, ZRL20152282 (HMAS 0278317, **holotype**).

Habit and habitat: Scattered on soil in forest.

Distribution: Tibet (China).

GenBank numbers: ITS = MG763129, LSU = MG765264, TEF1-α = MG765266.

Notes: *Agaricus langensis* (HMAS 0278317) belongs to a clade called Xan III (Thongklang et al. 2014; Parra et al. 2018) which is present (but not always indicated) in all previous multigene trees of *Agaricus* sect. *Xanthodermatei* (Zhao et al.

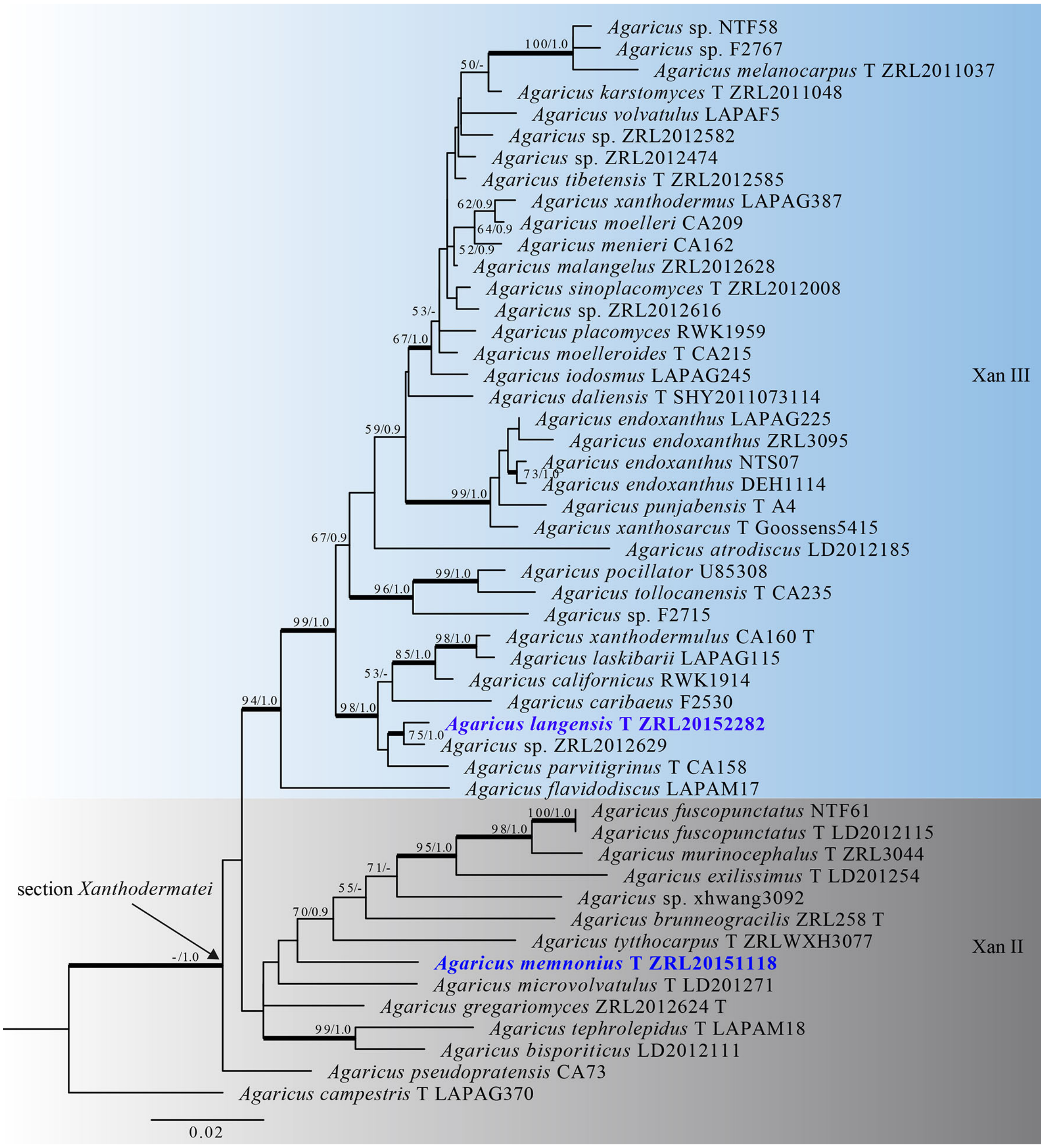


Fig. 119 Maximum likelihood tree of *Agaricus* sect. *Xanthodermatei* based on LSU, TEF1-α and ITS sequences with *Agaricus campestris* (LAPAG370) as the outgroup taxon. The bootstrap values and Bayesian posterior probabilities more than 50%/0.90 (BS/BYPP) are indicated at the nodes. The branches in bold mean the related PP > 0.95, "T" refers to sequences from type specimen

2016, Zhou et al. 2016, Parra et al. 2018) and which includes in our tree *A. flavidodiscus* L.A. Parra et al., *A. langensis* and 32 other species (Fig. 119). The new species forms a sister lineage with *Agaricus* sp. (ZRL2012629) with moderate support (75% ML and 1.00 BYPP) in our phylogenetic analyses (Fig. 119). *Agaricus parvitigrinus* Guinb. & Callac resembles *A. langensis* in the field, because both have small to medium sized basidiomes, a convex pileus covered by greyish fibrillose scales. However, *A. langensis* has larger basidiospores than those of *A. parvitigrinus* (5.8 × 3.7 µm; Parra 2013). *Agaricus menieri* Bon, *A. xanthodermulus* Callac & Guinb. and *A. xanthodermus* Genev. have similar sized basidiospores, but have distinct cheilocystidia (Parra 2013), a feature lacking in *A. langensis*. *Agaricus tibetensis* J.L. Zhou & R.L. Zhao also has small to medium sized basidiomes, same sized basidiospores as *A. langensis*, and no cheilocystidia (or rare in *A. tibetensis*), and both species originated from Tibet (Zhou et al. 2016). However, their ITS sequences differ at 33 base positions, and the molecular phylogeny also indicates that they are different species.

Based on the phylogenetic analyses and morphological characteristics, we introduce this new species, which is

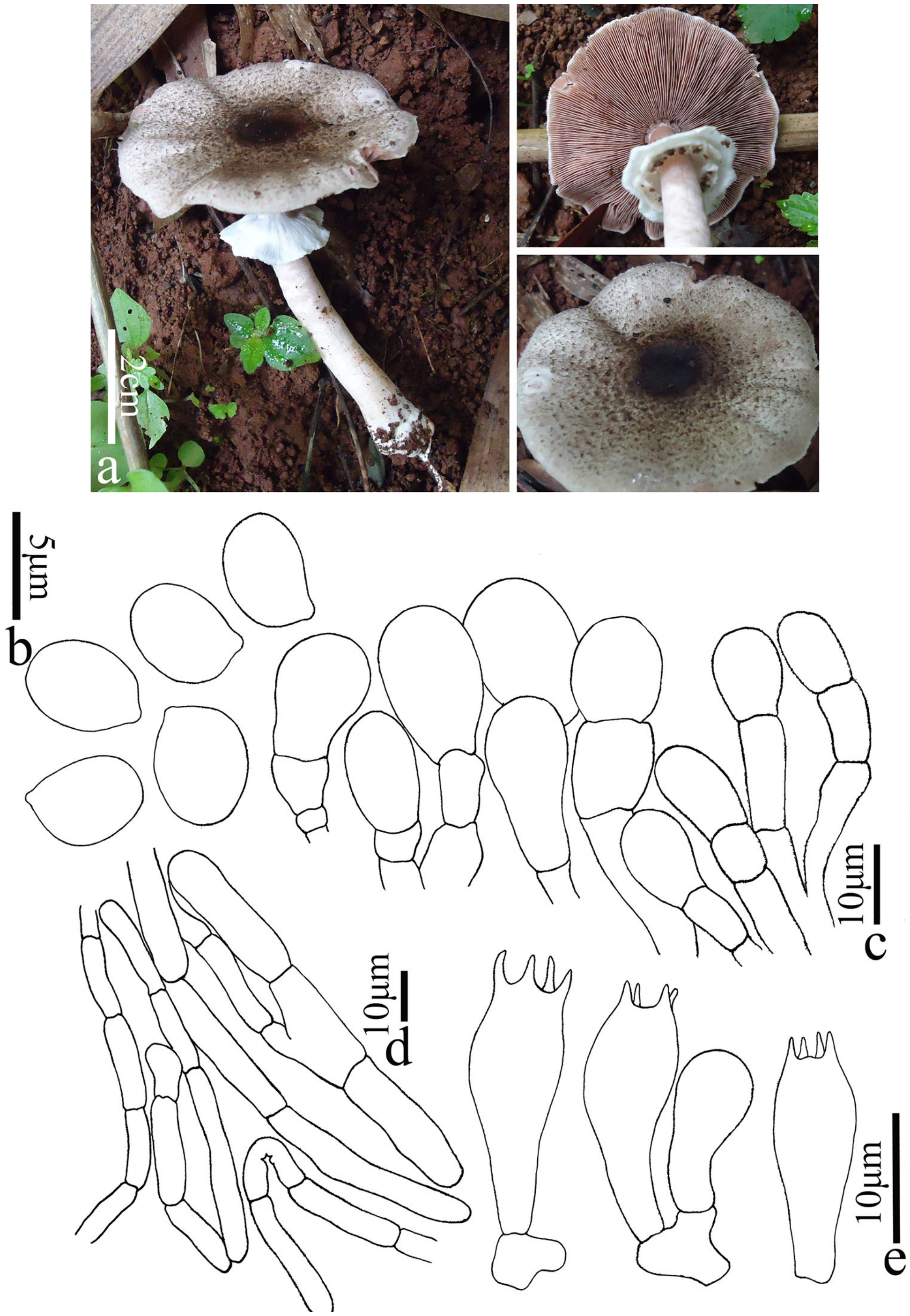


Fig. 120 ***Agaricus memnonius*** (HMAS 0278359, **holotype**). **a** Basidiome in the field. **b** Basidiospores. **c** Cheilocystidia. **d** Pileipellis hyphae. **e** Basidia. *Scale bars* **a** = 2 cm, **c–e** = 10 µm, **b** = 5 µm

characterized by its distinct phylogenetic position in sect. *Xanthodermatei*, small to medium sized basidiomes, relatively large basidiospores and absence of cheilocystidia.

Coprinus Pers.

Traditionally, *Coprinus* comprised all coprinoid species (black spore print and mature lamellae, plicate-sulcate pileus) and it was the type genus of the family *Coprinaceae* Overeem & Weese. On the basis of earlier phylogenetic studies, Redhead et al. (2001) transferred most *Coprinus* species into four genera of the new family *Psathyrellaceae* Vilgalys et al. *Coprinus comatus* (O.F. Müll.) Pers., and a few related species remained in *Coprinus*, which was transferred to family *Agaricaceae* (Moncalvo et al. 2002; Vellinga 2004). *Coprinus* species have rather small to large basidiomes with squamulose pileus, ring-like partial veil and deliquescent lamellae. A phylogenetic tree is presented in Fig. 122.

Coprinus trigonosporus Tkalčec & Mešić, ***sp. nov.***

MycoBank number: MB826852; *Facesoffungi number*: FoF05719, Fig. 123

Etymology: The species is named after its basidiospores that are often rounded triangular in frontal view.

Holotype: CNF 1/6594

Pileus up to 24 mm broad and 32 mm high when still closed, 32–46 mm broad at maturity, ellipsoid to oblong at first, later obtusely conical to subapplanate with broad subumbonate centre, often radially splitting, when young entirely covered with a dense, white universal veil forming imbricate, rather large scales with mostly upturned lower edge, later veil splitting up into patches of different sizes (from one scale to group of scales) except at the centre, surface strongly plicate-sulcate, white at first, becoming pink brown to vinaceous brown and soon black, margin sometimes with few small, white, appendiculate remnants of partial veil at maturity. *Lamellae* free, crowded, broad, often sinuous when young, white at first, later turning pink to vinaceous brown, soon becoming black, weakly deliquescent. *Stipe* 34–56 × 5.5–10 mm, tapering upwards or subcylindrical, with subbulbous, obconical, buried base (up to 15 mm wide), white, central, hollow, dry, ± tomentose when young, (sub) glabrous at maturity, partial veil remaining as a white, narrow ring at the top of the base. *Context* white. *Odour and taste* fungoid. *Spore print* black. *Basidia* 30–62 × 12–24 µm, clavate, 4-spored, thin-walled or moderately thick-walled (up to 1 µm), first hyaline, at maturity partially (in the middle part) or entirely with pale to dark brown parietal pigment, surrounded by 6–12 hymenophysalides (pseudoparaphyses). *Hymenophysalides* 15–42 × 6–14 µm, clavate, thin-walled, sometimes moderately thick-walled (up to 0.8 µm), hyaline to pale brown. *Basidiospores* [500/5/1] (9.3–)10.7–*14.6*–18.6(–20.8) × (8.1–)9.6–*11.8*–14.3(–15.1) × (7.8–)8.5–*10*–11.6(–12.3) µm, averages of different basidiomes 13.9–15.3 × 11.7–12.2 × 9.8–10.3 µm, Q_f = 0.9–*1.2*–1.7, Q_s = 1.2–*1.4*–1.8, av. Q_f = 1.1–1.3, av. Q_s = 1.4–1.5, rounded triangular, cordiform, ovoid or subglobose in frontal view (rarely ellipsoid), with rounded to flat base and rounded apex, ovoid to ellipsoid in side view, flattened, smooth, moderately thick-walled (up to 1 µm), with 1.5–3.5 µm wide, slightly to strongly eccentric, rarely central germ-pore (sometimes ring-like protruding), medium to dark brown in H_2O and KOH, semitransparent, non-amyloid and non-dextrinoid. *Pleurocystidia* absent. *Cheilocystidia* 16–58 × 11–28 µm, broadly to narrowly clavate, thin-walled, hyaline. *Pileipellis* a cutis, composed of repent, thin-walled, 5–15 µm wide, subhyaline to brown hyphae with intracellular pigment. *Veil cells on the pileus* 12–170 × 2–38 µm, cylindrical to inflated, in chains, often constricted at the septa, occasionally branched, sometimes with individual, simple, subglobose to finger-like excrescences, thin-walled, rarely moderately thick-walled (up to 0.8 µm), smooth, rarely finely encrusted, hyaline. *Stipitipellis* a cutis of parallel, repent, thin-walled, hyaline, 1.5–10 µm wide hyphae. *Clamp connections* absent; pseudoclamps present on some septa in veil, pileipellis and trama.

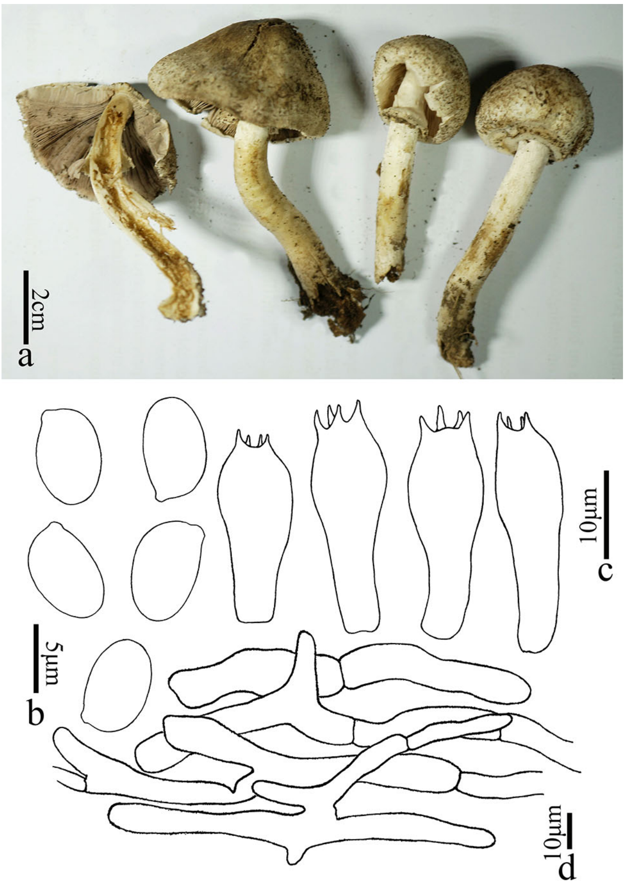


Fig. 121 ***Agaricus langensis*** (HMAS 0278317, **holotype**). **a** Basidiomes in the laboratory. **b** Basidiospores. **c** Basidia. **d** Pileipellis hyphae. *Scale bars* **a** = 2 cm, **c, d** = 10 µm, **b** = 5 µm

Material examined: SAUDI ARABIA, Jizan Province, village, 8 km S from Harub, 17°22′03″N, 42°52′10″E, 257 m a.s.l., on sandy soil in a courtyard, 22 September 2010, leg. M. Čerkez, CNF 1/6594 (**holotype**).

Habit and habitat: In group (approximately 20 basidiomes), on sandy soil with some sheep dung, among scattered herbaceous plants and bushes in a courtyard.

Distribution: So far known only from the type locality in the Kingdom of Saudi Arabia, Jizan Province.

GenBank numbers: ITS = MH422561, LSU = MH422563.

Notes: Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using ITS sequence for our new species is *Coprinus vosoustii* Pilát [GenBank no. JF907844, similarity = 627/668(94%), Gaps = 9/668(1%)]. Phylogenetic analysis based on the ITS sequence data of *Coprinus sensu stricto* shows that *C. trigonosporus* formed a distinct lineage and clustered with *C. vosoustii* and

C. sterquilinus (Fr.) Fr.. Morphologically, *C. trigonosporus* is best characterised by a considerable number of cordiform and rounded triangular basidiospores. Other species in the genus have ellipsoid or ovoid basidiospores (van de Bogart 1976; Moreno and Heykoop 1998; Cacialli et al. 1999; Uljé 2005; Crous et al. 2016b). The rather peculiar microscopic characteristic of *C. trigonosporus* is the large number of hymenophysalides (6–12) surrounding the basidium.

Amanitaceae E.-J. Gilbert

Amanitaceae is defined as those agarics having bilateral, divergent lamellae trama and a longitudinally acrophysalidic stipe context. The family comprises five genera, *Amanita* Pers., *Catatrama* Franco-Mol., *Limacella* Earle, *Limacellopsis* Zhu L. Yang et al. and *Myxoderma* Fayod ex Kühner (Cui et al. 2018). In this family, *Amanita* is the most species-rich genus (Bas 2000; Tulloss 2005; Yang 2005; Cui et al. 2018). More than 1000 species have been described worldwide with ca. 600 accepted names; about 60 taxa have been reported from India (Yang 2000; Bhatt et al. 2003; Tulloss and Yang 2016).

Amanita Pers

Amanita was recently discussed by Ariyawansa et al. (2015a), Tulloss and Yang (2016), Tulloss et al. (2016) and Cui et al. (2018). We follow the latest treatment and updated accounts of *Amanita* in Tulloss and Yang (2016), Tulloss et al. (2016), Tibpromma et al. (2017) and Cui et al. (2018). Two novel species (belonging to *Amanita* sect. *Amanita* and *A.* sect. *Vaginatae*), collected from the north-western part of Indian Himalaya are introduced together with their morphology and phylogenetic placements (Figs. 128, 131). In addition, *A. altipes* and *A. melleialba* are reported from Thailand for the first time, which was established based on morphology and DNA sequence analyses of LSU and RPB2 regions (Fig. 124).

Amanita altipes Zhu L. Yang, M. Weiss & Oberw., Mycologia 96(3): 636 (2004)

Facesoffungi number: FoF04857, Fig. 125a

Holotype: China, Yunnan Province, Lijiang Country, Laojunshan, altitude 3800 m., on soil under *Abies*, *Betula*, *Picea*, *Quercus* and/or *Salix*, 14 August 2000, Zhu L. Yang 2915, KUN-HKAS 36609.

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1978).

Basidiomes medium-sized. *Pileus* 70 mm in wide, parabolic when young, convex to plano-convex, depressed at centre, broadly umbonate, yellowish to yellow (3A4–7), pale yellow toward margin, often with dark yellow to brownish (5D6–8) over disk, viscid when moist; universal veil mostly over disc as felty, floccose patches, 2–5 mm wide, thick, yellowish to yellow to dirty yellow (3A2–5); margin tuberculate-striate (0.13–0.41R), non-appendiculate. *Lamellae* 2–4 mm broad, free to nearly free, crowded to plentiful, white to yellowish (2A1–3); lamellulae of 2–5 lengths, crowed, truncate; context white, hollow in centre. *Stipe* 150 × 16 mm. (length includes bulb), with tapering upward, yellowish (3A2–4), becoming whitish toward stipe base, often covered with yellow to yellowish (3A4–6) squamules above partial veil, white, with yellowish to whitish squamules or fibrils under partial veil, white (1A1). *Bulb* subglobose to ovate, 8–32 mm diam., white. *Universal veil on stipe base* as very short volval limb on bulb margin, floccose patches or warts near apex of bulb, yellow to yellowish (3A6–8). *Partial veil* subapical,

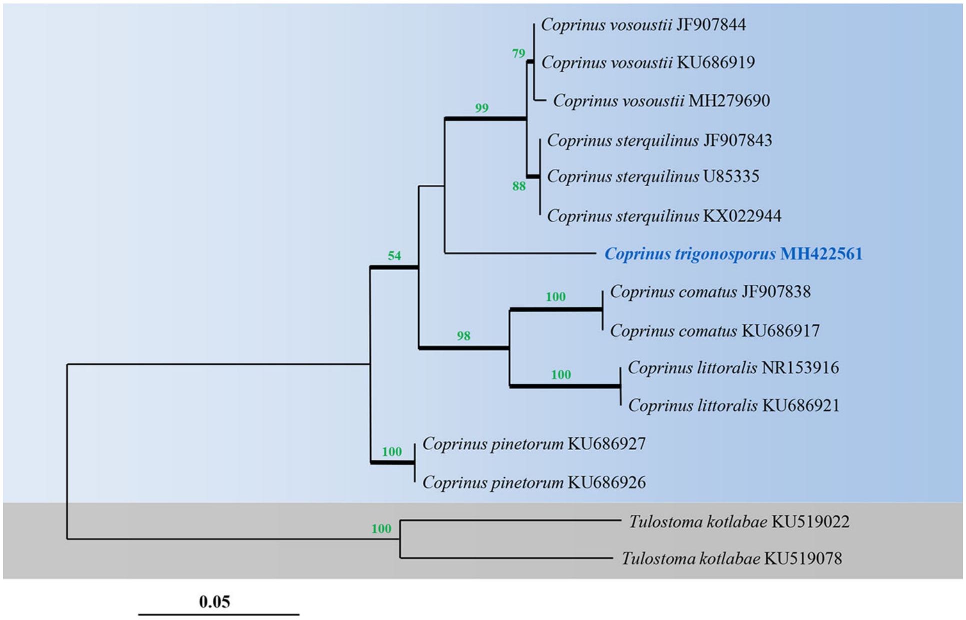


Fig. 122 Maximum likelihood phylogenetic tree of *Coprinus trigonosporus* and closely related species based on ITS sequence dataset and calculated with MEGA6.0 software (Tamura et al. 2013). The new species is shown in blue. Maximum likelihood bootstrap values greater than 50% are indicated at the nodes. The tree is rooted with *Tulostoma kotlabae* and *T. niveum*. The bar indicates the number of nucleotide substitutions per site

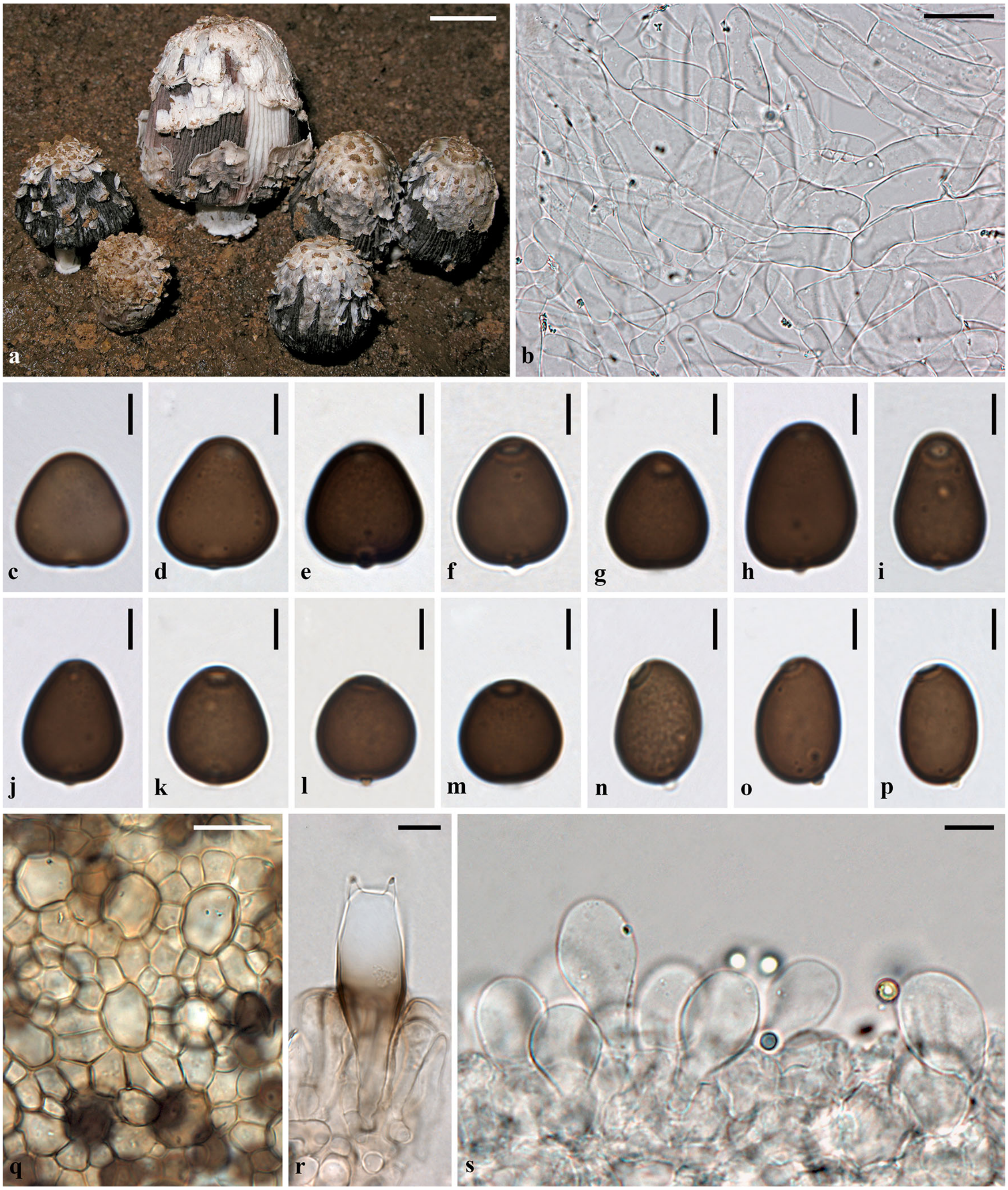


Fig. 123 ***Coprinus trigonosporus*** (CNF 1/6594, **holotype**). **a** Basidiomes. **b** Veil on the pileus. **c–p** Basidiospores. **q**, **r** Basidia surrounded by hymenophysalides. **s** Cheilocystidia. *Scale bars* **a** = 10 mm, **b** = 30 µm, **c–p** = 5 µm, **q** = 20 µm, **r, s** = 10 µm

membranous, 18 mm below apex of stipe, surface yellowish, with a yellow edge. *Odour* indistinct. *Lamellar trama* bilateral, divergent; mediostratum 50–60 µm wide; filamentous hyphae 1.8–8 µm wide, branching, hyaline, of abundant fusiform to subellipsoid, inflated cells (60–90 × 12–33 mm); vascular hyphae not observed. *Subhymenium* 30–50 µm thick; inflated cells dominating, in 2–3 layers, ovoid to subellipsoid, 10–25 × 8–18 µm, subtended by concatenated partially inflated hyphal segments. *Basidia* 32–70 × 10–14 µm, narrowly clavate to clavate, mostly 4-spored, occasionally 2-spored, with sterigmata up to 7 µm long; clamps absent. *Basidiospores* [60/1/1] (7.5–)8–10(–11) × (7–)7.5–9.5(–10) µm, (Q = 1–1.1(–1.2); Q'= 1.07 ± 0.06), smooth, hyaline, colourless, thin-walled, inamyloid, globose to subglobose, rarely broadly ellipsoid, apiculus rather variable, sublateral, very prominent to rather small, cylindric to truncate-conic; contents monoguttulate or occasionally granular; white in deposit. *Lamellar edge* sterile; filamentous hyphae 3–7 µm wide, hyaline, colourless or pale yellow, thin-walled; inflated cells dominating, mostly globose to subglobose and sometimes ovoid, 15–25 × 10–18(–24) µm, colourless, thin-walled. *Pileipellis* up to 155 µm thick; upper layer (70–130 µm thick) strongly gelatinized, composed of interwoven, thin-walled, colourless, filamentous hyphae 3–8 µm wide; lower layer (50–65 µm thick) composed of compactly arranged, filamentous hyphae 3–8 µm wide; vascular hyphae rare. *Universal veil on pileus* filamentous hyphae 2.5–6.2 µm wide, branching, with slightly inflated elements; inflated cells very abundant to nearly dominant, globose to subglobose to ovoid or ellipsoid to subfusiform (45–90 × 15–30 µm), in chains of 2–4, thin-walled, colourless vascular hyphae occasional. *Universal veil on stipe base* composed 5–6 irregularly arranged elements; filamentous hyphae very abundant 2.2–15 µm wide; inflated cells abundant to very abundant, fusiform to long ellipsoid, 40–80 × 10–35 µm, colourless or with intracellular pale brown pigment, thin- to slightly thick-walled, terminal or in chains of 2–3 and then terminal, becoming rare toward inner layer; filamentous hyphae abundant; vascular hyphae occasional. *Stipe trama* longitudinally acrophysalidic; filamentous hyphae 2.2–14 µm wide; acrophysalides subfusiform to clavate, 250–450 × 25–40 µm; vascular hyphae rare. *Partial veil* filamentous hyphae 2–5 µm wide, gelatinized, branching, hyaline, inflated cells terminal, thin-walled, ellipsoid to long ellipsoid, 15–70 × 10–24 µm, colourless, or with intracellular pale brown pigment, thin-walled; vascular hyphae rare. *Clamp connections* absent in all parts of basidiomes.

Material examined: THAILAND, Lampang Province, Along road number 1252, 18.935, 99.390833, elev.1450 m, 14 June 2013, B. Thongbai, BZ201342 (MFLU 14-0065).

Host and habitat: Solitary in forests dominated by *Fagaceae.*

Distribution: Known from China and Thailand.

GenBank numbers: LSU = MH716040, RPB2 = MH727686.

Notes: *Amanita altipes*, originally described from southwestern China by Yang et al. (2004), resembles several species in the section *Amanita*, such as *A. elata* (Massee) Corner & Bas, *A. gemmata* (Fr.) Bertillon, *A. orientigemmata* Zhu L. Yang & Yoshim. Doi, *A. russuloides* (Peck) Sacc., and *A. xylinivolva* Tulloss et al. *Amanita altipes* shares some morphological similarities with these yellow to yellowish species which have been discovered in either Europe or Asia. Molecular analyses indicate that *A. altipes* is a distinct species closely related to *A. melleialba*. The combined gene phylogenetic analyses indicate that Thai *A. altipes* sequences clustered with *A. altipes* sequences from China with 100% ML support (Fig. 124).

Amanita flavoalba Mehmood & R.P. Bhatt, ***sp. nov.***

MycoBank number: MB820829; *Facesoffungi number*: FoF04390, Figs. 126, 127

Etymology: Referring to the yellow centre and whitish margin of the pileus.

Holotype: CAL 1405.

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1978).

Basidiomes small to medium-sized. *Pileus* 40–60 mm wide, initially hemispherical then convex to plane, slightly umbonate, yellow to vivid yellow or cadmium yellow (2A7–8) over centre, white to yellowish white (1A2–2A2) toward margin, viscid to sub-viscid when moist, shiny; context 3–4 mm thick, thinning slowly toward margin, white, unchanging when bruised or exposed; margin striate (0.1–0.2R), non-appendiculate. *Universal veil on pileus* as membranous to sub-membranous patches, 2–4 mm wide, white or snow white (1A1), distributed irregularly over the pileus surface. *Lamellae* free to narrowly adnate, leaving decurrent line on stipe, crowded (8–10 lamellae/10 mm at margin), white, unchanging, 3–8 mm broad. *Lamellulae* truncate to subtruncate, plentiful, in several lengths. *Stipe* 70–95 × 5–7 mm (length includes bulb), nearly cylindric or slightly tapering upward, slightly flaring at apex, white to yellowish white (1A2), finely fibrillose above and below annulus; context white, unchanging when cut or bruised, stuffed. *Partial veil* medium to subapical, membranous, white. *Bulb* 17–19 × 15–17 mm, subglobose to ovoid, remnants of universal veil on top of bulb white, sub-membranous to shaggy or as cottony patches. *Odour* indistinct. *Taste* not recorded. *Spore print* white. *Macrochemical test* no reaction to 5% KOH on pileal surface and context. *Subhymenium* w_{st}*-near* = 25–40 µm; w_{st}*-far* = 38–55 µm thick, with basidia arising from short inflated hyphal segments up to 8 × 10 µm. *Hymenophoral trama* bilateral, divergent; w_{cs} = 30–45 µm, composed of long ellipsoid to subfusiform inflated cells (up to 65 × 30 µm), filamentous hyphae 3–7 µm wide, thin-walled, colourless, hyaline. *Basidia* (42–)45–55(–60) × (10–)10.5–11.5(–12) µm, thin-walled, colourless; sterigmata 3–4 µm long; clamp connections not observed at the base of basidia. *Basidiospores* [60/3/2](8–)8.5–10.5(–11) × (7–)7.5–9(–9.5) µm, (L = 9.5 µm; W = 8.3 µm; Q = (1.09–)1.11–1.17(–1.21); Q' = 1.14), subglobose, sometimes broadly ellipsoid, thin-walled, hyaline, smooth, non-amyloid, apiculus sublateral, up to 1.5 µm high; contents monoguttulate. *Lamellae edge* sterile, with inflated, clavate or subglobose to pyriform cells, 14–35 × 8–13 µm, dominating, thin-walled, colourless. *Pileipellis* 110–130 µm thick, in two layers; upper layer 40–50 µm thick, slightly gelatinized, colourless, filamentous hyphae 2–4 µm wide, subradially arranged to interwoven; lower layer 70–80 thick, filamentous hyphae 2–5 µm wide, subradially to densely arranged with yellowish brown

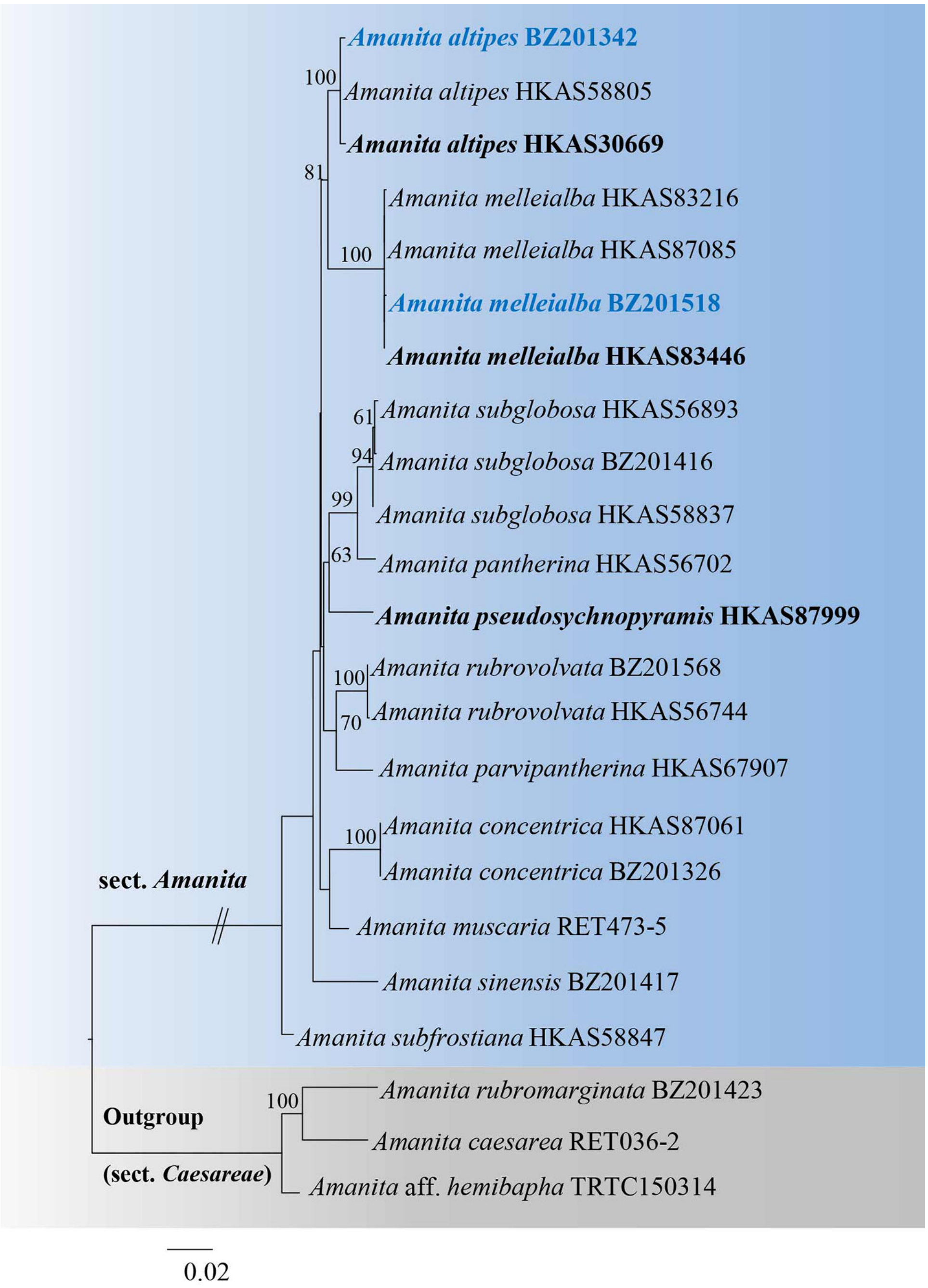


Fig. 124 Phylogenetic tree of *Amanita* species inferred from a combine LSU and RPB2 sequence dataset using maximum likelihood. Bootstrap values (BS) ≥ 50% are shown above the branches. The first records of *Amanita* species from Thailand in this study are in blue font. Voucher collection identifiers are provided after each species name. Type specimens are indicated in bold

intracellular pigment, thin-walled. *Universal veil on pileus* filamentous hyphae 3–7 µm wide, dominating, hyaline; inflated cells globose to subglobose 20–50 × 26–47 µm, broadly ellipsoid to ellipsoid or fusiform, 37–64 × 12.5–20 µm, thin-walled, colourless, hyaline. *Pileus context* filamentous hyphae 5–8 µm wide, colourless, hyaline, thin-walled, inflated cells 30–90 × 10–30 µm, colourless, thin-walled; vascular hyphae not observed. *Universal veil on stipe base* filamentous; hyphae 4–9 µm wide, dominating, branching, hyaline, thin-walled; inflated cells subglobose to ovoid 18–36 × 21–37 µm, broadly ellipsoid to subclavate 39–74 × 12.5–20 µm, abundant to very abundant. *Partial veil* filamentous hyphae 2–4 µm wide, branching, thin-walled, colourless, hyaline, with inflated cells up to 25 × 13 µm. *Stipe context* longitudinally acrophysalidic; acrophysalides dominating 190–280 × 26–36 µm, filamentous hyphae (3–7 µm wide). *Clamp connections* absent in all tissues.

Material examined: INDIA, Uttarakhand, Bageshwar District, Dhakuri, 2570 m, N30°04.962′ E79°55.159′, 2 August 2016, T. Mehmood, TM 16-1249 (CAL 1405,

Fig. 125 Basidiomes. **a** *Amanita altipes*. **b** *Amanita melleialba*. *Scale bars* 10 cm

holotype); *ibid*., Dhakuri, 3 August 2016, T. Mehmood, TM 16-1280.

Host and habitat: On ground under *Abies pindrow* (Royle ex D. Don) Royle in temperate coniferous forest

Distribution: Indian Himalaya.

GenBank numbers: LSU = KY861748 (CAL 1405), MF695813 (TM 16-1280).

Notes: A combination of macro- and micromorphological features like inamyloid basidiospores and bulbous stipe base place *A. flavoalba* in *Amanita* [subg. *Amanita*] sect. *Amanita* (Yang 1997).

Amanita flavoalba is distinct from other known species of *Amanita* sect. *Amanita* by a combination of characteristics: smaller basidiomes, yellow to vivid yellow pileus centre and whitish to yellowish white toward pileus margin, membranous to submembranous universal veil on pileus, subglobose basidiospores, universal veil on the pileus composed of abundant filamentous hyphae mixed with scattered inflated cells. In the field, *A. flavoalba* is easily recognized by its yellow pileus with yellowish white margin, easily detachable universal veil on pileus in the form of membranous to submembranous patches and its occurrence under *Abies pindrow*. The presence of subglobose basidiospores, very abundant filamentous hyphae mixed with scattered inflated cells in universal veil on the pileus are also quite striking.

Amanita flavoalba might be confused with *A. melleialba* Zhu L. Yang et al. (originally described from China), however, the latter possesses a honey pileus with longer marginal striation, subconical to granular universal veil remnants on pileus, ellipsoid to sometimes broadly ellipsoid basidiospores (7.5–9.5 × 6–7 µm, with Q = 1.41) and it occurs in subtropical forests dominated by plants of *Fagaceae* (Ariyawansa et al. 2015a).

Amanita flavoalba is similar to *A. pseudosychnopyramis* Yang Y. Cui et al., but the latter has yellowish brown to brownish pileus, universal veil remnants as conical to pyramid, grey to brownish grey warts and it occurs in subtropical forests of *Fagaceae* (Ariyawansa et al. 2015a).

Amanita parvipantherina Zhu L. Yang et al. and *A. subparvipantherina* Zhu L. Yang et al. are easily segregated from *A. flavoalba* by the universal veil remnants on pileus in the form of subconical to granular warts (Yang et al. 2004; Ariyawansa et al. 2015a). *Amanita parvipantherina* also has broadly ellipsoid to ellipsoid basidiospores (8.5–11.5 × 6.5–8.5 µm, Q = 1.38; Yang et al. 2004) and *A. subparvipantherina* has broadly ellipsoid to ellipsoid basidiospores (9–11.5 × 6.5–8 µm, with Q = 1.38; Ariyawansa et al. 2015a). *Amanita flavoalba* resembles *A. altipes* by its yellowish pileus but *A. altipes* pileus has a brownish tinge and its basidiospores are globose to subglobose (8–10 × 7.5–9.5 µm, with Q = 1.07; Yang et al. 2004). *Amanita elata* (originally described from Singapore) differs from *A. flavoalba* by its pale dingy to ochraceous buff pileus with very faint sulphur-yellow tinge, exannulate stipe, smaller basidiospores (7–8.5 × 6.8–7.7 µm) and its occurrence in tropical forests (Corner and Bas 1962).

Our molecular phylogenetic analysis shows closeness (though well separated in Fig. 128) with a few taxa (in *Amanita* sect. *Amanita*) like *A. xylinivolva* (originally described from Colombia; GenBank no. FJ890036), *A. crenulata* Peck (originally described from the USA; GenBank no. HQ539687) and *A. breckonii* Thiers & Ammirati (originally reported from the USA; GenBank no. KJ535440).

Fig. 126 ***Amanita flavoalba*** (CAL 1405, **holotype**). **a–e** Fresh basidiomes in the field and base camp. **f** Basidiospores. **g, h** Basidia and element of subhymenium. **i** Elements of universal veil from pileus surface. *Scale bars* **a** = 10 mm, **f–i** = 20 µm

Amanita xylinivolva can be easily separated by its basidiomes without a pileal umbo, white to off-white to dingy grey volval remnants, whitish buff lamellae, marked to abrupt bulb and microscopically, globose to subglobose basidiospores with comparatively lower Q value (8–10.2 × 7.2–9.5 µm, Q′ = 1.08; Tulloss et al. 1992). *Amanita crenulata* has a brownish beige to greyish pileus, universal veil on pileus as flocculose to subpyramidal warts and subglobose to broadly ellipsoid basidiospores (Q′ = 1.08) (Peck 1900). *Amanita breckonii* has ellipsoid to elongate basidiospores (9.8–12.8 × 6.2–8.7 µm, Q′ = 1.65) and clamp connections at the base of basidia (Thiers and Ammirati 1982). Macro- and micromorphology coupled with the LSU-based phylogenetic analysis corroborate *A. flavoalba* as a novel species.

Amanita melleialba Zhu L. Yang, Qing Cai & Yang Y. Cui, in Ariyawansa et al., Fungal Divers: https://doi.org/10.1007/s13225-015-0346-5, [163] (2015), Fig. 125b

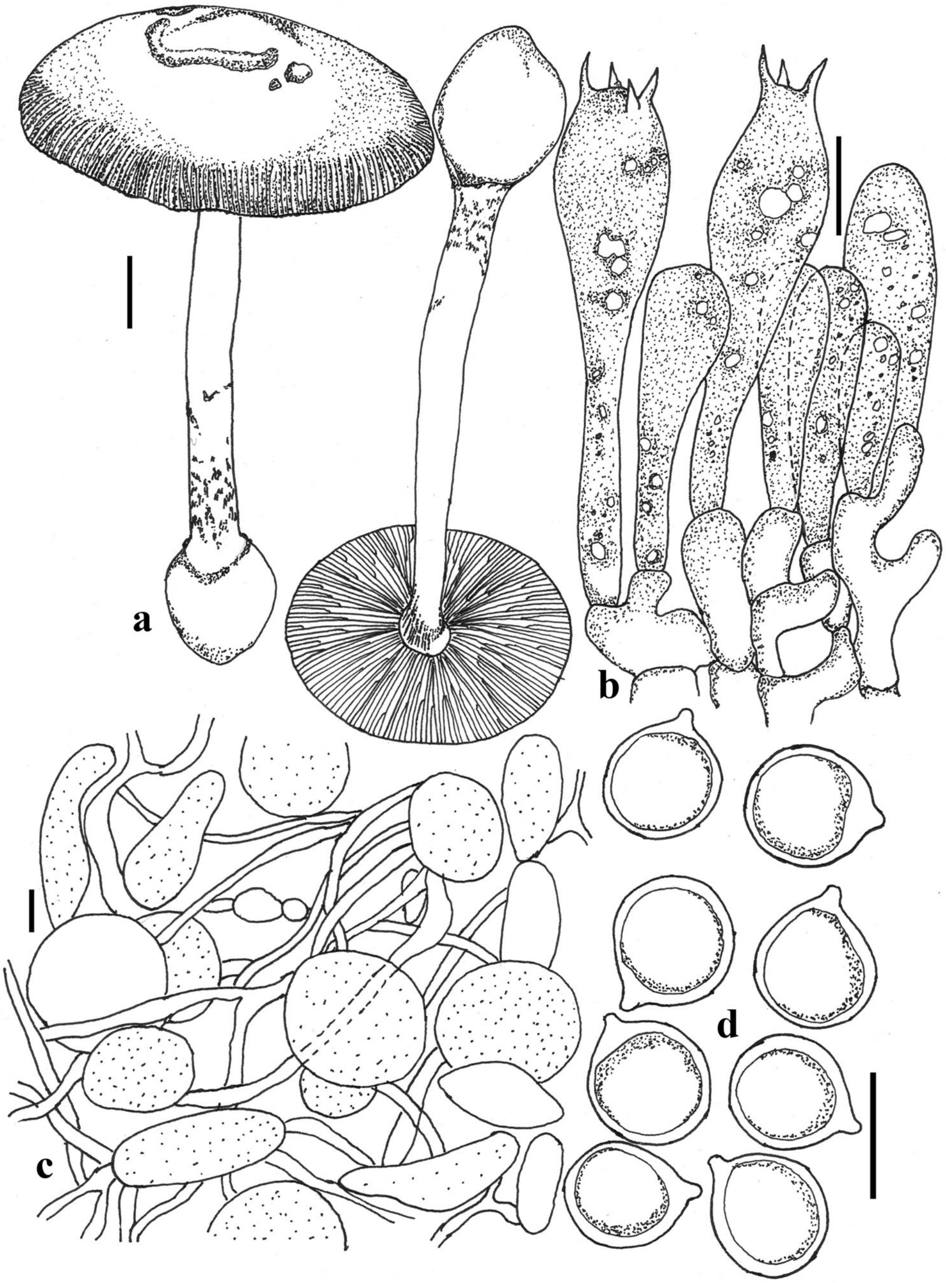


Fig. 127 ***Amanita flavoalba*** (CAL 1405, **holotype**). **a** Basidiomes. **b** Basidia and element of subhymenium. **c** Elements of universal veil from pileus surface. **d** Basidiospores. *Scale bars* **a** = 10 mm, **b–d** = 10 μm

Holotype: CHINA, Yunnan Province, Puer City, Caiyanghe Nature Reserve, *Fagaceae* (elev. 1300 m), 11 July 2014, G. Wu 1339 (HKAS 83446).

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1978).

Basidiomes small-sized. *Pileus* 30–48 mm wide, parabolic when young, planoconvex to plane at maturity, depressed at centre, yellowish (4A3–4) to yellow (3B5–6), becoming yellowish to whitish (3A2) toward margin, slightly viscid when moist; universal veil mostly over disc, scarce towards margin, as granular or small warts dirty white (5B2), cream to yellowish (4A2–3), honey; margin tuberculate-striate (0.4–0.6R), non-appendiculate. *Lamellae* 2–4 mm broad, free to nearly free, crowded, white (1A1); lamellulae of 3–4 lengths, truncate. *Stipe* 40–75 × 4–7 mm (length includes bulb), slightly tapering upward, white (1A1) to dull white ground (1A2), often covered with floccose squamules above partial veil, white (1A1), floccose squamules to granules under partial veil, white (1A1); context stuffed to nearly hollow in centre, thin, white (1A1). *Bulb* subglobose to napiform, 6–12 mm wide, white (1A1). *Universal veil on stipe base* as very short volval limb on bulb margin and floccose squamules to granules dirty white (1A2). *Partial veil* subapical, membranous, 15–30 mm below apex of stipe, white (1A1) to cream (1A2), with a yellow floccose edge. *Odour* indistinct. *Lamellar trama* bilateral, divergent; mediostratum 30–60 µm wide; filamentous hyphae 1.8–8 µm wide, branching, hyaline, with slightly inflated elements; vascular hyphae not observed. *Subhymenium* 30–60 µm thick; inflated cells dominating, in 3–4 layers, subglobose to ovoid, 10–19 × 8–17 µm, subtended by concatenated partially inflated hyphal segments. *Basidia* 32–50 × 10–14 µm, narrowly clavate to clavate, mostly 4-spored, occasionally 2-spored, with sterigmata up to 5 µm long; clamps absent. *Basidiospores* [60/1/2] (7.2–)7.3–9.4(–10) × (5.3–)6.5–7(–7.3) µm, Q = 1.2–1.28(–1. 56); Q’ = 1.4 ± 0.06, smooth, hyaline, colourless, thin-walled, inamyloid, ellipsoid, sometimes broadly ellipsoid; apiculus rather variable, sublateral, very prominent to rather small, cylindric to truncate-conic; contents monoguttulate or occasionally granular; white in deposit. *Lamellar edge* sterile; filamentous hyphae 3–7 µm wide, hyaline, colourless or pale yellow, thin-walled; inflated cells dominating, mostly globose to subglobose and sometimes ovoid, 9–30 × 9–18(–24) µm, colourless, thin-walled. *Pileipellis* up to 155 µm thick; upper layer (50–70 µm thick) strongly gelatinized, composed of interwoven, thin-walled, colourless, filamentous hyphae 3–8 µm wide; lower layer (50–85 µm thick) composed of compactly arranged, filamentous hyphae 3–8 µm wide; vascular hyphae rare. *Universal veil on pileus* filamentous hyphae, 2.5–6.2 µm wide, branching, with slightly inflated elements; inflated cells very abundant to nearly dominant, globose to subglobose to ovoid or ellipsoid to subfusiform (20–60 × 10–30 µm), in chains of 2–4, thin-walled, colourless; vascular hyphae occasional. *Universal veil on stipe base* composed of two layers; inflated cells abundant to very abundant, fusiform to ellipsoid, 20–40 × 10–30 µm, colourless or with intracellular pale brown pigment, thin- to slightly thick-walled, terminal or in chains of 2–3 and then terminal, becoming rare toward inner layer; filamentous hyphae abundant; vascular hyphae occasional. *Stipe trama* longitudinally acrophysalidic; filamentous hyphae 2.2–15 µm wide; acrophysalides subfusiform to clavate, 120–350 × 25–45 µm; vascular hyphae rare. *Partial veil* filamentous hyphae 2–5 µm wide, gelatinized, branching, hyaline, inflated cells terminal, thin-walled, ellipsoid to long ellipsoid, 15–65 × 10–28 µm, colourless, thin-walled; vascular hyphae rare. *Clamp connections* absent in all parts of basidiomes.

Material examined: THAILAND, Chiang Rai Province, Chiang-khong District, Huay-sor Subdistrict, Nensomburn Village, 5 August 2015, B. Thongbai, BZ201518 (MFLU 15-3316).

Habit and habitat: Gregarious in forests dominated by *Fagaceae.*

Distribution: Known from China and now Thailand.

GenBank numbers: LSU = MH716041, RPB2 = MH727687.

Notes: *Amanita melleialba* belongs to subg. *Amanita* sect. *Amanita.* It was originally described from southwestern and central China. In the field, the distinguishing morphological characteristics of *A. melleialba* include its small basidiomes, universal veil mostly over disc as granular or small warts as well as stipe base. *Amanita melleialba* is very similar to *A. parvipantherina*, also known from China. However, *A. parvipantherina* has larger basidiospores (8.5–11.5 × 6.5–8.5 µm) and is distributed in mixed forests with *Pinus yunnanensis* (Yang et al. 2004; Yang 2005, 2015, Ariyawansa et al. 2015a). Combined-gene phylogenetic analyses show that Thai *A. melleialba* cluster with *A. melleialba* strains from China with 100% ML support (Fig. 124).

Amanita subtropicana Mehmood & R.P. Bhatt, ***sp. nov.***

MycoBank number: MB824531; *Facesoffungi number*: FoF04391, Figs. 129, 130

Etymology: Referring to the subtropical region of Uttarakhand, the type locality.

Holotype: CAL 1660

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1978).

Basidiomes small to medium-sized. *Pileus* 30–65 mm wide, olive brown (5F4–5) yellowish brown (5F6–8) to brown (6E4) over centre, honey yellow to khaki (4D4–6) toward margin, initially hemispherical, then convex to plano-convex, slightly umbo, dry, shiny; context 8–12 mm thick, white, unchanging when cut or bruised; margin tuberculate-striate, up to 14 mm wide, non-appendiculate. *Universal veil remnants on pileus* as felted, subconical to subpyramidal warts. *Lamellae* free, crowded, (8–12 per 10 mm at margin), 5 mm broad, initially white (1A1), fading yellowish white (1B2) with age. *Lamellulae* truncate, unevenly distributed. *Stipe* 90–160 × 10–20 mm, nearly cylindrical, slightly tapering upward, with apex slightly expended, initially white (5A1), covered with white farinose squamules; context white, hollow, unchanging. *Partial veil* absent. *Universal veil remnants on stipe base* white (1B1) to yellowish white (1C1), felted warts, mostly in complete ring, sometimes irregularly distributed. *Odour* indistinct. *Taste* not recorded. *Spore print* white. *Subhymenium* w_{st}*-near* = 25–40 µm; w_{st}*-far* = 45–60 µm; basidia arising from subglobose to irregular shaped cells, 6–16 × 4–14 µm. *Hymenophoral trama* bilateral, divergent; w_{cs} = 36–55 µm wide, with inflated (clavate to fusiform) cells, 40–60 × 10–14 µm; filamentous, undifferentiated hyphae 3–7 µm wide, thin-walled, colourless, hyaline. *Basidia* (32–)46–60(–68) × (12–)13–15(–16) µm, 2- to 4-spored, thin-walled, colourless; sterigmata 3–5 µm long; clamp connections not observed

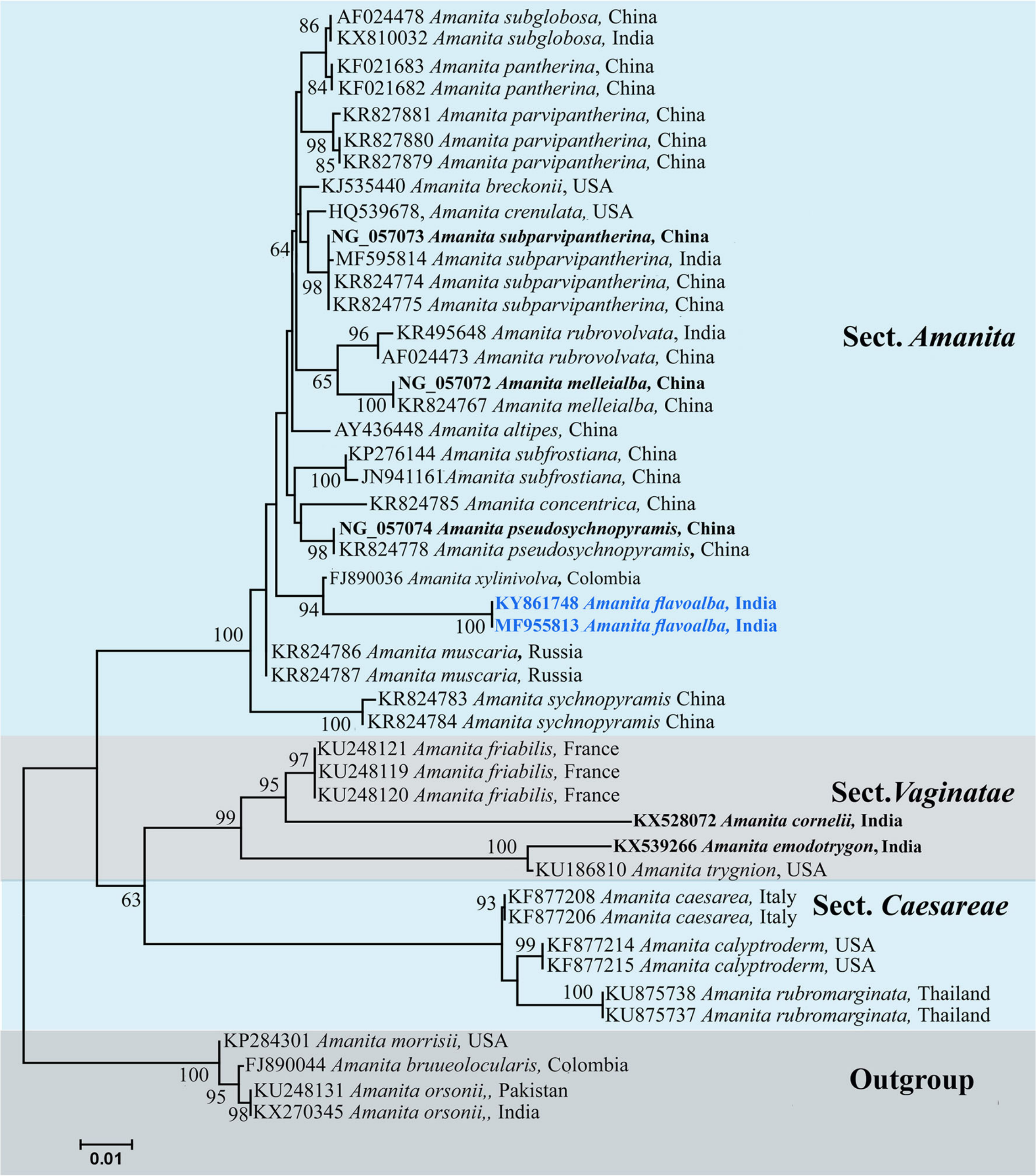


Fig. 128 Maximum likelihood phylogram of *Amanita* showing the position of *Amanita flavoalba*. Phylogenetic analysis was conducted in MEGA 6.0 (Tamura et al. 2013) based on LSU sequence data. Bootstrap support values (> 50%) obtained from maximum likelihood analysis are shown above or below the branches at nodes. New taxon is highlighted in blue. Type specimens are indicated in bold. *Amanita morrisii* Peck, *A. brunneolocularis* Tulloss & Franco-Mol. and *A. orsonii* Ash. kumar & T.N Lakh. were used as the outgroup taxa

at the base of basidia. *Basidiospores* [80/4/2] (7–)8.5–11(–12) × (5.5–)6–8(–8.5) µm, (L = 10.5 µm; W = 7.5 µm; Q = (1.19–)1.33–1.47(–1.6); Q' = 1.41), broadly ellipsoid to ellipsoid, non-amyloid, hyaline, thin-walled, smooth, apiculus sublateral, up to 1.7 µm high; contents monoguttulate. *Lamellar edge cells* sterile with inflated cells, subglobose to pyriform, 20–48 × 18–36 µm, thin-walled, colourless, hyaline or sometimes with yellowish brown pigments. *Pileipellis* 80–140 µm thick, in two layers; gelatinized suprapellis, 25–50 µm thick, composed of compactly arranged filamentous, undifferentiated hyphae 2–5 µm wide, thin-walled, colourless, hyaline; ungelatinized subpellis, 55–90 µm thick, composed of filamentous, undifferentiated hyphae 3–7 µm wide, radially arranged with yellowish brown intracellular pigments. *Pileus trama* filamentous, undifferentiated hyphae 3–8 µm wide; with broadly ellipsoid to ellipsoid cells, 30–65 × 10–20 µm. *Universal veil on pileus* with inflated cells globose to subglobose, 20–44 × 18–38 µm, broadly ellipsoid to ellipsoid, 16–62 × 12–38 µm; filamentous, undifferentiated hyphae 3–6 µm wide. *Universal veil on stipe* base is similar to that of pileus surface. *Stipe context* longitudinally acrophysalidic; acrophysalides 118–224 × 24–32 µm; filamentous, undifferentiated hyphae 2–10 µm wide, thin-walled hyaline. *Clamp connections* absent in all tissues.

Material examined: INDIA, Tehri Garwhal, Byasi, 510 m, N30°04.00′ E78°28.09′, 9 August 2015, T. Mehmood, TM 15-915 (CAL 1660, **holotype**); *ibid.*, Byasi, 18 August 2017, T. Mehmood, TM 17-1574.

Habit and habitat: Solitary to scattered, on ground under *Shorea robusta* C. F. Gaertn. (*Dipterocarpaceae*) in subtropical mixed forest.

Distribution: Indian Himalaya.

GenBank numbers: LSU = MG913204 (TM 17-1574); MG923799 (TM 15-915).

Notes: In the field, *Amanita subtropicana* is distinct from other known species of *Amanita* sect. *Vaginatae* by a combination of macroscopic characteristics: olive brown to yellowish brown pileus over centre, honey yellow to khaki colour towards margin which is covered by felted, subconical, subpyramidal to warty universal veil remnants on the pileal surface and broadly ellipsoid to ellipsoid basidiospores and putative association with *Shorea robusta* in subtropical broadleaf forest. *Amanita ceciliae* (Berk. & Broome) Bas, *A. liquii* Zhu L. Yang et al., *A. griseofolia* Zhu L. Yang, and *A. cinctipes* Corner & Bas are species of sect. *Vaginatae* which are somewhat similar to *A. subtropicana* on the basis of friable universal veil at the stipe base.

Amanita ceciliae, a European species, can be easily segregated from *A. subtropicana* by its yellow brown to grey-brown or olive-brown pileus with greyish to brownish universal veil remnants (Phillips 1990; Breitenbach and Kränzlin 1995). *Amanita liquii*, originally described from southwestern China, differs from *A. subtropicana* by its dark brown to blackish pileus with dark universal veil remnant and globose to subglobose basidiospores. Furthermore, it is associated with *Abies* and *Picea* (Yang et al. 2004). *Amanita griseofolia* differs by its grey to brownish grey pileus and felted to verrucose universal veil and globose to subglobose basidiospores (10–13.5 × 9.5–13 µm; Yang 2004). *Amanita cinctipes* (originally described from Singapore) is distinct from *A. subtropicana* by its mouse grey to greyish brown pileus with abundant universal veil remnants on the base of the stipe forming 2–4 rings and globose to subglobose basidiospores (Corner and Bas 1962).

Three Indian species, *Amanita cornelii* Mehmood et al., *A. emodotrygon* Mehmood et al. and *A. rajendrae* Mehmood et al. (GenBank no. KX528072, KX539266 and MF170174, respectively, in Fig. 131) of sect. *Vaginatae* are easily segregated from *A. subtropicana* by their distinct saccate universal veil on stipe base (Das et al. 2017b; Tibpromma et al. 2017).

Initial BLASTn search results of LSU sequence from Indian collection (TM 17-1574) against the NCBI database exhibited 87% similarity with 100% query coverage of *Amanita subtropicana* to "*Amanita* sp. Aus09" (GenBank no. KY349232). Phylogenetically (Fig. 131), *A. subtropicana* might have some closeness with *Amanita* sp. (Aus09), *A. madagascariensis* L.P. Tang et al. and *A. strobilaceovolvata* (Beeli) E.-J. Gilbert. Unfortunately, no morphological description of *Amanita* sp. (Aus09) is available for comparison of important morphological characteristics. *Amanita madagascariensis* originally described from East Africa can easily be separated by its dirty white or dull white pileus covered with greyish to brownish grey universal veil remnants and occurrence under *Eucalyptus* (Tang et al. 2015). *Amanita strobilaceovolvata*, originally described from the Congo, has a yellow to pale yellow pileus, a strobiloid saccate universal veil and subglobose to broadly ellipsoid basidiospores (8–10 × 7–9 µm) (Gilbert 1940; Tang et al. 2015).

Hygrophoraceae Lotsy

The family *Hygrophoraceae* contains 25 genera and over 600 species (Lodge et al. 2014). Most species in the family prefer a humicolous habitat, except for a few that are lignicolous, ectomycorrhizal, or on mosses (Griffith et al. 2002).

Hygrocybe (Fr.) P. Kumm

Hygrocybe is cosmopolitan in distribution (Senthilarasu et al. 2010). Currently, 457 species are listed as legitimate in Index Fungorum and MycoBank (2019). The genus is characterized by the presence of variously coloured basidiomes with waxy lamellae, absence of veilar remnants on the pileus margin as well as stipe, and white, inamyloid, smooth basidiospores (Boertmann 1995; Babos et al. 2011; Lodge et al. 2014; Hosen et al. 2016). Most species predominantly grow on soil, except for a few found on tree trunks or on logs (Lodge et al. 2006).

Hygrocybe lucida K. Acharya & A.K. Dutta, ***sp. nov.***

MycoBank number: MB826973; *Facesoffungi number*: FoF05720, Figs. 132, 133

Etymology: Refers to the bright colouration of the pileus.

Holotype: CUH AM123

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1978).

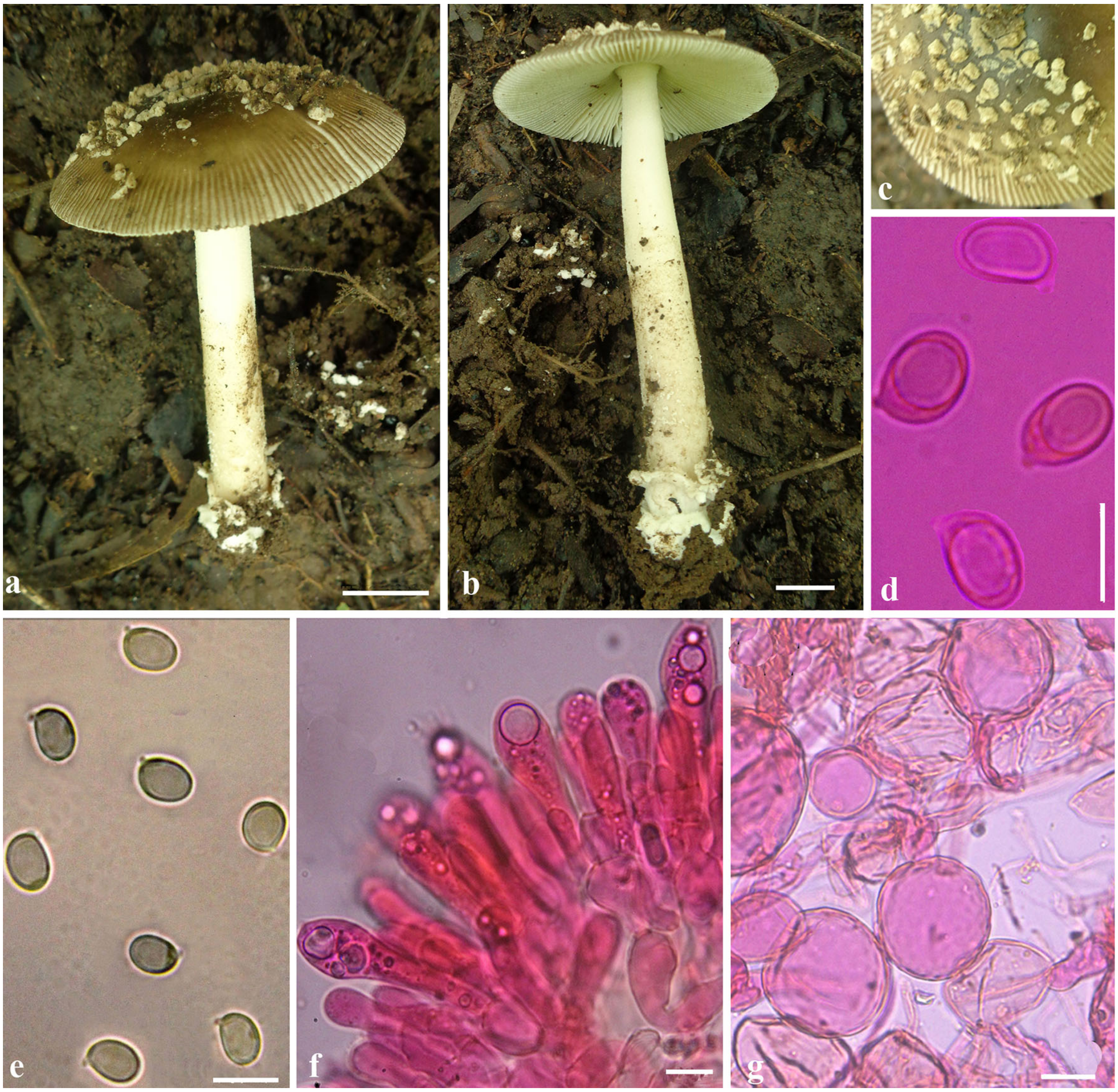


Fig. 129 ***Amanita subtropicana*** (CAL 1660, **holotype**). **a, b** Fresh basidiomes in the field. **c** Universal veil remnants on pileus surface. **d, e** Basidiospores. **f** Basidia and element of subhymenium. **g** Elements of universal veil on pileus surface. *Scale bars* **a, b** = 10 mm; **c–g** = 20 µm

Basidiomes small to medium-sized. *Pileus* 6–23 mm diam., convex to broadly convex when young, becoming somewhat infundibuliform at maturity; surface somewhat sticky when moist, greyish orange (5B5–6) to orange (6A6–7) or reddish orange (7A7) with a slightly darker (7A8, 7B8) disc when young, becoming light orange (6A5) to orange (6A6–7) with reddish orange (7A7, 7B7) to orange-red (8A7, 8B7–8) centre, no colour change on bruising or with age, smooth and glabrous, often slightly fibrillose; margin at first entire, turning wavy at maturity. *Lamellae* ca. 2–3 mm broad, adnexed to broadly adnate, thick, white (1A1), regular, often forked towards margin from half-way to the stipe, distant, with lamellulae of 1–2 lengths; edge concolorous with the sides, smooth. *Stipe* 4–11 × 1.5–3 mm, central, orange (5A6–7) to deep orange (5A8) or greyish orange (5B6), cylindrical, rarely slightly broader towards the apex, mostly glabrous, semi moist, often slightly fibrillose, hollow. *Odour and taste* indistinct. *Lamellar trama* regular, made up of 3.5–7.5 µm broad, cylindrical, IKI-, thin-walled, hyaline, hyphae, individual compartments 29–76 µm long, tubuliform elements absent. *Basidia* dimorphous; macrobasidia 50–53(–58) × 5–7(–8.5) µm, narrowly clavate to cylindric-clavate, thin-walled, with refractive oleaginous contents, 4-spored; microbasidia 32–35(–40) × 4–5(–7) µm, narrowly clavate, thin-walled, with refractive contents, 4-spored. *Basidioles* 32–39(–58) × 5–6(–7) µm, narrowly clavate, thin-walled, hyaline, with refractive contents. *Basidiospores* vaguely dimorphous; macrospores 9–10–*10.3*(–10.8) × (6–)6.5–*7*–7.2 µm, Q = 1.4–*1.45*–1.5, ellipsoid, hyaline, thin-walled, inamyloid, with refractive oleaginous

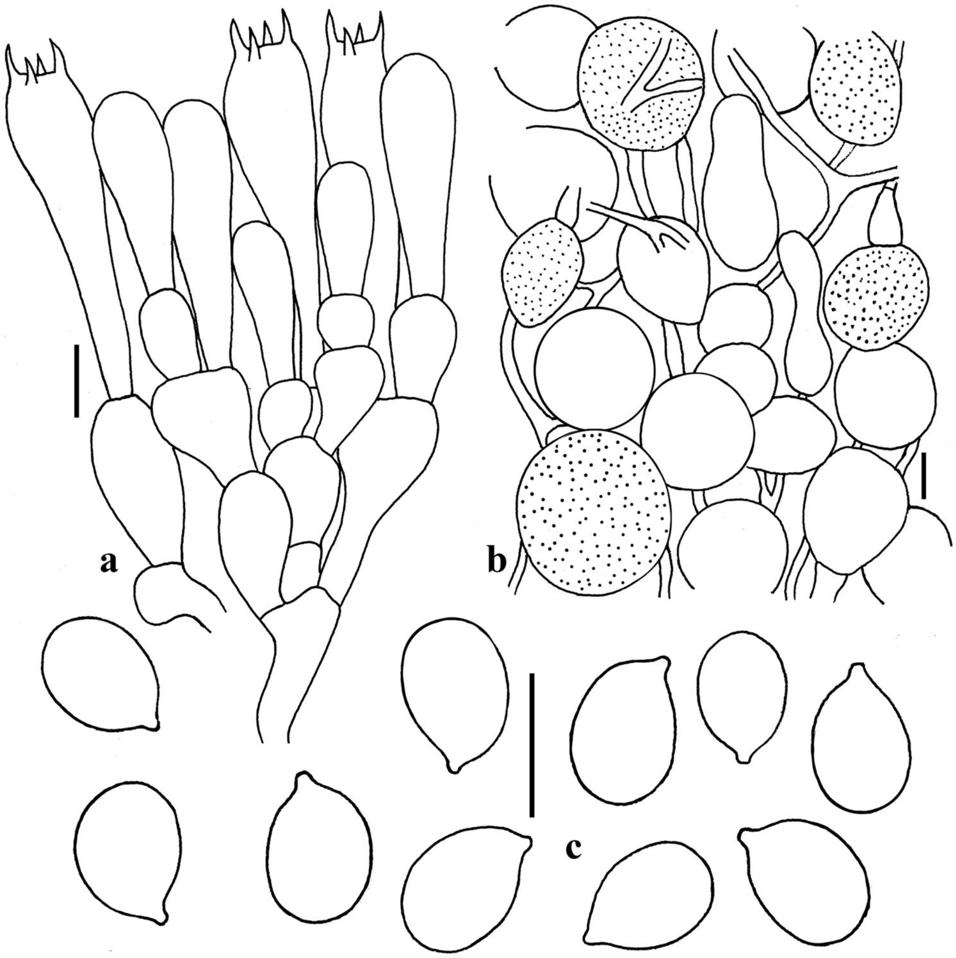


Fig. 130 ***Amanita subtropicana*** (CAL 1660, **holotype**). **a** Basidia and element of subhymenium. **b** Elements of universal veil from pileus surface. **c** Basidiospores. *Scale bars* **a** = 10 mm, **b–d** = 10 µm

contents when viewed in KOH, not constricted at the middle; microspores (6.4–)7–*7.2*–7.5(–7.9) × (3.9–)5–*5.5*–6.5(–6.8) µm, Q = 1.1–*1.3*–1.8 µm, subglobose to ellipsoid, hyaline, thin-walled, IKI-, with few refractive oleaginous contents in KOH, not constricted at the middle. *Lamellar edge* fertile. *Cheilo-* and *pleurocystidia* absent. *Pileipellis* an ixotrichodermium, made up of erect, mostly unbranched to often branched, cylindrical hyphae, (5–)7–10(–15) µm broad, hyaline, IKI-, thin-walled, hyphal end often broader. *Pileus tramal hyphae* 7–9 µm broad, hyaline, IKI-, thin-walled. *Stipitipellis* an ixocutis with thin-walled hyphae, 3.5–5.5 µm wide, hyaline. *Stipe trama* hyphae 7–8 µm broad, interwoven, hyaline, thin-walled, IKI-. *Caulocystidia* absent. *Clamp connections* present in all parts of the basidiome including the base of basidia.

Material examined: INDIA, West Bengal, North-24-Parganas, near Basirhat, 22°39′10.0″N, 88°52′00.3″E (alt. 9 m), 9 August 2015, K. Acharya & A.K. Dutta, CUH AM123 (**holotype**); *ibid.*, North-24-Parganas, Basirhat, 22°38′36.1″N, 88°53′35.3″E (alt. 9 m), 12 August 2015, K. Acharya & A.K. Dutta, CUH AM126.

Habit and habitat: Uncommon, solitary or scattered, on humus-rich soil.

Distribution: India.

GenBank numbers: ITS = MH599084 (CUH AM123); ITS = MH599083 (CUH AM126).

Notes: The distinguishing features of *Hygrocybe lucida* include small basidiome size, a convex (when young) to somewhat infundibuliform (at maturity), orange to reddish orange pileus that does not change colour on bruising or with age; white, adnexed to broadly adnate lamellae; an orange or greyish orange stipe; dimorphous basidiospores and basidia; absence of cheilo- and pleurocystidia; an ixotrichodermium-type pileipellis; regular lamellae trama composed of short hyphal elements (29–76 µm long); an ixocutis-type stipitipellis; absence of caulocystidia; and presence of clamp connections in all parts of the basidiome. This combination of features place the present species in sect. *Firmae* of subgen. *Pseudohygrocybe* (Pegler and Fiard 1978; Pegler 1986; Cantrell and Lodge 2001; Lodge and Ovrebo 2008). The morphological placement is further supported by the molecular phylogenetic analysis based on ITS sequence data (Fig. 134).

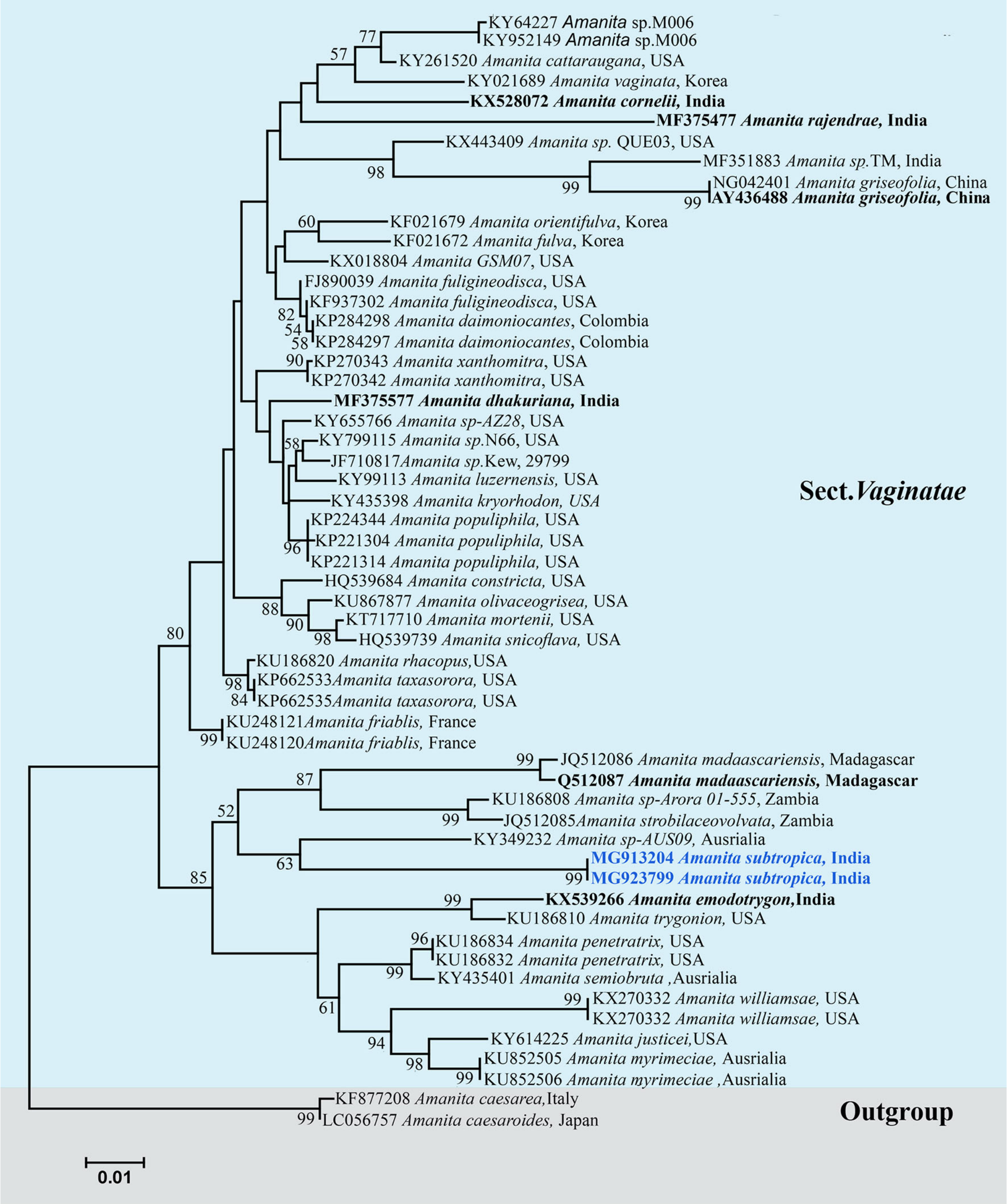


Fig. 131 Maximum likelihood phylogram of *Amanita* showing the position of *Amanita subtropicana*. Phylogenetic analysis was conducted in MEGA 6.0 (Tamura et al. 2013) based on LSU sequence data. Bootstrap support values (> 50%) obtained from maximum likelihood analysis are shown above or below the branches at nodes. The new taxon is highlighted in blue and bold on the tree. Type specimens are in bold. *Amanita caesareoides* Lj.N. Vassiljeva and *A. caesarea* (Scop.) Pers. were used as the outgroup taxa

Within sect. *Firmae*, species with more or less similar size of the macrospores include *Hygrocybe alwisii* (Berk. & Broome) Pegler, *H. diversicolor* (Petch) Pegler, and *H. earlei* (Murrill) Pegler. *Hygrocybe alwisii*, previously reported from India, and differing by a larger pileus (45–55 mm), adnexed to almost free lamellae, a longer stipe (60–70 mm), and a repent epicutis type of pileipellis (Pegler 1986; Leelavathy et al. 2006). *Hygrocybe diversicolor* has a larger pileus (up to 50 mm) that is olivaceous brown to blackish brown with appressed squamulose surface, longer stipe (30–35 mm), purplish grey to purplish black, and epicutis type of pileipellis (Pegler 1986).

Hygrocybe earlei, a species known only from Cuba and Trinidad, has a pileus that is initially campanulate and becomes expanded with a broad low umbo, and free to adnexed lamellae. *Hygrocybe* cf. *earlei*, previously known only from Panama, has an umbonate pileus, pale yellow lamellae with white edge, a pure white, much longer stipe (up to 40 mm), smaller macrobasidia (24–46 µm long) and microbasidia (22–30 µm long), and presence of an intermittent thin gelatinous coating in the pileipellis (Lodge and Ovrebo 2008).

Hygrocybe batistae Singer, described from Brazil and later found in Colombia and Puerto Rico, has similarly coloured basidiomes but differs by its rugulose to rugose pileus, caespitose basidiomes, and presence of coralloid hyphae in the pileipellis (Lodge and Pegler 1990; Cantrell and Lodge 2001; Lodge et al. 2014). *Hygrocybe neofirma* S.A. Cantrell & Lodge also has similarly coloured basidiomes but has a star-shaped perforation at the pileus centre, light yellow to brilliant yellow lamellae, and larger macrospores (12.8–17.6 × 8–10.4 µm; Cantrell and Lodge 2001).

Hygrocybe hypohaemacta (Corner) Pegler, previously placed within sect. *Firmae* and recently transferred to sect. *Velosae* based on phylogenetic analysis by Lodge et al. (2014), appears to be close to *H. lucida* in some morphological characteristics. However, *H. hypohaemacta* has a convex to plano-convex pileus that is covered by a thick (up to 1.5 mm) greyish gluten, discolorous lamellae with pale golden edge, longer stipe (up to 60 mm), somewhat differently sized macrospores (7–11 × 5–8 µm), presence of polymorphic cheilocystidia, and an epicutis-type pileipellis (Pegler and Fiard 1978).

Hygrocybe trinitensis (Dennis) Pegler and *H. siparia* (Berk.) Singer are comparable in having similar smaller pilei (Pegler and Fiard 1978). *Hygrocybe trinitensis* differs by the presence of coral red lamellae that are broadly adnate with a decurrent tooth, a longer stipe (up to 50 mm), smaller macrospores (7–9 × 4.5–5.5 µm, Q = 1.56), smaller macro- and micro-basidia, and an epicutis-type pileipellis that contains red vacuolar pigments. *Hygrocybe siparia*, described from Brazil, has an umbilicate pileus with squamulose surface, lamellae with a decurrent tooth, longer macrospores (10–13 µm long, Q = 1.53), and smaller macro-basidia (40–48 µm long).

Among phylogenetically related taxa (Fig. 134), *Hygrocybe firma* (Berk. & Broome) Singer differs by its yellow pileus, strongly decurrent lamellae, and longer macrospores (11–18 µm long) (Berkeley and Broome 1871; Young and Mills 2002). *Hygrocybe andersonii* Cibula & N.S. Weber, originally described from Horn Island of Mississippi, has densely cespitose growth habit, brownish orange to deep orange lamellae, longer stipe (up to 42 mm long) reddish brown, and large bacilliform basidiospores (14–20.7 × 3.8–5.6 µm; Cibula and Weber 1996).

Fig. 132 ***Hygrocybe lucida*** (CUH AM123, **holotype**). Basidiomes in the field (lamellae facing side, in inset). *Scale bars* 10 mm. Photos by A.K. Dutta

Marasmiaceae Roze ex Kühner

Marasmiaceae is a family of pale-spored agarics. It has a worldwide distribution and comprises about 54 genera and 1590 species (Kirk et al. 2008). Several of these taxa were previously considered under *Tricholomataceae sensu lato* (Moncalvo et al. 2002; Matheny et al. 2006). Most species are saprobes that play a leading role in nutrient-recycling and form prominent components of forest ecosystems (Cannon and Kirk 2007). A novel species, *Marasmius indojasminodorus* is introduced within *Marasmiaceae*. An updated phylogenetic tree of ITS sequence data based on maximum likelihood and Bayesian inference analyses of the genus *Marasmius* is provided (Fig. 135). Detailed literature and updated accounts of *Marasmius* were provided by Wannathes et al. (2009) and Tibpromma et al. (2017).

Marasmius Fr.

We follow the latest treatment and updated accounts of *Marasmius* in Komura et al. (2016) and Tibpromma et al. (2017).

Marasmius indojasminodorus A.K. Dutta, K. Acharya & K. Das, ***sp. nov.***

MycoBank number: MB820566; *Facesoffungi number*: FoF03247, Figs. 136, 137

Etymology: Refers to an Indian look-a-like of the Thai taxon *Marasmius jasminodorus*

Holotype: CAL 1514

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1978).

Pileus 12–21 mm diam., conical to convex when young, becoming broadly convex at maturity, often with a small

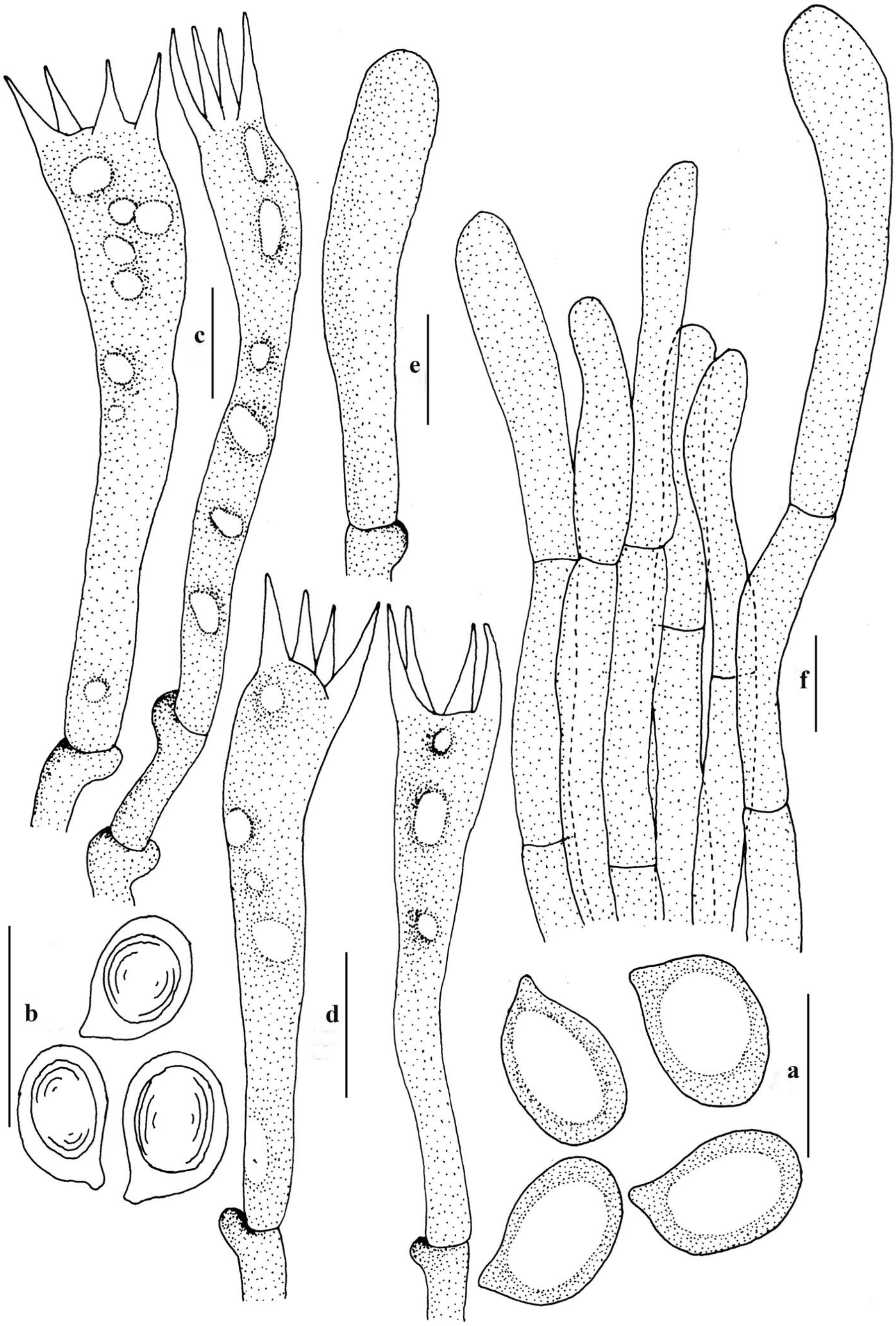


Fig. 133 ***Hygrocybe lucida*** (CUH AM123, **holotype**). **a** Macrospores. **b** Microspores. **c** Macrobasidia. **d** Microbasidia. **e** Basidioles. **f** Pileipellis hyphae. *Scale bars* **a–f** = 10 µm. Drawings by A.K. Dutta

umbonate centre, smooth to minutely pruinose, moist to semi moist, hygrophanous; disc rugulose, olive-brown (4D5–8) or light brown (5D7) to yellowish brown (5D–E8, 5F7–8), turning translucent with KOH; margin smooth when very young, rugulose-striate in age, slightly paler, yellowish brown (5D4–6, 5E4–5), turning translucent with KOH. *Lamellae* 2–2.5 mm broad, adnexed, subdistant (L = 14–16, l = 2–3), white (1A1) to cream, non-marginate, concolorous, non-intervenose. *Stipe* 15–40 × 1–1.5 mm, central, cylindrical, hollow, glabrous to slightly velutinous, non-insititious, overall white when young, at maturity apex becoming white to cream, base light brown (6D6) to brown (6D8), strigose at base, yellowish white to brownish white. *Context* 1 mm broad at centre, gradually thinner towards margin, creamy white, turning translucent with KOH. *Odour* strong, fragrant, sweet, like jasmine. *Taste* slightly bitter. *Lamellar trama* composed of 6–7(–7.5) µm broad, interwoven, cylindrical, hyaline, dextrinoid, non-gelatinous, thin- to thick-walled hyphae. *Basidia* not observed. *Basidioles* 21–22.5(–26) × (4–)6–6.5(–7.5) µm, fusoid to clavate, hyaline, thin-walled. *Basidiospores* (6.5–)8–*8.7*–10(–10.5) × 3.5–*3.7*–4 µm, Q = 1.8–*2.4*–2.8, ellipsoid, often curved in profile, hyaline, inamyloid, thin-walled. *Pleurocystidia* absent. *Cheilocystidia* composed of *Siccus*-type broom cells; main body 10–12(–15) × (3.5–)6–7(–7.5) µm, clavate to subclavate, hyaline, thin- to moderately thick-walled; apical setulae (3–)6.5–7(–9.5) µm long, cylindrical, acute to obtuse, yellowish in KOH, thick-walled. *Pileipellis* hymeniform, consisting of *Siccus*-type broom cells; main body (10–)12.5–14(–16.5) × (5–)6.5–7(–8) µm, cylindrical to clavate or broadly clavate, hyaline, inamyloid, thin- to moderately thick-walled; apical setulae (3.5–)5–7(–10.5) µm long, cylindrical, obtuse, yellowish with KOH, thick-walled. *Pileus trama* hyphae 3.5–5.5 µm broad, interwoven, cylindrical, often branched, hyaline, dextrinoid, thin-walled. *Stipitipellis* hyphae 3.5–4.5 µm broad, parallel, yellowish, cylindrical, dextrinoid, thin-walled. *Stipe trama* hyphae 4–7(–9) µm broad, parallel, hyaline, dextrinoid, cylindrical, non-gelatinous, thin- to moderately thick-walled. *Caulocystidia* of two types: a) abundant non-setulose cells, (17–)28–32(–36) × 6–7(–11) µm, cylindrical to irregular in outline, often seldom branched, rarely bilobed at apex, thin- to moderately thick-walled; b) *Siccus*-type brooms cells with main body 20–21.5(–25) × 3.5–4.5(–5) µm, uncommon, scattered, cylindrical to irregular in outline, hyaline, thin-walled; apical setulae 10–12.5 µm, cylindrical to irregular in outline, thin- to moderately thick-walled. *Clamp connections* present in all the tissues.

Material examined: INDIA, West Bengal, Howrah District, Acharya Jagadish Chandra Bose Indian Botanic Garden, 22°33′35.3″N, 88°17′21.5″E (alt. 12.2 m), 23 September 2015, A.K. Dutta & S. Paloi, AKD 135/2015 (CAL 1514, **holotype**); *ibid.*, 22°33′38.4″N, 88°17′22.6″E (alt. 15.1 m), 23 September 2015, A.K. Dutta & S. Paloi, AKD 139/2015 (CAL 1515).

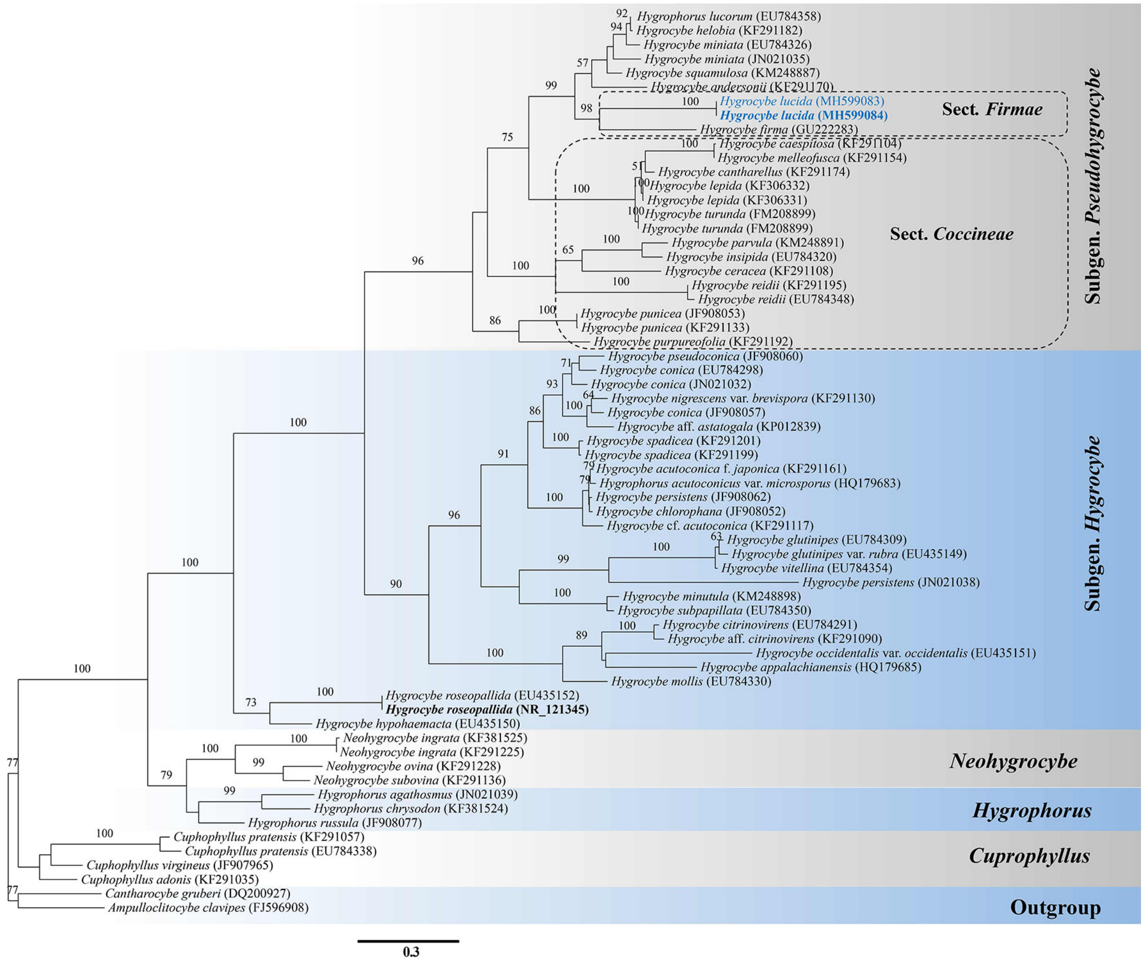


Fig. 134 Phylogram generated from maximum likelihood (RAxML) analysis using a GTR + I+G model of nucleotide evolution based on ITS sequence dataset. *Ampulloclitocybe clavipes* and *Cantharocybe gruberi* were used as the outgroup taxa following Lodge et al. (2014). Maximum likelihood bootstrap support values greater than 50% are indicated above or below the nodes. Sequences used in this study mostly have been sampled from a previous study of Lodge et al. (2014). The newly generated sequences are placed in blue font to highlight its phylogenetic position in the tree. GenBank accession numbers for all of the sequences are indicated in the tree

Host and habitat: Uncommon, scattered to gregarious, on dead and decayed leaves and wood of dicotyledonous plants.

GenBank numbers: ITS = KY785172, LSU = KY785174 (CAL 1514); ITS = KY785171, LSU = KY785173 (CAL 1515).

Notes: The most distinctive combination of features of *Marasmius indojasminodorus* includes a small to medium sized (12–21 mm diam.), convex to broadly convex, rugulose-striate yellowish brown pileus with a rugulose, olive brown to light brown or yellowish brown disc; adnexed, subdistant (14–16), white to cream, lamellae with lamellulae of 2–3 lengths; a non-insititious, glabrous to slightly velutinous stipe coloured white to cream at apex and light brown to brown at base, with yellowish white to brownish white basal mycelium; strong, sweet, jasmine like odour; ellipsoid basidiospores with a mean size of 8.7 × 3.7 µm (Q = 1.8–2.8); *Siccus*-type cheilocystidia with main body 10–15 × 3.5–7.5 µm; absence of pleurocystidia; and two types of caulocystidia, *Siccus*-type in combination with numerous non-setulose cells, cylindrical to irregular in outline (17–36 × 6–11 µm). This combination of features undoubtedly place the present taxon within *Marasmius* ser. *Atrorubentes* of sect. *Sicci* (Wannathes et al. 2009).

Among taxa that possess jasmine-like odour, *Marasmius jasminodorous* Wannathes et al. (Wannathes et al. 2009), described from Northern Thailand, differs by its colouration of pileus (dark reddish brown towards disc with light brown to brownish orange margin), basal mycelium of the stipe (brownish orange), and larger basidiospores with a mean range of 10.1 × 3.6 µm (Q_m = 2.8). *Marasmius odoratus* V.A. Farook & Manim., recently described from Kerala state of India, primarily differs by the presence of “*Globulares*-type” cells in the pileipellis and is categorized under sect. *Globulares* (Farook and Manimohan 2015).

Among other similar species belonging to sect. *Sicci*, and phylogenetically close taxa (Fig. 135), *M. midnapurensis* A.K. Dutta et al., described from India, primarily differs from *M. indojasminodorus* by the absence of jasmine-like odour, longer basidiospores (10.7–15 µm long, Q_m = 3), comparatively broader main-body of cheilocystidia (up to 10 µm broad), and longer (up to 50 µm), and non-setulose caulocystidia (Dutta et al. 2014). The Indonesian taxon, *M. araucariae* var. *siccipes* Desjardin et al. differs by its non-rugulose pileus, orange brown all over or with darker disc, discolorous lamellae with orange-brown edge, glabrous stipe, absence of any fragrant odour, and distinctly longer (11–12 × 3–4 µm), subfusoid basidiospores (Desjardin et al. 2000). *Marasmius ochroleucus* Desjardin & E. Horak, described from New Caledonia and subsequently reported from Northern Thailand, primarily differs by its light yellow to cream pileus, much crowded (L = 20–24, l = 3–4), and intervenose lamellae, and presence of only one type of caulocystidia shaped cylindrical to fusoid-ventricose (Wannathes et al. 2009). The Korean taxon *M. occultatiformis* Antonín et al. has brownish orange to brownish red pileus and slightly paler towards margin, presence of more lamellae (L = 25) finely pubescent towards edge, whitish basal mycelium, somewhat differently sized basidiospores (mean of 7.8 × 4 µm, Q = 1.95), and absence of caulocystidia (Antonín et al. 2012). *Marasmius araucariae* Singer, described from Argentina, has castaneous-ferruginous or ferruginous pileus, more lamellae (16–24), comparatively longer stipe (up to 70 mm long) with fulvous-white basal mycelium, absence of any odour, larger basidiospores (9–12.5 × 2.7–4.5 µm), and only one type of caulocystidia, subcylindric, 50 × 5.5 µm (Singer 1976). *Marasmius napoensis* Singer differs by its larger pileus (up to 60 mm diam.) with deeply sulcate margin, distant lamellae, longer stipe (60–77 mm long), absence of any strong odour, and presence of only *Siccus*-type caulocystidia (Singer 1976).

Marasmius pellucidus Berk. & Broome, although phylogenetically related as revealed in Fig. 135, possess *Globulares*-type of cells in the pileipellis and is categorized under a sect. *Globulares* (Wannathes et al. 2009). The other distinguishing features of *M. pellucidus* from that of *M. indojasminodorus* includes a plano-campanulate to almost applanate pileus, ivory to pale orange towards disc with white to cream or pale yellowish white margin, and presence of comparatively more lamellae (up to 26; Wannathes et al. 2009).

Omphalotaceae Bresinsky

The family *Omphalotaceae* was proposed by Bresinsky in Kämmerer et al. (1985) to accommodate the genera *Omphalotus* Fayod and *Lampteromyces* Singer. The members of the family are characterized by fleshy, brightly coloured and often luminescent basidiomes with a glabrous or fibrillose pileus, decurrent lamellae, central or eccentric stipe devoid of any veil, hyaline, smooth, globose or ellipsoid and inamyloid basidiospores, clavate basidia often intergrading with cystidioles, the absence of cystidia and monomitic hyphal system with clamp connections (Cannon and Kirk 2007). Species of *Omphalotaceae* are saprobic or necrotrophic on wood or litter (Moncalvo et al. 2002). Moncalvo et al. (2002), in their broad systematic treatment of the euagarics using LSU sequence, observed that several genera that were traditionally classified in various families or tribes of *Agaricales* (Singer 1986) and *Caripia montagnei*, a reduced form that was generally placed in the *Stereales* (Hawksworth et al. 1995) were clustered together in *Omphalotaceae* clade together with lentinuloid and omphalotoid species. In their overview of phylogeny of

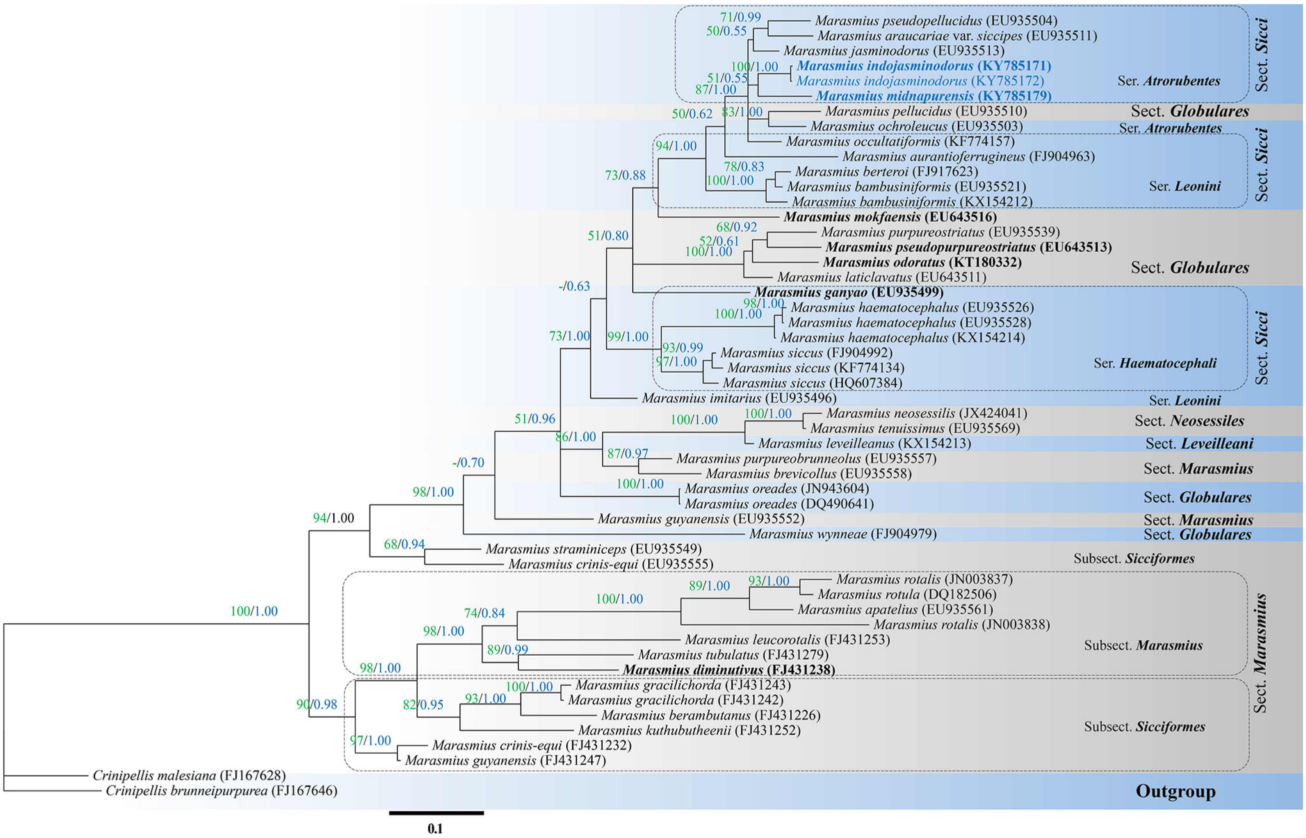


Fig. 135 Consensus phylogram (50% majority rule) obtained from MCMC analysis of one million generations from a Bayesian inference analysis based on ITS region for *Marasmius* taxa and two outgroup sequences (*Crinipellis brunneipurpurea* and *C. malesiana*). Maximum likelihood (RAxML) bootstrap support (left) ≥ 50% and Bayesian posterior probabilities (right) ≥ 0.50 are indicated above the nodes. Sequences used in this study mostly have been sampled from a previous study (Tan et al. 2009; Wannathes et al. 2009). The newly generated previously described type specimen sequence of *Marasmius midnapurensis* and the sequences of the newly described taxa for the present study are placed in blue font to highlight its phylogenetic position in the tree. Ex-type strains are in bold. GenBank accession numbers for all of the sequences are indicated in the tree

Fig. 136 ***Marasmius indojasminodorus*** (CAL 1514, **holotype**). *Scale bar* 5 mm. Photo by A.K. Dutta

major clades of *Agaricales*, Matheny et al. (2006) recovered *Omphalotaceae* as monophyletic family.

Marasmiellus Murrill

Marasmiellus is a predominantly tropical and subtropical genus that encompasses more than 400 species known worldwide (Wilson and Desjardin 2005; Blanco-Dios 2015). Traditionally, the genus had been placed in family *Tricholomataceae* (Singer 1986). While Kirk et al. (2008) treated it in the *Marasmiaceae*, DNA-based molecular phylogenetic studies of Moncalvo et al. (2002) and Wilson and Desjardin (2005) indicated that this genus belongs to the *Omphalotaceae*. *Marasmiellus* is characterized by collybioid, omphalioid or pleurotoid basidiomes, slightly decurrent, intervenose lamellae, smooth, white or off-white and inamyloid basidiospores, and pileipellis or stipipellis showing a Rameales-structure (Singer 1973; Pérez-De-Gregorio et al. 2011). Most of the species are saprobes occurring on dead and rotting plant material and some are host specific. A few species are found on living hosts. According to Wilson and Desjardin (2005), the genus is polyphyletic. In the course of our studies on the agarics of Kerala State, India, we came across a remarkable species of *Marasmiellus*. It is formally described here as a new

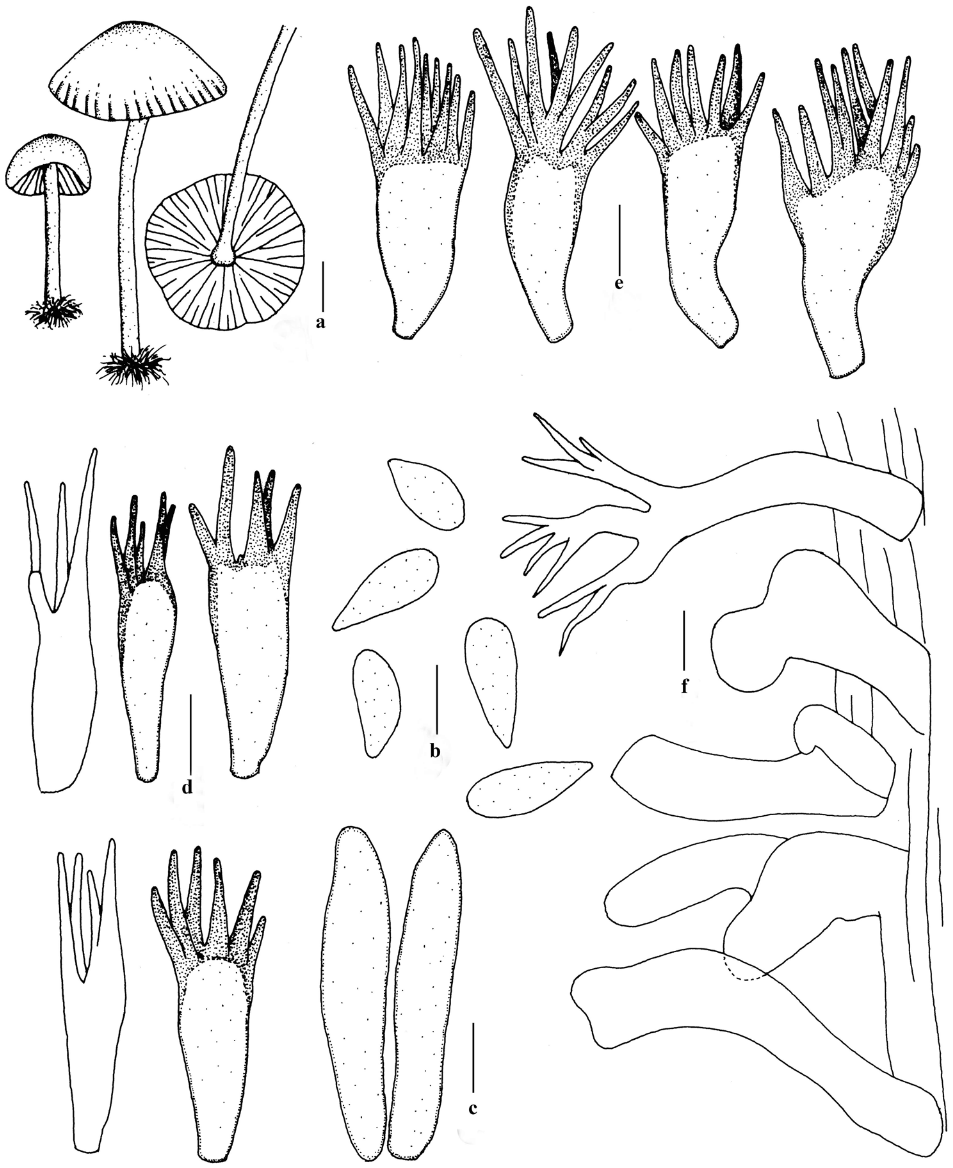


Fig. 137 ***Marasmius indojasminodorus*** (CAL 1514, **holotype**). **a** Basidiomes. **b** Basidiospores. **c** Basidioles. **d** *Siccus*-type cheilocystidia. **e** *Siccus*-type cells of the pileipellis. **f** Caulocystidia showing setulose and non-setulose cells. *Scale bars* **a** = 5 mm, **b–f** = 5 µm. Drawings by A.K. Dutta

species based on both morphology and molecular phylogeny (Fig. 138).

Marasmiellus bicoloripes K.P.D. Latha, K.N.A Raj & Manim., ***sp. nov.***

MycoBank number: MB820689; *Facesoffungi number*: FoF03251, Figs. 139, 140

Etymology: Referring to the bicoloured stipe of the basidiomes.

Holotype: CAL 1524.

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1978) and the Online Auction Color Chart (Anonymous 2004).

Basidiomes small, somewhat omphalinoid. *Pileus* 5–20 mm diam., initially convex, becoming plano-convex with a small umbo surrounded by a shallow depression at maturity; surface brown (6F4/OAC733) all over when young, becoming greyish brown (6D3/OAC730) at the centre and brownish beige (6E3/OAC723) towards the margin, not hygrophanous, faintly pellucid-striate, appressed-fibrillose all over; margin decurved to somewhat straight, initially entire, becoming somewhat wavy. *Lamellae* adnate or subdecurrent, somewhat thick and waxy, often furcate and anastomosing, close, brownish orange (6E2/OAC724), up to 2 mm wide, with lamellulae of 2–3 tiers; edge finely torn, concolorous with the sides. *Stipe* 12–14 × 1–2 mm, central, terete, equal or slightly tapering towards the base, solid; surface initially white all over, becoming dark grey (5E1, 5F1/OAC904) towards the base at maturity, appressed-fibrillose all over. *Odour* and *taste* not distinctive. *Lamellar trama* subregular, hyphae 3–9 µm wide, hyaline, thin-walled, inamyloid. *Subhymenium* poorly developed pseudoparenchymatous. *Basidia* 20–31 × 4–6 µm, clavate or occasionally pedicellate clavate, hyaline, thin-walled, 4- or 2-spored; sterigmata up to 5 µm long. *Basidiospores* 4–8 × 3–4(–5) (6.5 ± 1.5 × 3.5 ± 0.6) µm, Q = 1.3–2.7, Q_m = 1.9, oblong-ellipsoid, pip-shaped or subfusiform, often with a stretched-out apicular end, with prominent guttules, hyaline, inamyloid, smooth, thin-walled. *Lamellar edge* heterogeneous. *Pleurocystidia* absent. *Cheilocystidia* 20–32 × 4–8 µm, scarce, scattered, versiform: clavate with short or long, apical diverticulate projections or with a mucronate apex, cylindrical with a mucronate apex, utriform with a rostrate apex or flexuous, thin-walled, hyaline. *Pileus trama* interwoven; hyphae 3–10 µm wide, hyaline, thin-walled, inamyloid. *Pileipellis* a differentiated cutis with occasional nodulose-diverticulate hyphae; hyphae 3–18 µm wide, with a yellowish brown plasmatic pigment and strong, yellowish brown spiral encrustions, thin- to slightly thick-walled. *Stipitipellis* an epicutis; hyphae 3–6 µm wide, hyaline or with a yellowish brown plasmatic pigment, thick-walled (up to 1 µm thick), often giving rise to short or long, sometimes diverticulate side branches, 17–108 × 3–5 µm, slightly thick-walled towards the base. *Caulocystidia* absent. *Clamp connections* observed on all hyphae.

Material examined: INDIA, Kerala State, Ernakulam District, Pooyamkutty, 22 November 2014, K.P.D. Latha, DKP331 (CAL 1524, **holotype**).

Host and habitat: In small group among on a decaying twig.

GenBank numbers: ITS = KY807129, LSU = KY817233.

Notes: *Marasmiellus bicoloripes* is characterised by omphalinoid basidiomes with a greyish brown, faintly striate and fibrillose pileus, brownish orange, anastomosing and somewhat thick and waxy lamellae, a white stipe turning dark grey towards the base, oblong-ellipsoid to subfusiform basidiospores, a hymenium devoid of pleurocystidia, a heterogeneous lamellar edge with scattered cheilocystidia, a cutis-type pileipellis with occasional nodulose-diverticulate hyphae, an epicutis-type stipitipellis with frequent nodulose-diverticulate hyphae and presence of clamp connections. Owing to the combination of characteristics such as the stipe tending to greyish at the base, the cutis-type pileipellis with occasional diverticulate hyphae and the short basidiospores (less than 10.4 µm), this species can be placed either in sect. *Candidi* (Bat.) Sing. or in sect. *Dealbati* Sing. (Singer 1986) of *Marasmiellus*.

Marasmiellus cibodasensis Retnowati, an Indonesian species described invalidly by Retnowati (2012), differs in having a flattened pileus with a wrinkled surface, subdistant, non-anastomosing lamellae, an apically tapered, granulose and bulbous stipe which is not darkening towards the base, ellipsoid basidiospores, a fertile lamellar edge devoid of cheilocystidia and a gregarious habit on wood. *Marasmiellus rhizomorphigenus* Antonín et al., known from Republic of Korea (Antonín et al. 2010), differs in having a greyish to whitish pileus with a pubescent to tomentose surface, whitish to pale yellowish and distant lamellae, a stipe with a pubescent to furfuraceous surface, presence of rhizomorph, larger basidiospores (13.5–17 × 4.5–6.5 µm), well-developed, larger hymenial cystidia (34–70 × 8–14 µm) and presence of pileo- and caulocystidia. *Marasmiellus koreanus* Antonín et al. also described from Republic of Korea (Antonín et al. 2010), has larger, robust basidiomes with a brownish orange, rugulose pileus, light yellow lamellae, whitish to light yellow stipe, versiform cheilocystidia and stipitipellis with copious caulocystidia. *Marasmiellus candidus* (Fr.) Singer, a widespread species in Europe (Noordeloos 1995), differs in having a pure white, pruinose to tomentose pileus with a grey-brown centre, a pruinose stipe with a bulbous base, oblong to cylindrical and larger basidiospores [(10.5–)11.5–15(–17.5) × (7.5–)8.0–12.5 µm], copious and larger cheilocystidia (45–90 × 6–12.5 µm), an irregular cutis-type pileipellis with a transition to a trichoderm and the stipitipellis with caulocystidia.

The phylogenetic trees inferred from the ML and BI analyses of the ITS sequence dataset show identical topology and the ML phylogram is presented in Fig. 138. The tree reveals two distinct clades, the Tetrapyrgos and the Marasmiellus clades, as shown by Wilson and Desjardin (2005) and subsequently confirmed by Antonín et al. (2010). *Marasmiellus bicoloripes* nests in the Tetrapyrgos clade with 82% ML and 1.00 BYPP support. Within this clade, *M. bicoloripes* together with collections of *M. rhizomorphigenus*, *M. tenerrimus* (Berk. & M.A. Curtis) Singer and *M. candidus* formed a cluster where *M. bicoloripes* was found to be a lineage distinct from other species with significant support (73% ML and 1.00 BYPP). It has to be emphasized here that the clade Tetrapyrgos does not exactly correspond to the genus *Tetrapyrgos* as the latter is primarily characterised by tetrahedral basidiospores and a stipe arising from a basal pad (Honan et al. 2015) while some species including *M. bicoloripes* and *M. candidus* that form part of the clade Tetrapyrgos do not show these features.

Psathyrellaceae Vilgalys et al.

Based on molecular studies, Redhead et al. (2001) introduced the family *Psathyrellaceae* to accommodate the genera *Psathyrella* (Fr.) Quél. and *Lacrymaria* Pat., together with related species in the polyphyletic genus *Coprinus sensu lato*, which were transferred to the genera *Coprinellus* P. Karst., *Coprinopsis* P. Karst. or *Parasola* Redhead et al. A few species related to *Agaricus* remained in *Coprinus sensu stricto*. Therefore, the concept of family *Coprinaceae* Overeem & Weese was abandoned and

Coprinus sensu stricto was transferred to *Agaricaceae* Chevall. Afterwards, several smaller genera were included in *Psathyrellaceae*. Kirk et al. (2008) consider the family to contain 12 genera.

Coprinopsis P. Karst.

Coprinopsis is a large genus that contains around 200 species (Kirk et al. 2008). They are saprotrophic on soil, wood, vegetable refuse, dung or burnt ground, and produce agaricoid, rather fragile basidiomes which are often short lived and/or deliquescent, with black to blackish spore deposit (Vesterholt 2012). The phylogenetic tree is presented in Fig. 141.

Coprinopsis kubickae (Pilát & Svrček) Redhead, Vilgalys & Moncalvo, in Redhead et al., Taxon 50(1): 229 (2001)

Facesoffungi number: FoF05721, Fig. 142

Basionym: Coprinus kubickae Pilát & Svrček, Česká Mykol. 21: 142 (1967).

Holotype: Czechoslovakia, on culm of *Juncus*.

Pileus up to 10 mm wide when expanded, sphaerical at first, then ellipsoid to ovoid, paraboloid, convex, finally applanate or plano-concave with revolute margin, plicate-sulcate except at the centre, whitish to pale brown when young, then pinkish, finally brownish grey except brownish central disc, non-deliquescent, covered with scarce, minute, brownish to brown flocculose veil. *Lamellae* free, distant, L = 22–34, l = 1–3, white at first, becoming pinkish, then reddish brown with whitish and flocculose edge, finally brown-black and deliquescent. *Stipe* 16–28 × 0.8–1.2 mm, cylindrical or gradually thickened towards the base, which is often (sub) bulbose or with basal disc (up to 2 mm wide), central, hollow, dry, minutely fibrillose-floccose, often tomentose at the base, white. *Odour* and *taste* not observed. *Spore print* brown-black. *Basidia* 14–31 × 9–12 µm, clavate, 4-spored, thin-walled, hyaline, surrounded by 5–8 hymenophysalides (pseudoparaphyses). *Basidiospores* [100/2/1] 8–*9.6*–11.1 × 6.9–*8.2*–9.3 µm, Q = (1–)1.05–*1.17*–1.30(–1.38), mostly subglobose, broadly ellipsoid or ovoid, but also globose and ellipsoid, not flattened, with rounded to slightly conical base and rounded apex, smooth, thin-walled to moderately thick-walled (up to 0.7 µm), with 1.2–1.8 µm wide (inner diameter), central to eccentric germ-pore, medium rusty brown in H_2O and NH_4OH, medium brown in KOH, but soon becoming medium brown grey, semi-transparent, non-amyloid and non-dextrinoid. *Cheilocystidia* 30–90 × 9–24 µm, narrowly utriform to utriform, oblong, subcylindrical, conical or narrowly clavate, thin-walled to moderately thick-walled (up to 0.7 µm), hyaline, scattered. *Pleurocystidia* 50–110 × 13–24 µm, similar to cheilocystidia, but somewhat more elongated, mostly narrowly utriform, narrowly conical or subcylindrical, scattered. *Veil* composed of 2–6 µm broad, branched, thin-walled, rather sparsely diverticulate, hyaline to light yellowish brown hyphae, mostly with minutely to coarsely encrusted, light to dark brown pigment. *Pileipellis* a cutis, composed of repent, hyaline, thin-walled, 1.5–5 µm wide hyphae. *Stipitipellis* a cutis of parallel, repent, thin-walled, hyaline, 1–8 µm wide hyphae, sparsely diverticulate, with ascending hyphal tufts in places. *Clamp connections* present and abundant in all tissues.

Material examined: CROATIA, Karlovac County, Fishpond Draganići, 10 km NE from Karlovac, 45°33′40″N, 15°38′21″E, 107 m a.s.l., 7 September 2013, leg. M. Čerkez, CNF 1/6614.

Host and habitat: Solitary or in small groups on dead *Phragmites*, *Typha*, *Juncus*, *Carex*, *Glyceria* and *Acorus* species in wet habitats, as well as on rich soil and rotten straw in greenhouses (Uljé 2005; Nagy 2007; Gierczyk et al. 2011). From Canada reported on wood submerged in an alkali lake (Anastasiou 1967; as *Coprinus amphibius* Anastasiou). Our collection was collected on wet remnants of *Phragmites australis*, on the marshy edge of a fishpond.

Distribution: Known from about 15 European countries and Canada, rare.

GenBank number: ITS = MH422562.

Notes: *Coprinopsis kubickae* is primarily characterized by its branched, diverticulate and thin-walled veil elements, presence of clamp connections, smooth, globose to broadly ellipsoid, not flattened spores, rather small basidiomes and by living on plant (almost always herbaceous) remnants in wet habitats. Morphologically (according to branched and diverticulate veil), it belongs to section *Alachuani* (Singer) D.J. Schafer. However, the morphological concept of section *Alachuani* is not supported by molecular data and several *Alachuani* species are mixed with species of sections *Atramentarii* (Fr.) D.J. Schafer and *Lanatuli* (Fr.) D.J. Schafer in our ITS based phylogram (Fig. 141). Still, *Coprinopsis kubickae* nests in the clade with the rest of *Alachuani* species. We report *Coprinopsis kubickae* as new to Croatian mycobiota.

Boletales E.-J. Gilbert

Boletaceae Chevall.

Boletaceae is an important Basidiomycete family with a global distribution, most of which form ectomycorrhizal associations with trees. Most species have been described from temperate regions, and little research had been carried out on tropical boletes before 2010. In the past decade, however, phylogenetic analyses based on multigene dataset and including tropical taxa, have greatly improved our understanding of the systematics of the group, with many new genera and species being published (e.g., Halling et al. 2012; Hosen et al. 2013; Wu et al. 2015, 2016; Henkel et al. 2016). This molecular revolution has left a number of *Boletaceae* species (especially in the large genus *Boletus*)

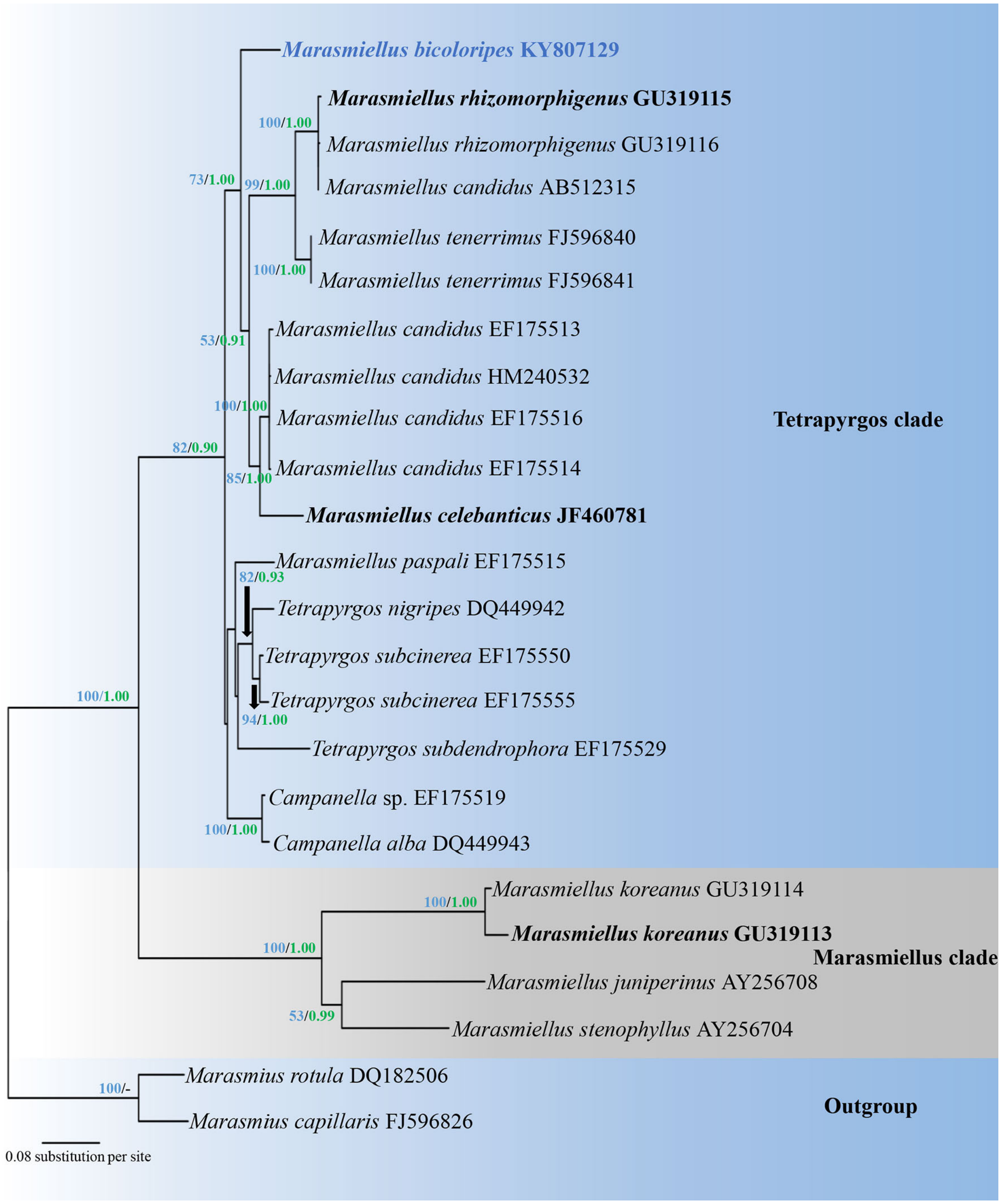


Fig. 138 Phylogram derived from maximum likelihood (RAxML) analysis using ITS sequence dataset. Maximum likelihood (RAxML) bootstrap support (left) ≥ 50% and Bayesian posterior probabilities (right) ≥ 0.90 BYPP are indicated above the nodes. *Marasmiellus bicoloripes* is highlighted in blue. *Marasmius rotula* and *M. capillaris* are selected as the outgroup taxa

to be re-examined and recombined in the light of modern classification of the family. A novel species, *Baorangia major* is introduced based on distinct morphological characteristics coupled with phylogenetic analysis of a combined ATP6, RPB2, and TEF1-α dataset (Fig. 143). Two new combinations, *Baorangia rufomaculata* and *Lanmaoa pallidorosea* are also designated in this study.

Baorangia G. Wu & Zhu L. Yang

Baorangia was first recognized by Wu et al. (2014, as 'clade 51'), and later formally described by Wu et al. (2015). Typical characteristics are a thin hymenophore that is 3–5 times thinner than the pileus context, yellow tubes and pores that stain blue when bruised, a light yellow context that slowly stains pale blue when cut, and a

Fig. 139 ***Marasmiellus bicoloripes*** (CAL 1524, **holotype**). **a, b** Basidiomes in the field. *Scale bars* **a, b** = 10 mm. Photos by K. P. Deepna Latha

trichodermium to interwoven trichodermium pileipellis (Wu et al. 2015). Three species are recorded in the genus, *B. bicolor* (Kuntze) G. Wu et al., *B. emilei* (Barbier) Vizzini et al. and *B. pseudocalopus* (Hongo) G. Wu & Zhu L. Yang, which is the generic type (Kirk et al., continuously updated).

Baorangia major Raspé & Vadthanarat, ***sp. nov.***

MycoBank number: MB824250; *Facesoffungi number*: FoF05722, Figs. 144, 145

Etymology: The specific epithet "*major*" from Latin, refers to the size of mature basidiomes, the largest in the genus.

Holotype: MFLU 12-0040

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1978).

Basidiomes large when mature. *Pileus* (7–)16–22(–23) cm diam., at first hemispherical to convex, becoming convex to plano-convex and sometimes slightly depressed at the centre, greyish red (11C–E5) to greyish ruby (12B–E5), more rarely greyish pink (around 10A3), paler in spots and in age; margin involute at first, later inflexed, slightly exceeding; concolorous or abruptly paler (yellowish white; 2A2); surface even, dry, dull, subtomentose; context 1.7–3.8 cm thick half-way to the margin, firm at first, soft in age, off-white to yellowish white (1A2), slightly marmorated above the hymenophore, blueing when bruised, sometimes only weakly, then slowly getting yellow (3A5–6) with time, as in worm wounds. *Stipe* central, terete, cylindrical to subclavate (4.8–)5.2–8.5(–15) × 1.5–3.3(–4.5) cm; surface finely and densely dotted, subceraceous, dull, with off-white to pale yellow basal tomentum; context solid, yellowish white (2A2) at the top, more intensely yellow towards the base, marmorated, often with dark red spots, especially in the lower half, quickly and intensely blueing when cut. *Hymenophore* tubulate, decurrent; tubes 2–5 mm long, not separable, yellow (2–3A7), sometimes stained red at places (old bruises) or when old, quickly and intensely blueing when bruised; pores 2–5 mm wide at mid-radius when mature, mostly angular, elongated and radially arranged near the stipe, yellow (2A8), quickly and intensely blueing when bruised, sometimes reddish when very old. *Odour* fungoid to slightly fruity. *Taste* mild, fungoid. *Spore print* olive-brown. *Macrochemical reactions*: KOH pale orange on pileus and stipe, paler on context, null or merely slightly orangish on hymenium; NH_4OH null. *Basidia* 4-spored, (36–)36–*42.2*–55(–55) × (8.5–)8.5–*9.3*–11(–11) µm (n = 20), narrowly clavate, sometimes curved, hyaline, with sterigmata up to 5 µm long, without basal clamp connection. *Basidiospores* (6–)7.5–*8.1*–9(–10) × (4–)4–*4.6*–5(–5.5) µm Q = (1.44–)1.5–*1.8*–2.1(–2.4) [*N* = 5/5/265]. From the type (7.5–)8–*8.6*–9.5(–9.5) × (4–)4–*4.5*–5(–5) µm, Q = (1.6–)1.69–*1.9*–2.13(–2.13) [n = 55], ellipsoid to ovoid, thin-walled, smooth, yellowish to greenish hyaline in water, KOH or NH_4OH, yellowish in Melzer's reagent. *Cheilocystidia* thin-walled, hyaline, of two different shapes, the first clavate to broadly clavate, (21–)21–*29.3*–37(–37) × (11.5–)11.5–13.1–15(–15) µm, the second fusiform to broadly fusiform, (26–)26–*38.9*–57(–57) × (10–)10–*13.3*–15(–15) µm. *Pleurocystidia* infrequent, fusiform to narrowly fusiform with obtuse apex, (44–)44–*54.4*–70(–70) × (8–)8–*9.5*–12(–12) µm, thin-walled, hyaline. *Hymenophoral trama* divergent, 90–112 µm wide, composed of 4–10 µm wide, hyaline hyphae, with regular mediostratum 30–45 µm wide. *Pileipellis* a trichoderm to tangled trichoderm, 170–190 µm thick, made of moderately interwoven and somewhat anastomosing, thin-walled, hyaline hyphae; terminal cells

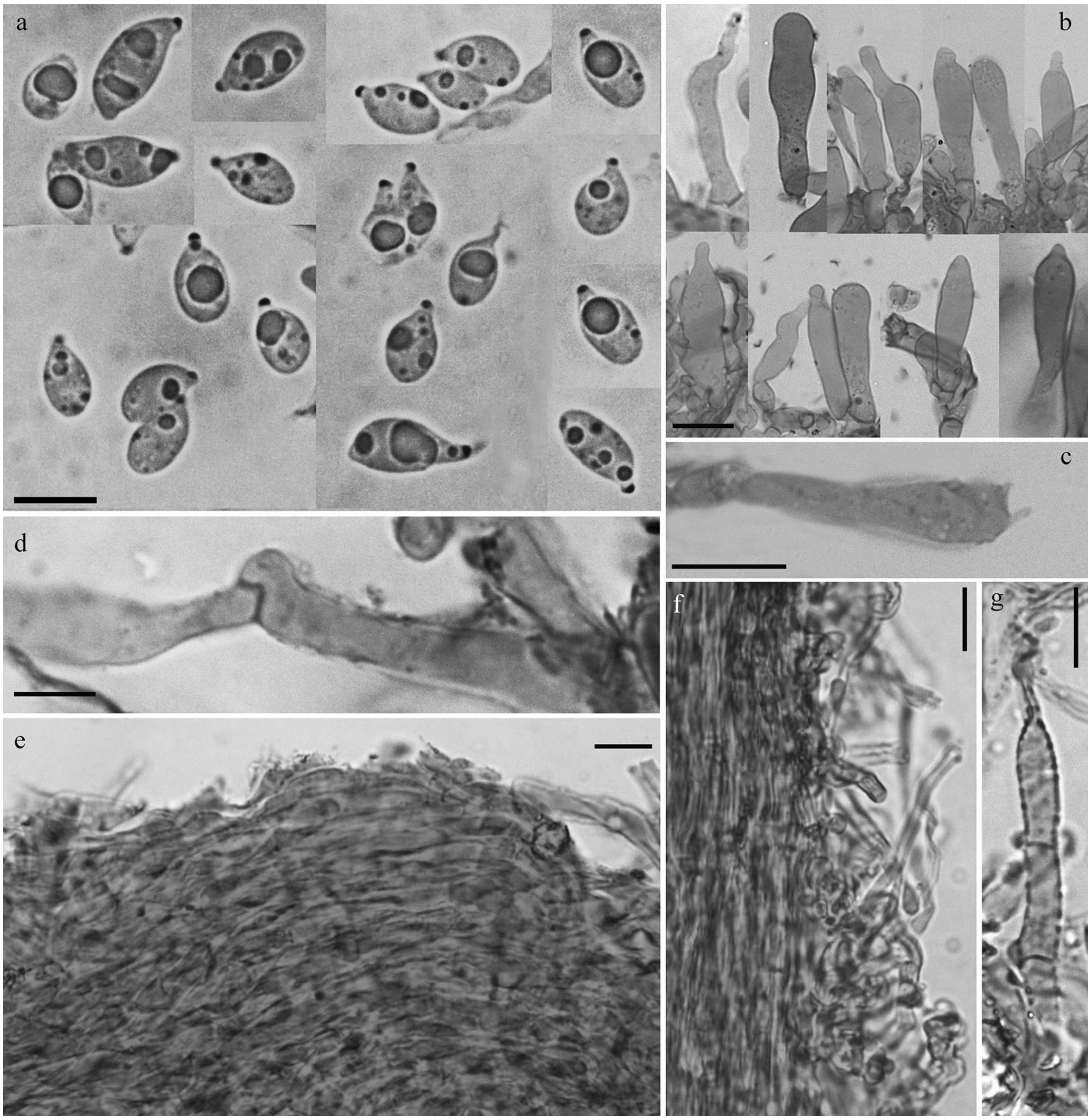


Fig. 140 ***Marasmiellus bicoloripes*** (CAL 1524, **holotype**). **a** Basidiospores. **b** Cheilocystidia. **c** Basidium. **d** Clamped hypha of pileipellis. **e** Pileipellis. **f** Stipitipellis. **g** Pileipellis hypha showing spiral encrustations. *Scale bars* **a–c** = 10 µm, **d–g** = 20 µm. Photos by K. P. Deepna Latha and K. N. Anil Raj

cylindrical with rounded apex, 20–58 × 4–9 µm, mostly hyaline to slightly pale yellowish brown at places in KOH. *Pileus context* made of moderately interwoven, hyaline, thin-walled hyphae, 4–13 µm wide. *Stipitipellis* a hymeniderm, 62–88 µm thick, mostly composed of basidiole-like cells, 12–43 × 4–10 µm. *Caulocystidia* infrequent, of three shapes, the first clavate to broadly clavate, (13–)*23.8*(–31) × (10–)*12.5*(–15) µm, thin-walled, hyaline, the second fusiform to broadly fusiform, (21–)*31.5*(–45) × (9.5–)*11.6*(–15), thin-walled, hyaline, and the third cylindrical, slightly curved, mostly hyaline, at places slightly yellowish brown in KOH. *Stipe context* composed of parallel, 4–12 µm wide, hyaline and somewhat anastomosing hyphae. *Clamp connections* not seen in any tissue.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, around Mushroom Research Center, N19°07.1′–E98°44.0′, elev. 900 m, 2 July 2010, P. Sysouphanthong, OR070 (MFLU!, BR!); *ibid.*, N19°07.2′–E98°43.9′, elev.915 m, 17 June 2011, O. Raspé & S.C. Karunarathna, OR197 (MFLU!, BR!); N19°06.5′–E98°44.5′, elev.1075 m, 18 June 2011, O. Raspé & S.C. Karunarathna, OR209 (MFLU, **holotype**; BR, **isotype**); N19°06.6′–E98°44.5′, elev.1055 m, 7 June 2012, O. Raspé & K. Wisitrassameewong, OR404; N19°07.2′–E98°43.9′, elev. 910 m, 29 July 2013, O. Raspé & B. Thongbai,

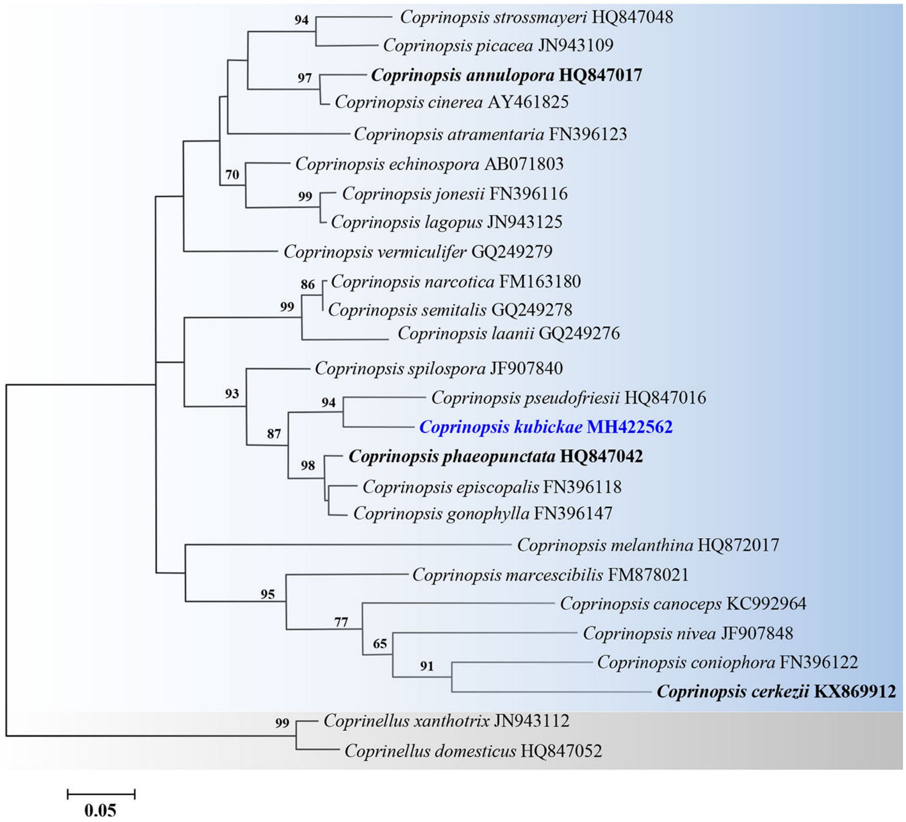


Fig. 141 Maximum likelihood phylogenetic tree of *Coprinopsis kubickae* and related species based on ITS sequence alignment, calculated with MEGA6 software (Tamura et al. 2013). The sequence obtained in this study is shown in blue. Ex-type strains are indicated in bold. Maximum likelihood bootstrap values greater than 50% are indicated at the nodes. The tree is rooted with *Coprinellus xanthothrix* and *C. domesticus*. The bar indicates the number of nucleotide substitutions per site

OR657 (MFLU!, BR!); CHINA, Yunnan Province, Cangyuan County, Banhongxiang, along the road, N23°18.6′–E99°05.3′, elev. 1010 m, 10 July 2012, O. Raspé & R.L. Zhao OR486 (HMAS).

Habit and habitat: Mostly gregarious, sometimes fasciculate or solitary, on soil in forests dominated by *Lithocarpus* spp., *Castanopsis* spp., sometimes mixed with *Dipterocarpus* spp.

Distribution: Known from Chiang Mai Province, Thailand and Yunnan Province, China.

GenBank numbers: ATP6 = MG897421, RPB2 = MG897441, TEF1-α = MG897431 (OR209, **holotype**); ATP6 = MG897422, RPB2 = MG897442, TEF1-α = MG897432 (OR404), ATP6 = MG897423, RPB2 = MG897443, TEF1-α = MG897433 (OR486).

Notes: *Baorangia major* can easily be recognised in the field by its large basidiomes when mature, decurrent hymenophore with large, angular, radially arranged (at least near the stipe), and 1–3 times compound pores, red stipe that immediately and intensely turns blue when injured or merely touched. In their diagnosis of *Baorangia*, Wu et al. (2015) mentioned "context which stains pale blue slowly when cut". While this fits *B. major* pileus context, it does not fit its stipe context, which quickly and intensely stains blue when cut. *Baorangia bicolor* (Kuntze) G. Wu et al. and *B. rufomaculata* (see below) somewhat resembles *B. major*, but the latter can easily be distinguished by the large angular pores and intense blueing.

Baorangia rufomaculata (Both) Raspé & Vadthanarat, ***comb. nov.***

MycoBank number: MB824251; *Facesoffungi number*: FoF05723, Fig. 146

Basionym: *Boletus rufomaculatus* Both, Bull. Buffalo Soc. Nat. Sci. 36: 221 (1998)

Holotype: USA, Western New York, under *Fagus grandifolia* Ehrh., *Quercus rubra* L., *Tsuga canadensis* (L.) Carrière and *Acer saccharum* Marshall, Both 2831 (BUF).

Basidia 4-spored, (21–)21–*24.6*–31(–31) × (8–)8–*8.9*–10(–10) µm, clavate, hyaline, sterigmata 3–5 µm long, without basal clamp connection. *Basidiopores* (9–)9–*10.6*–12(–12.5) × (3.5–)3.5–*3.9*–4.5(–4.5) µm Q = (2.1–)2.3–*2.7*–3.2(–3.6) [*N* = 50], subcylindrical with slight suprahilar depression, thin-walled, smooth, slightly greenish to yellowish hyaline in water, yellowish hyaline in 5% KOH or NH_4OH, brownish yellow in Melzer's reagent. *Cheilocystidia* (18–)18–*31.4*–45(–45) × (6–)6–*7.9*–10(–10) µm, frequent, fusiform to broadly fusiform, thin-walled, hyaline. *Pleurocystidia* (42–)42–*59.5*–72(–72) × (7–)7–*8.2*–9.5(–9.5) µm, infrequent, narrowly fusiform, thin-walled, hyaline. *Hymenophoral trama* regular to slightly divergent, 90–190 µm wide, composed of (3–)5–7(–12) µm wide hyaline hyphae. *Pileipellis* a subcutis to tangled

Fig. 142 ***Coprinopsis kubickae*** (CNF 1/6614). **a** Basidiomes. **b** Veil on the pileus. **c** Basidiospores. **d–f** Cheilocystidia. *Scale bars* **a** = 5 mm, **b** = 30 µm, **c–f** = 10 µm

trichoderm, 120–220 µm thick, made of loosely to moderately interwoven, thin-walled, hyaline hyphae; terminal cells cylindrical with rounded apex, 22–45 × 5–8 µm, mostly hyaline, at places yellowish hyaline in KOH. *Pileus context* made of moderately interwoven hyaline, thin-walled hyphae, 3–12 µm wide. *Stipitipellis* a hymeniderm, 85–120 µm thick; terminal cells clavate to narrowly clavate with rounded apex, thin-walled, 14–47 × 3–12 µm; below the hymeniderm parallel, hyaline hyphae anastomosing at places. *Stipe context* composed of parallel, branched, hyaline, thin-walled hyphae, 7–14 µm wide. *Caulocystidia* rare, 23–30 × 7–9 µm, fusiform or clavate, thin-walled, hyaline. *Clamp connections* not seen in any tissue.

Material examined: USA, New York, Erie Co., Town of Orchard Park, Chestnut Ridge Park, N42°43.1′–W78°45.3′, elev. 330 m, 6 August 1997, E. Both 4144 (CFMR).

Distribution: North America.

GenBank numbers: ATP6 = MG897415, RPB2= MG897435, TEF1-α = MG897425.

Notes: The specimen we studied (Both 4144) was already sequenced by Nuhn et al. (2013) for LSU, RPB1, and TEF1-α genes, but under the wrong number “4414”. Our TEF1-α sequence is 100% identical to the one published by Nuhn et al. (2013), except for the insertion of an “N” at position 215 in the latter, which is likely an artefact. Our measurements of microscopic characteristics slightly deviate from the original description of Both (1998). However, the specimen we studied was collected and identified by Both from the type locality. Therefore, we are confident that it belongs to the same species.

Lanmaoa G. Wu & Zhu L. Yang

The genus *Lanmaoa* was recognized by Wu et al. (2014, as ‘clade 49’), and later formally described by Wu et al. (2015). The typical characteristics of the genus are a thin hymenophore which is 3–5 times thinner than the pileus context and stains blue when bruised, a light yellow context that slowly stains pale blue when cut, and an interwoven trichodermium to subcutis pileipellis (Wu et al. 2015). Seven species are recorded in the genus, *L. angustispora* G. Wu & Zhu L. Yang, *L. asiatica* G. Wu & Zhu L. Yang (generic type), *L. carminipes* (A.H. Sm. & Thiers) G. Wu et al., *L. flavorubra* (Halling & M. Mata) G. Wu et al., *L. fragrans* (Vittad.) Vizzini et al., *L. pseudosensibilis* (A.H. Sm. & Thiers) G. Wu et al. and

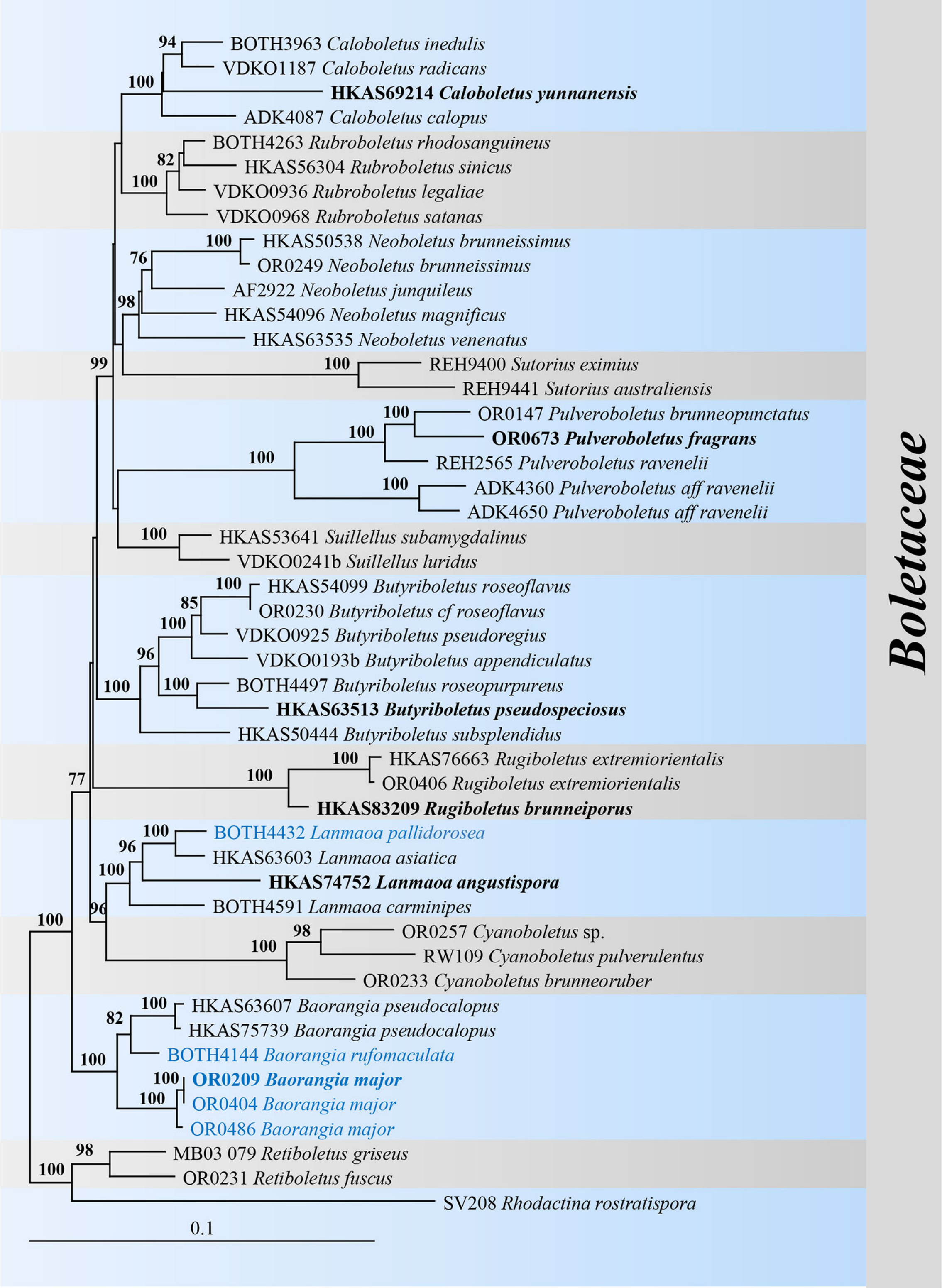


Fig. 143 Maximum likelihood tree inferred from three-gene dataset (ATP6, RPB2 and TEF1-α). *Retiboletus griseus*, *R. fuscus*, and *Rhodactina rostratispora* were used as the outgroup taxa. Sequences retrieved from GenBank were originally published in Halling et al. (2012), Wu et al. (2014, 2015, 2016), Zhao et al. (2014a, b), Raspé et al. (2016), and Vadthanarat et al. (2018). Maximum likelihood bootstrap values greater than 70% are indicated at the nodes. The bar indicates the number of nucleotide substitutions per site. Type specimens are indicated in bold. Newly generated sequences are in blue

Fig. 144 ***Baorangia major*** basidiomes in the field. **a, b** OR209 (**holotype**). **c** OR404. **d** OR486. *Scale bars* 3 cm

L. roseocrispans Bessette et al. (Kirk et al., continuously updated).

Lanmaoa pallidorosea (Both) Raspé & Vadthanarat, ***comb. nov.***

MycoBank number: MB824252; *Facesoffungi number*: FoF05724, Fig. 147

Basionym: *Boletus pallidoroseus* Both, Bull. Buffalo Soc. nat. Sci. 36: 218 (1998).

Holotype: USA, New York, on ground under *Quercus rubra* and *Fagus grandifolia*, Both 3026 (BUF).

Basidiospores and *basidia* not observed on the immature specimen studied. *Cheilocystidia* (14–)14–*19.4*–25(–25) × (5–)5–*6.5*–8(–8) µm, frequent, fusiform, thin-walled, hyaline. *Pleurocystidia* (28–)28–*33.9*–39(–39) × (6.5–)6.5–*7.9*–9(–9) µm, infrequent, narrowly fusiform, thin-walled, hyaline. *Hymenophoral trama* divergent, 110–175 µm wide, composed of (3.5–)4–7(–12) µm wide hyaline hyphae. *Pileipellis* a trichoderm, 220–300 µm thick, composed of thin-walled, hyaline hyphae; terminal cells cylindrical with rounded apex, 28–70 × 4–8 µm, mostly hyaline, at places brownish to yellowish hyaline in KOH. *Pileus context* made of strongly interwoven, hyaline, thin-walled hyphae, 4–6 µm wide. *Stipitipellis* a hymeniderm, 55–80 µm thick, composed of pointing out, clavate, thin-walled terminal cells 13–28 × 4–9 µm, which are mixed with caulocystidia. *Stipe context* composed of interwoven, sub-irregular, thin-walled, hyaline hyphae, 4–9 µm wide. *Caulocystidia* of two types, the first one very frequent, fusiform to broadly fusiform, (19–)19–*28.4*–39(–39) × (7–)7–*8.4*–11(–11.5) µm, thin-walled, hyaline, the second one infrequent, broadly clavate, (11–)11–*20.5*–27(–27) × (7–)7–*9.4*–11(–11) µm, thin-walled, hyaline. *Clamp connections* not seen in any tissue.

Material examined: USA, New York, Erie Co., Orchard Park, Chestnut Ridge Park, N42°43.1′–W78°45.3′, elev. 330 m, 19 August 2000, E. Both 4432 (CFMR).

Distribution: North America.

GenBank numbers: ATP6 = MG897417, RPB2 = MG897437, TEF1-α = MG897427.

Notes: Although the specimen we examined is immature and we could not check basidiospore and basidia dimensions, we are confident that it belongs to the species described by Both (1998). Indeed, it was collected and identified by E. Both himself from the type locality.

Cantharellales Gäum.

Clavulinaceae Donk

Clavulinaceae was established by Donk (1933) as a tribe, but later Donk (1961) raised the tribe to the rank of family. The family *Clavulinaceae* comprises four genera, *Burgella* Diederich & Lawrey, *Clavulina* J. Schröt., *Membranomyces* Jülich and *Multiclavula* R.H. Petersen (Kirk et al. 2008). We follow the treatment and updated

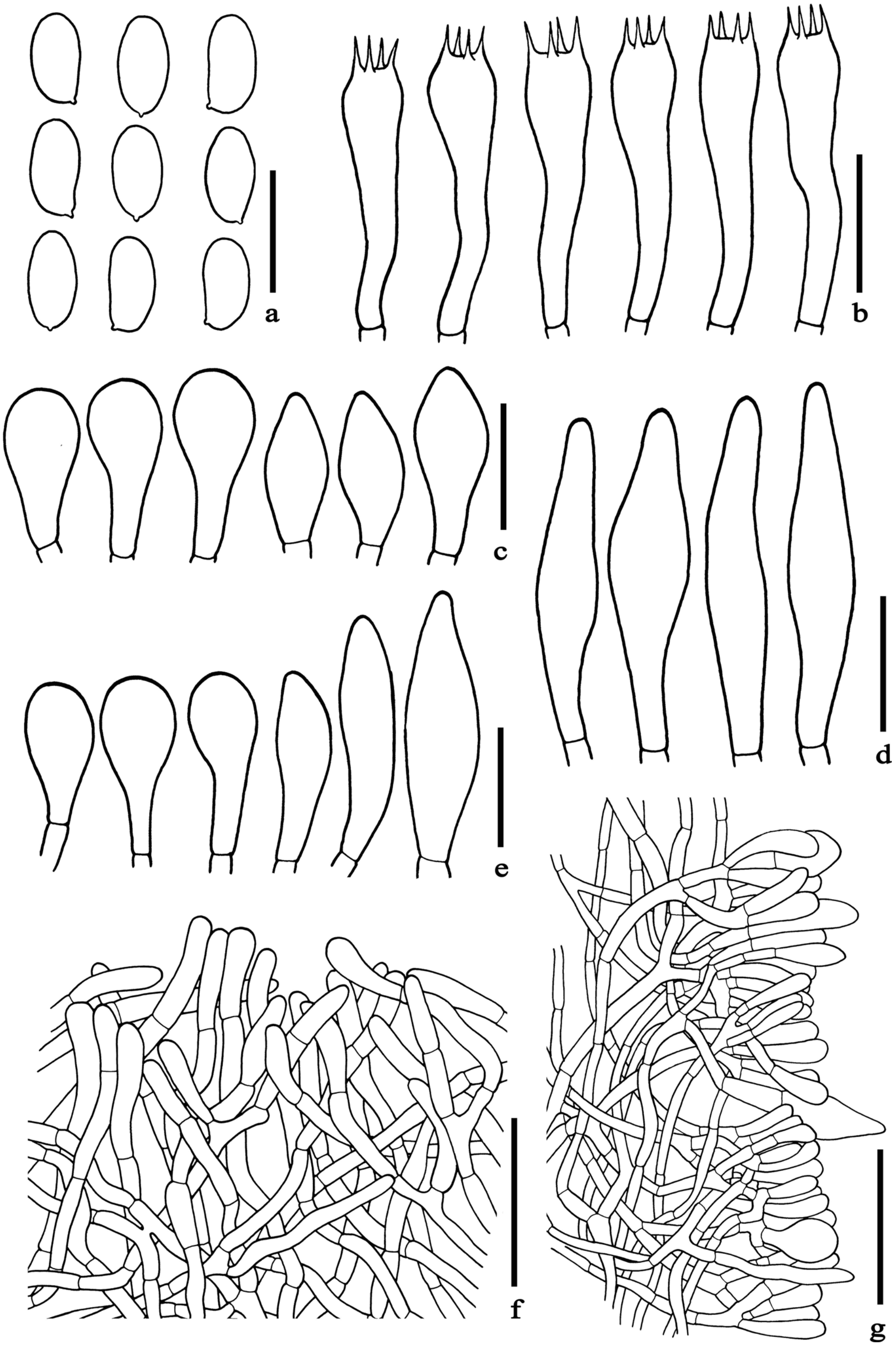


Fig. 145 ***Baorangia major*** microscopic features. **a** Basidiospores. **b** Basidia. **c** Two types of cheilocystidia. **d** Pleurocystidia. **e** Two types of caulocystidia. **f** Pileipellis. **g** Stipitipellis. *Scale bars* **a** = 10 µm, **b–e** = 20 µm, **f, g** = 50 µm. All drawings were made from the type OR209

accounts of *Clavulinaceae* in He et al. (2016) and Tibpromma et al. (2017). A novel species, *Clavulina thindii* is introduced based on distinct morphology and maximum likelihood phylogeny of ITS sequence data (Fig. 148).

Clavulina J. Schröt.

Clavulina is distributed worldwide and characterized by clavarioid to coralloid, occasionally resupinate and effused, simple or branched basidiomes, monomitic hyphal system, with clamp connections in most species; smooth, hyaline, subglobose to broadly ellipsoid basidiospores usually with one large guttule; basidia with two or up to six cornuted sterigmata and often develop a transversal septum (Corner 1950, 1970; Petersen 1988a; Henkel et al. 2005, 2011; Uehling et al. 2012a; He et al. 2016). Species of *Clavulina* occur in forests dominated by ectomycorrhizal (ECM) trees of the leguminous genera (*Fabaceae*) (Henkel et al. 2011). Approximately 82 species have been described in the genus *Clavulina* (Corner 1950, 1970; Thind 1961; Petersen 1967, 1983, 1985, 1988a, b; Thind and Sharda 1984; Roberts 1999; Thacker and Henkel 2004; Henkel et al. 2005, 2011; Douanla-Meli 2007; Duhem and Buyck 2007; Trappe and Castellano 2007; Olariaga and Salcedo 2012; Uehling et al. 2012a, b; Wartchow 2012; He et al. 2016).

Clavulina thindii U. Singh, ***sp. nov.***

MycoBank number: MB824527; *Facesoffungi number*: FoF04878, Figs. 149, 150

Etymology: To commemorate Prof. K.S. Thind for his contribution to Indian mycobiota.

Holotype: CAL 1661

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1978).

Basidiomes 41–66 × 30–49 mm, coralloid, terrestrial, profusely branched, solitary to scattered; sterile stipe 12–28 × 7–12 mm, white to greyish white, glabrous; fertile branches 30–38 × 2.5–4.5 mm, forming 4–7 ranks in multiple planes, branching pattern polychotomous to dichotomous-ascending, initially violet white to pale violet (16A2–3), maturing to lilac grey to lilac (16B2–3), wax white to greyish yellow (2B3–4) with drying, smooth; hymenium ripening over distal two-thirds of basidiomes, amphigenous, interface with stipe clearly demarcated; apices rounded-acuminate to irregularly coronate or blunt, concolorous with branches when young, becoming brownish orange (6C8) at maturity; context subsolid to hollow, concolorous with branches. *Taste* and *Odour* pleasant. *Basidiospore deposit* not obtained. *Basidia* 22–48 × 6–10 µm, subcylindrical to subclavate or clavate, with numerous granular contents, post-partial septa observed on some basidia, basally clamped, 2-spored; sterigmata up to 7 µm long, cornuted; basidioles numerous, subcylindrical to clavate. *Hymenophoral tramal hyphae* sub-regular to irregular; noninflated tramal hyphae 5–8 µm, smooth, thin-walled, hyaline, lacking internal contents; inflated tramal hyphae 11–15 µm, smooth, thin-walled, hyaline, lacking internal contents. *Cystidia* absent. *Basidiospores* 6.5–*7.5*–8 × 6–*6.4*–7 µm (n = 30, Q = 1.07–*1.15*–1.25), subglobose to broadly ellipsoid, smooth, pale yellow in KOH, inamyloid, with one translucent guttule; apicules up to 1 µm long. *Clamp connections* present.

Material examined: INDIA, Uttarakhand, Pauri Garhwal District, Gangoti-Adwani forest, alt. 1948 m, N 30°05.799′ E 078°43.927′, 3 October 2016, U. Singh, US 1428 (CAL 1661, **holotype**); *ibid*., 31 August 2017, U. Singh, US 1585.

Host and habitat: Solitary to scattered, on ground, under trees of *Acacia dealbata* A. Cunn. in mixed temperate forest.

Distribution: Known only from India.

GenBank numbers: ITS = MG892054 (US 1428); ITS = MG892055 (US 1585).

Notes: *Clavulina thindii* is distinct from all other species of *Clavulina* by the ITS sequence data and combination of morphological features: violet to lilac profusely branched basidiomes (42–66 × 38–49 mm) with white to greyish white stipe and rounded-acuminate to irregularly coronate or blunt apices, subsolid to hollow context, subglobose to broadly ellipsoid basidiospores, cylindrical to subclavate basidia with two cornuted sterigmata, absence of cystidia, noninflated to inflated tramal hyphae and presence of clamp connections.

In field, *Clavulina thindii* may appear similar to *C. livida* Shu Z. Yan et al. with both species possessing large sized, branched basidiomes with rounded-acuminate apices which turn brown at maturity, smooth basidiospores with one large guttule, subcylindrical to clavate basidia with sometimes post-partial septa, absence of cystidia, noninflated to inflated tramal hyphae and presence of clamp connections. However, the latter has greyish basidiomes with olive stipe, larger (11.6–12.9 × 10.7–12.5 µm), globose to subglobose basidiospores and larger basidia (51.5–76.5 × 7–12.3 µm) (He et al. 2016).

Clavulina amethystina (Bull.) Donk shares similarities with *C. thindii* in having lilac to violet, branched basidiomes with obtuse to blunt apices, but the former has completely lilac to violet basidiomes (the stipe of *Clavulina thindii* is white to greyish white), becoming dark grey with age and ellipsoid (Lm/Wm ≈ 1.55–1.62) basidiospores (Corner 1950; Olariaga et al. 2009).

Clavulina cinerea (Bull.) J. Schröt, *C. rugosa* (Bull.) J. Schröt, *C. coralloides* (L.) Schröt. (= *C. cristata*), *C. subrugosa* (Cleland) Corner and *C. samuelsi* R.H. Petersen are also closely related to *C. thindii*. However, these five species show morphological differences from *C. thindii*. *Clavulina cinerea* differs from *C. thindii* by its white to dark grey basidiomes with acute to blunt apices, indistinct or not well-delimited stipe due to basitonic branching and ovoid (Lm/Wm = 1.1–1.3) basidiospores (Bulliard 1788; Olariaga et al. 2009). *Clavulina rugosa* is distinguished by its simple to sparsely branched, white basidiomes, noncristate and normally obtuse apices and relatively larger basidiospores (9–14 × 8–12 µm, Lm × Wm = 9.9–10.6 × 8.2–8.8) (Corner 1950; Olariaga et al. 2009). *Clavulina coralloides* differs from *C. thindii* by its white to grey basidiomes with not well-delimited stipe due to basitonic branching, cristate apices, comparatively larger and subglobose basidiospores (7–11 × 6.5–10 µm) (Holmskjold 1790; Corner 1950; Olariaga et al. 2009). *Clavulina subrugosa* can be separated from *C. thindii* by its simple or filiform to flattened branched, white to pale greyish brown basidiomes and rather large basidiospores (6.8–8.6 × 5.8–7.2 µm) (Corner 1950; Petersen 1988a).

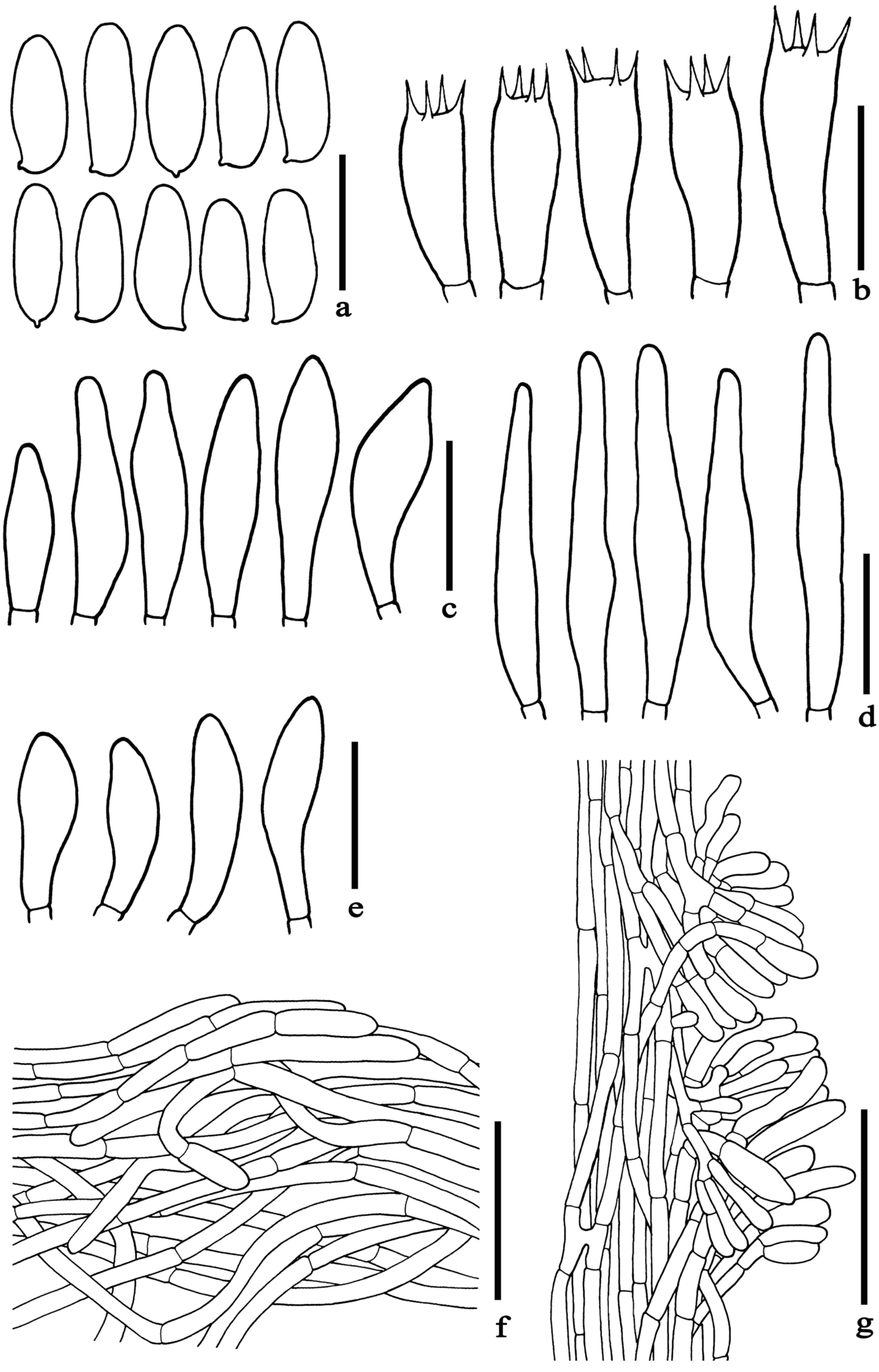


Fig. 146 ***Baorangia rufomaculata*** microscopic features. **a** Basidiospores. **b** Basidia. **c** Cheilocystidia. **d** Pleurocystidia. **e** Caulocystidia. **f** Pileipellis. **g** Stipitipellis. *Scale bars* **a** = 10 µm, **b–e** = 20 µm, **f, g** = 50 µm. All drawings were made from Both 4144

Clavulina samuelsii differs from *C. thindii* in having tilleul buff fruiting body, comparatively larger basidiospores (7.2–9.4 × 6.1–7.6 µm) and presence of cystidia (Petersen 1988a).

Clavulina mussooriensis Corner et al. (an Indian species) shares similarities with *C. thindii* in possessing profusely branched basidiomes and sometimes subglobose basidiospores but the former has cream-white to greyish brown basidiomes with cristate to acute apices and larger

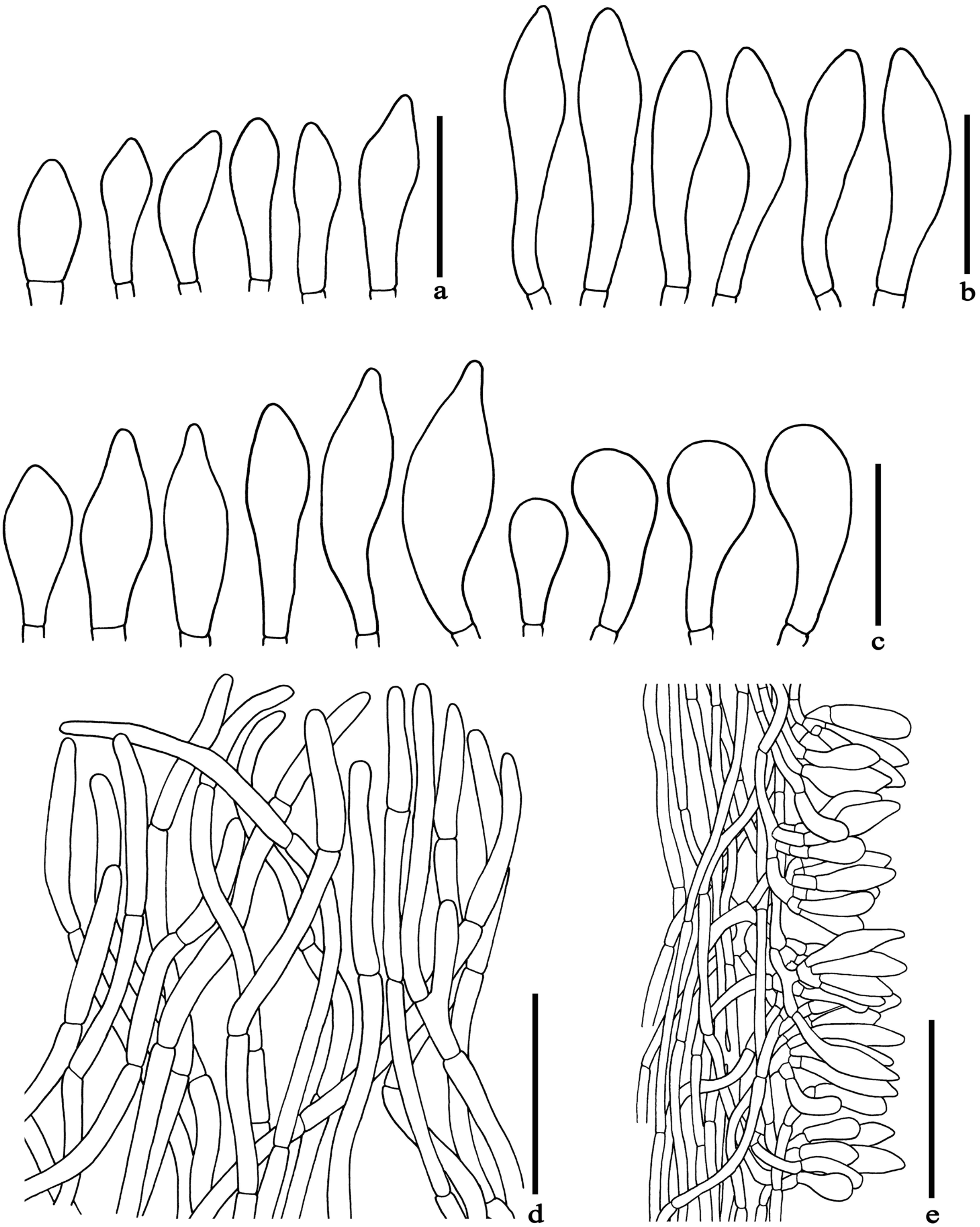


Fig. 147 ***Lanmaoa pallidorosea*** microscopic features. **a** Cheilocystidia. **b** Pleurocystidia. **c** Two types of caulocystidia. **d** Pileipellis. **e** Stipitipellis. *Scale bars* **a–c** = 20 µm, **d, e** = 50 µm. All drawings were made from Both 4432

basidiospores (7–9 × 5.6–8 µm) (Corner et al. 1958). *Clavulina limosa* K.S. Thind & Sharda (also originally reported from India) differs from *C. thindii* by simple (unbranched), slimy, creamish white to pallid-cream basidiomes and globose to subglobose basidiospores (Thind and Sharda 1984).

Thind (1961) reported *Clavulina amethystinoides* (Peck) Corner from India, but the conspecificity has not yet been verified with help of sequence data from the Indian collections. *Clavulina amethystinoides* shares some similarities with *C. thindii* in possessing violet basidiomes and 2-spored basidia, but differs in having simple or sparsely branched basidiomes, comparatively larger and globose to subglobose basidiospores (9–12.3 × 8.8–10.5 µm). Moreover, *C. amethystinoides* (originally reported from USA) differs from *C. thindii* by having simple or irregular branches, slightly palmate branching, pale drab, pinkish tan, fawn or very pale lilac basidiomes, pale livid flesh, eventually blackening tips with distinctly different colour and larger basidiospores (7–10 × 6–8 µm) (Corner 1950).

Clavulina thindii is commonly collected and consumed by local villagers. 'Angalchyun' (fingers like mushroom) is the vernacular name used for this species in the local language (Garhwali). However, inhabitants refer this vernacular name (Angalchyun) for all clavarioid fungi. The ITS dataset consisting of 49 sequences (including our isolates: US 1428, represented by GenBank no. MG892054 and US 1585, represented by GenBank no. MG892055) of *Clavulina* and *Hydnum* L. was analyzed by maximum likelihood phylogenetic inference (Fig. 148). Two sequences isolated from Indian materials appear to be nested amongst other sequences of *Clavulina* and form a distinct clade being sister to Chinese collections of *C. livida* (represented by KU219603, KU219604, KU219605 and KU219606). The combination of morphological features and phylogenetic analysis indicates that *Clavulina thindii* is a new species, distinct from all the known taxa of *Clavulina*.

Polyporales Gäum.

Phanerochaetaceae Jülich

The family *Phanerochaetaceae* was described by Jülich (1981) with *Phanerochaete* as generic type, and also including the genera *Meruliopsis* Bondartsev, *Phlebiopsis* Jülich and *Scopuloides* (Massee) Höhn. & Litsch. This family was characterized by mostly resupinate basidiome, thick-walled hyphae, often without clamps, basidia narrowly clavate and spores hyaline, smooth and thin-walled (Larsson 2007; Ryvarden and Melo 2014; Yuan et al. 2017). Justo et al. (2017) revised the family on the basis of molecular and morphological data and, in addition to *Phanerochaete*, they include the following thirteen genera: *Bjerkandera* P. Karst., *Donkia* Pilát, *Hapalopilus* P. Karst., *Hyphodermella* J. Erikss. & Ryvarden, *Oxychaete* Miettinen, *Phaeophlebiopsis* Floudas & Hibbett, *Phanerina* Miettinen, *Phlebiopsis* Jülich, *Pirex* Hjortstam & Ryvarden, *Porostereum* Pilát, *Rhizochaete* Gresl. et al., *Riopa* D.A. Reid and *Terana* Adans. Most of these genera are corticioid and rarely polyporoid, with the hyphal system monomitic or sometimes dimitic, and most have hyphae without clamps; cystidia are often present and spores are thin-walled, hyaline and smooth. All species of this family produce a white-rot.

Phanerochaete P. Karst.

Phanerochaete is a genus of widespread corticioid fungi that causes white rot on all kinds of decayed wood and plays a key role in forest ecosystems. The genus contains 167 legitimate names (MycoBank 2019). Since 2008 eight new species and one subspecies have been described (Nakasone 2008; Ghobad-Nejhad et al. 2015; Floudas and Hibbett 2015; Liu and He 2016; Sádlíková and Kout 2017; Spirin et al. 2017), and six new combinations have been proposed (Nakasone 2008; Hjortstam et al. 2009; Melo et al. 2012; Floudas and Hibbett 2015; Volobuev et al. 2015; Miettinen et al. 2016).

Phanerochaete was described by Karsten (1889) to accommodate *Thelephora alnea* Fr. and *T. odora* Fr., and therefore based on two elements, without designation of a type. Cooke (1953) considered *T. alnea* as generic type and later *Corticium decolorans* (= *Phanerochaete velutina*) was chosen as lectotype by Eriksson et al. (1978a). Recently, Spirin et al. (2017) reinstated *T. alnea* as the generic type. Long neglected, *Phanerochaete* was reintroduced by Donk (1957) with the two initial species. Several years later, the taxonomy of the genus was discussed by Donk (1962), Parmasto (1968), Eriksson et al. (1978b) and Burdsall (1985). Donk (1962) amended *Phanerochaete*, recognizing that the generic limits were uncertain and suggesting that other taxa should be included. Parmasto (1968) accepted twenty species separated in two subgenera, *Phanerochaete* and *Phanericium* Parm.; cystidiate and acystidiate species, respectively. Eriksson et al. (1978b) recognized twelve species in Northern Europe divided into three groups, *Phanerochaete velutina* group (= subgen. *Phanerochaete*), *P. tuberculata* group (= subgen. *Phanericium* Parm.), and *P. septocystidiata* group, the last one with only one species characterized by cystidia regularly septate. Burdsall (1985) recognized 42 species in three subgenera, *Phanerochaete, Phanericium,* and *Scopuloides* (Massee) Burdsall, the latter with cystidia and subiculum usually distinct.

Phylogenetic studies carried out in *Phanerochaete sensu* Burdsall (1985) showed that the genus is polyphyletic (De Koker et al. 2003; Wu et al. 2010a) and its species are distributed in nine phylogenetic linages across the phlebioid clade within order *Polyporales* (Floudas and Hibbett 2015). According to Floudas and Hibbett (2015) one of these linages, *Phanerochaete sensu stricto*, includes species mostly found in the subgenus *Phanerochaete sensu* Burdsall (1985).

From a morphological point of view, the species included in the *Phanerochaete sensu stricto* clade in Floudas and Hibbett (2015) and in our LSU analysis (Figs. 151, 152) are characterized by their basidiomes being resupinate, membraceous, white, yellowish orange, or red to brown; the subiculum well-developed and the margin mostly fibrillose, with or without cordons. The hyphal

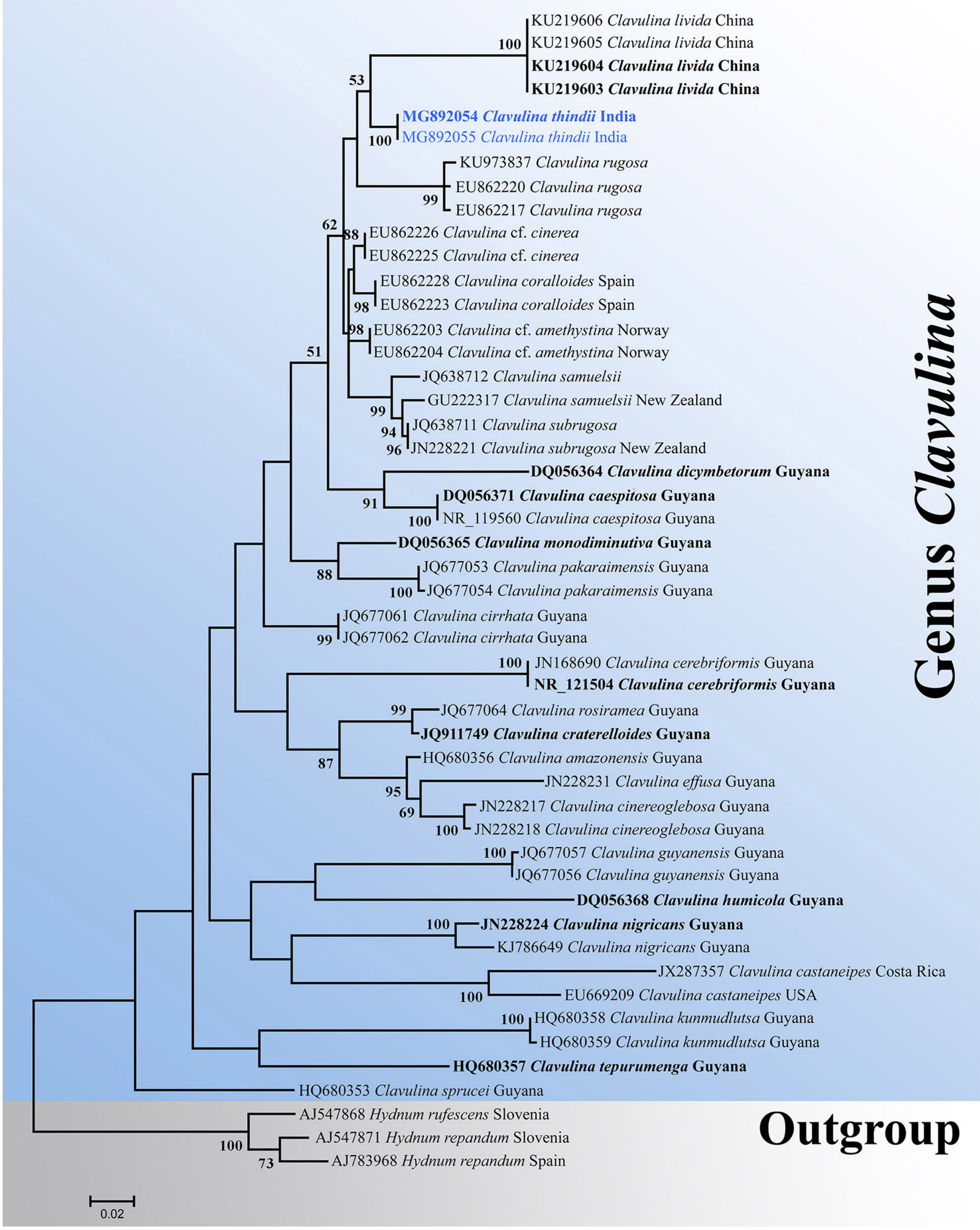


Fig. 148 Maximum likelihood phylogeny of *Clavulina* showing the position of novel species *Clavulina thindii* (shown in blue and bold). The ITS sequence dataset was aligned with online version of MAFFT v. 7 (Katoh and Standley 2013) and no manual editing was done within the alignment. One-thousand bootstrap replicates were analyzed to obtain nodal support values. Analysis was conducted with MEGA 6.0 (Tamura et al. 2013). *Hydnum rufescens* and *H. repandum* were used as the outgroup taxa. Maximum likelihood bootstrap values greater than 50% are indicated at the nodes. The bar indicates the number of nucleotide substitutions per site. Ex-type strains are indicated in bold

system is monomitic; the subicular hyphae thin to thick-walled, loosely interwoven, simple septate or with scattered single to multiple clamps; the subhymenial hyphae thin-walled, without clamps. The cystidia are cylindrical to subulate, thin-walled to almost metuloid, without a basal

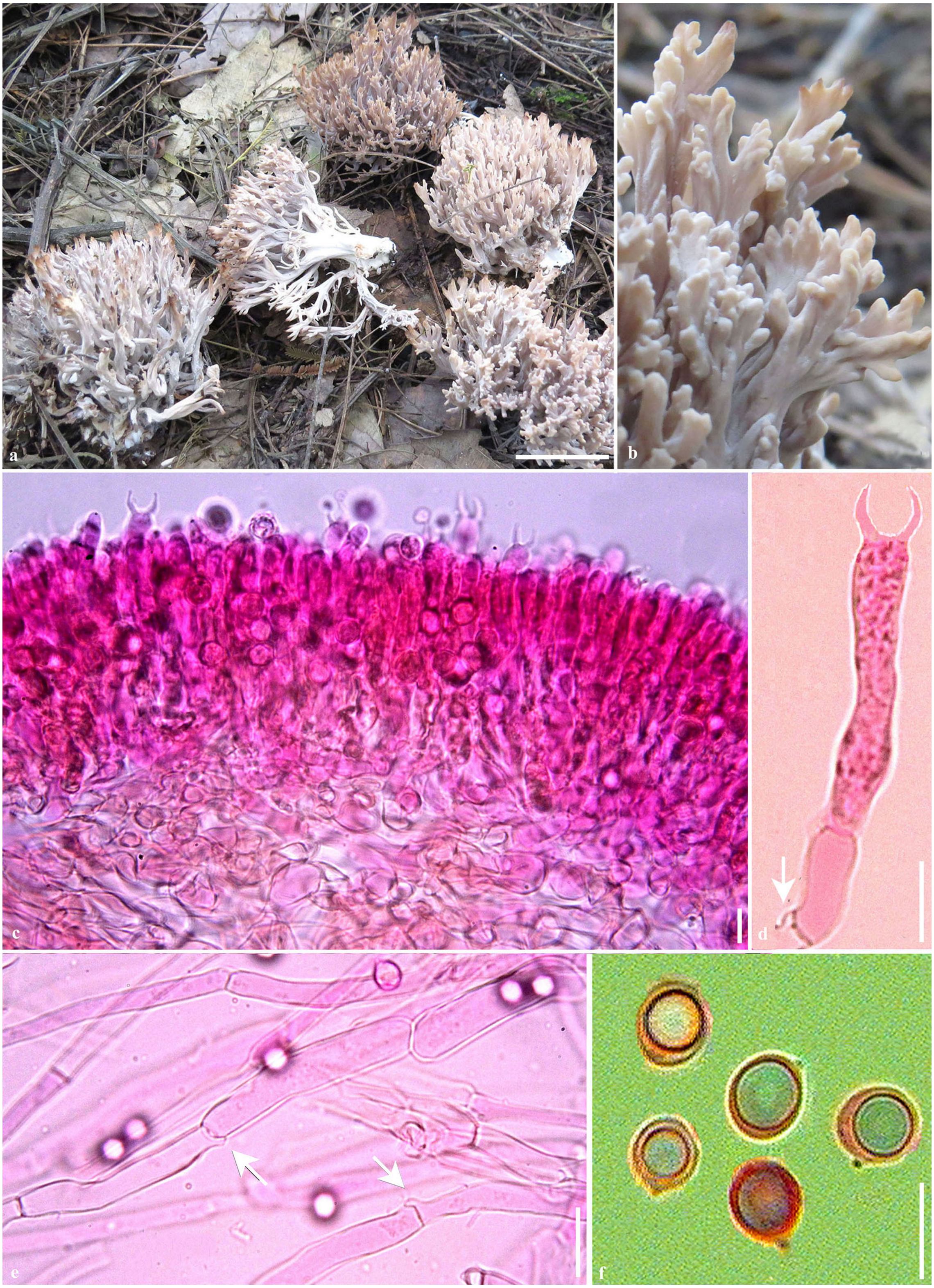


Fig. 149 ***Clavulina thindii*** (CAL 1661, **holotype**). **a** Fresh basidiomes. **b** Apices of basidiome. **c** Transverse section through hymenium. **d** Basidium with post-partial septa and basal clamp (indicated by white arrow). **e** Hymenophoral tramal hyphae showing clamps (indicated by white arrows). **f** Basidiospores. *Scale bars* **a** = 20 mm, **c–f** = 10 µm

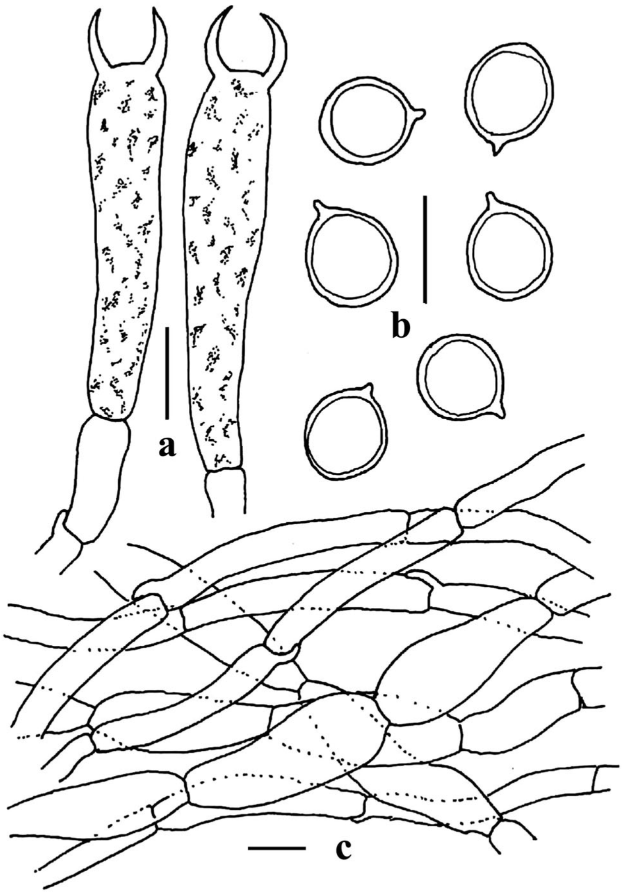


Fig. 150 *Clavulina thindii* (from holotype). **a** Basidia. **b** Basidiospores. **c** Hymenophoral tramal hyphae showing clamps. *Scale bars* **a–c** = 10 μm

clamp. Spores are thin-walled, inamyloid and non dextrinoid.

We follow the treatment and updated accounts of Floudas and Hibbett (2015) and Miettinen et al. (2016); the new species, *Phanerochaete australosanguinea* is introduced.

Phanerochaete australosanguinea Telleria, M. Dueñas & M.P. Martín, ***sp. nov.***

MycoBank number: MB825276; *Facesoffungi*: FoF05725, Figs. 153, 154

Etymology: From Latin "*australis*" which means southern and "*sanguinea*" refers to the morphological similarity of this species with *Phanerochaete sanguinea* (Fr.) Pouzar

Holotype: 20102Tell, MA-Fungi 91309

Colour codes follow: ISCC-NBS Centroid Colour Charts (Kelly and Judd 1976)

Basidiomes resupinate, orbicular to confluent, membranaceous, closely adnate; hymenophore smooth to slightly cracked in mature specimens; brownish orange (54. Br O–37. m r O) when young, in mature specimens orange yellow (70. l. OY–71. m. OY); the edge especially differentiated by dark reddish orange (38. d. r O). *Margin* fibrillose and white; with well-developed dark strands sometimes present. *KOH 3% reaction* (+) turning green that quickly change to brown. *Subiculum* byssoid, white to cream, lighter in colour than the hymenophore. *Hyphal system* monomitic. *Subicular hyphae* thick-walled, loosely interwoven, sparsely branched, growing parallel to the substrate, (5–)8–10 μm wide, sometimes with orange brown content, with single clamps. *Subhymenial hyphae* thin-walled and short-celled, branched, densely interwoven, growing perpendicular to the substrate, 3–5 μm wide. *Cystidia* thin-walled, cylindrical to tapering, sometimes with secondary septa, 44–66 × 4–5 μm. *Basidia* narrowly cylindrical to claviform, four sterigmata, 40–46 × 4–5 μm. *Spores* ellipsoid, 4.5–5.5 × 3–3.5 μm, thin-walled, sometimes with oil drops in the protoplasm, Q (L/W) = 1.29.

Material examined: CHILE, Los Lagos, Palena, Hornopirén, comuna Hualainhué, Huinay Biological Reserve, path to Cerro del Tambor, 42°22′54″S 72°24′53″W, 202 msl, on unidentified wood, 8 May 2013, M. Dueñas, M.P. Martín & M.T. Telleria, 20102Tell., (MA-Fungi 91309, **holotype**); *ibid.*, 20098Tell. (MA-Fungi 91308); 20114Tell. (MA-Fungi 91310).

Host and habitat: Known from the Valdivian temperate rain forest, Chilean Patagonia, South America, growing on decayed wood and associated with white rot.

GenBank numbers: ITS = MH233925, LSU = MH233928 (20098Tell., MA-Fungi 91308); ITS = MH233926, LSU = MH233929, (20102Tell., MA-Fungi 91309, **holotype**); ITS = MH233927 (20114Tell., MA-Fungi 91310).

Notes: Based on LSU analyses (Fig. 151), *Phanerochaete australosanguinea* clusters into the *Phanerochaete sensu stricto* clade in the *P. sanguinea* complex, according to the maximum likelihood phylogeny of the concatenated ITS, LSU, RPB1 and RPB2 obtained by Floudas and Hibbett (2015). Most species of this complex cause red–orange staining of the substrate, such as *P. australosanguinea* (Fig. 153c). In the LSU analyses, *P. australosanguinea* is a sister species of *P. sanguineocarnosa* Floudas & Hibbett. Morphologically, this is corroborated by both species sharing well-developed dark strands, the KOH reaction turning quickly green changing to brown on the basidiome; the subicular hyphae having developed clamps, and cystidia in both species are cylindrical, tapering to the apex, with secondary septa and of similar size. However, the spores are ellipsoid to broadly ellipsoid in *P. australosanguinea* (Q = 1.29), while those of *P. sanguineocarnosa*, described by Floudas and Hibbett (2015), are sub-ellipsoid to ellipsoid (Q = 1.8).

In the ITS analyses (Fig. 152), *Phanerochaete australosanguinea* also clusters in the *P. sanguinea* complex. However, the newly generated sequences are very distinct from those of the *P. sanguinea* complex of Floudas and Hibbett (2015). These authors included mainly species and specimens from the Northern hemisphere (except one sequence from Tasmania). The three collections from Chile form a basal and highly supported group (99% ML, 97% MP and 1.00 PP) indicating that *P. australosanguinea* is distinct from other species of the *P. sanguinea* complex by its geographical distribution. So far, *P. australosanguinea* has been reported from Valdivian temperate rain forest in Chilean Patagonia, where it is probably frequent and could have been confused with *P. sanguinea* (Fr.) Pouzar reported from the Patagonian Andes forest of Southern Argentina by Greslebin and Rajchenberg (2003).

Russulales Kreisel ex P.M. Kirk et al.

Russulaceae Lotsy

Russulaceae is one of the most speciose, and morphologically diverse ectomycorrhizal mushroom families (Miller et al. 2006; Hyde et al. 2016). This family has a worldwide distribution of more than 1200 species (Kirk et al. 2008). Multigene molecular phylogenetic analyses consistently recovered this family as a monophyletic clade which is now comprised of four genera: *Russula* Pers., *Lactarius* Pers., *Lactifluus* (Pers.) Roussel and *Multifurca* Buyck & Hofstetter (Buyck et al. 2008, 2010). We follow the treatments and the updated accounts of taxa in *Russulaceae* in Li et al. (2016), Hyde et al. (2016, 2017), De Crop et al. (2017) and Tibpromma et al. (2017). Four novel species viz. *Lactarius olivaceopallidus*, *Lactifluus midnapurensis*, *Russula choptae* and *R. uttarakhandia* are introduced in *Russulaceae* based on morphological distinctiveness and phylogenetic support. An updated phylogenetic tree of *Lactarius*, *Lactifluus*, *Russula* subg. *Russula* and subg. *Incrustatula* are provided. Detailed discussion and reviewed literatures were provided in Li et al. (2016), Hyde et al. (2016, 2017), De Crop et al. (2017) and Tibpromma et al. (2017).

Lactarius Pers.

Lactarius is one of the most prevalent agarics which form obligate symbiotic associations with many wide spread genera of trees (Verbeken et al. 2001; Le et al. 2007; Das and Verbeken 2011; Verbeken and Nuytinck 2013; Das et al. 2015; Hyde et al. 2016; Uniyal et al. 2017). Multigene based phylogenetic studies resulted segregation of paraphyletic *Lactarius sensu lato* into *Lactifluus* Pers. (Roussel) and *Lactarius* (including all angiocarpic species). *Lactarius sensu novo* consists of three cosmopolitan subgenera: *Lactarius* subg. *Lactarius*, *L.* subg. *Plinthogalus* (Burl.) Hesler & A. H. Sm. and *L.* subg. *Russularia* (Fr. ex Burl.) Kauffman (Verbeken and Nuytinck 2013; Das et al. 2015). Recent studies indicate the high species richness within *L.* subg. *Lactarius* in the Indian Himalayan region (Sharma and Das 2003; Das and Sharma 2005; Das and Verbeken 2011; Das 2013; Das et al. 2015; Uniyal et al. 2017). A novel species within *L.* subg. *Lactarius* sect. *Uvidi*, collected from Himalayan temperate forest (India) is presented here with morphological details and ITS phylogeny (Fig. 155).

Lactarius olivaceopallidus Uniyal, ***sp. nov.***

MycoBank number: MB820694; *Facesoffungi number*: FoF04839, Figs. 156, 157

Etymology: Due to pale olive colour of basidiomes.

Holotype: CAL 1401

Colour codes follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978).

Pileus 21–88 mm diam., convex, centrally depressed, finally infundibuliform, olive yellow (3C6) at centre, greyish yellow (4C4–7) toward margin, paler at margin, surface slimy to gelatinous, viscid at centre, sticky when dry, azonate to faintly zonate near margin, pale yellow (3A3) then yellow (3A7) with 30% KOH; margin decurved to inrolled. *Lamellae* yellowish white (1A2), pale yellow (3A2) in age, often with greyish yellow (4B4) spots, greyish violet (15D5) on bruising, adnate to broadly adnate, close (10–17 L + l/cm), including lamellulae), some forked near stipe, lamellulae numerous. *Stipe* 21–45 × 10–23 mm, yellowish white (4A2) to pale yellow (4A3), spotted with light yellow (4A5) scrobiculi, stuffed to hollow. *Context* up to 14 mm thick in pileus, yellowish white (1A2), pale yellow (3A3) with KOH, pale yellow (3A2) in stipe, immediately turning violet (15C6) on exposure. *Latex* yellowish white (3A2), rather abundant, immediately turning dull lilac (15C3) on gills, context, white paper and after 2–3 minutes on glass slide. *Odour* pleasant. *Taste* acrid. *Basidia* 51–72 × 9.5–16 µm, subclavate, 2–4-spored, sterigmata 5–9 µm long. *Basidiospores* 7.5–*8.7*–9.5 × 7–*7.7*–8.5 µm, (n = 40, Q = 1.06–*1.12*–1.21), subglobose to broadly ellipsoid; ornamentations amyloid, 1.7–2 µm high, mostly composed of broad ridges with wavy to even margin, triangular narrow ridges with round apices and small isolated warts, forming a dense incomplete reticulum; plage distally amyloid. *Pleuromacrocystidia* 51–113 × 9–17.5 µm, abundant, subclavate to fusiform, mostly round to blunt and acute apices, sometimes mucronate, contents dense. *Pleuropseudocystidia* up to 9 µm thick, nonemergent, cylindrical with rounded nonforked apex. *Lamellae edge sterile* composed of cheilomacrocystidia and marginal cells. *Cheilomacrocystidia* 34–63 × 8.5–12 µm, broadly fusiform, round to blunt apex. *Marginal cells* 13–23 × 4–6 µm, cylindric to subfusiform with rounded apex. *Hymenophoral trama* mainly composed of sphaerocytes and abundant lactifers, lactifers up to 14 µm wide. *Pileipellis* an ixocutis, 300–630 µm thick, composed of densely packed septate

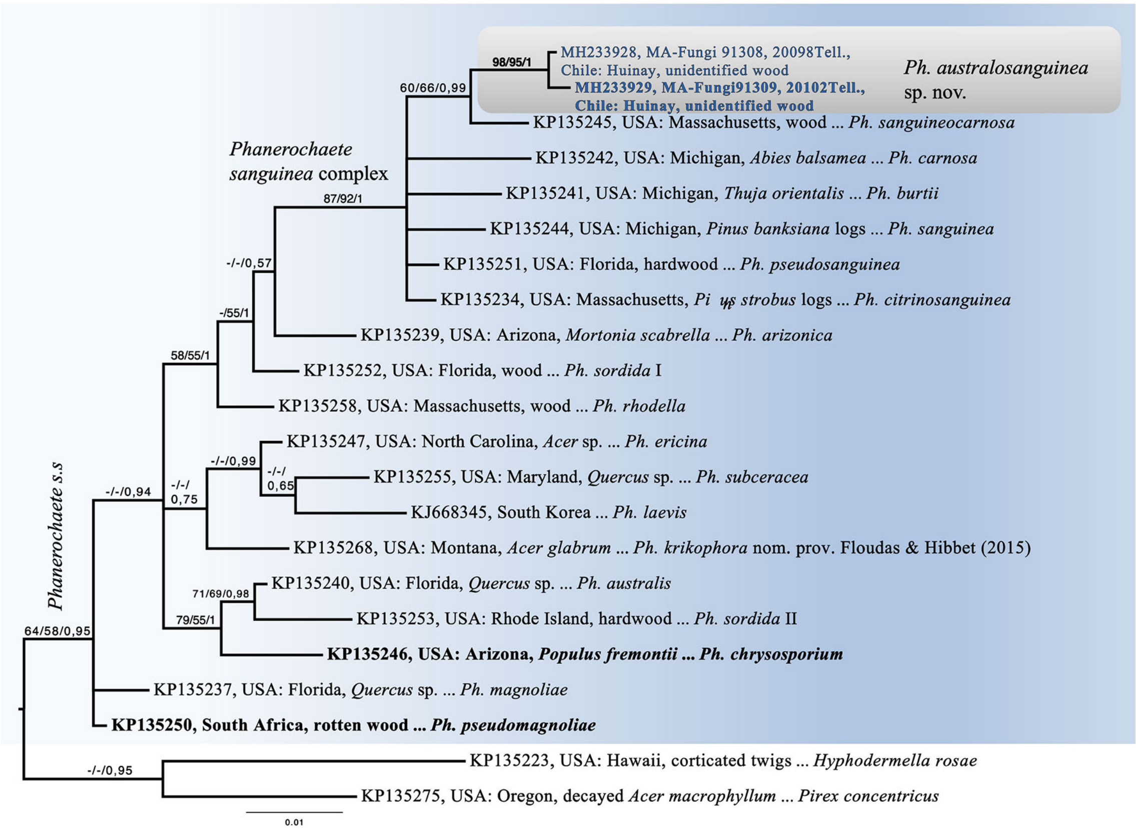


Fig. 151 Phylogram generated from Bayesian inference analysis of LSU sequence data of species of *Phanerochaete sensu stricto* from Floudas and Hibbett (2015) and the new species is marked in grey square. Maximum parsimony and maximum likelihood bootstrap support ≥ 50% (10.000 replicates both), and Bayesian posterior probabilities ≥ 0.50 BYPP are shown above the nodes. The tree is rooted with *Pirex concentricus* and *Hyphodermella rosae*. Newly generated sequences are in blue, types are in bold

hyphae, often shriveled, forming bundles in outer parts, 1–4 µm thick. *Lactifers in pilear trama* up to 11 µm wide. *Stipitipellis* an ixocutis, 65–102 µm thick, hyphae 1–4 µm wide, septate, not shriveled.

Material examined: INDIA, Uttarakhand, Pauri Garhwal, Chaubatta, alt 1904 m, N30° 09.681′ E78° 51.222′, 19 July 2016, P. Uniyal, PU-1110 (CAL 1401, **holotype**); *ibid.*, Pauri Garhwal, Chaubatta, 16 July 2016, P. Uniyal, PU 15-1090.

Host and habitat: Gregarious, under *Quercus leucotrichophora* A. Camus in temperate mixed forest.

GenBank numbers: ITS = KY440363 (CAL1401), ITS = MF741705 (PU 15-1090).

Notes: *Lactarius olivaceopallidus* differs from other members of *Lactarius* sect. *Uvidi* due to presence of pale olive basidiomes, abundant yellowish white latex, very high (≤ 2 µm) ornamentations of basidiospores and very thick (≤ 630 µm) ixocutis type of pileipellis. The combination of characteristics like viscid to slimy, azonate to slightly zonate pileus, ixocutis pattern of pileipellis and presence of white latex turning dull lilac on exposure undoubtedly place the present taxon in *Lactarius* sect. *Uvidi*.

In the field, *Lactarius olivaceopallidus* can easily be recognized by its pale olive basidiome, slimy to gelatinous pilear surface, pale yellow lamellae turning lilac when damaged, scrobiculate stipe surface and yellowish white latex that immediately changes into lilac on gills. Microscopically, very thick pileipellis (≤ 630 µm) and basidiospores with very high prominences (up to 2 µm) in form of a dense incomplete reticulum are also distinct.

Studies have suggested that poor molecular resolution in *Lactarius* sect. *Uvidi* has been a problem, as species in this group are dissimilar but genetically very close (Das et al. 2015; Barge et al. 2016). Species of *L.* sect. *Uvidi* in present study are well-separated (Fig. 155) from species belonging to other sections of *L.* subg. *Lactarius*. Two collections of the present species *L. olivaceopallidus* (CAL1401 and PU 15-1090) are distinctly separated in a relatively long branch from its closely related species. Morphologically, *L. olivaceopallidus* can be confused with *L. uvidus* (Fr.) Fr. (GenBank no. KJ742416, KJ742417; Fig. 155), *L. violascens* (J. Otto) Fr. and *L. aspideus* (Fr.) Fr. But, *L. uvidus* (originally described from Europe) differs in having greyish pink to light vinaceous grey pileus, cream to pale pinkish buff lamellae, larger basidiospores

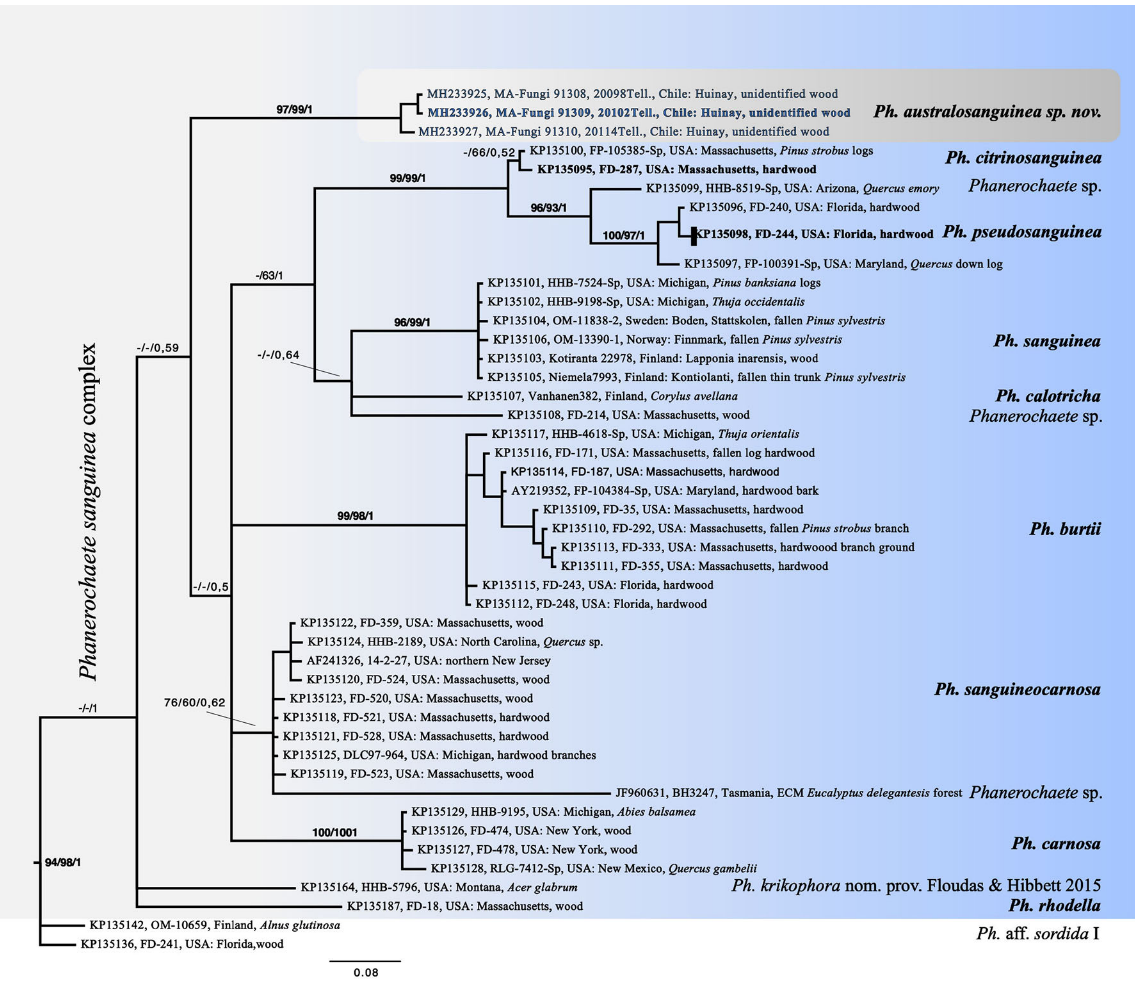


Fig. 152 Phylogram generated from Bayesian inference analysis of ITS sequence data of species of *Phanerochaete sanguinea* complex from Floudas and Hibbett (2015) and the new species is marked in grey square. Maximum parsimony and maximum likelihood bootstrap support ≥ 50% (10,000 replicates both), Bayesian posterior probabilities ≥ 0.50 BYPP are shown above the nodes. The tree is rooted with three *Phanerochaete* species

(8.4–11.3 × 6.6–8.5 µm), with shorter ornamentations (up to 0.7 µm) in form of rounded warts and obtuse broad ridges forming an incomplete reticulum. *Lactarius violascens* (originally reported from Europe) shares similarity in occurrence under deciduous trees but quite different due to greyish buff to brownish violet, azonate or zonate pileus, extracellular pigmentation in pileipellis appearing as dark brown granules and larger basidiospores (7.6 – 11.3 × 6.4–8.5 µm) (Heilmann-Clausen et al. 1998). Like *L. olivaceopallidus*, a pale basidiome is also present in *L. aspideus* (originally reported from Europe) which differs from *L. olivaceopallidus* due to smaller (10–70 mm in diam.) pileus, non-scrobiculate stipe, unchanging latex on isolation from flesh, shorter ornamentations (up to 0.5 µm) in basidiospores, zebroid pattern forming complete to nearly complete reticulum and very thin (40–70 µm) pileipellis (Heilmann-Clausen et al. 1998).

Lactarius salicis-reticulatae Kühner (GenBank no. KR090958, KR090959; Fig. 155) is another lilac staining species which is also phylogenetically close (94% similarity for 93–96% query coverage using BLAST) to the present novel species, however, it has subdistant to distant lamellae, mild tasting watery white latex, association with *Salix* and larger basidiospores (8.5–11.5 × 8–10 µm) (Barge and Cripps 2016).

Genetically, *Lactarius repraesentaneus* Britzelm. (GenBank no. KR090950, KR090954, KR090948, KR090953, JF908312 and KR090952; Fig. 155) is the closest relative (only 95–96% similarity for 93–96% query coverage using BLAST) to *L. olivaceopallidus*, but morphology of the two species is very different. *Lactarius repraesentaneus* (originally reported from Europe) has orange-yellow to honey pileus and conspicuously bearded pileus margin (hairs up to 5 mm long). Moreover, *L. repraesentaneus* is reported growing in ecological

Fig. 153 ***Phanerochaete australosanguinea*** (20102Tell., MA-Fungi 91309, **holotype**). **a** Basidiome dry specimen. **b** Strands, dry specimen. **c** Substrate stained red. **d** Basal hyphae thick-walled with clamp. **e** Probasidia and cystidium. **f** Basidium stained in congo red. **g** Cystidium with secondary septa stained in congo red. **h** Spores. *Scale bars* **a–c** = 1 cm, **d–h** = 10 μm

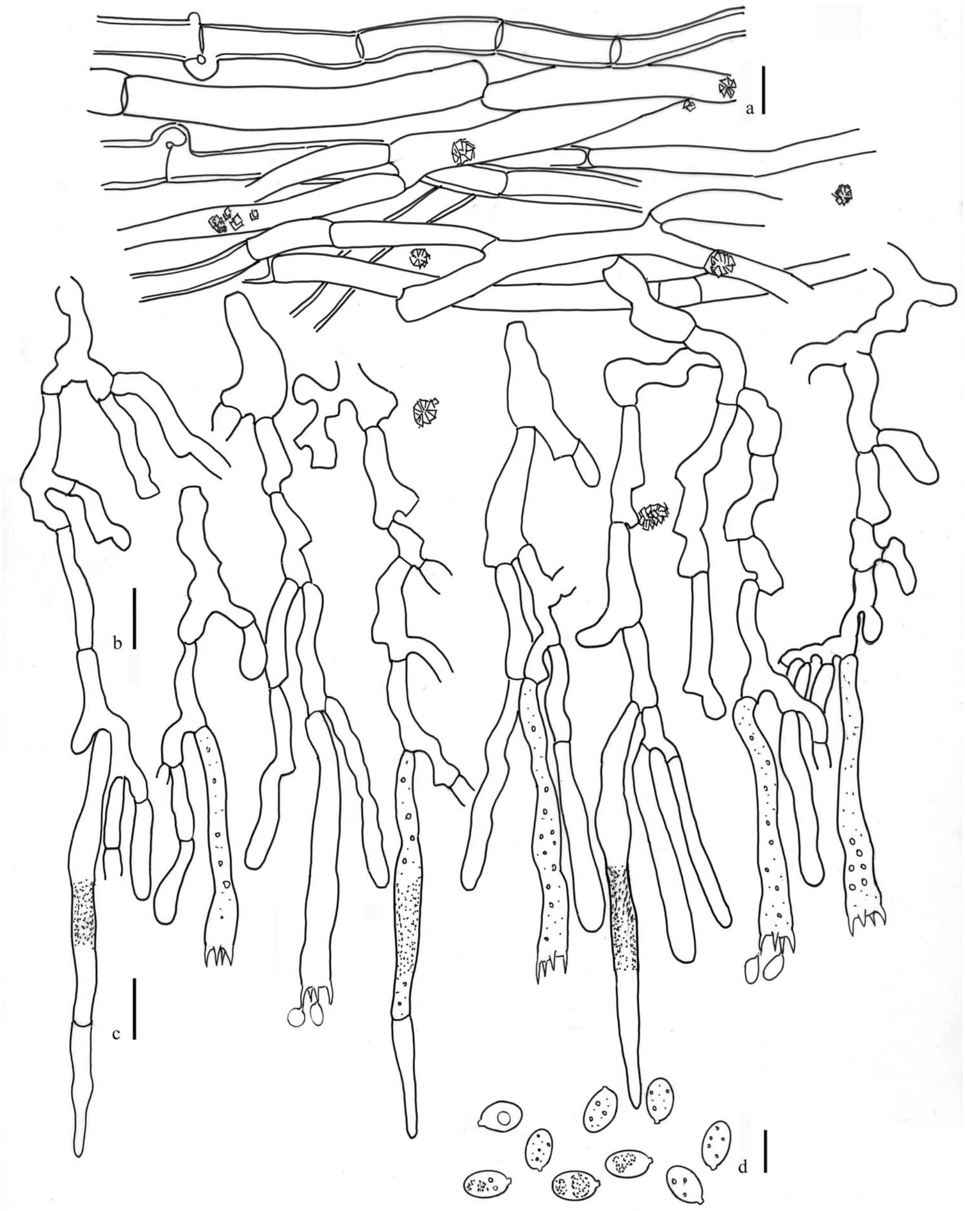


Fig. 154 ***Phanerochaete australosanguinea*** (20102Tell., MA-Fungi 91309, **holotype**). **a** Basal hyphae thin- to thick-walled with clamps. **b** Subhymenial hyphae. **c** Hymenium with probasidia, basidia and cystidia. **d** Spores. *Scale bars* **a–d** = 10 μm

association with *Picea*, *Betula* and *Salix* in temperate to arctic-alpine areas of North America and Europe. Microscopically, it has longer basidiospores (8–10.5 μm) with shorter (≤ 1 μm high) ridges and ixotrichoderm type of pileipellis. Phylogenetic analyses have suggested 99.4% similarity of *L. repraesentaneus* with *L. dryadophilus* Kühner (GenBank no. KR090901), which is very similar to *L. repraesentaneus* (Barge et al. 2016). *Lactarius dryadophilus* (originally reported from Europe) is also genetically close to *L. olivaceopallidus* (95% similarity for 94% query coverage using BLAST) but quite different due to white to pale yellow pileus with bearded margin and larger basidiospores (9.3–11.8 × 7.2–9.2 μm) having very low (≤ 0.3 μm high) ornamentations (Heilmann-Clausen et al. 1998; Barge et al. 2016).

In Asia, *Lactarius* sect. *Uvidi* is represented by *L. formosus* H.T. Le & A.Verbeken and *L. pyriodorus* K. Das & Verbeken. *Lactarius formosus* (originally reported from Thailand) is distinct from the present taxon by possessing greyish yellow to yellowish buff, zonate, scaly pileus with bundles of glutinous hairs and cutis to trichoderm type of thick (120–140 μm) pileipellis (Le et al. 2007). *Lactarius pyriodorus* K. Das & Verbeken (originally reported from Indian Himalaya) cannot be mistaken in the field for *L. olivaceopallidus* as the former displays brown vinaceous pileus, watery white latex, distinctive pear-like fruity odour and association with *Abies*. Microscopically, *L. pyriodorus* has larger basidiospores (8–8.9–10.5 × 6.9–7.5–8.8 μm), with lower (≤ 1.1 μm high) prominences and thinner (≤ 320 μm) pileipellis (Das et al. 2015).

Lactifluus (Pers.) Roussel

We follow the latest treatment and updated account of *Lactifluus* in De Crop et al. (2017) and Hyde et al. (2017). The new species *Lactifluus midnapurensis* is introduced in *Lactifluus* subgen. *Lactifluus* (Burl.) Hesler & A.H. Sm (Fig. 158).

Lactifluus midnapurensis S. Paloi & K. Acharya, ***sp. nov.***

MycoBank number: MB820587; *Facesoffungi number*: FoF03248, Figs. 159, 160

Etymology: The specific epithet refers to the type locality, Purba Midnapur (India).

Holotype: CAL 1516

Colour codes follow: Methuen handbook of colour (Kornerup and Wanscher 1978).

Pileus 11–48 mm diam., convex to broadly convex with an umbo when young, becoming plain to infundibuliform or applanate with a slight umbo toward centre at maturity, semi-moist to dry when young, dry and shiny at maturity, smooth, becoming slightly wavy and translucent with maturity, margin incurved at young stage, brown (5E4; 6E4) to yellowish brown (5E5) toward centre, brownish grey (5C2; 6D2) at early stage, becoming finally white (1A1) toward margin at maturity, no colour change on bruising, turns orange to reddish orange with guaiacol, negative in phenol, SV and KOH; context 1 mm toward centre, < 1 mm toward margin, white (1A1), no colour change on exposed in air. *Partial veil* present at the young stage, white (1A1), but disappear when mature. *Lamellae* ca. 3 mm broad, decurrent, distant, white (1A1), negative in phenol and KOH; edge even, regular, concolorous; lamellae two to three of length, forked toward margin. *Stipe* 8–43 × 2–5 mm, central when young, becoming central or excentric when mature, semi-moist at early stage, becoming dry and shiny when mature, smooth, grey (4C1) to golden grey (4C2) or brownish grey (4D2) when young, becoming white (1A1) at maturity, turns light yellowish brown on bruising at early stage but no change when mature, orange to orange-red with guaiacol, negative with KOH, phenol and SV; context hollow, white (1A1), no colour change on exposed in air. *Latex* water-like (transparent), no colour change up to 5 minutes in exposed on air. *Odour* unknown. *Taste* mild. *Spore print* white. *Lamellar trama* mainly composed of irregularly arranged sphaerocytes, hyphae and lactiflus hyphae. *Basidia* (43–)46.5–*51.5*–53.7(–57.2) × (7.1–)8–*8.9*–10(–11) µm, clavate to subclavate, hyaline, thin-walled, oil droplets present when viewed KOH, 4-spored; sterigmata 3.6–7.2 × 1–2.7 µm. *Basidiospores* 5.5–*6.5*–7.1(–8) × (5–)6–*6.6*–6.9(–7.5) µm, (n = 30) Q = 1.02–*1.07*–1.12, globose to subglobose, ornamentation amyloid, composed of short (0.3–0.6 µm) and long warts (1.5–2.0 µm), interconnected by a ridge line, forming a complete reticulum, sometimes connected line are shown wing-like pattern in side view, suprahilar spot amyloid or not. *Lamellae edge sterile* mainly composed of numerous cheilocystidia. *Cheilocystidia* 27–48.5 × 4.5–7.5 µm, subclavate to subcylindrical with mostly capitate apex, hyaline, thin-walled, oil droplet present when viewed with KOH. *Pleuromacrocystidia* 43–61 × 7.5–11 µm, rare toward cap margin but abundant toward cap centre, mostly appendiculate or mucronate, hyaline, thin-walled. *Pleuropseudocystidia* 2–4.5 µm in diam., abundant, cylindrical to subcylindrical with capitate or obtuse apex, dense with cytoplasmic component. *Pileipellis* a palisade, context made up with unequal, irregular shaped sphaerocytes and loosely arranged hyphal cells, branched, septet; distantly 2-layers, 30.6–46.2 µm deep, subpellis non-gelatinous, composed of tightly arranged globose to subglobose or irregular shaped cell, 11.6–19.7 × 10.7–17.9 µm, thin-walled, 2–4-celled deep; suprapellis composed of erect to sub-erect hyphal cell, 14.3–39.4 × 3.6–7.1 µm, hyaline, thin-walled, 2–3-celled, underling attached with the subpellis region of globose cells, non-gelatinized. *Stipitipellis* a palisade, 52.2–85.6 µm deep, upper layer composed of thin-walled, septet (up to 4 times) hyphae, 4.5–7.5 µm in diam., hyphal end subulate or obtuse, underling 2–3 globose like cells.

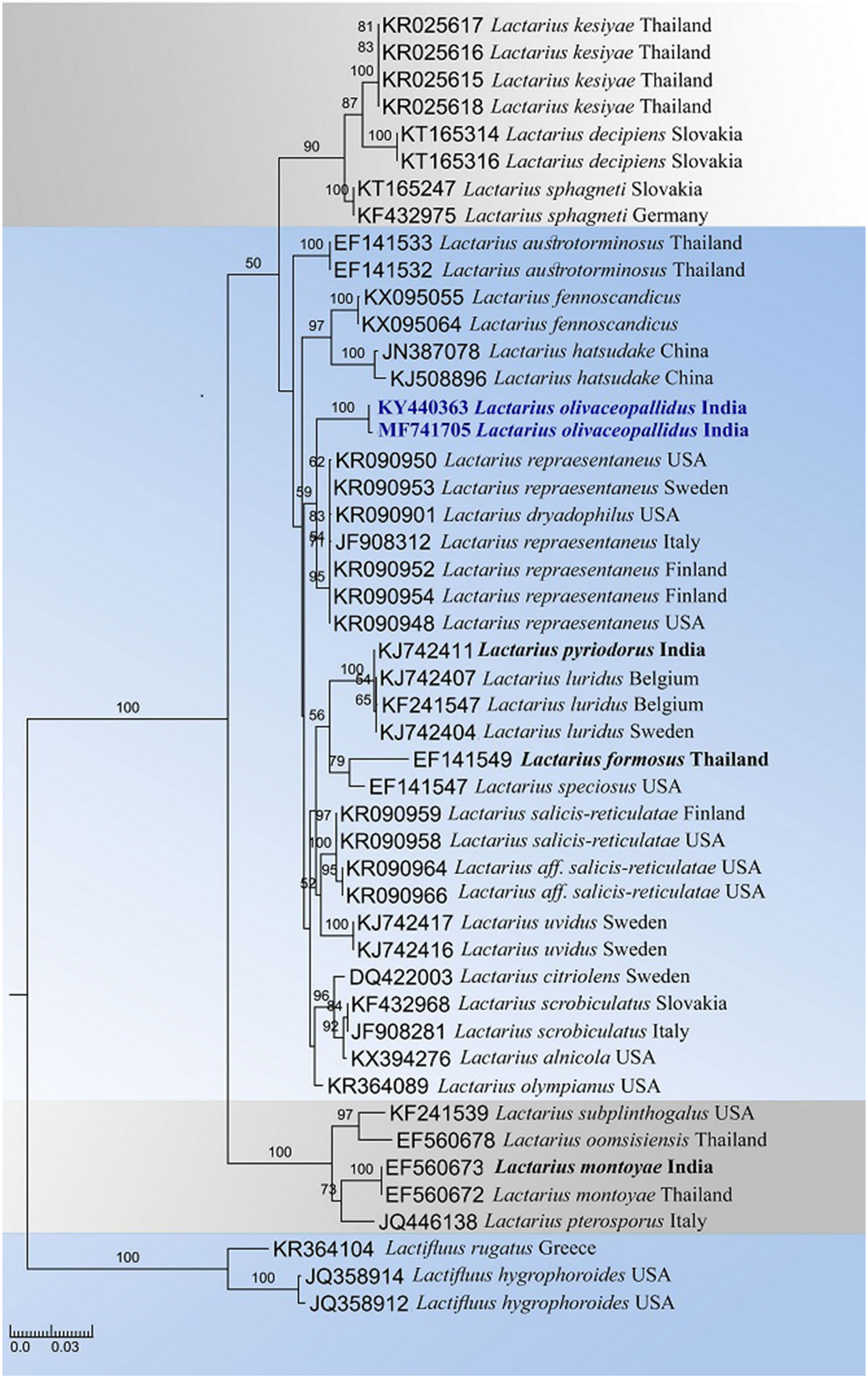
Material examined: INDIA, West Bengal, Purba Midnapur, Kasafaltalya, 21°43′0.552′′ N, 87°30′26.6472″E, S. Paloi & K. Acharya, 23 August 2015, SOUMITRA-22 (CAL 1516, **holotype**); *ibid.*, 21°43′6.222′′N, 87°30′7.9524′′E, S. Paloi & A.K. Dutta, 27 August 2015, SOUMITRA-40 (CAL 1523).

Habit and habitat: Common, solitary or gregarious, growing under *Shorea robusta* C.F. Gaertn. tree (*Dipterocarpaceae*).

GenBank numbers: ITS = KY785175, LSU = KY785177 (CAL 1516, **holotype**); ITS = KY785176, LSU = KY785178 (CAL 1523).

Notes: The diagnostic features of the newly described species includes small to medium sized (11–48 mm in diam.), convex to infundibuliform or applanate pileus, brownish grey to white that turns reddish orange with guaiacol; distant lamellae, white; slightly excentric stipe; watery latex (transparent); white spore print; mild taste; globose to subglobose basidiospores with a mean size of 7.1 × 6.6 µm, $Q_m = 1.07$, ornamentation composed of warts (up to 2 µm), interconnected with each other forming complete reticulate; pileipellis a palisade type. This combination of characteristics undoubtedly place *Lactifluus midnapurensis* under subg. *Lactifluus* sect. *Gerardii* (Stubbe et al. 2010; De Crop et al. 2017).

Lactifluus midnapurensis appears to be related to *L. coniculus* (Stubbe & Verbeken) Verbeken, described from Sri Lanka growing in association with *Shorea* sp. However, *L. coniculus* differs by cigar brown to snuff brown pileus,


81
KR025617 Lactarius kesiyae Thailand
83
KR025616 Lactarius kesiyae Thailand
100
KR025615 Lactarius kesiyae Thailand
87
KR025618 Lactarius kesiyae Thailand
100
KT165314 Lactarius decipiens Slovakia
KT165316 Lactarius decipiens Slovakia
90
100
KT165247 Lactarius sphagneti Slovakia
KF432975 Lactarius sphagneti Germany
50
100
EF141533 Lactarius austrotorminosus Thailand
EF141532 Lactarius austrotorminosus Thailand
100
KX095055 Lactarius fennoscandicus
97
KX095064 Lactarius fennoscandicus
100
JN387078 Lactarius hatsudake China
KJ508896 Lactarius hatsudake China
100
KY440363 Lactarius olivaceopallidus India
MF741705 Lactarius olivaceopallidus India
62
KR090950 Lactarius repraesentaneus USA
59
KR090953 Lactarius repraesentaneus Sweden
83
KR090901 Lactarius dryadophilus USA
54
71
JF908312 Lactarius repraesentaneus Italy
95
KR090952 Lactarius repraesentaneus Finland
KR090954 Lactarius repraesentaneus Finland
KR090948 Lactarius repraesentaneus USA
KJ742411 Lactarius pyriodorus India
100
64
KJ742407 Lactarius luridus Belgium
65
KF241547 Lactarius luridus Belgium
100
56
KJ742404 Lactarius luridus Sweden
79
EF141549 Lactarius formosus Thailand
EF141547 Lactarius speciosus USA
97
KR090959 Lactarius salicis-reticulatae Finland
100
KR090958 Lactarius salicis-reticulatae USA
95
KR090964 Lactarius aff. salicis-reticulatae USA
52
KR090966 Lactarius aff. salicis-reticulatae USA
100
KJ742417 Lactarius uvidus Sweden
KJ742416 Lactarius uvidus Sweden
DQ422003 Lactarius citriolens Sweden
96
84
KF432968 Lactarius scrobiculatus Slovakia
92
JF908281 Lactarius scrobiculatus Italy
KX394276 Lactarius alnicola USA
KR364089 Lactarius olympianus USA
97
KF241539 Lactarius subplinthogalus USA
EF560678 Lactarius oomsisiensis Thailand
100
100
EF560673 Lactarius montoyae India
73
EF560672 Lactarius montoyae Thailand
JQ446138 Lactarius pterosporus Italy
100
KR364104 Lactifluus rugatus Greece
100
100
JQ358914 Lactifluus hygrophoroides USA
JQ358912 Lactifluus hygrophoroides USA
0.0 0.03

◀**Fig. 155** Phylogeny of *Lactarius olivaceopallidus* inferred from maximum likelihood analysis of ITS sequence dataset using RAxMLGUI 1.5 (Silvestro and Michalak 2012). Multiple sequence alignment was performed using MAFFT v.7 (Katoh and Standley 2013) with default settings. Alignment was manually edited with Bioedit v 7.2.5 (Hall 1999). To change the multiple alignment format, Alignment Transformation Environment (ALTER) was used (Glez-Peña et al. 2010). One-thousand bootstrap replicates were analyzed to obtain nodal support values. TreeGraph2 was used for visualization of the phylogram (Stöver and Müller 2010). The novel species is shown in blue and type strains are in bold. Species of sister genus *Lactifluus* were selected as the outgroup taxa

solid stipe context, comparatively larger basidiospores (7.1–10.2 × 6.4–8.8 µm) with ornamentation like interconnected conical to triangular, round to acute warts and absence of pleuromacrocystidia (Stubbe et al. 2012b).

Within the same section, among taxa with similar sized basidiospores, colouration of the latex and growth in association to *Dipterocarpus* plants, *Lactifluus limbatus* (Stubbe & Verbeken) Stubbe (described from Malaysia) is a phylogenetically close taxon (Fig. 158). *Lactifluus limbatus* has a larger pileus (30–60 mm), brownish grey towards centre and grey towards margin, greyish brown lamellar edge, spore ornamentation up to 0.8 µm high and absence of pleuromacrocystidia (Stubbe et al. 2012a, b). *Lactarius atrovelutinus* J.Z. Ying frequently encountered from China and Malaysia, has a dark black-brown pileus, cream (young) to yellow (mature) lamellae, latex that turns pink or brownish pink on drying, presence of fruity or sweet odour, absence of pleuromacrocystidia and very thick pileipellis (80–100 µm; Ying 1991). *Lactarius conchatulus* Stubbe & Verbeken, described from northern Thailand (alt. 1300 m), has smaller pileus (2–7 mm diam.) that turns pale yellow on bruising, subdecurrent lamellae, and broadly ellipsoid basidiospores (Q = 1.08–1.35) with up to 0.9 µm long ornamentation (Stubbe et al. 2012a, b).

Being a well representative member of the sect. *Gerardii*; *Lactifluus bicolor* (Massee) Verbeken, distributed in Malaysia and Singapore, differs from *L. midnapurensis* in having a larger pileus (20–80 mm diam.), dark brown or fuliginous, longer stipe (10–80 mm), and larger basidiospores (7.5–9.6 × 6.4–8.6 µm) with a ornamentation up to 0.3–0.5 µm high (Massee 1914; Stubbe et al. 2012a, b). A taxon with similar pileus colouration, *L. leae* Stubbe & Verbeken differs by its very larger pileus (35–120 mm in diam.), somewhat differently sized basidiospores (6.6–12.1 × 5.9–9.1 µm), ornamentation up to 0.5–1 µm high and absence of macrocystidia (Stubbe et al. 2012a, b).

Russula Pers.

Russula is species-rich and one of the most thoroughly monographed genera of fungi that is mainly ectomycorrhizal with a diverse range of plants in deciduous or evergreen, broadleaf or coniferous woods, scrubland and even meadows from tropical to subalpine areas and has a cosmopolitan distribution (Knudsen and Borgen 1982; Singer 1986; Buyck et al. 1996; Rawla 2001; Das and Sharma 2005; Das et al. 2006a, b, Das et al. 2010, Das et al. 2013, Das et al. 2014, 2017a, b; Miller et al. 2012; Li et al. 2013, 2015; Hyde et al. 2016; Ghosh et al. 2016, 2017; Ghosh and Das 2017). Species within this genus are known by the combination of their conspicuous and fleshy basidiomes, colourful fragile pileus, amyloid warty basidiospores, abundant sphaerocytes in a heteromerous trama that can make these fungi brittle, absence of latex and the hyphae that lack clamp connections (Romagnesi 1967; Singer 1986; Sarnari 1998, 2005). *Russula* has 10 subgenera namely: *R.* subg. *Compactae*, *R.* subg. *Heterophyllidia*, *R.* subg. *Ingratula*, *R.* subg. *Amoenula*, *R.* subg. *Incrustatula* and *R.* subg. *Russula*, *R.* subg. *Archaea*, *R.* subg. *Brevipes*, *R.* subg. *Malodora* and *R.* subg. *Crassotunicata* Buyck & V. Hofstetter (Sarnari 1998; Hongsanan et al. 2015; Das et al. 2017b). Here, two novel species (belonging to subg. *Incrustatula* and *Russula*) collected from the northwestern part of Indian Himalaya are described with morphological details and phylogenetic placement (Figs. 161, 162).

Russula choptae A. Ghosh & K. Das, ***sp. nov.***

MycoBank number: MB824343; *Facesoffungi number*: FoF04953, Figs. 163, 164

Etymology: Referring to Chopta in Uttarakhand (India), the type locality.

Holotype: CAL 1658

Colour codes follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978).

Basidiomes 34–112 mm in height, small to medium sized. *Pileus* 6–48 mm in diam., hemispheric when young, convex, plano-convex, expanding to applanate when mature, centre slightly depressed with age, finely wrinkled and areolate at maturity; margin decurved to plane with maturity, entire, slightly tuberculately striate, dry (viscid when moist), peeling 1/4 from the edge, brownish red (9C6–8) at young stage, pale red (9–10A3), pastel red (9–10A4–5) to madder red (9A6–7), intermixed with pink, orange to yellowish tinge of coral red (9B7) at the centre, pinkish white (9A2), pale red to pastel red (9A3–4) towards the margin; pale yellow to pastel yellow (2A3–4) with KOH. *Pileus context* greyish white (1B1), 2–4 mm thick, unchanging after bruising, turning reddish brown (8D6–7) with guaiacol. *Lamellae* adnexed to subdecurrent, crowded (10–16/cm), chalky white to yellowish white (1A1–2) with maturity, up to 3 mm thick, narrowing towards the margin, forked near the stipe apex, middle of lamellae and near cap margin, entire, edges concolorous, unchanging when bruised. *Lamellulae* present in different lengths (up to 5 series). *Stipe* 37–88 × 6–13 mm,

Fig. 156 ***Lactarius olivaceopallidus*** (CAL 1401, **holotype**). **a, c** Fresh basidiomes in field and basecamp. **b** Latex on gills. **d** Transverse section through thick pileipellis. **e** Hyphal arrangement in pileipellis. **f, g** Pleurocystidia. **h** Cheilocystidia and marginal cells. **i** Pseudocystidia. **j, k** SEM images of basidiospores. *Scale bars* **a** = 20 mm, **d** = 100 µm, **e, g–i** = 10 µm, **f** = 25 µm, **j–k** = 2 µm

cylindrical to subclavate, central, dry, smooth, brittle, pale red, pastel pink to pink rose (11A3–5) with white (1A1) to yellowish white (1A2) areas or orange white to pale orange (5A2–3) tinge at the base; turning reddish brown (8D6–7) with guaiacol. *Stipe context* stuffed to hollow, dirty white, unchanging after bruising but reddish brown (8D6–7) and greyish green (27C4–5) with guaiacol and KOH respectively. *Taste* acrid. *Spore print* yellowish white. *Subhymenium layer* up to 28 µm thick, pseudoparenchymatous. *Basidia* 30–40 × 9–14 µm, 4-spored, cylindrical, subclavate to clavate, sterigmata up to 6 µm long. *Basidiospores* (6.9–)7–*7.4*–7.9(–8) × (6–)6.1–*6.6*–7 µm, [n = 30, Q = (1–)1.06–*1.13*–1.2(–1.31)], subglobose to broadly ellipsoid, rarely globose and ellipsoid, composed of amyloid warts becoming linked as small crests and thick ridges, forming an incomplete network, intermixed with isolated warts (up to 1 µm) in height;

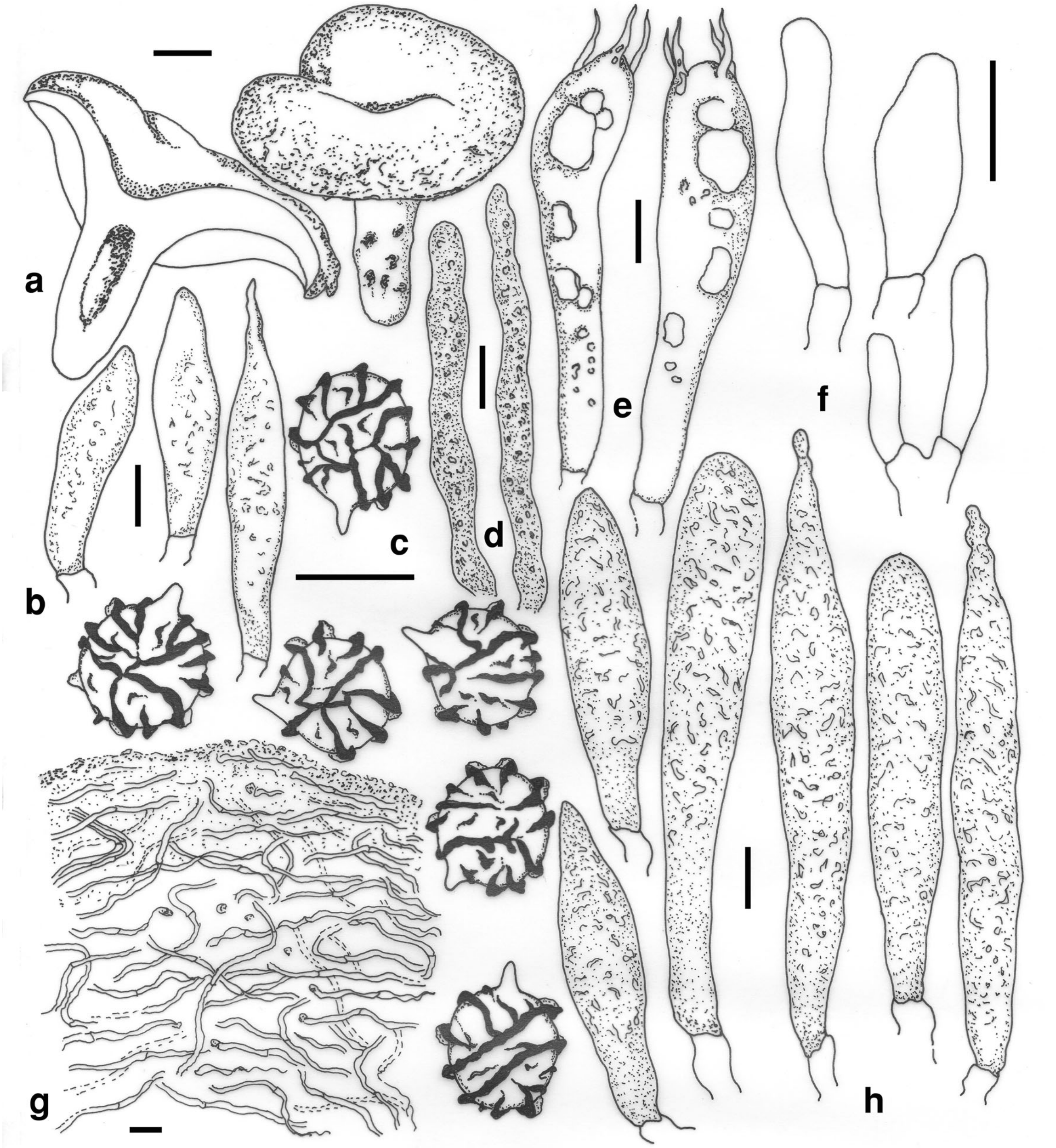
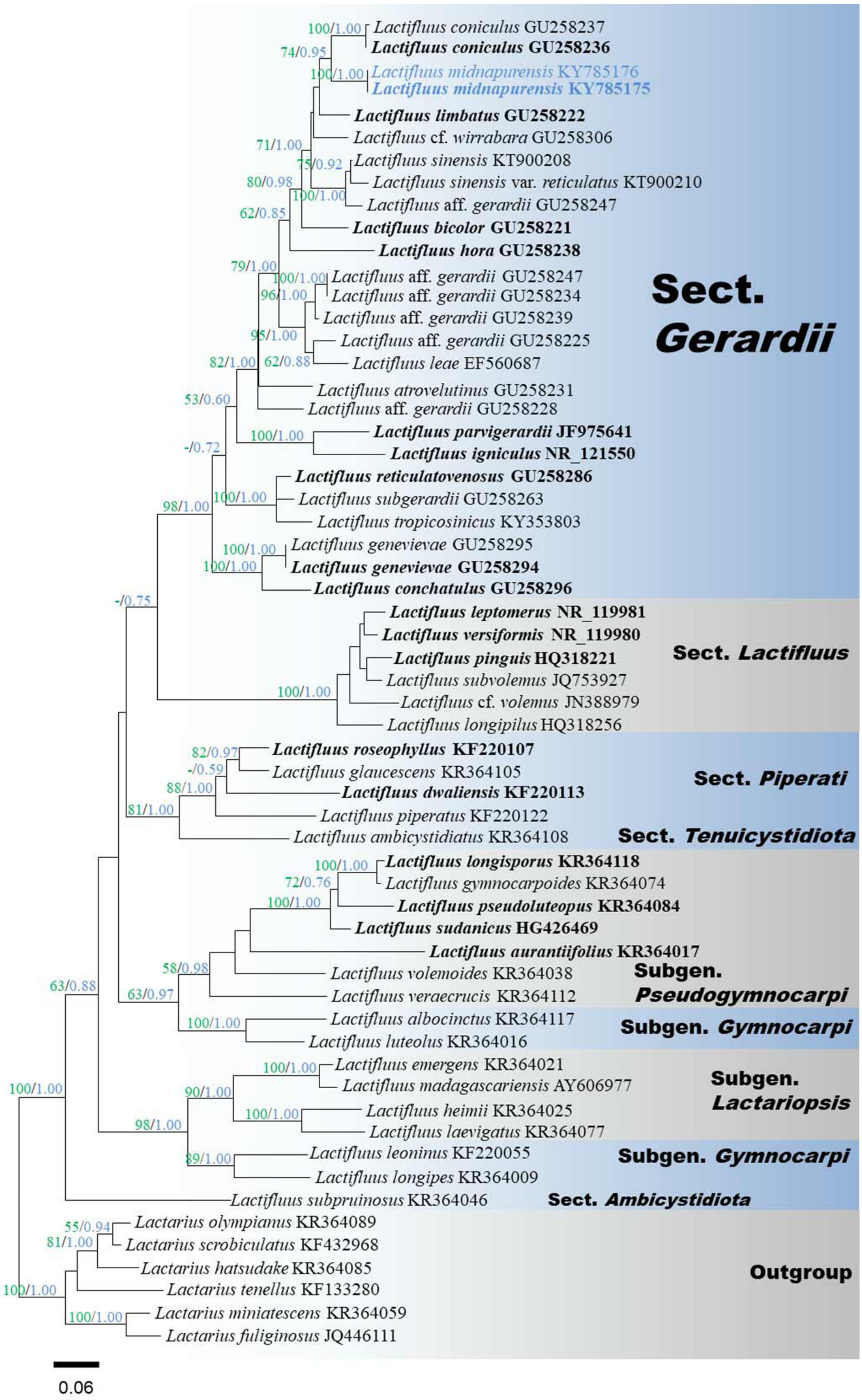


Fig. 157 ***Lactarius olivaceopallidus*** (CAL 1401, **holotype**). **a** Fresh/dissected basidiomes. **b** Cheilocystidia. **c** Basidiospores. **d** Pseudocystidia. **e** Basidia. **f** Marginal cells. **g** Pileipellis. **h** Pleurocystidia. *Scale bars* **a** = 20 mm, **b–h** = 10 µm

suprahilar plage inamyloid, apiculi up to 2 µm high. *Pleurocystidia* (35–)45–*64*–80(–96) × (7–)7.5–*10*–12(–13) µm, abundant, cylindrical to subclavate with capitate, appendiculate, pointed, mucronate, moniliform or rounded apex, emergent up to 47 µm, completely filled with dense, finely crystalline content in congo red, turning grey-black with sulphovanillin (SV). *Lamellar edge* fertile with basidia and cystidia. *Cheilocystidia* (30–)35–*45.5*–56(–61) × (6–)7–*9*–11(–12) µm, cylindrical to subclavate with mostly rounded apex, completely filled with dense, finely crystalline content in congo red, turning grey-black with sulphovanillin (SV). *Pileipellis* orthochromatic in cresyl blue, a trichoderm, up to 260 µm thick, two-layered and sharply delimited from the underlying sphaerocytes of the context; distinctly divided in a 120–160 µm deep, suprapellis of erect to suberect hyphal ends and pileocystidia, containing branched, septate, hyphal endings, and underneath this suprapellis a 140–100 µm deep, subpellis of interwined, more or less horizontally oriented hyphae. *Hyphal extremities* near the cap margin composed of a single or a few cells only; the terminal cells subcylindrical to cylindrical, with rounded or obtuse tips, measuring (15–)18–*24*–30(–34) × (2.5–)3–*3.5*–4(–5) µm; subterminal cells


100/1.00
Lactifluus coniculus GU258237
Lactifluus coniculus GU258236
74/0.95
100/1.00
Lactifluus midnapurensis KY785176
Lactifluus midnapurensis KY785175
Lactifluus limbatus GU258222
71/1.00
Lactifluus cf. wirrabara GU258306
75/0.92
Lactifluus sinensis KT900208
80/0.98
Lactifluus sinensis var. reticulatus KT900210
100/1.00
Lactifluus aff. gerardii GU258247
62/0.85
Lactifluus bicolor GU258221
Lactifluus hora GU258238
79/1.00
100/1.00
Lactifluus aff. gerardii GU258247
96/1.00
Lactifluus aff. gerardii GU258234
Lactifluus aff. gerardii GU258239
95/1.00
Lactifluus aff. gerardii GU258225
82/1.00
62/0.88
Lactifluus leae EF560687
Lactifluus atrovelutinus GU258231
53/0.60
Lactifluus aff. gerardii GU258228
100/1.00
Lactifluus parvigerardii JF975641
Lactifluus igniculus NR_121550
-/0.72
Lactifluus reticulatovenosus GU258286
100/1.00
Lactifluus subgerardii GU258263
98/1.00
Lactifluus tropicosinicus KY353803
100/1.00
Lactifluus genevievae GU258295
100/1.00
Lactifluus genevievae GU258294
Lactifluus conchatulus GU258296
Sect. Gerardii
-/0.75
Lactifluus leptomerus NR_119981
Lactifluus versiformis NR_119980
Lactifluus pinguis HQ318221
Lactifluus subvolemus JQ753927
100/1.00
Lactifluus cf. volemus JN388979
Lactifluus longipilus HQ318256
Sect. Lactifluus
82/0.97
Lactifluus roseophyllus KF220107
-/0.59
Lactifluus glaucescens KR364105
88/1.00
Lactifluus dwaliensis KF220113
81/1.00
Lactifluus piperatus KF220122
Lactifluus ambicystidiatus KR364108
Sect. Piperati
Sect. Tenuicystidiota
100/1.00
Lactifluus longisporus KR364118
72/0.76
Lactifluus gymnocarpoides KR364074
100/1.00
Lactifluus pseudoluteopus KR364084
Lactifluus sudanicus HG426469
Lactifluus aurantiifolius KR364017
58/0.98
Lactifluus volemoides KR364038
63/0.88
63/0.97
Lactifluus veraecrucis KR364112
Subgen. Pseudogymnocarpi
100/1.00
Lactifluus albocinctus KR364117
Lactifluus luteolus KR364016
Subgen. Gymnocarpi
100/1.00
Lactifluus emergens KR364021
100/1.00
Lactifluus madagascariensis AY606977
90/1.00
100/1.00
Lactifluus heimii KR364025
98/1.00
Lactifluus laevigatus KR364077
Subgen. Lactariopsis
89/1.00
Lactifluus leoninus KF220055
Lactifluus longipes KR364009
Subgen. Gymnocarpi
Lactifluus subpruinosus KR364046
Sect. Ambicystidiota
55/0.94
Lactarius olympianus KR364089
81/1.00
Lactarius scrobiculatus KF432968
Lactarius hatsudake KR364085
100/1.00
Lactarius tenellus KF133280
100/1.00
Lactarius miniatescens KR364059
Lactarius fuliginosus JQ446111
Outgroup
0.06

◀ **Fig. 158** Phylogram generated from maximum likelihood (− InL = 10343.610778) (RAxML) analysis using a GTR + I + G model of nucleotide evolution based on ITS sequence dataset for 47 *Lactifluus* and six outgroup sequences (*Lactarius scrobiculatus*, *L. olympianus*, *L. hatsudak*, *L. miniatescens*, *L. fuliginosus*, *L. tenellus*). Maximum likelihood bootstrap support values (left) greater than 50% and Bayesian posterior probabilities (right) greater than 0.50 BYPP are indicated above the nodes. Sequences used in this study mostly have been sampled from a previous study (Stubbe et al. 2010, 2012a, b). The newly described taxon is indicated in blue and ex-type strains are indicated in bold. Classification of the subgenus and sections follows De Crop et al. (2017)

subcylindrical to cylindrical; in the cap centre, terminal cells subcylindrical to cylindrical, with rounded or obtuse tips, measuring (19–)20–*25*–29(–35) × 3–*4*–4.5(–5) µm; subterminal cells cylindrical. *Pileocystidia* near the pileus margin aseptate, short to very long, measuring (2.5–)4–*5*–6(–7) µm broad, subcylindrical to cylindrical, sometimes with lateral projections, obtuse-rounded or sometimes swollen apex, almost completely filled with dense granular content in congo red, distinctly grey-black in sulfovanillin (SV), without incrustations. *Pileocystidia* near the pileus centre aseptate, short to very long, measuring (3)4–*5*–6(–8) µm broad, slightly larger, subcylindrical to cylindrical, sometimes with lateral projections, obtuse-rounded or swollen or sometimes forked apex, almost completely filled with dense granular content in congo red, distinctly grey-black in sulfovanillin (SV), without incrustations. *Clamp connections* and *laticiferous hyphae* absent from all tissues.

Material examined: INDIA, Uttarakhand, Rudraprayag District, Chopta, N30°28.997′ E79°10.298′, alt. 2632 m, under *Quercus* sp., 24 July 2016, A. Ghosh, AG 16-1186 (CAL, **holotype;** GUH, **isotype**); *ibid*., N30°28.693′ E79°11.636′, alt. 2315 m, under *Quercus* sp., 25 August 2016, A. Ghosh, AG 16-1363; Pabdhar, N30°29.376′ E79°09.673′, alt. 2356 m, under *Quercus* sp., 25 July 2016, A. Ghosh, AG 16-1206; Bageshwar District, Dhakuri, N30°04.970′ E79°55.134′, alt. 2586 m, under *Quercus* sp., 2 August 2016, A. Ghosh (AG 16-1269, **paratype**); Baniyakund, N30°28.998′ E79°10.657′, alt. 2614 m, under *Quercus* sp., 7 August 2017, A. Ghosh, AG 17-1529; Baniyakund, N30°29.091′ E79°10.400′, alt. 2565 m, under *Quercus* sp., 8 August 2017, A. Ghosh, AG 17-1549.

Host and habitat: Growing caespitose, under *Quercus* sp. (*Fagaceae*) in mixed forests dominated by *Quercus*, *Rhododendron* (*Ericaceae*) and *Abies* (*Pinaceae*).

GenBank numbers: ITS = MG897815 (AG 16–1186); ITS = MG925207 (AG 16–1363).

Notes: The combination of macro- and micromorphological features such as, taste being usually acrid or very acrid, epicutis containing well characterized dermatocystidia, yellowish white spore print, often pinkish or lilac stipe, mostly adnate or subdecurrent lamellae and red pilei growing in deciduous forests place *Russula choptae* under subg. *Russula* sect. *Russula* subsect. *Sardoninae* (Sarnari 1998).

In the field *Russula choptae* is distinct from other species of this group by its brownish red, pale red, pastel red to madder red finely wrinkled pileus with intermixed of pink, orange to yellowish tinge of coral red at the centre, long and slim stipe with yellowish white (1A2) areas or orange white to pale orange (5A2–3) tinge at the base; lamellae with bifurcate, different lengths at the apex of stipe, lamellulae with different lengths (up to 5 series); stipe cuticle and context turns reddish brown and greyish green with guaiacol and KOH, respectively, and micromorphologically it is separated from allied species by different types of cystidial apex (capitate, appendiculate, pointed, mucronate, moniliform or rounded) and basidiospores with warts that are linked as small crests and thick ridges, forming an incomplete network and intermixed with isolated warts.

Based on the BLASTn search in NCBIs GenBank nucleotide database, the closest hit using ITS sequences (AG 16-1186 and AG 16-1363) is *Russula* sp. (voucher HKAS 78400 GenBank no. KF002784) collected from China. Unfortunately, there is no micro- and macromorphological details available for this Chinese collection in published literature. Our phylogeny (Fig. 161) shows *R. choptae* as sister to this unknown Chinese *Russula* sp.

In subsect. *Sardoninae*, three species *Russula persicina* Krombh., *R. exalbicans* (Pers.) Melzer & Zvára and *R. gracillima* Jul. Schäff. (also appeared to be close in ITS phylogeny in Fig. 161) resemble *R. choptae*. However, *R. persicina*, originally reported from Europe, has larger pileus (40–100 mm), widely spaced rather sinuate lamellae, basidiospores, mostly with isolated warts (0.8 µm) with few crests (Galli 1996; Sarnari 1998; Kränzlin 2005; Knudsen et al. 2012). *Russula exalbicans* (originally reported from Europe), differs in having larger (50–100 mm diam.), rose-red, pink, vinaceous, rapidly becoming paler to almost entirely greenish white pileus usually with a trace of pink at the extreme margin, firm white stipe which soon becomes grey with age or in wet weather, frequent 0–1-septate dermatocystidia, larger basidiospores (7–10 × 5–7 µm) with low (up to 0.75 µm high) ornamentations and ochre spore print (Pearson 1950; Galli 1996; Sarnari 1998; Kränzlin 2005). *Russula gracillima* (also reported from Europe), differs from *R. choptae* in possessing moderately spaced lamellae, presence of abundant, broad (5–10 µm) dermatocystidia and basidiospores with isolated blunt warts (Rayner 1985; Galli 1996; Sarnari 1998; Kränzlin 2005; Knudsen et al. 2012; Kibby 2014). *Russula renidens* Ruots. et al., another taxon in subsect. *Sardoninae* and originally reported from Europe, has bright crimson red, blood-red to copper red

Fig. 159 ***Lactifluus midnapurensis*** (CAL 1516, **holotype**). **a** Fresh basidiomes in the field. **b** Basidiome showing lamellae side. **c** SEM microphotograph of basidiospores. **d** Pleurocystidia. **e** Pileipellis. *Scale bars* **a, b** = 10 mm, **c** = 5 µm, **d** = 20 µm, **e** = 10 µm

larger pileus (35–80(–100) mm), sulcate margin with age, some intervening lamellae, cylindric to clavate stipe (40–100 × 10–22 mm), basidiospores with low ornamentation (up to 0.5 µm) consisting of small warts with some clusters or ridges, 0–2-septate and slender to clavate dermatocystidia (Galli 1996; Sarnari 1998; Knudsen et al. 2012).

Five more taxa of this subsection, *Russula sanguinea* Fr., *R. queletii* Fr., *R. sardonia* Fr., *R. torulosa* Bres. and *R. thindii* K. Das & S.L. Mill. also differ from *R. choptae*. *Russula sanguinea*, originally reported from Europe, has a coniferous habitat especially under pines and elliptical larger basidiospores (7–9 × 6–7 µm), with ornamentation consisting mostly of solitary warts which are somewhat elongated (only a few with connections) (Rayner 1985; Sarnari 1998; Kränzlin 2005; Knudsen et al. 2012). *Russula queletii* (originally reported from Europe) can be distinguished by presence of a combination of characteristics i.e. vinaceous red to violet pileus and stipe, strong fruity odour and changing of pilear context to light vinaceous red with $FeSO_4$ (Rayner 1985; Saini and Atri 1989; Sarnari 1998; Kränzlin 2005; Knudsen et al. 2012). Similarly, *R. sardonia*, originally reported from Europe, differs in having dark violaceous purple, reddish purple or livid vinaceous pileus, sometimes with greyish olivaceous or with yellowish patches; solid and firm stipe; slightly larger basidiospores (7–9 × 6–7 µm) and is mycorrhizal with *Pinus* on acid soil (Sarnari 1998; Knudsen et al. 2012). *Russula torulosa* (originally reported from Europe) possess purple-violet, purple-red, violet-red or dark red pileus sometimes with lighter ochraceous or olivaceous spots, often blackish at centre; solid and firm stipe; larger basidiospores (7.2–9.5 × 5.6–7.3 µm) with low ornamentations (0.4–0.6 µm) and is found mostly under *Pinus* sp. (Sarnari 1998; Knudsen et al. 2012). *Russula thindii* (originally reported from India) is distinct by its larger pileus (38–77 mm diam.), pale yellow spore print and larger basidiospores (7.5–*9*–10 × 6–*7*–8 µm), with ornamentation composed mostly of isolated conical to spinoid warts being occasionally connected by fine connectors (Das et al. 2014).

In Eastern Asia, *Russula choptae* might be confused with *R. chiui* G.J. Li & H.A.Wen, *R. zhejiangensis* G.J. Li & H.A. Wen and *R. minutula* var. *minor* Bi (originally described from China). However, *R. chiui* differs in having brightly red tinged pileus, white stipe, septate pileocystidia, densely reticulate larger basidiospores [(8–)8.5–10(–10.5) × 7–8(–8.5) µm] and sterile lamellar edge (Li et al. 2015). *Russula zhejiangensis* has a purely white stipe, isolated conical to obtuse warts in basidiospores, shorter pleurocystidia (35–74 × 6–11 µm) with mostly rounded or mucronate apex, sterile lamellar edge and 0–3-septate pileocystidia (Li et al. 2011). *Russula minutula* var. *minor*, described in Guangdong Province of South China, differs by its white to yellowish gills, white stipe, isolated spinoid basidiospores and shorter pleurocystidia (Bi and Li 1986; Li et al. 2011).

Russula uttarakhandia A. Ghosh & K. Das, ***sp. nov.***

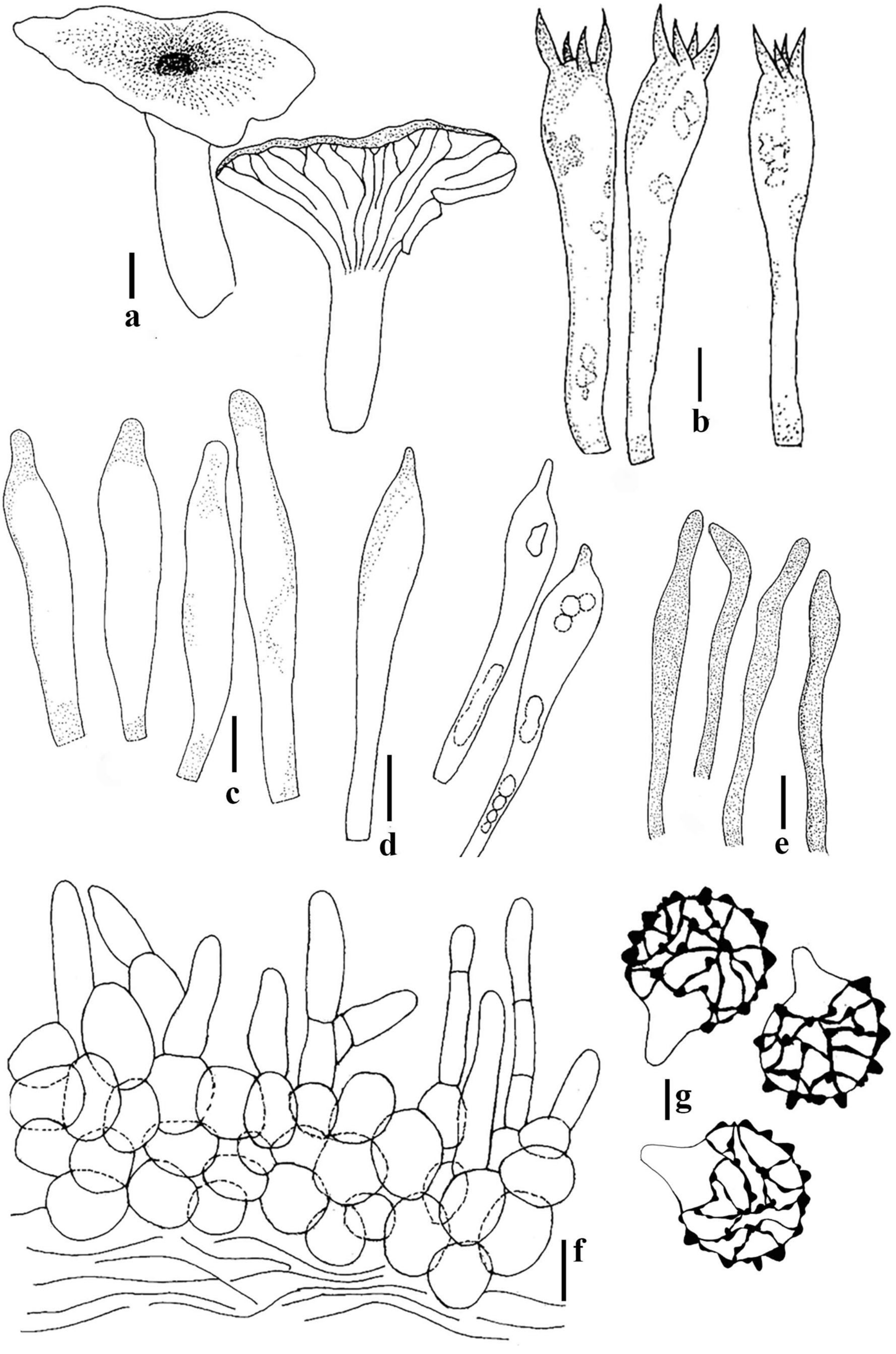
MycoBank number: MB820834; *Facesoffungi number*: FoF04954, Figs. 165, 166

Etymology: Referring to the name of an Indian state, Uttarakhand from where the species was collected.

Holotype: CAL 1537

Colour codes follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978).

Basidiomes 70–90 mm high. *Pileus* 45–60 mm diam., planoconvex to applanate with slightly depressed centre, margin decurved to plane with maturity, entire, tuberculately striate, surface dry, viscid when moist, gelatinous, glossy, pinkish white or reddish white (10A2) to venetian pink (10A3) and centrally olive yellow (2B6–7) to greyish yellow (2A4–6), discoloring to colourless with KOH, cuticle peeling 1/3 of the radius, chalky white (1–2A1) beneath the cuticle; pileus context chalky white (1–2A1), unchanging on bruising. *Lamellae* adnate to adnexed, close to rather crowded (7–10 cm at pileus margin), chalky white (1A1), entire, with concolorous edges, unchanging when bruised. *Lamellulae* present, in 2 series. *Stipe* 55–70 × 10–12 mm, cylindric, central, dry, smooth, longitudinally striate, brittle, chalky white (1–2A1) turning pink or red rose (11A3–5) with guaiacol; stipe context hollow, chalky white (1–2A1), unchanging when bruised but pink or red rose (11A3–5) sometimes after the applications of guaiacol. *Odour* indistinctive. *Taste* mild. *Spore print* yellowish white (2A2). *Hymenophoral trama* mainly composed of large nests of sphaerocytes and few hyphal elements. *Subhymenium* layer up to 15 µm thick, pseudoparenchymatous. *Basidia* (26–)28.5–*33*–37(–45) × (9–)12–*14*–15.6 µm, 4-spored, clavate, sterigmata up to 6 µm long. *Basidiospores* (6–)6.5–*7*–8(–9) × (5–)5.5–*6*–6.8(–7) µm, [n = 40, Q = (1–)1.1–1.2(–1.3)], broadly ellipsoid to subglobose, rarely globose and ellipsoid; ornamentation amyloid, composed of isolated spines (up to 1.1 µm high), suprahilar plage amyloid; apiculus up to 2 µm high. *Pleurocystidia* (48–)50–*59*–67(–71) × 7–*10*–12(–14) µm, cylindrical, subclavate to clavate with capitate, rounded, moniliform, appendiculate (appendages up to 23 µm long) or blunt apex; emergent up to 35 µm, partly filled with heteromorphous, mostly thick coarsely crystalline content in congo red, sulphovanillin (SV) negative. *Lamellae edge* fertile with basidia. *Cheilocystidia* not found. *Pileipellis* up to 65 µm thick, metachromatic in cresyl blue, not sharply delimited from the underlying spherocytes of the context, an ixotrichoderm type, distinctly divided in a 15–18 µm deep and gelatinized suprapellis of erect or ascending hyphal ends and primordial hyphae, gelatinous layer


a
b
c
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g

◀**Fig. 160** ***Lactifluus midnapurensis*** (CAL 1516, **holotype**). **a** Basidiomes. **b** Basidia. **c** Pleuromacrocystidia. **d** Cheilocystidia. **e** Pleuropseudocystidia. **f** Pileipellis. **g** Basidiospores. *Scale bars* **a** = 10 mm, **b–f** = 10 µm, **g** = 2 µm. Drawings by S. Paloi

containing branched, septate, hyphal endings, and underneath this suprapellis, 50–47 µm deep, subpellis of interwined, compact, more or less horizontally oriented hyphae. *Hyphal extremities* near the cap margin composed of a single or a few cells only; the terminal cells subcylindrical, subclavate to clavate with tapered base, measuring (22–)25–*31*–37(–41) × (3–)4–*5*–6(–7) µm, with rounded or obtuse tips, subterminal cells cylindrical; in the cap centre, terminal cells slightly shorter in length, subcylindrical, subclavate to clavate with tapered base, measuring (20–)21–*26*–30(–38) × (3–)4–*5*–6(–7) µm, with rounded or obtuse tips; subterminal cells cylindrical. *Primordial hyphae* comparatively longer than the other extremities and often protruding or repent on the cap surface, occurring mostly singly, composed of 5–*7*–9(–10) µm broad, cylindrical cells, obtuse apex, thick-walled (up to 1 µm thick); incrustations present. *Clamp connections and laticiferous hyphae* absent from all tissues.

Material examined: INDIA, Uttarakhand, Rudraprayag District, Baniyakund, alt 2634 m, N30°28.914′ E79°10.854′, 17 July 2015, A. Ghosh, AG 15-670 (CAL 1537, **holotype**); *ibid.*, alt 2560 m, N30°29207′ E79°10.258′, 24 July 2016, A. Ghosh, (AG 16-1190 **paratype**).

Habitat and distribution: Under *Quercus* sp. in mixed forests dominated by *Quercus*, *Rhododendron* and *Abies*.

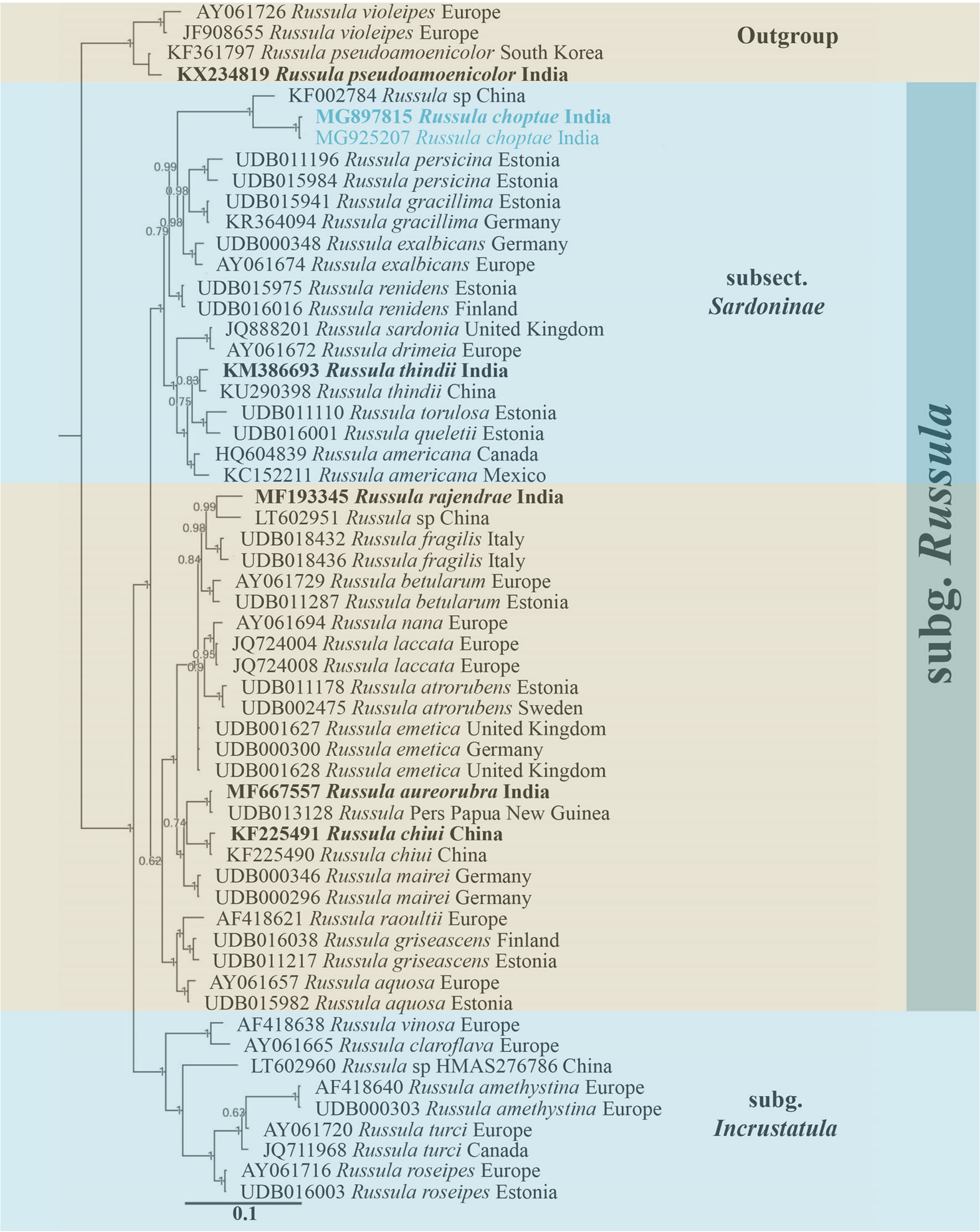
GenBank numbers: ITS = KY873997 (CAL 1537); ITS = MF684758 (AG 16-1190).

Notes: The combination of macro- and micromorphological features such as: epicutis with primordial hyphae, absence of dermatocystidia, mild taste, yellow to ochre spore print, nonpruinose cap and epicutis with clavate hyphal ends undoubtedly place *Russula uttarakhandia* under subg. *Incrustatula*, sect. *Amethystinae* subsect. *Chamaeleontinae* (Sarnari 1998). In the field *R. uttarakhandia* is distinct from other known species of this group by its pinkish white or reddish white to venetian pink and centrally olive yellow to greyish yellow gelatinous, glossy pileus; stipe that turns pink or red rose after sometime with application of guaiacol, pale yellowish cream spore print. Micromorphologically, it is separated from allied species by the combination of various shapes of cystidial apex (distinctively appendiculate cystidia with long appendages up to 23 µm long).

Based on the BLASTn search in NCBIs GenBank nucleotide database, the closest hit using ITS sequences of *Russula uttarakhandia* (collection numbers AG 15-670 and AG 16-1190) is *Russula* sp. (voucher HMAS 277786 collected from China, GenBank no. LT602960), showing 96% similarity with 98% query coverage. Unfortunately, there is no morphological details available for this Chinese collection in any published literature. Our phylogeny (Fig. 162) clearly shows that *R. uttarakhandia* is genetically closer and sister to unknown Chinese *Russula* sp. (LT602960).

In subsection *Chamaeleontinae*, *Russula postiana* Romell and *R. risigallina* (Batsch) Sacc. also appeared to be close in ITS phylogeny with *R. uttarakhandia* (Fig. 162). But, *R. postiana* (originally reported from Europe), differs from *R. uttarakhandia* by its herbage green to yellowish green, smooth, shining pileus; bright ochre yellow lamellae, heavily encrusted primordial hyphae, slightly larger basidiospores (8–10.2 × 7–8 µm) and its occurrence under coniferous trees (Galli 1996; Kibby 2014). *Russula risigallina* (also originally reported from Europe), differs from *R. uttarakhandia* by its red or orange pileus often with paler yellow centre (sometimes entirely yellowish opaque), strongly intervened egg yellow to almost orange lamellae and deep yellow spore print (Galli 1996; Sarnari 2005; Kibby 2014). Another taxon of this subsect., *R. lutea* (Huds.) Gray (also appeared in the BLASTn search), originally reported from Europe, separated from *R. uttarakhandia* by its entirely yellow, apricot or coral pileus, deep ochre gills and deep ochraceous spore print (Rayner 1985; Kibby and Fatto 1990).

Considering the cap colouration, *R. uttarakhandia* may also be confused in the field with *R. gracillima* Jul. Schäff., *R. cremeirubra* Murrill, *R. robertii* J. Blum, *R. nitida* (Pers.) Fr. and *R. decipiens* (Singer) Svrcek. However, *R. gracillima* (originally described from Europe) possess moderately spaced lamellae, a little acrid taste, presence of abundant broad dermatocystidia (5–10 µm) and basidiospores with isolated blunt warts (Rayner 1985; Galli 1996; Sarnari 1998; Chou and Wang 2005; Kibby 2014). *Russula cremeirubra* (originally reported from Florida) has rather distant straw coloured lamellae, basidiospores with amyloid warts connected by fine lines or connectors which combine to form few meshes and broken reticulum, pilear hyphae (2–6 µm broad) with acute to rounded apex (Murrill 1945; Hesler 1960; Kibby and Fatto 1990; Fatto 1998). *Russula robertii* (originally described from Europe) has 1–2-septate, slender dermatacystidia (3–5 µm broad) and spores with many crests and connectives forming partial to complete reticulum (Sarnari 2005; Kibby 2014). *Russula nitida* (originally reported from Europe) has pale straw-yellow gills, sometimes with reddish edge near the cap margin, larger basidiospores (8–10.5(–12) × 6.5–8(–9) µm) with rather sharp spines (up to 1.2 µm high), isolated or variously connected, and abundant dermatocystidia with 1–3 septation (Rayner 1985; Galli 1996; Sarnari 2005).


AY061726 Russula violeipes Europe
JF908655 Russula violeipes Europe
KF361797 Russula pseudoamoenicolor South Korea
KX234819 Russula pseudoamoenicolor India
Outgroup
KF002784 Russula sp China
MG897815 Russula choptae India
MG925207 Russula choptae India
0.99
UDB011196 Russula persicina Estonia
UDB015984 Russula persicina Estonia
0.98
UDB015941 Russula gracillima Estonia
0.98
KR364094 Russula gracillima Germany
0.79
UDB000348 Russula exalbicans Germany
AY061674 Russula exalbicans Europe
UDB015975 Russula renidens Estonia
UDB016016 Russula renidens Finland
subsect.
Sardoninae
JQ888201 Russula sardonia United Kingdom
AY061672 Russula drimeia Europe
KM386693 Russula thindii India
0.83
KU290398 Russula thindii China
0.75
UDB011110 Russula torulosa Estonia
UDB016001 Russula queletii Estonia
HQ604839 Russula americana Canada
KC152211 Russula americana Mexico
subg. Russula
MF193345 Russula rajendrae India
0.99
LT602951 Russula sp China
0.98
UDB018432 Russula fragilis Italy
UDB018436 Russula fragilis Italy
0.84
AY061729 Russula betularum Europe
UDB011287 Russula betularum Estonia
AY061694 Russula nana Europe
JQ724004 Russula laccata Europe
0.95
JQ724008 Russula laccata Europe
0.9
UDB011178 Russula atrorubens Estonia
UDB002475 Russula atrorubens Sweden
UDB001627 Russula emetica United Kingdom
UDB000300 Russula emetica Germany
UDB001628 Russula emetica United Kingdom
MF667557 Russula aureorubra India
UDB013128 Russula Pers Papua New Guinea
0.74
KF225491 Russula chiui China
KF225490 Russula chiui China
0.62
UDB000346 Russula mairei Germany
UDB000296 Russula mairei Germany
AF418621 Russula raoultii Europe
UDB016038 Russula griseascens Finland
UDB011217 Russula griseascens Estonia
AY061657 Russula aquosa Europe
UDB015982 Russula aquosa Estonia
AF418638 Russula vinosa Europe
AY061665 Russula claroflava Europe
LT602960 Russula sp HMAS276786 China
AF418640 Russula amethystina Europe
UDB000303 Russula amethystina Europe
0.63
AY061720 Russula turci Europe
JQ711968 Russula turci Canada
AY061716 Russula roseipes Europe
UDB016003 Russula roseipes Estonia
subg.
Incrustatula
0.1

◀**Fig. 161** The ITS sequence of the newly generated *Russula* species (*Russula choptae*) plus those acquired from GenBank, UNITE database and relevant literature, were aligned with the help of AliView (Larsson 2014) using default settings. Sequences of ITS were phylogenetically analyzed using Bayesian inference analysis (BI). Bayesian inference was computed independently twice in MrBayes v.3.2.2 (Ronquist et al. 2012). The best-fit substitution model of nucleotide evolution (TIMef) was carried out in MrModeltest 3.7 (Posada and Crandall 1998). Posterior probabilities (PP) were calculated in two simultaneous runs with Markov chain Monte Carlo (MCMC) algorithm (Larget and Simon 1999). Markov chains were run for 1000000 generations, saving a tree every 100th generation. Default settings in MrBayes were used for the incremental heating scheme for the chains (3 heated and 1 cold chain), unconstrained branch length [unconstrained: exponential (10.0)] and uninformative topology (uniform) priors. The analysis was terminated when the average standard deviation of split frequencies fell below 0.01. The first 25% of trees were discarded as burn-in (Hall 2004). The convergence of runs was visually assessed using Trace function in Tracer version 1.6 (Rambaut et al. 2013). The novel species having GenBank no. MG897815 and MG925207 (ITS) are shown in blue and bold on the tree and ex-type strains are in bold. *Russula pseudoamoenicolor* and *R. violeipes* are considered as the outgroup taxa

Russula decipiens (belonging to subg. *Russula*), originally reported from Europe has slightly infundibuliform pileus, yellowish white stipe that slightly becomes grey on bruising, acrid taste and presence of aseptate, subclavate to clavate dermatocystidia (Rayner 1985; Sarnari 1998).

In field, *Russula uttarakhandia* may be confused with *R. rajendrae* A. Ghosh & K. Das (originally described from India and also collected from Uttarakhand, Rudraprayag District, Baniyakund), but the latter possess an acrid taste, numerous pileocystidia in cuticle and belongs to subg. *Russula* (Ghosh and Das 2017).

Considering the acystidiate aspect of pileipellis and mild taste (key characters of subg. *Incrustatula*), *Russula uttarakhandia* is also similar to other taxa of subg. *Incrustatula* reported from India viz. *R. sharmae* K. Das et al., *R. dafianus* K. Das & J.R. Sharma, *R. dhakuriana* K. Das et al., *R. hookeri* S. Paloi et al. and *R. kewzingensis* K. Das et al. However, *R. sharmae* (reported for the first time from West District of Sikkim) possess red to scarlet with yellow blotched larger pileus (70–140 mm), absence of lamellulae, smaller basidiospores (6.8–*7.3*–7.9 × 6–*6.6*–7 μm) and palisade to trichopalisade type of pileipellis (Das et al. 2013). *Russula dafianus* (reported from Dafia Dhura, Uttarakhand) has smaller basidiomes (35–45 mm), yellowish white to pale yellow lamellae and encrusted pilear hyphae (Das and Sharma 2005). *Russula dhakuriana* (reported from Dhakuri, Uttarakhand) has more robust basidiomes (pileus 80–120 mm diam., stipe 50–125 × 20–28 mm), longer basidiospores (6.5–10.2 × 6–7.7 μm) and pleurocystidia (60–115 × 7–12 μm) and cellular nature to the subpellis (Das et al. 2006a). *Russula hookeri* (reported from Darjeeling Hill, Eastern Himalaya) has small to medium basidiomes (20–35 mm), greyish red to greyish rose pileus with brownish red centre, concolorous stipe; smaller basidiospores (5.4–7.2 × 4.5–6.4 μm) and white spore print (Paloi et al. 2015). *Russula kewzingensis* (reported from Kewzing, Sikkim Himalaya) has deep and intense red pileus, red-flushed stipe and pseudoparenchymatous nature of subpellis (Das et al. 2017b).

Stereaceae Pilát

The family *Stereaceae* was proposed by Pilát (1930) with *Stereum* Hill ex Pers. as generic type. This family is one of the most widespread and diverse in the *Russulales*, together with *Russulaceae*. It includes species with basidiome appressed, effuse-reflexed or discoid, rarely stalked; pileus often zoned; monomitic or dimitic hyphal system; hymenophore smooth to tuberculate; basidia and spores hyaline, smooth, amyloid or non-amyloid. The family comprises species that grow in exposed positions, such as dead branches still attached to hardwood or conifer trees, causing white rot (Miller et al. 2006; Larsson 2007).

Aleurodiscus Rabenh. ex J. Schröt.

Aleurodiscus is one of the largest genera in *Stereaceae*. It was proposed by Rabenhorst (1874) without diagnosis, and validated by Schröter in (1888), with *Peziza amorpha* Pers. (≡ *Aleurodiscus amorphus* (Pers.) J. Schröt.) as type species. Pilát (1926) included *Aleurodiscus* corticioid fungi with large basidia and large spores, as well as variable sterile elements and this concept was largely accepted (Bourdot and Galzin 1912, 1928; Burt 1918). Lemke (1964a, b) considered the genus to be artificial and proposed to exclude species with inamyloid spores, and described the following new genera: *Aleurocystidiellum* Lemke, *Aleurocorticium* Lemke and *Licrostroma* Lemke.

On the basis of morphological and molecular data, Wu et al. (2000) described *Acanthofungus* Sheng H. Wu et al. with *Acanthofungus rimosus* Sheng H. Wu et al. as type species, and *Neoaleurodiscus* Sheng H. Wu with *Neoaleurodiscus fujii* Sheng H. Wu as type species. From a phylogenetic perspective, Wu et al. (2001) analyzed the limits of *Aleurodiscus sensu lato* and the monophyly of previously segregated genera, concluding that *Aleurocystidiellum* and *Acanthobasidium* are monophyletic. However, subsequent studies (Larsson and Larsson 2003; Miller et al. 2006; Larsson 2007) have shown that *Aleurocystidiellum* does not belong to *Stereaceae*. Wu et al. (2001) set the boundaries of *Aleurodiscus sensu stricto* and confirmed that *Aleurodiscus sensu lato* is paraphyletic.

According to Wu et al. (2001), *Aleurodiscus sensu lato* includes species with highly variable characteristics; these are not congruent and usually overlap, so the species in *Aleurodiscus sensu lato* show all possible combinations of spore surface from smooth or ornamented, presence or absence of acanthophyses, and hyphae with clamps or

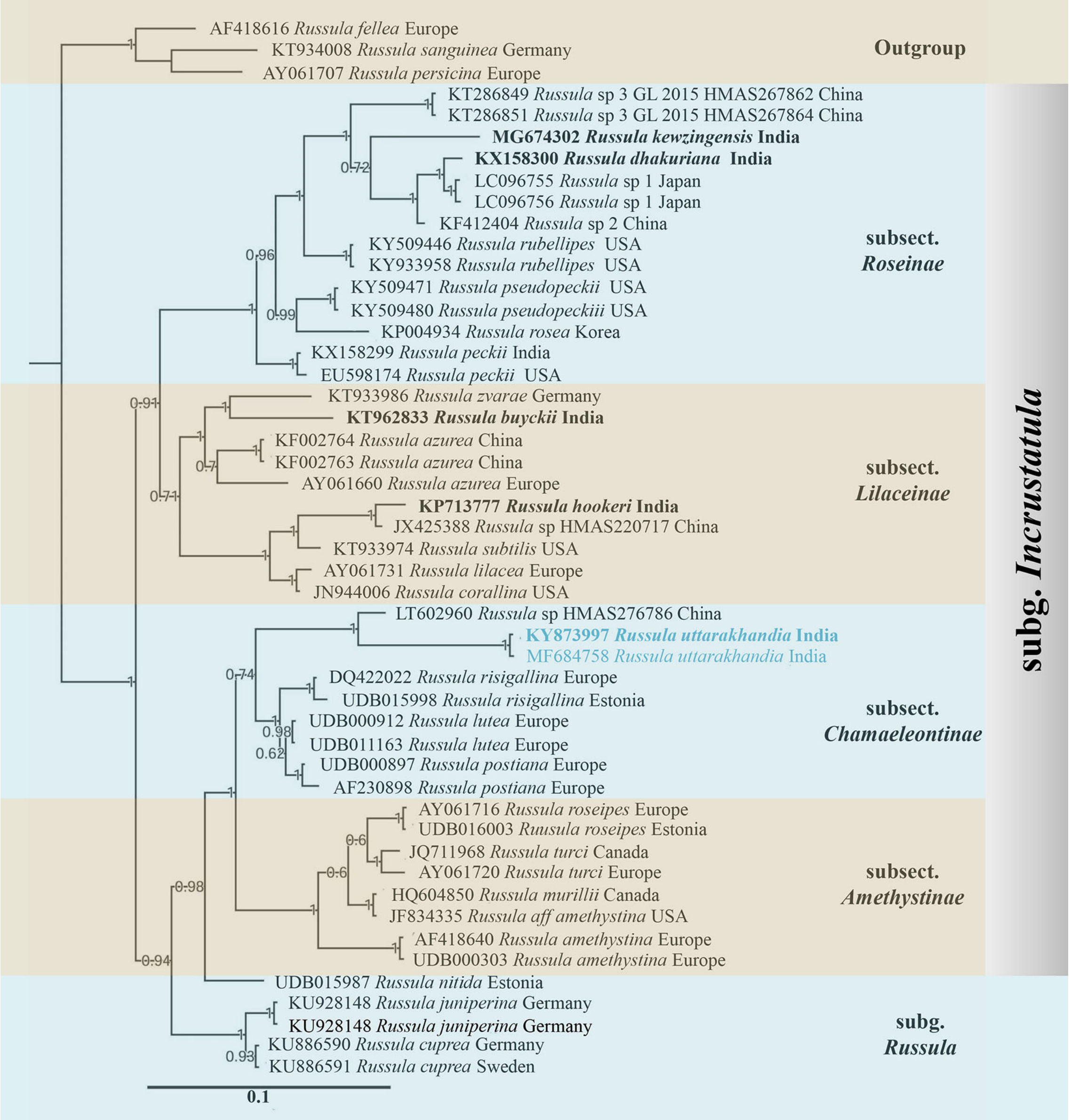


Fig. 162 The ITS sequence of the newly generated *Russula uttarakhandia* plus those acquired from GenBank, UNITE database and relevant literature, were aligned with the help of AliView (Larsson 2014) using default settings. Sequences of ITS were phylogenetically analyzed using Bayesian inference analysis (BI). Bayesian inference was computed independently twice in MrBayes v.3.2.2 (Ronquist et al. 2012). The best-fit substitution model of nucleotide evolution (TIMef) was carried out in MrModeltest 3.7 (Posada and Crandall 1998). Posterior probabilities (PP) were calculated in two simultaneous runs with Markov chain Monte Carlo (MCMC) algorithm (Larget and Simon 1999). Markov chains were run for 1000000 generations, saving a tree every 100th generation. Default settings in MrBayes were used for the incremental heating scheme for the chains (3 heated and 1 cold chain), unconstrained branch length [unconstrained: exponential (10.0)] and uninformative topology (uniform) priors. The analysis was terminated when the average standard deviation of split frequencies fell below 0.01. The first 25% of trees were discarded as burn-in (Hall 2004). The convergence of runs was visually assessed using Trace function in Tracer version 1.6 (Rambaut et al. 2013). The novel species having GenBank no. KY873997 and MF684758 (ITS-rDNA) are shown in blue and ex-type strains are in bold. *Russula fellea*, *R. sanguinea* and *R. persicina* are considered as the outgroup taxa

simple-septate. The novel species, *Aleurodiscus patagonicus* is introduced following the treatment in Wu et al. (2001), Dai and He (2016), and Dai et al. (2017b, c).

Aleurodiscus patagonicus Nogal, Telleria, M. Dueñas & M.P. Martín, ***sp. nov.***

MycoBank number: MB823981; *Facesoffungi number*: FoF05726, Figs. 167, 168

Etymology: Named after the Chilean Northern Patagonian region where the holotype and paratypes were collected.

Fig. 163 ***Russula choptae*** (AG 16–1186, **holotype**). **a–e** Fresh and dissected basidiomes in the field. **f, g** Radial section through pileipellis showing elements. **h** Image of basidiospores under SEM. **i–k** Transverse section through lamellae showing pleurocystidia. **l** Transverse section through lamellae showing cheilocystidia. *Scale bars* **b** = 55 mm, **f** = 25 µm, **g** = 10 µm, **h** = 2 µm, **i** = 25 µm, **j–l** = 10 µm

Holotype: 19609Tell., MA-Fungi 90714

Colour codes follow: ISCC-NBS Centroid Colour Charts (Kelly and Judd 1976).

Basidiomes first discoid then confluent; margin determinate, involute; hymenophore smooth to slightly reticulate, pale orange yellow to medium orange yellow (73. p. OY–71. m. OY). *Hyphal system* monomitic; hyphae thick-

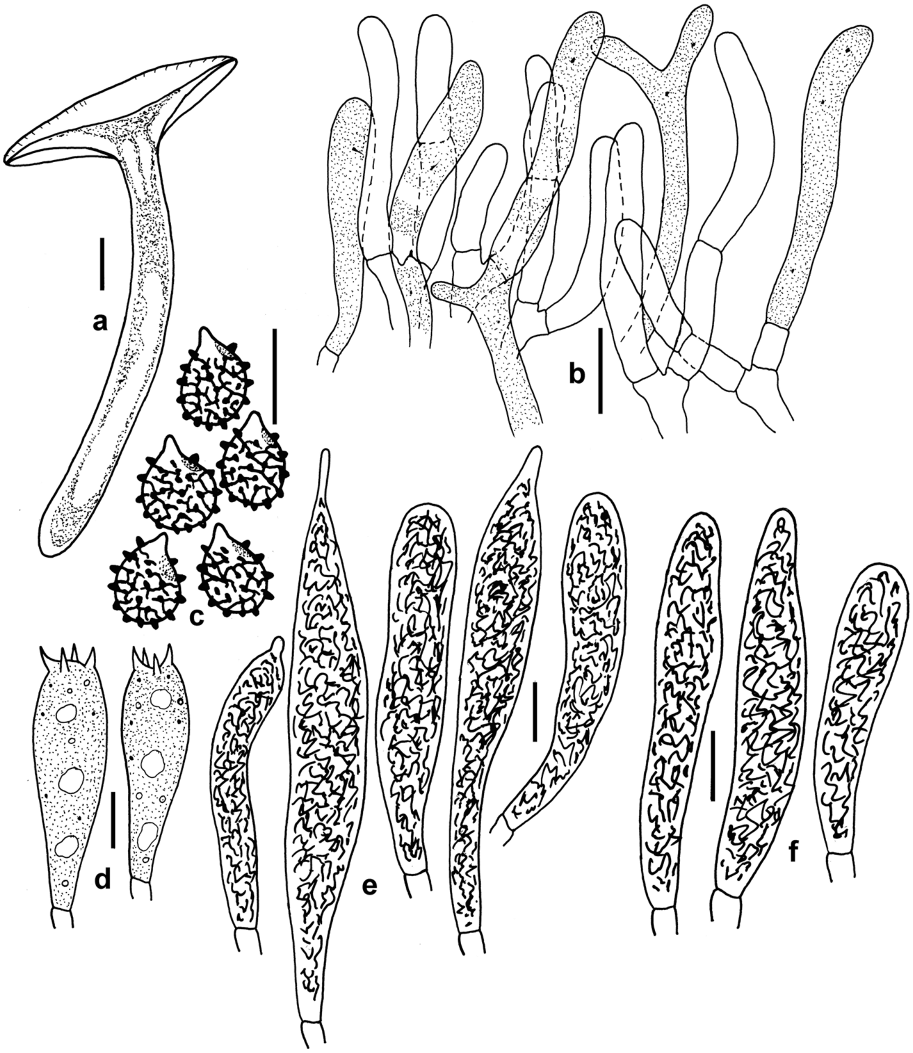


Fig. 164 ***Russula choptae*** (AG 16-1186, **holotype**). **a** Dissected basidiome. **b** Radial section through pileipellis. **c** Basidiospores. **d** Basidia. **e** Pleurocystidia. **f** Cheilocystidia. *Scale bars* **a** = 10 mm, **b–f** = 10 µm

walled, 3–6 µm wide; paraphysoid hyphae cylindrical, occasionally branched, with scattered clamps, 3–5 µm wide. *Basidia* clavate, thin-walled, stalked, with basal clamp, 150–190 × (22 −)24–27 µm, with four sterigmata, 5–7 µm wide. *Basidiospores* citriform, smooth, thin-walled, hyaline, strongly amyloid, 19–22(−24) × 14–16 µm, Q = 1.38.

Material examined: CHILE, Palena, Comuna Hualaihué, Huinay Reserve, path to Cerro del Tambor, 42°22′44″S, 72°24′25″W, 100 m asl., on unidentified wood, 7 May 2013, M. Dueñas, M.P. Martín & M.T. Telleria, 19609Tell. (MA-Fungi 90714, **holotype**); *ibid.*, 14537MD (MA-Fungi 90713); Comuna Hualaihué, Base Paula, path of Geyser, on unidentified wood, 42°24′16.1″S, 72°44′0.59″W, 52 msl., 28 May 2012, M. Dueñas, M.P. Martín & M.T. Telleria, 14080MD (MA-Fungi 90711).

Habitat and distribution: On unidentified wood in Valdivian temperate rainforest in Chilean Northern Patagonian region.

Additional material examined: *Aleurodiscus limonisporus*—AUSTRALIA, Victoria, Cumberland falls, on *Nothofagus cunninghamii* (*Nothofagaceae*), 6 June 1954, A. Miller (PDD 16691, **isotype**); NEW ZEALAND, Bay of Plenty, Te Urewera, Tarapounamu, west of road, on decaying branch, 19 May 2005, B. Paulus & M. Fletcher (PDD 83502); Te Urewera, Tarapounamu, east of road, on decaying wood, 17 May 2005, B. Paulus (PDD 83552); Te Urewera, Tarapounamu, west of road, on fallen branch, 19 May 2005, B. Paulus & M. Fletcher (PDD 83553); Buller, North of Reefton, Perseverance Bridge, 5 May 2001, E. Johannesen (PDD 72991); Paparoa National Park, Bullock Creek Farm, on *N. fusca*, 26 April 1987, P.K. Buchanan (PDD 55241); Paparoa Ranges, Tiropahi Walk, on *N. menziesii*, 27 April 1987, P.K. Buchanan (PDD 55264); Victoria Forest Park, east of Maruia, on *N. menziesii*, 22 April 1986, R.E. Beever (PDD 53413); Canterbury, Arthur's Pass National Park, Dobson Nature Walk, on *Olearia capillaris* (*Asteraceae*), 20 November 1988, P.K.

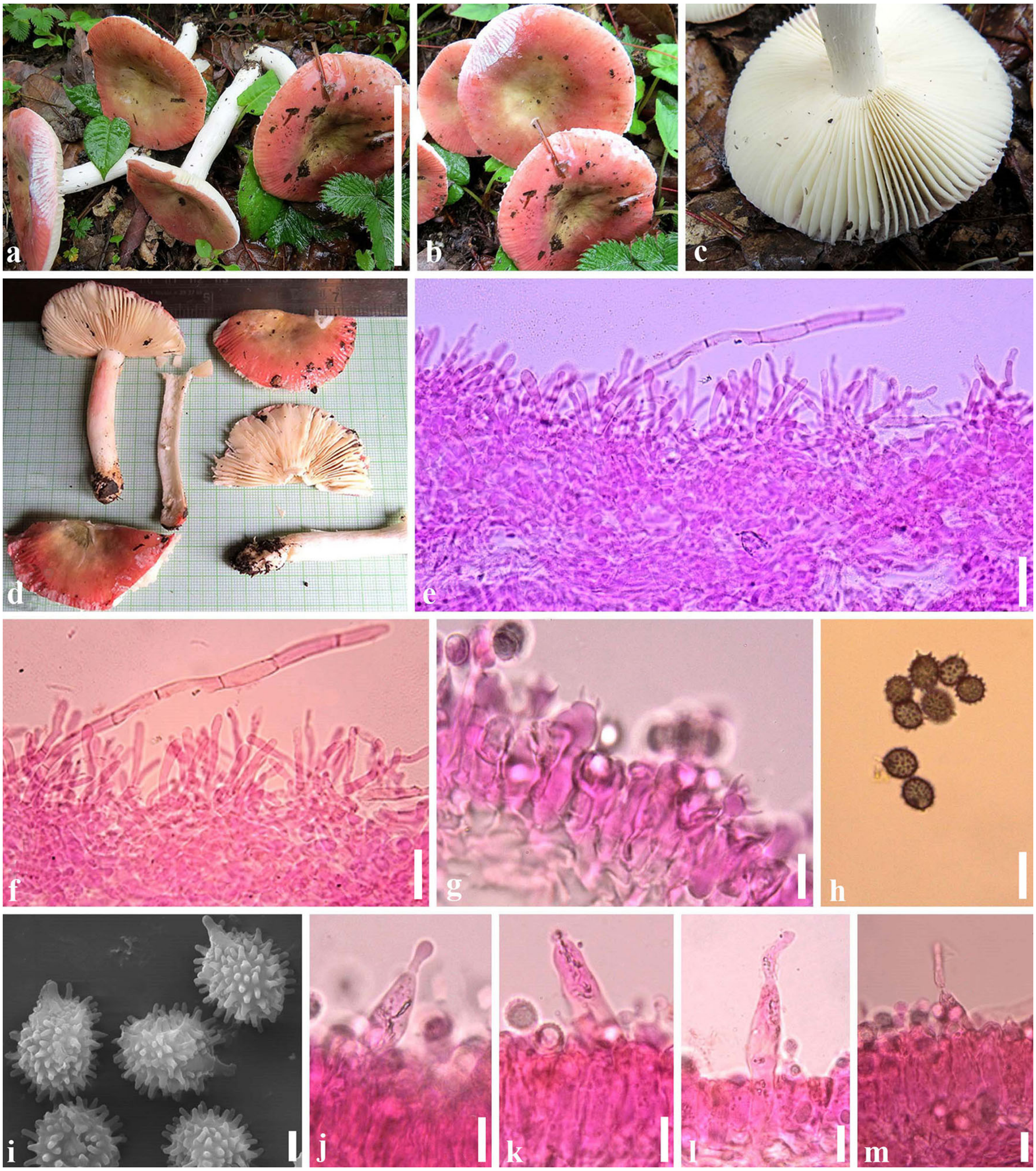


Fig. 165 ***Russula uttarakhandia*** (CAL 1537, **holotype**). **a–d** Fresh basidiomes in the field. **e, f** Radial section through pileipellis showing elements. **g** Basidia. **h** Basidiospores. **i** SEM image of basidiospores. **j–m** Transverse section through lamellae showing pleurocystidia. *Scale bars* **a** = 80 mm, **e–h** = 10 µm, **i** = 2 µm, **j–m** = 10 µm

Buchanan (PDD 55021); Jollie's Bush Reserve, Christchurch, on standing dead tree, 4 July 2010, J.A. Cooper (PDD 95980); Gisborne, Moanui Conservation Area, 38°24′24.84″S, 177°23′58.92″E, on *Nothofagus*, 13 May 2013, S.R. Pennycook (PDD 97004); Hawke's Bay, Upper Mohaka River, Kaimanawa Range, on *Nothofagus fusca*, May 1953, J.M. Dingley (PDD 12600); Nelson, Abel Tasman National Park, Hardwoods Hole, on decaying branch of *N. solandri*, 15 April 2008, A.J. O'Donnell & B.C. Paulus (PDD 94131); Kahurangi National Park, Flora Saddle, on decaying bark, 14 April 2008, A.J. O'Donnell & B.C. Paulus (PDD 94144); Murchison, on *N. fusca*, April 1956, S.D. & P.J. Brook (PDD 17122); Southland, Porakino Valley, on bark of *N. solandri*, 7 May 2012, Lloyd (PDD 96617); Wairarapa, Tararua Forest Park, Mt Holdsworth, Gentle Annie Track, on *N. fusca*, 10 May 2007, A.J. O'Donnell (PDD 92582); Tararua Forest Park, Mt Holdsworth, Donnelly Flat track, on decaying branch, 10 May 2007, B.C. Paulus (PDD 92616); Tararua Forest Park, Mt Holdsworth track, on decaying wood, 7 May 2007, G.

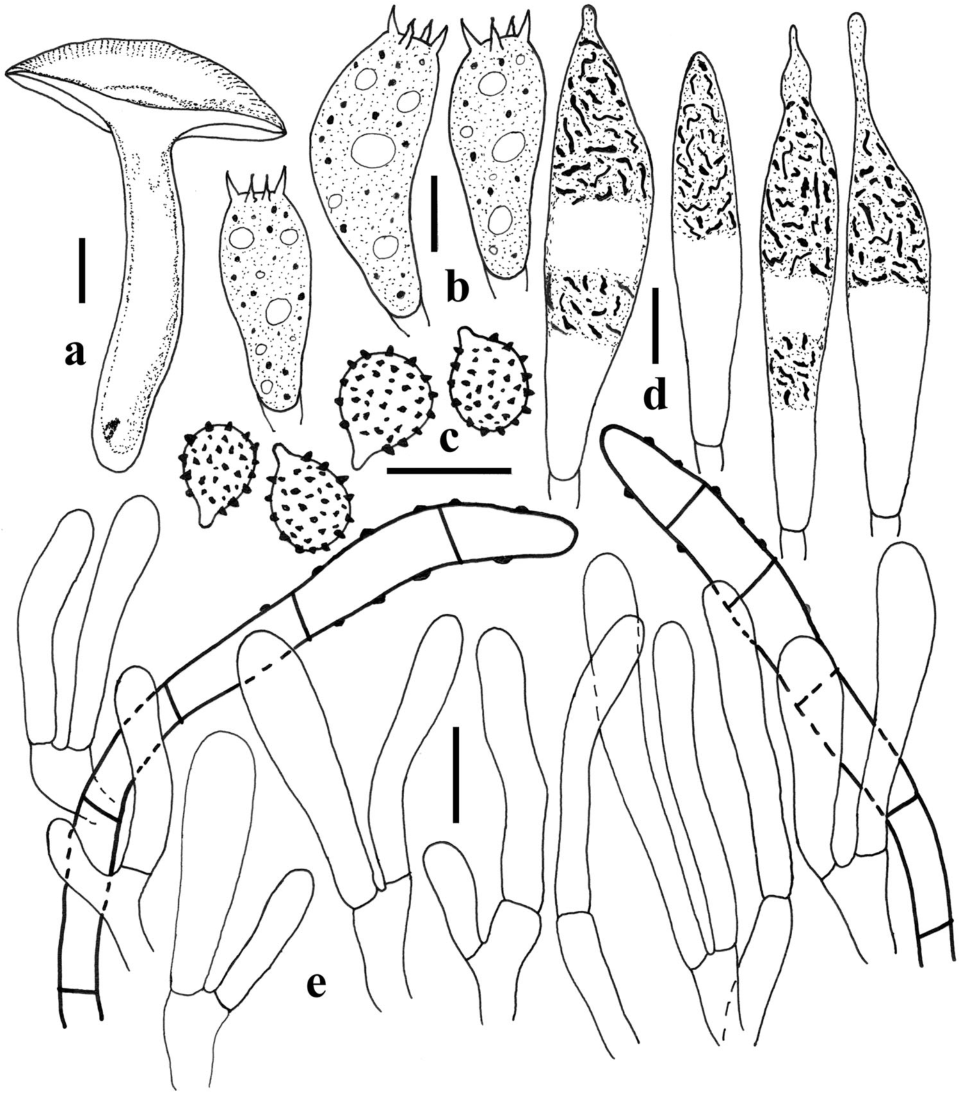


Fig. 166 ***Russula uttarakhandia*** (CAL 1537, **holotype**). **a** Dissected basidiome. **b** Basidia. **c** Basidiospores. **d** Pleurocystidia. **e** Radial section through pileipellis. *Scale bars* **a** = 10 mm, **b–e** = 10 µm

Gates & D. Ratkowsky (PDD 92829); Wellington, Kaimanawa Range, on *N. menziesii*, April 1955, J.M. Dingley (PDD 15227); Mangatorutoru Stream, on *N. solandri* var. *cliffortioides*, March 1948, J.M. Dingley (PDD 7452); Tongariro National Park, on *N. solandri* var. *cliffortioides*, February 1951, G.H. Cunningham (PDD 15230); Ohakune, Lake Surprise Track, on *Nothofagus* sp., April 1935, E.E. Chamberlain (PDD 15229); Whakapapa-iti Stream, Ruapehu, on *N. solandri* var. *cliffortioides*, Sep 1955, J.M. Dingley (PDD 15355): Whakapapa-iti Stream, Tongariro National Park, on *N. solandri* var. *cliffortioides*, January 1951, J.M. Dingley (PDD 11188); Turangi, near Beggs Pool, Kaimanawa Range, on *Weinmannia racemosa* (*Cunoniaceae*), 25 May 1970, J.M. Dingley (PDD 28631); Westland, Granville Forest, Orwell Creek, Ahaura, on *N. fusca*, 2 April 1963, J.M. Dingley (PDD 20997). *Aleurodiscus* sp.–Otago Lakes, Beyond Paradise, on *Nothofagus* small branch, 7 May 2016, P. Catcheside (PDD 110288) [identified as *A. limonisporus*]. Unidentified–Glacier Burn Track, on *Nothofagus*, 8 May 2016, A. Chinn (PDD 109766) [identified as *A. limonisporus*].

GenBank numbers: ITS = MF631175, LSU = MF631191 (MA-Fungi 90711); ITS = MF631176, LSU = MF631192 (MA-Fungi 90713); ITS = MF631177, LSU = MF631193 (MA-Fungi 90714); ITS = MF631152, LSU = MF631178 (PDD 7452); ITS = MF631153 (PDD 12600); ITS = MF631154 (PDD 15229); ITS = MF631155 (PDD 15230); ITS = MF631156, LSU = MF631179 (PDD 16691); ITS = MF631157 (PDD 17122); ITS = MF631158 (PDD 28631); ITS = MF631159 (PDD 53413); ITS = MF631160 (PDD 55021); ITS = MF631161 (PDD 55241); ITS = MF631162 (PDD 72991); ITS = MF631163 (PDD 83502); ITS = MF631164, LSU = MF631180 (PDD 83552); ITS = MF631165, LSU = MF631181 (PDD 92582); ITS = MF631166, LSU = MF631182 (PDD 92616); ITS = MF631167, LSU = MF631183 (PDD 92829); ITS =

MF631168, LSU = MF631184 (PDD 94131); ITS = MF631169, LSU = MF631185 (PDD 94144); ITS = MF631170, LSU = MF631186 (PDD 95980); ITS = MF631171, LSU = MF631187 (PDD 96617); ITS = MF631172, LSU = MF631188 (PDD 97004); ITS = MF631173, LSU = MF631189 (PDD 109766); ITS = MF631174, LSU = MF631190 (PDD 110288).

Notes: Phylogenetic analysis based on a combined ITS and LSU sequence dataset (Fig. 169) shows that *Aleurodiscus patagonicus* clusters within *Stereaceae*, far away from the *Aleurodiscus sensu stricto* clade, which includes only *A. amorphous* (Pers.) J. Schröt. (type species) and *A. grantii* Lloyd (Wu et al. 2001). *Aleurodiscus sensu lato* is paraphyletic; sequencing shows species of apparently unrelated genera intermingled with the species of *Aleurodiscus sensu lato* (Wu et al. 2001, 2010b; Larsson and Larsson 2003; Binder et al. 2005; Miller et al. 2006). In the phylogeny (Fig. 169), *A. patagonicus* groups in a highly supported clade (99% ML, 99% MP and 1.00 PP), which is sister to the *A. limonisporus* D.A. Reid clade and this relationship is also highly support (92% ML, 90% MP and 1.00 BYPP).

Aleurodiscus patagonicus is similar to *A. limonisporus.* Both species have a monomitic hyphal system, cylindrical paraphysoid hyphae, and characteristic citriform smooth spores. However, *A. patagonicus* differs in the following characteristics: clamps present in paraphysoid hyphae, longer and wider basidia, with basal clamp, and, spores with higher length/width ratio, as well as, in the geographical distribution (Table 3). *Aleurodiscus patagonicus* is reported from Chilean Northern Patagonia, while *A. limonisporus* occurs in Australia (Reid 1955) and New Zealand (McKenzie et al. 2000).

Trechisporales K.H. Larsson

Hydnodontaceae Jülich

Hydnodontaceae was described by Jülich (1981) with *Hydnodon* Banker as generic type, and includes *Brevicellicium* K.H. Larss. & Hjortstam, *Cristelloporia* I. Johans. & Ryvarden and *Trechispora* P. Karst. *Hydnodon* is now considered as a synonym of *Trechispora* (Ryvarden 2002). This family was characterized by the resupinate, effused-reflexed or pileate basidiome, hymenophore smooth to hydnoid or poroid, as well as by the ampulate septa, short cylindrical basidia and ornamented spores. The family concept was revised by Larsson (2007), on the basis of morphological and molecular data, and *Brevicellicium*, *Fibriciellum* J. Erikss. & Ryvarden, *Fibrodontia* Parmasto, *Luellia* K.H. Larss. & Hjortstam, *Porpomyces* Jülich, *Subulicystidium* Parmasto, *Trechispora* and *Tubulicium* Oberw. were included.

Trechispora P. Karst.

Trechispora was erected by Karsten (1890) to include only one species, *Trechispora onusta* P. Karst. (= *Trechispora hymenocystis*). This genus was characterized by its adnate basidiomes, poroid hymenophore, with hyaline and ornamented spores. *Trechispora* was treated by Bondartsev and Singer (1941), and Rogers (1944, 1951), and the initial description was amended by Liberta (1966) to include species with clamped hyphae, ampulate septa and smooth spores. Liberta (1973), in his monograph, introduced new morphological criteria for species delimitation, such as shape and size of spores, as well as the spore surface (smooth or ornamented), hyphal system (monomitic or dimitic), and hymenophore configuration (smooth, poroid or hydnoid), and this species concept was followed in all subsequent treatments. Larsson (1994, 1995a, b, 1996) gave detailed micromorphological studies, described new taxa, proposed new combinations and recognized the morphology of crystal deposits on subicular hyphae as a reliable character for species delimitation.

Most species of *Trechispora* have been described from boreal and temperate zones, growing on deeply decayed wood and other debris on the ground, although Matssura and Yashiro (2010) reported an insect-fungus association between a termite species (*Reticulotermes termites*) and an undescribed trechisporoid fungus (*Trechispora* sp.) from Japan. *Trechispora* contains 82 legitimate names (Index Fungorum 2019). According to Hjortstam and Ryvarden (2007), 27 species have been reported from tropical and subtropical areas. *Trechispora echinospora* sp. nov. is introduced from Equatorial Guinea.

Trechispora echinospora Telleria, M. Dueñas, I. Melo & M.P. Martín, ***sp. nov.***

MycoBank number: MB825275; *Facesoffungi number*: FoF05727, Fig. 171

Etymology: From Latin "*echinus*" which means hedgehog and *spore*; referring to the characteristic ornamented spores with straight prickles

Holotype: 13858Tell., MA-Fungi 82485

Colour codes follow: ISCC-NBS Centroid Colour Charts (Kelly and Judd 1976).

Basidiomes resupinate, effused, confluent, adnate; hymenophore farinaceous to grandinioid, yellowish grey (93. y Grey) to cream (92. y White–89. p. Y). *Margin* not differentiated and strands not seen. *Hyphal system* monomitic. *Subicular hyphae* thin-walled, loosely interwoven, moderately branched, straight, 1–2 µm wide, long-celled, with clamps and ampullate septate, up to 4 µm wide. *Sphaerocysts* thin-walled, with basal clamp, (11–)15–18 µm diam., sometimes present. *Subhymenial hyphae* thin-walled, branched, short-celled, isodiametric, up to 6 µm wide, with clamps in all septae. *Crystals* not seen. *Basidia* short-cylindrical to urniform, four sterigmata,

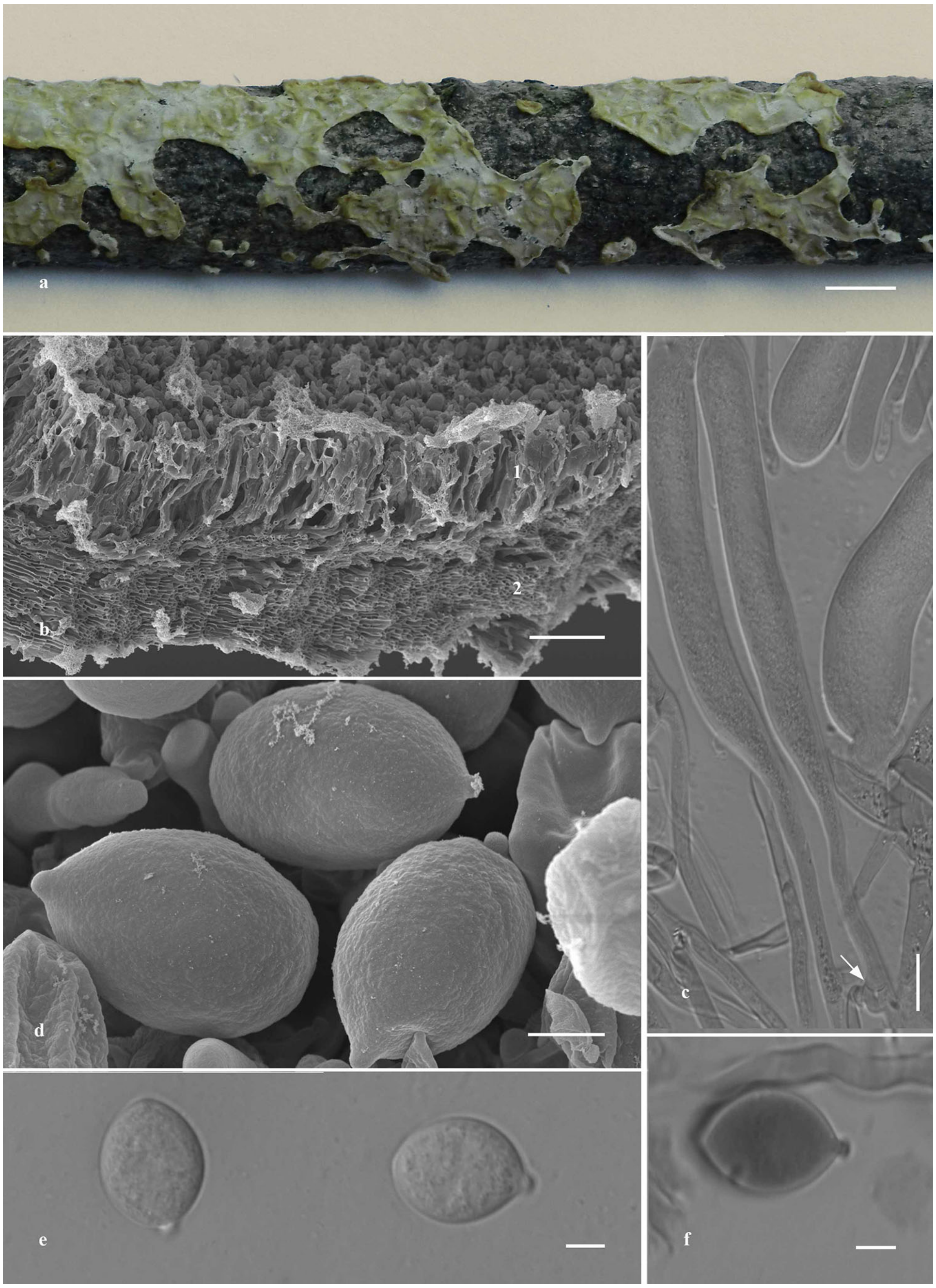


Fig. 167 ***Aleurodiscus patagonicus*** (19609Tell., MA-Fungi 90714, **holotype**). **a** Basidiome. **b** Section of basidiome under SEM; hymenial layer (1), basal layer (2). **c** Probasidia with basal clamp. **d** Spores under SEM. **e**, **f** Basidiospores. *Notes* scanning electron microscope (SEM) was used after coating basidiome samples in gold with Balzers SCD 004 sputter coater with a Hitachi S-3000 N SEM. *Scale bars* **a** = 5 mm, **b** = 50 µm, **c** = 10 µm, **d–f** = 5 µm

13–16(–17) × 5–6 µm, with basal clamp. *Spores* globose, 4–5 µm (excluding the ornamentation), thin-walled, echinulate with straight prickles up to 1 µm long, sometimes with one oil drop in the protoplasm, Q (L/W) = 1.02.

Material examined: EQUATORIAL GUINEA, Centro Sur Province, road Niefang to Evinayong, next to Nkumekie, on *Oxythenantera abyssinica* (*Poaceae*), 7 December 1990, M.T. Telleria, 13858Tell. (MA-Fungi 82485, **holotype**); *ibid.*, 13861Tell. (MA-Fungi 82486); 13870Tell. (MA-Fungi 91312).

Habitat and distribution: Only known from the type locality in the Continental Region (Mbini) of Equatorial Guinea, West Tropical Africa, on dead stem of bamboo (*Oxythenantera*, *Poaceae*)

GenBank numbers: ITS = JX392845, JX392847, LSU = JX392846, JX392848, JX392849 (13858Tell., MA-Fungi 82485, **holotype**); ITS = JX392853, JX392850, JX392852, LSU = JX392851, JX392854 (13861Tell., MA-Fungi 82486).

Notes: In the framework of our study Telleria et al. (2013), a number of ITS and LSU sequences of

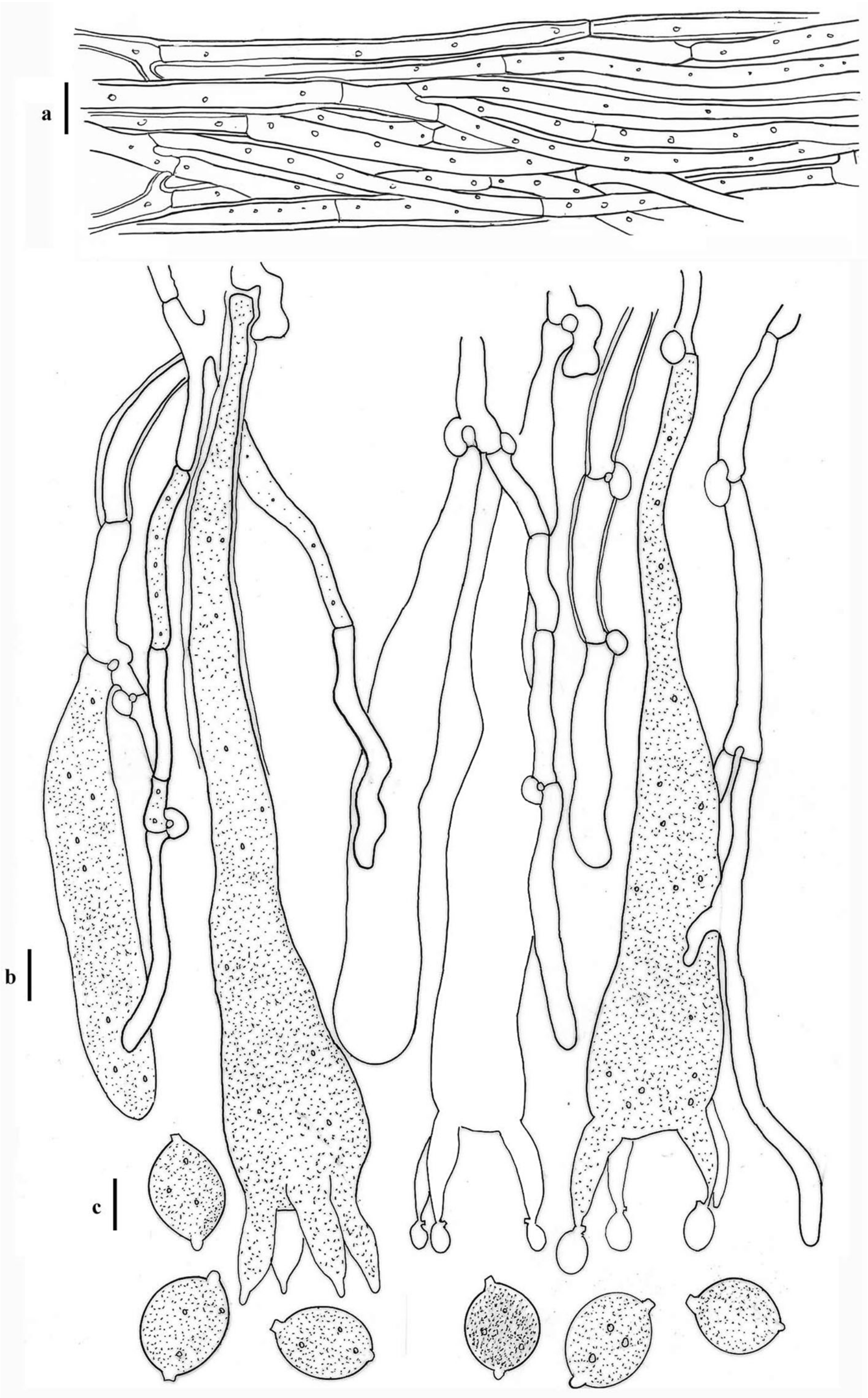


Fig. 168 ***Aleurodiscus patagonicus*** (19609Tell., MA-Fungi 90714, **holotype**). **a** Basal layer. **b** Hymenial layer with basidia and paraphysoid hyphae. **c** Basidiospores. Line drawings were made with a Leyca DM2500 microscope with aid of a drawing tube by M. Dueñas. *Scale bars* = 10 µm

Trechispora obtained by our team were deposited in GenBank under *Trechispora* sp. because many specimens were collected in tropical areas, and require a thorough study of their morphology to clearly identify them to the species level.

In this paper, ITS sequences from 13858Tell. and 13861Tell. collected during our study of the corticoid fungi from Equatorial Guinea (Centro Sur Province), growing on *Oxythenantera abyssinica* (A.Rich.) Munro, were compared with sequences available in the EMBL/GenBank/DDBJ (Cochrane et al. 2011) and UNITE (Abarenkov et al. 2011; Kõljalg et al. 2013) databases, mainly from Larsson et al. (2004), Lutzoni et al. (2004), Krause et al. (2011), Brazee et al. (2012, 2014), Sjökvist et al. (2012), Telleria et al. (2013), and Ordynets et al. (2015). The sequences were analyzed under maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference (BI). The BI tree is shown in Fig. 170, including the MP and ML bootstrap values, as well as the posterior probabilities. The five sequences from these collections, group together in a highly supported clade (85% MP, 99% ML and 1.00 BYPP), sister group of the clade formed by *Trechispora araneosa* (Höhn. & Litsch.) K.H. Larss., *T. farinacea* (Pers.) Liberta, *T. hymenocystis* (Berk. & Broome) K.H. Larss. and *T. mollusca* (Pers.) Liberta, although this relationship is not well-supported. These collections from Equatorial Guinea show unique morphological characteristics, such as the spores being globose and echinulate with straight prickles, striking under SEM (Fig. 171). The morphological characteristics and molecular phylogenetic results, its habitat on dead stem of bamboo, and its geographical distribution led us to propose the new species, *T. echinospora*.

Subclass Auriculariomycetidae Jülich

Auriculariales J. Schröt.

Auriculariaceae Fr. Ex Lindau

Auriculariaceae, typified by *Auricularia mesenterica* (Dicks.) Pers. (= *Helvella mesenterica* Dicks.), belongs to *Auriculariales* and comprises nine genera and 155 species (Kirk 2017). The family includes species with resupinate, effused-reflexed, hydnoid, cerebriform and pileate basidiomes; thin or thick-walled probasidia and metabasidia, both varying from globose to cylindrical and thin-walled basidiospores that germinate by tubes or producing conidia (Lowy 1971; Martin 1952). The most common genera of *Auriculariaceae* are *Auricularia* Bull., *Heterochaete* Pat., *Exidia* Fr., *Eichleriella* Bres., *Exidiopsis* (Bref.) A. Møller and *Hirneolina* (Pat.) Bres.

Tremellochaete Raitv.

Tremellochaete was described by Raitviír (1964) with *T. japonica* (Lloyd) Raitv. (= *Exidia japonica* Lloyd) as the type species and comprises two legitimate species (Kirk 2017). The genus is characterized by tough-gelatinous basidiomes, often becoming softer with age, varying from tuberculate-erumpent and effused-tuberculate; papillate hymenium, papillae heavily encrusted with irregular, hyaline crystals; metabasidia with 2- or 4-celled; and allantoid-suballantoid, hyaline, aseptate basidiospores. *Tremellochaete* is similar to *Exidia*, which has fewer papillae (Raitviír 1964), and has been considered a synonym of the latter. However, *Tremellochaete* was reinstated after morphological and phylogenetic analyses (Malysheva and Spirin 2017). We follow the treatments and updated accounts in Malysheva and Spirin (2017). The new species, *T. atlantica* is introduced based on phylogenetic analysis of a combined ITS and LSU sequence dataset coupled with morphological characteristics (Fig. 172).

Tremellochaete atlantica Alvarenga, ***sp. nov***.

MycoBank number: MB823716; *Facesoffungi number*: FoF05728, Fig. 173

Etymology: The name refers to the phytophysiognomy where it was collected.

Holotype: URM 90199

Colour codes follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978).

Basidiomes yellowish to greyish or brown (1B, 2A, 5E, 4D) when fresh, greyish brown to yellowish brown (3F, 8E) when dry, foliose, 2.5–3 × 3.5 cm, gelatinous, densely papillate, papillae 50–107.5 × 40 µm, encrusted with irregular, hyaline crystals not dissolving in KOH, margin detaching from the substrate, marginal hairs present in tufts, 50–212 µm or absent, subhymenial hyphae with ochraceus, granular content. *Basidia* with complete septum, 2- or 4-celled, hyaline, ovoid, 9–12(–13) × 6–9(–10) µm, clamped at the base. *Basidiospores* allantoid to reniform, 7.8–10(–12) × 2–5 µm, thin-walled, IKI-. *Hyphal system* monomitic, hyphae clamped, thin-walled, hyaline, 1–2 µm in diam. *Cystidia* absent.

Material examined: BRAZIL, Pernambuco: Igarassu, Refúgio Ecológico Charles Darwin, May 2017, R.L.M. Alvarenga, RLMA 491 (URM 90198); *ibid.*, Pernambuco: Recife, Centro de Biociências, near the Departamento de Zoologia, Universidade Federal de Pernambuco, June 2017, R.L.M. Alvarenga, RLMA 477 (URM 90199 **holotype**; **isotype** in O).

GenBank numbers: ITS = MG594382, LSU = MG594384 (URM 90198); ITS = MG594381, LSU = MG594383 (URM 90199).

Notes: *Tremellochaete atlantica* is recognized by the marginal hairs ranging from 50–212 µm and the heavily encrusted papillae with hyaline, irregular crystals. It is similar to *T. japonica* and *T. nigerima* (Viégas) Spirin & V. Malysheva. *Tremellochaete japonica* (type locality Japan) differs by the darker basidiomes, fewer dark hyphae, smaller papillae (60–75 µm), absence of marginal hairs and slightly smaller basidiospores (9.5–12 × 4–4.5 µm) (Roberts 2006), while *T. nigerima* (type locality Brazil) has larger metabasidia and basidiospores (20–25 × 10–15 µm and 17–20 × 7–8 µm, respectively) (Viégas 1945).

Tremellochaete hispidula (Lowy) Raitv. (= *Exidia hispidula* Lowy, from USA) also has marginal hairs (up to 125 µm), but lacks clamps, has larger metabasidia [(7–)8–10 × (10–)12–16] and ovoid to allantoid basidiospores [(9–13(–14.5) × 5–7)] (Lowy 1957). This species, however, is illegitimate, because *Exidia hispidula* Berk. has priority over *E. hispidula* Lowy.

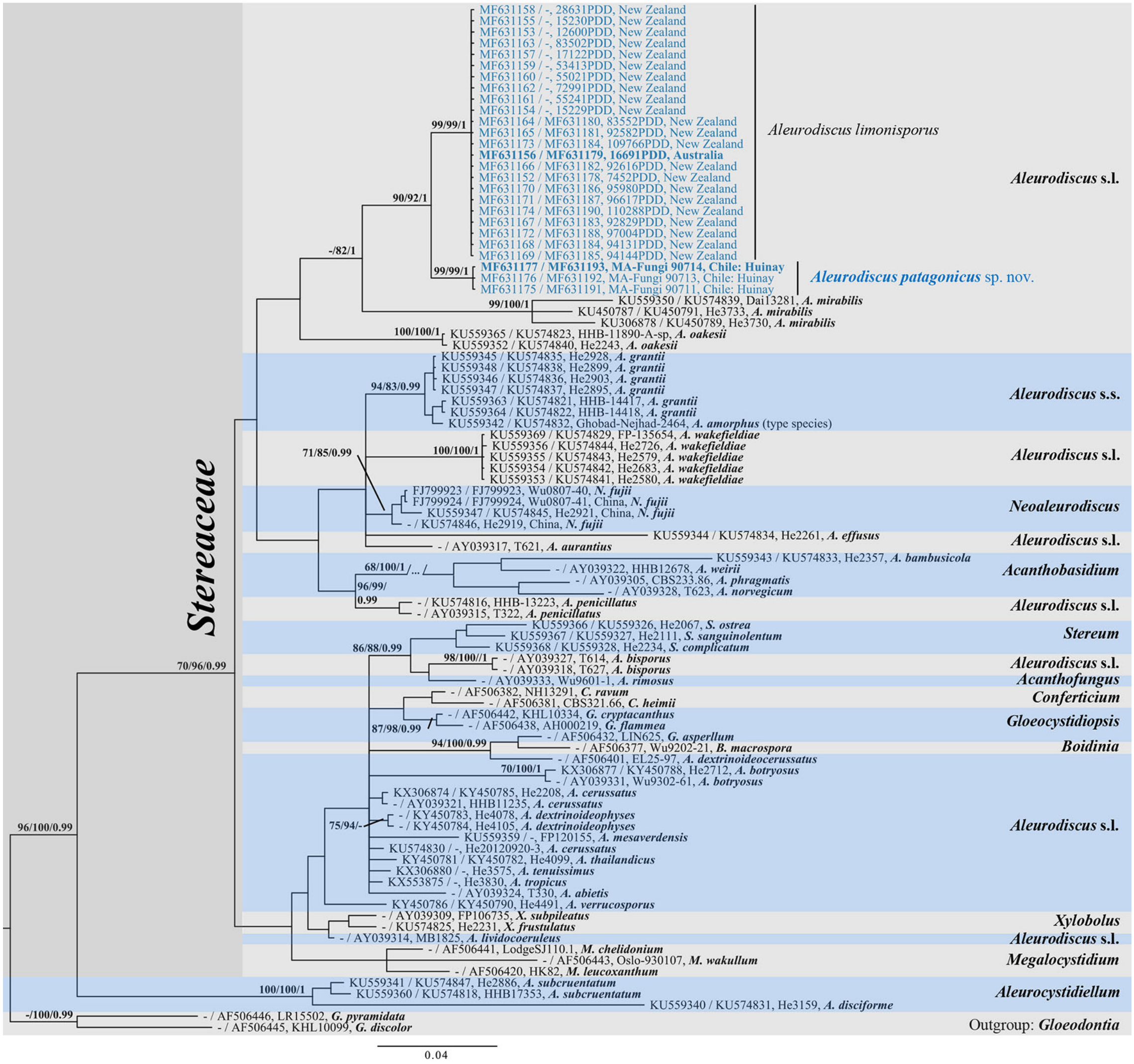


Fig. 169 Bayesian majority rule consensus topology based on a combined ITS and LSU DNA sequence dataset. Two *Gloeodontia* species were included as the outgroup taxa. Maximum parsimony and maximum likelihood bootstrap support (≥ 50%), and posterior probability (≥ 0.95 BYPP) are indicated above branches. Newly generated sequences are marked in blue and ex-type strains are in bold. Scale bar indicates substitution per site. Sequences were retrieved from EMBL Nucleotide Sequence Database (Cochrane et al. 2015), and they were published in Wu et al. (2001), Larsson and Larsson (2003), Wu et al. (b), Dai and He (2016), Dai et al. (2017a, b)

Table 3 Comparison of morphological characteristics and distribution between *Aleurodiscus patagonicus* and *A. limonisporus*

Morphology and distribution	*A. patagonicus*	*A. limonisporus*	ANOVA
Basidia length (µm)	150–190	130–160(−190)	**F = 31.26, p < 0.05**
Basidia width (µm)	(22 −)24–27	20–25(−26)	**F = 21.45, p < 0.05**
Basal clamp in basidia	Present	Absent	–
Spore length, L (µm)	19–22(−24)	20–24(−26)	F = 0.808, p = 0.379
Spore width, W (µm)	14–16	12–16	F = 4.195 p = 0.0532
Q Index, L/W	1.36–1.40	1.41–1.60	**F = 10.02, p < 0.05**
Distribution	Chile: Huinay Reserve	Australia, New Zealand	–

ANOVA analyses were performed to assess the significance of basidia and spore morphology using the function "aov" of the stats R package v 3.2.1 (R Core Team 2015)

Phylogenetic analysis of a combined ITS and LSU sequence dataset shows that *Tremellochaete atlantica* forms a well-resolved clade in *Tremellochaete* clade as a sister group to *T. japonica*, collected in Russia (Fig. 172).

Class Dacrymycetes Doweld

The classification of the families in Dacrymycetes follows Oberwinkler (2014), Zhao et al. (2016) and Shirouzu et al. (2017).

Dacrymycetales Henn.

Dacrymycetaceae J. Schröt.

Dacrymycetaceae was introduced by Schröter (1889), with the genera *Calocera* (Fr.) Fr., *Dacrymyces* Nees, *Dacryomitra* Tul. & C. Tul. and *Guepinia* Fr. Nowadays, according to Oberwinkler (2014) this family contains ten genera: *Arrhytidia* Berk. & M.A. Curtis, *Calocera*, *Dacrymyces*, *Dacryomitra*, *Dacryonaema* Nannf., *Dacryopinax* G.W. Martin, *Ditiola* Fr. (= *Guepinia*), *Femsjonia* Fr., *Guepiniopsis* Pat. and *Heterotextus* Lloyd.

The species included in this family are characterized by the form of basidiome: pustulate, cupulate, clavate, or sometimes branched; gelatinous when fresh and usually yellow or orange. The hyphal system is monomitic, the basidia bifurcate, with two well-developed sterigmata and the spores are usually septate germinating by conidia or germ tubes. All species are wood-decaying and cause brown rot (Oberwinkler 1993). The genera in this family have been delimited according to morphological criteria such as the shape of basidiome, the position of the hymenium, and presence or absence of a specialized cortex (Kobayasi 1939; McNabb 1973; Reid 1974). Phylogenetic studies (Weiß and Oberwinkler 2001; Shirouzu et al. 2007, 2009, 2013, 2017) showed that *Calocera*, *Cerinomyces*, *Dacrymyces*, and *Dacryopinax* are polyphyletic, suggesting that the traditional taxonomy should be revised.

We follow the treatment and updated accounts in Shirouzu et al. (2017) as well as following Reid (1974) for taking into account *Dacrymyces sensu lato*. The species of this genus are characterized by the basidiomes being gelatinous when fresh, at first pustular, becoming pulvinate, discoid or turbinate, sometimes stipitate; hymenium amphigenous, or restricted to the upper surface; hyphal system monomitic; hyphidia simple, or somewhat branched, with or without clamp connections; basidia clavate becoming bifurcate; spores cylindrical, ellipsoid, allantoid, ovate or subglobose, becoming variously septate at maturity and germinating by conidia or germ-tubes. The novel species, *Dacrymyces invisibilis* is introduced based on morphological characteristics coupled with ITS phylogenetic analyses (Fig. 174).

Dacrymyces invisibilis M. Dueñas, Telleria & M.P. Martín, ***sp. nov.***

MycoBank number: MB825361; *Facesoffungi number*: FoF05729, Figs. 175, 176

Etymology: From Latin "*invisibilis*" not visible, refers to dry basidiome difficult to see.

Holotype: 14597MD, MA-Fungi 91306.

Basidiomes pustulate at first, pulvinate to discoid, confluent, 0.5–3 mm diam., gelatinous, white, becoming varnish-layered when dry; hymenophore amphigenous, smooth; margin determinate. *Hyphal system* monomitic. *Hyphae* thin- to thick-walled, smooth, or incrusted, loosely interwoven, sparsely ramified, 2–4 µm wide, without clamps. *Basidia* 37–48 × 5–6 µm, hyaline, guttulate, subcylindrical to subclavate, without basal clamp, two sterigmata, 21–30 × 3 µm. *Spores* (14–)15–18 × 5–6(–7) µm ($\bar{x}$ = 15.8 × 5.95 µm), hyaline, ellipsoid, 3-septate at maturity, thin-walled, smooth, with oil drops, Q (L/W) = 2.65.

Material examined: CHILE, Los Lagos, Palena, comuna Hualaihué, Hornopirén, Huinay Biological Reserve, behind the hydroelectric power station, next to the beach, 42°22′53.4″S 72°24′55.6″W, on unidentified wood, 9 May 2013, M. Dueñas, M.P. Martín & M.T. Telleria, 14597MD, (MA-Fungi 91306, **holotyp**e); *ibid.*, CHILE, Los Lagos, Palena, comuna Hualaihué, Hornopirén, Huinay Biological Reserve, "Cementerio de los Alerces" experimental plot, 42°22′01.5″S 72°24′57.8″W, 50 msl, on unidentified wood, 10 May 2013, M. Dueñas, M.P. Martín & M.T. Telleria, 14617MD (MA-Fungi 91307).

Habitat and distribution: Known from the Valdivian temperate rainforest in the Chilean Northern Patagonian region, growing on unidentified wood.

GenBank numbers: ITS = MH230100 (14597MD, MA-Fungi 91306); ITS = MH230101 (14617MD, MA-Fungi 91307).

Notes: Previous ITS/LSU analyses (data not shown) of *Dacrymyces invisibilis*, and 119 homologous sequences from Shirouzu et al. (2017), included this taxon with *D. subantarcticensis* Burds. & Laursen described from New Zealand (Burdsall and Laursen 2004). However, morphological and molecular features clearly separate the two taxa. In this paper, a shorter and more accurate alignment is reported, including the species closest to *D. subantarcticensis* in Shirouzu et al. (2017): *D. aureosporus* Shirouzu & Tokum., *D. chrysospermus* Berk. & M.A. Curtis, *D. dictyosporus* G.W. Martin, *D. minor* Peck, *D. subalpinus* Kobayasi, *D. stillatus* Nees and *Guepiniopsis buccina* (Pers.) L.L. Kenn. In the UPGMA tree (Fig. 174) based on Kimura-2-parameters, the genetic distances proposed in Schoch et al. (2012) as barcode analyses, are shown, including the parsimony bootstrap and maximum likelihood support values, as well as the Bayesian posterior probabilities. The two collections from Chile form a well-supported group (81% MP, 78% ML and 1.00 BYPP) indicating that *D. invisibilis* is distinct from *D. subantarcticensis*. In addition, in this figure a small part of the alignment (around positions 189 and 246) is included to show some of the variable positions between these two

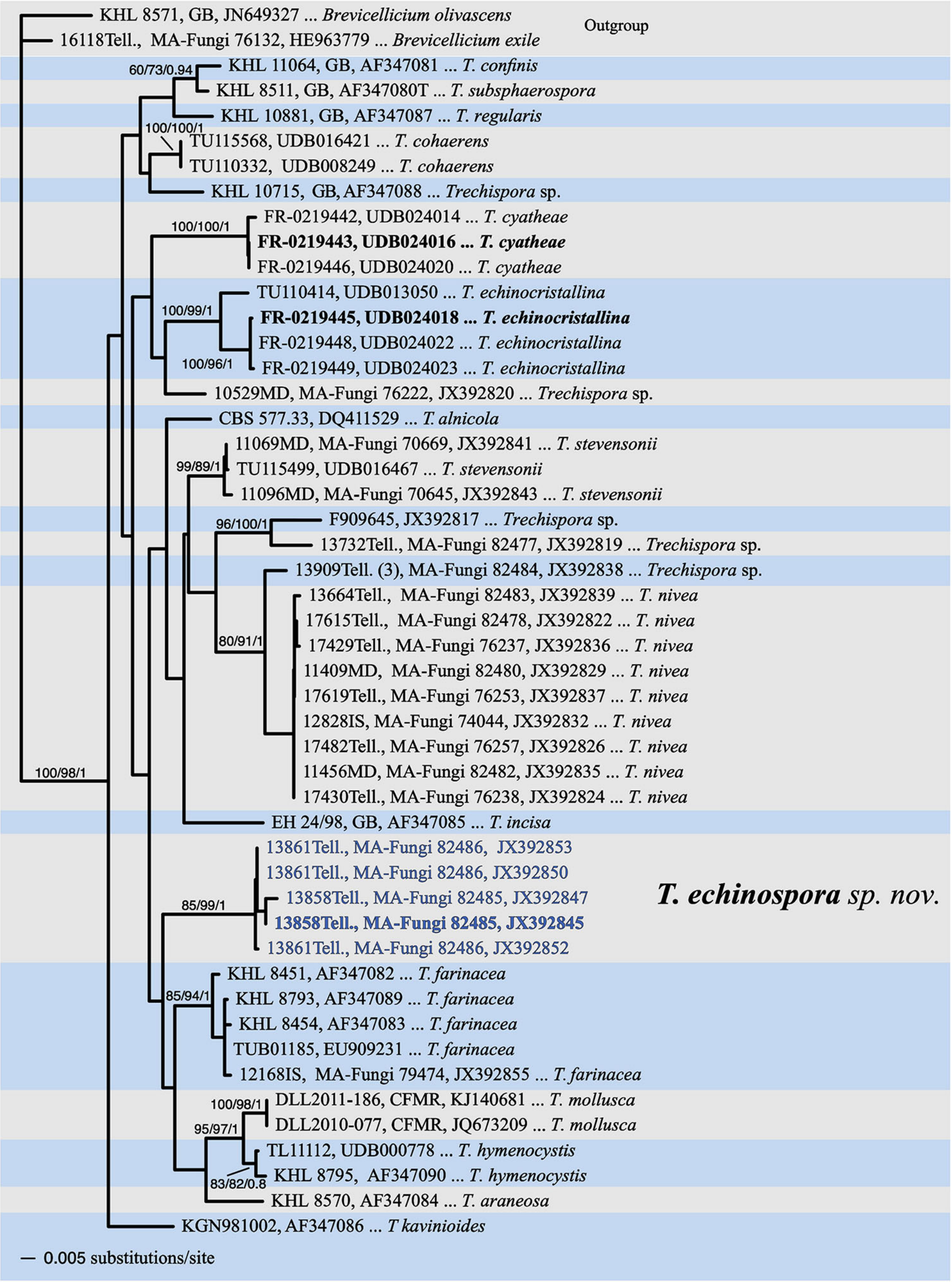


Fig. 170 Phylogram generated from Bayesian inference analysis of ITS sequence dataset of *Trechispora* sequences. Maximum parsimony and maximum likelihood bootstrap support values ≥ 50% (10,000 replicates both), and Bayesian posterior probabilities ≥ 80% are shown above the nodes. The tree is rooted with *Brevicellicium exile* and *B. olivascens.* Newly generated sequences are marked in blue and ex-type strains are in bold

species. *Dacrymyces invisibilis* and *D. subantarcticensis* have basidiomes nearly invisible when dry, and thin-walled spores, with three septa, but they differ in the size of basidia and spores, smaller in *D. subantarcticensis* (20–30 × 5 µm and 10–13 × 4.5–6 µm, respectively). *Dacrymyces subalpinus*, *D. aureosporus*, *D. chrysospermus* and *D. dictyosporus* form a subclade close to *D. subantarcticensis* and *D. invisibilis*; all of them have spores with more than three septa at maturity. *Dacrymyces subalpinus* and *D. aureosporus* are known only from Japan (Kobayasi 1939; Shirouzu and Hosoya 2017). *Dacrymyces chrysospermus* has been widely reported and *D. dityosporus* is known from Honduras, and Mexico (Lowy 1971).

Mucoromycota Doweld

We follow the latest treatment and updated accounts of Mucoromycota in Tedersoo et al. (2018) and Wijayawardene et al. (2018b).

Mucoromycetes Doweld

The classification of the families in Mucoromycetes follows Tedersoo et al. (2018) and Wijayawardene et al. (2018b).

Mucorales Fr.

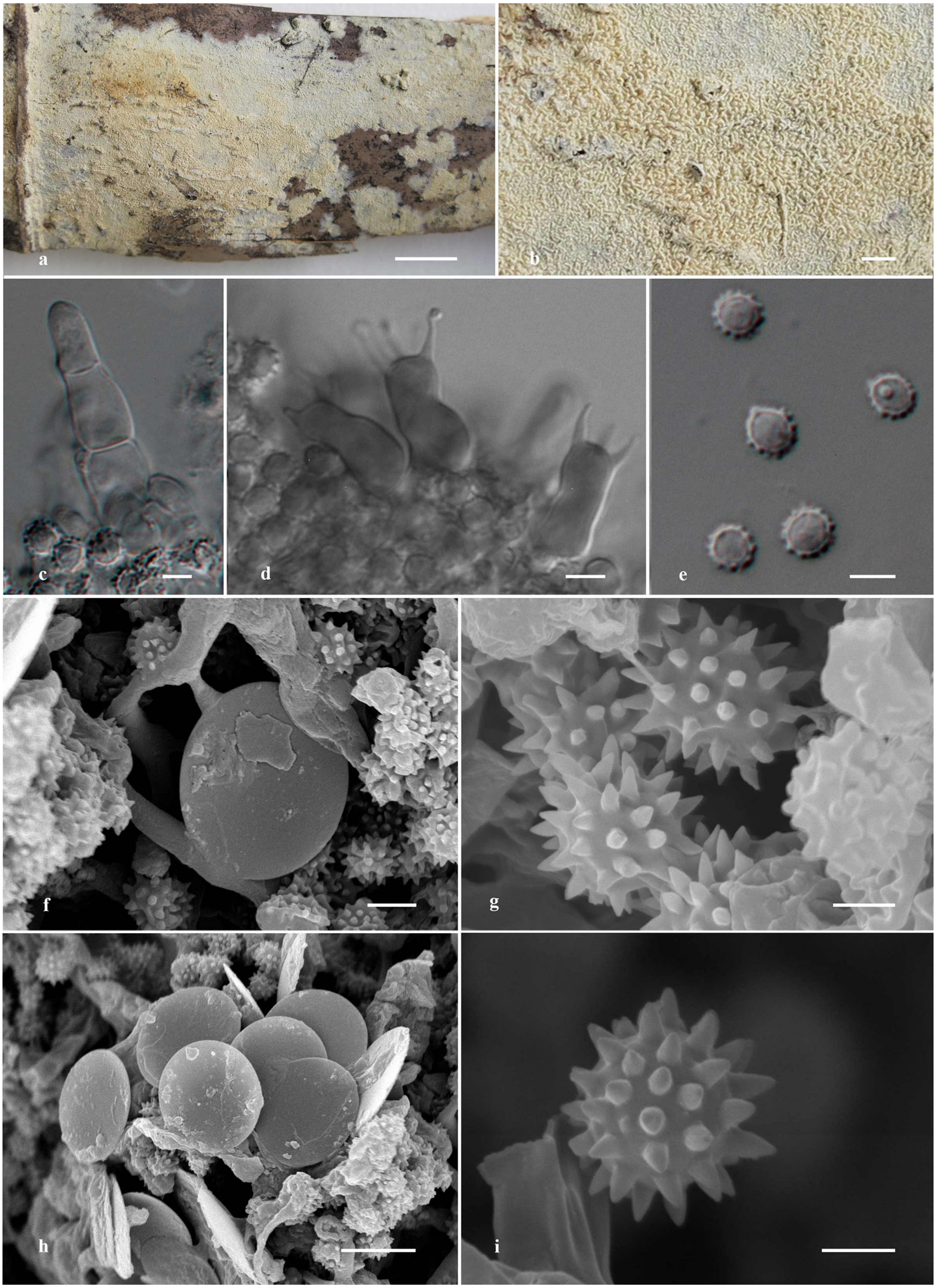


Fig. 171 ***Trechispora echinospora*** (13858Tell., MA-Fungi 82485, **holotype**). **a, b** Basidiome dry specimen. **c** Apical hypha of aculeus. **d** Basidia. **e** Spores. **f, h** Sphaerocysts (SEM). **g** Spores (SEM) of *T. echinospora* (13861Tell., MA-Fungi 82486). **i** Spores (SEM). *Scale bars* **a** = 1 cm, **b** = 5 mm, **c–f** = 5 µm, **g, i** = 2.5 µm, **h** = 10 µm

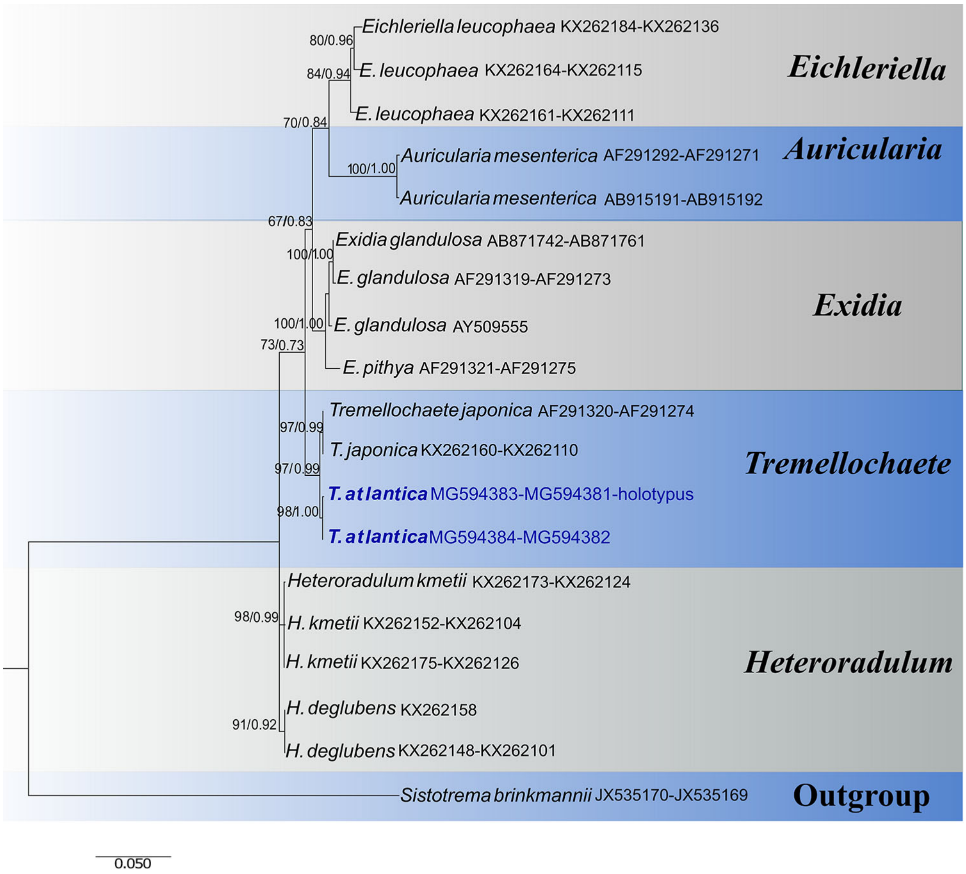


Fig. 172 Phylogenetic tree of the *Tremellochaete* obtained by analyses of DNA sequences. The phylogenetic tree was generated by partial concatenated analyses of the ITS and LSU sequence dataset. Only species with at least the LSU sequences were considered for the phylogeny. The sequences obtained in this study were aligned with other from GenBank in MEGA6 (Tamura et al. 2013) and edited using the Staden Package 2.0 software (Staden et al. 1998). *Sistotrema brinkmannii* (Bres.) J. Erikss. was used as outgroup taxa. Prior to phylogenetic analyses, the model of nucleotide substitution was estimated using Topali 2.5 (Milne et al. 2004). Bayesian inference analyses [two runs over 2 × 106 generations with a burn in value of 25% and maximum likelihood (1000 bootstrap)] were performed, respectively, in MrBayes 3.1.2 (Ronquist et al. 2012) and PhyML (Guindon and Gascuel 2003) launched from Topali 2.5, using the GTR + G model. Sequences obtained in this study are in blue. Support values are maximum likelihood (BSML) and Bayesian posterior probability (BYPP). Only support values of at least 50% are shown

Mucoraceae Dumort.

We follow the latest treatment and updated accounts of *Mucoraceae* in Spatafora et al. (2016), Tibpromma et al. (2017) and Wanasinghe et al. (2018). A high-level classification of *Mucoraceae* was updated by Tedersoo et al. (2018) based on an evolutionary ecological analysis.

Mucor Fresen.

The genus *Mucor* was described by Fresenius (1850), and comprises the largest number of species within the *Mucorales* (Benny et al. 2014). They are readily isolated from soil, fruits, vegetables, stored grains, insects or dung (Benny 2008). Several species are of great interest to the biotechnology industry because of their ability to produce proteolytic enzymes (de Souza et al. 2015), while some species are considered as the causal agents of cutaneous zygomycosis in humans (Ribes et al. 2000). During a study of *Mucorales* from fecal samples of praying mantis collected from the gardens of Chonnam National University, Gwangju, Korea, a new species of *Mucor* was isolated and is described here. Recently, only three new *Mucor* species have been reported in Korea: *M. koreanus* Hyang B. Lee et al. from tangerine fruit (Li et al. 2016); *M. stercorarius* Hyang B. Lee et al. from rat faeces (Tibpromma et al. 2017); and *M. fluvii* Hyang B. Lee et al. from freshwater (Wanasinghe et al. 2018) (Fig. 177).

Mucor orantomantidis Hyang B. Lee, P.M. Kirk & T.T.T. Nguyen, ***sp. nov.***

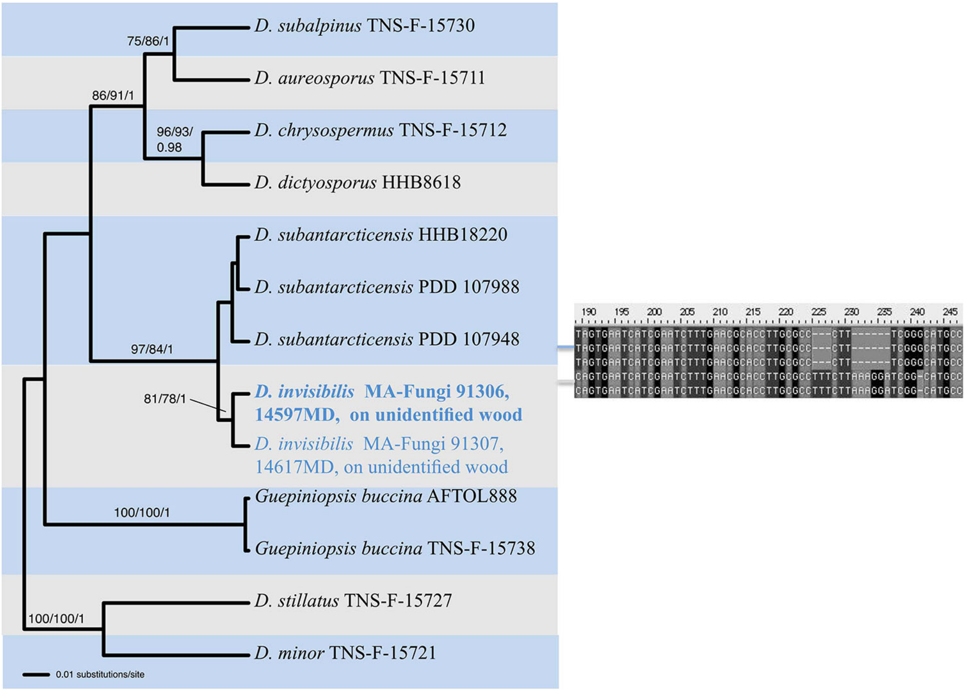
Index Fungorum number: IF555163; *Facesoffungi number*: FoF05733, Fig. 178

Etymology: The specific epithet "*orantomantidis*" refers to the origin of the fecal pellet of a praying mantis from which the species was first isolated.

Holotype: CNUFC-MID1-1

Fig. 173 ***Tremellochaete atlantica*** (URM 90199, **holotype**). **a** Basidiome when fresh. **b** Papillae encrusted with crystals. **c** Clamped hyphae of the context. **d, e** 2-celled, metabasidia, hyphae with ochraceus, granular content. **f, g** Basidiospores. *Scale bars* **a** = 1 cm, **b** = 1 mm, **c–g** = 10 µm. Photos by R.L. Alvarenga

Fig. 174 UPGMA tree based on Kimura-2-parameters of ITS sequence dataset of seleceted *Dacrymycetales* species from Shirouzu et al. (2017). Maximum parsimony and maximum likelihood bootstrap support values ≥ 50% (10,000 replicates) and Bayesian posterior probabilities ≥ 0.95 BYPP are shown above the nodes. The analyses were done without rooting the tree. The 189-246 positions in the alignment to *D. invisibilis* and *D. subantarcticensis* are shown. New species is indicated in blue bold



Colonies on SMA reaching 38–41 mm diam. at 25 °C after 3 days of incubation, yellowish; reverse yellow brownish. *Sporangiophores* 6.5–16.5 µm wide, arising from aerial hyphae, simple or sympodially branched, with short or long branches. *Sporangia* globose to subglobose, multispored, initially light yellow then turning brownish

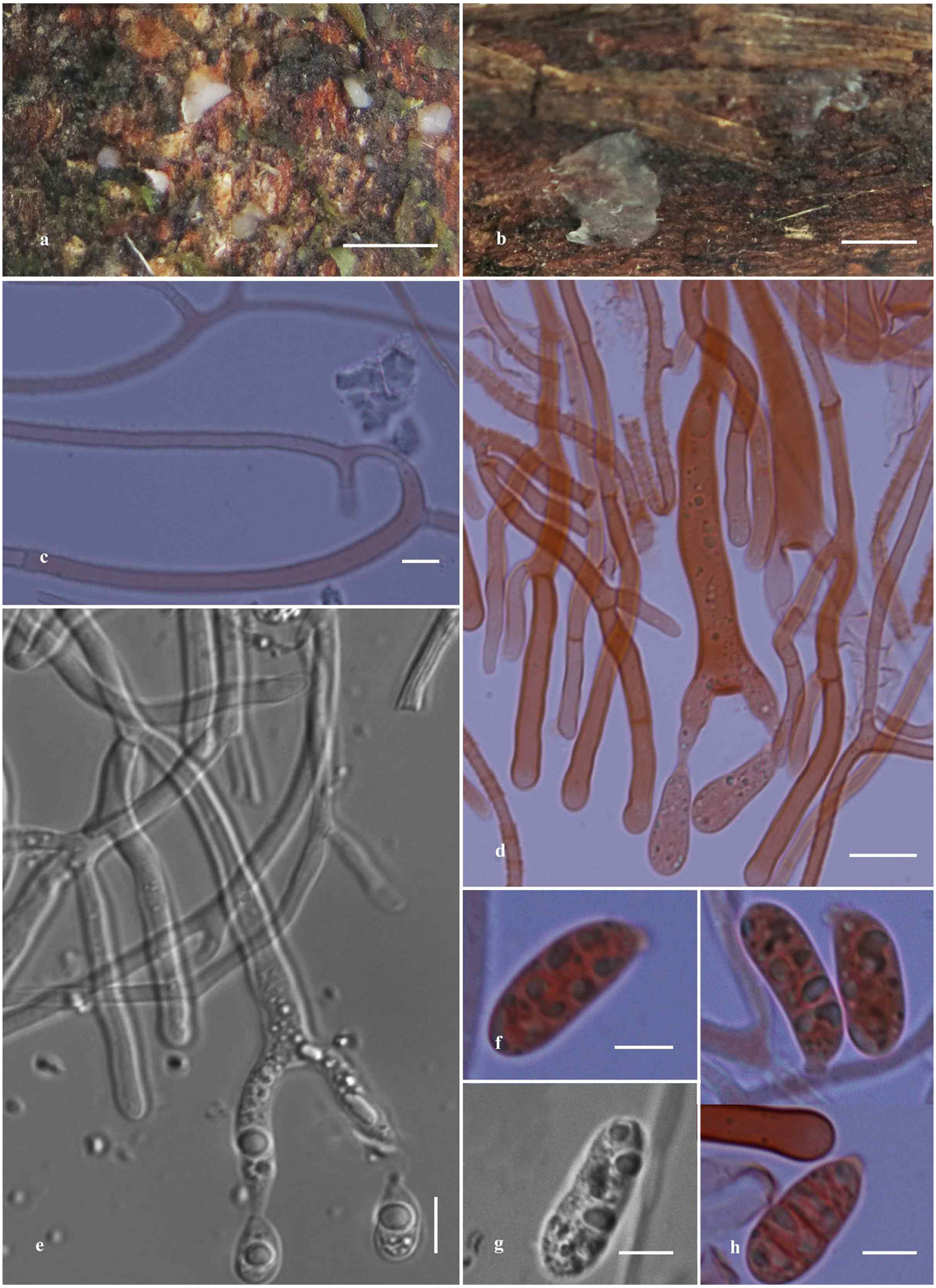


Fig. 175 ***Dacrymyces invisibilis*** (MA-Fungi 91306, **holotype**). **a, b** Appearance of basidiome on host surface. **c** Hyphae stained in congo red. **d** Basidia stained in congo red. **e** Basidia. **f–h** Spores. *Scale bars* **a, b** = 2 mm, **c** = 5 µm, d, **e** = 10 µm, **f–h** = 5 µm

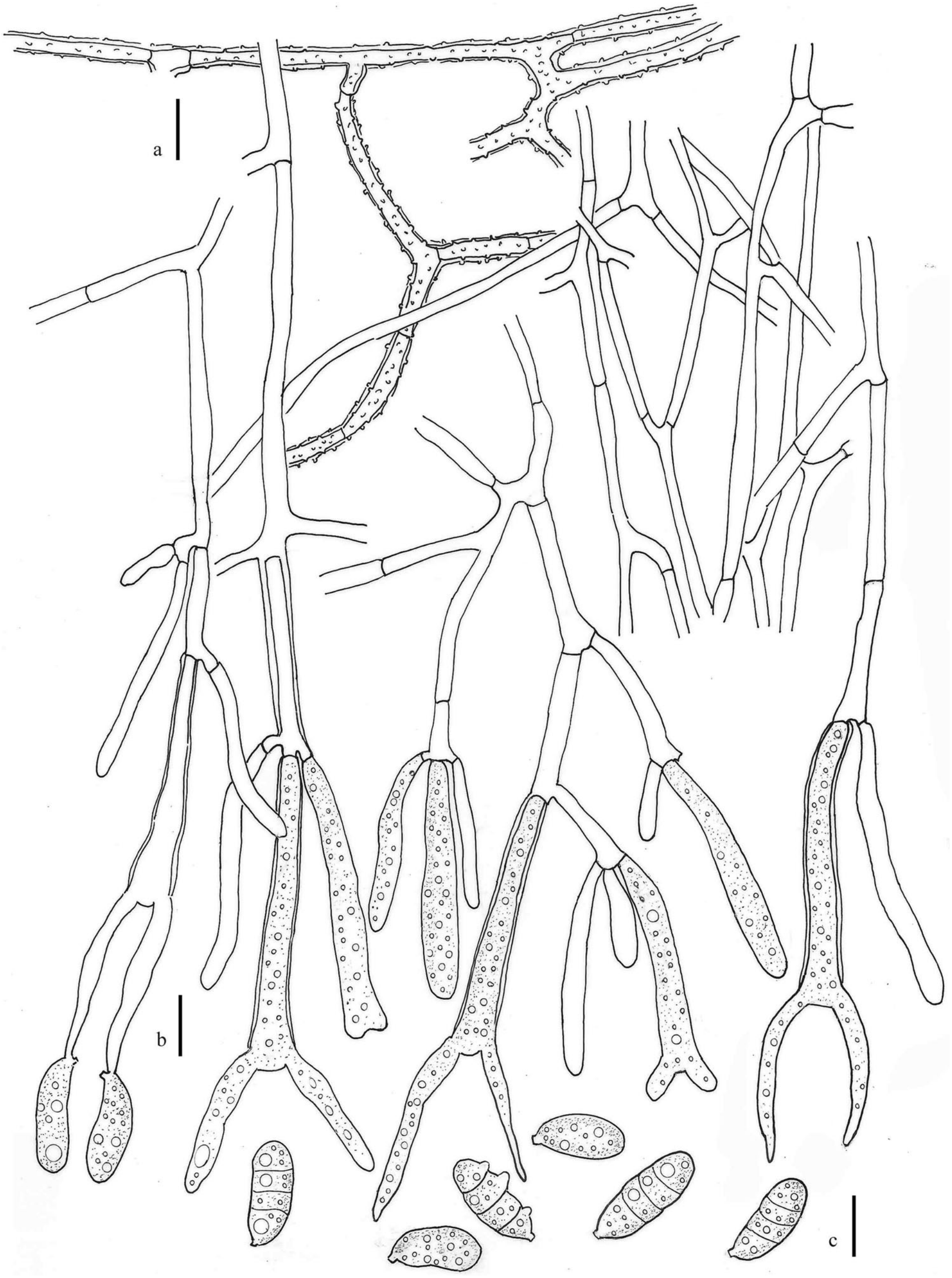


Fig. 176 ***Dacrymyces invisibilis*** (MA-Fungi 91306, **holotype**). **a** Hyphae. **b** Basidia. **c** Spores. *Scale bars* = 10 µm

yellow, 29.5–60.5 × 28.5–58.5 µm. *Columellae* globose to subglobose, ellipsoidal, 25–58.5 × 22.5–45.5 µm. *Sporangiospores* ellipsoidal, sometimes one side slightly flattened, 8–11.5 × 4.5–6 µm. *Chlamydospores* abundantly produced in aerial hyphae, in chains or irregular, globose, fusiform, barrel-shaped, or irregular in shape. *Zygospores* borne near the agar surface, reddish brown when young, later blackish brown, 38.5–60.5 × 31.5–49 µm.

Culture characteristics: The isolate grew over a wide range of temperatures with varying growth rates on SMA, PDA, and MEA of 12.5, 14.5, and 12 mm per 24 h, respectively. Optimal growth was observed around 25–30 °C, slow growth was observed below 10 °C, and no growth at 40 °C.

Material examined: REPUBLIC OF KOREA, Jeonnam Province, garden of Chonnam National University located in Gwangju (35° 09′ 16.99″N, 126° 54′ 56.02″E), from fecal sample of praying mantis, October 2017 (CNUFC-

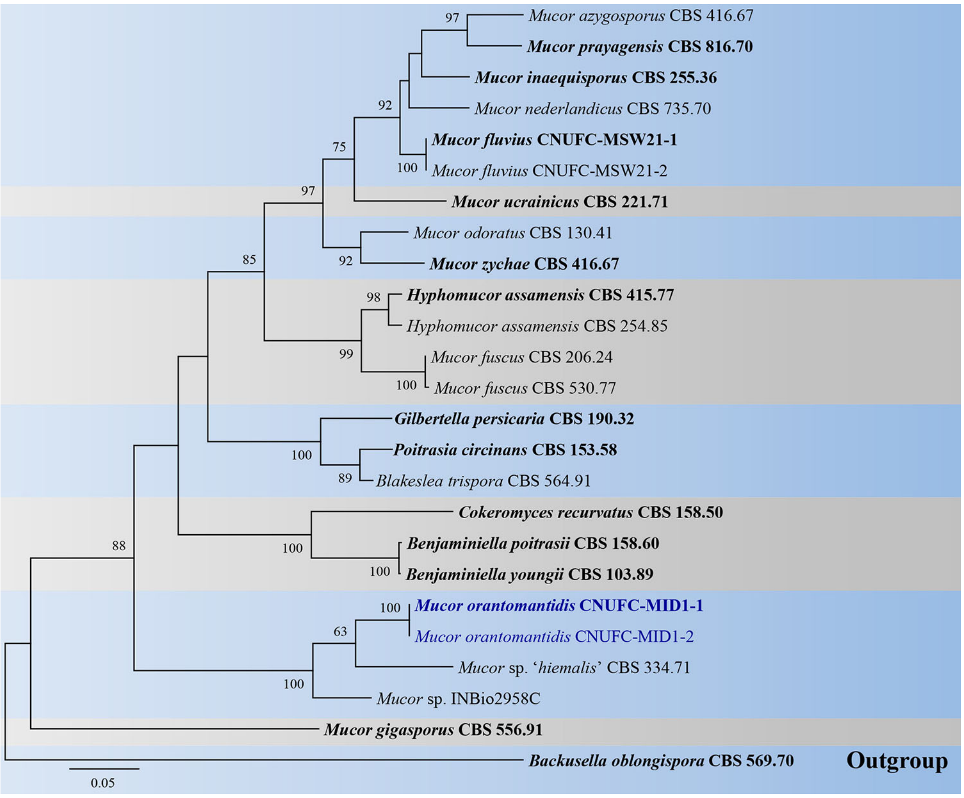


Fig. 177 Phylogenetic tree of *Mucor orantomantidis* (CNUFC-MID1-1 and CNUFC-MID1-2), and related species based on a maximum likelihood analysis of a combined ITS and LSU sequence dataset. The sequence of *Backusella oblongispora* was used as outgroup taxon. Numbers at the nodes indicate the bootstrap values (> 50%) from 1000 replications. The bar indicates the number of substitutions per position. New taxa are shown in blue and ex-type strains in bold

MID1-1, **holotype**); **isotype** in Korean Agricultural Culture Collection (KACC, Wanju, Korea); ex-type living culture, JMRC:SF:013605 (deposited at Jena Microbial Resource Collection, University of Jena and Leibniz Institute for Natural Product Research and Infection Biology, Jena, Germany and preserved as glycerol stock at -80 °C in the CNUFC).

GenBank number: ITS = MH594737, LSU = MH591457 (CNUFC-MID1-1); ITS = MH594738, LSU = MH591458 (CNUFC-MID1-2).

Notes: The phylogenetic analyses of a combined ITS and LSU sequence dataset (Fig. 177) show that *Mucor orantomantidis* belongs to *M. amphibiorum* group as defined by Walther et al. (2013). *Mucor orantomantidis* is closely related to *Mucor* sp. '*hiemalis*'. However, *M. orantomantidis* differs from *Mucor* sp. '*hiemalis*' by producing zygospores with equal or unequal suspensors, and by having larger sporangiospores. *M. orantomantidis* grows and sporulates at 35 °C, whereas, the maximum temperature for *Mucor* sp. '*hiemalis*' is around 30 °C. In addition, the strain forms a separate branch from other species of the genus, showing it represents a new species in the phylogenetic tree (Fig. 177).

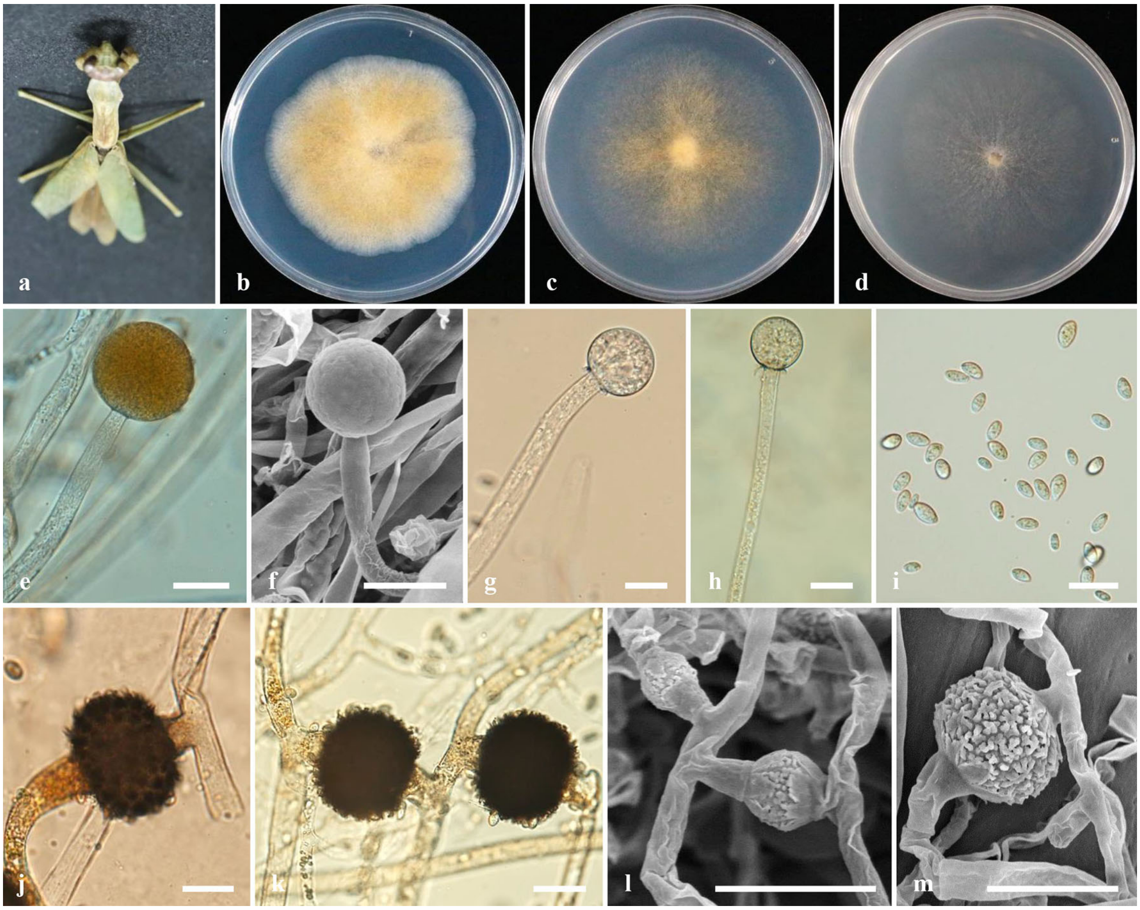


Fig. 178 ***Mucor orantomantidis*** (CNUFC-MID1-1, **holotype**). **a** A praying mantis. **b** Colony in potato dextrose agar. **c** Colony in synthetic mucor agar. **d** Colony in malt extract agar. **e, f** Sporangiophores and sporangia. **g, h** Columellae with collarette. **i** Sporangiospores. **j–m** Zygospores. (**e, g–k:** LM; **f, l, m:** SEM). *Scale bars* **e–k** = 20 µm, **l, m** = 50 µm

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References

Abarenkov K, Nilsson RH, Larsson KH, Alexander IJ, Eberhardt U, Erland S, Høiland K, Kjøller R, Larsson E, Pennanen T, Sen R, Taylor AF, Tedersoo L, Ursing BM, Vrålstad T, Liimatainen K, Peintner U, Kõljalg U (2011) The UNITE database for molecular identification of fungi—recent updates and future perspectives. New Phytol 186:281–285

Abdel-Wahab MA, Pang KL, Nagahama T, Abdel-Aziz FA, Gareth Jones EB (2010) Phylogenetic evaluation of anamorphic species of *Cirrenalia* with the description of eight new genera and four new species. Mycol Prog 9:537–558

Acero FJ, González V, Sánchez-Ballesteros J, Rubio V, Checa J, Bills GF, Salazar O, Platas G, Peláez F (2004) Molecular phylogenetic studies on the *Peroneutypa* based on rDNA-ITS sequences. Mycologia 96:249–259

Adams GC, Wingfield MJ, Common R, Roux J (2005) Phylogenetic relationships and morphology of *Cytospora* species and related teleomorphs (Ascomycota, *Diaporthales*, *Valsaceae*) from Eucalyptus. Stud Mycol 52:1–144

Adams GC, Roux J, Wingfield MJ (2006) *Cytospora* species (Ascomycota, *Diaporthales*, *Valsaceae*): introduced and native pathogens of trees in South Africa. Australas Plant Pathol 35:521–548. https://doi.org/10.1071/AP06058

Agnello C, Baglivo A, Carbone M (2013) Rivalutazione e tipificazione di *Peziza sicula* alla luce di raccolte effettuate nel Salento (Puglia-Italia). Boll A.M.E.R. 88(1):15–24

Agnello C, Baglivo A, Carbone M (2015) Typification of *Peziza sicula*. Ascomycete 7(1):30

Agnello C, Alvarado P, Loizides M (2018) *Sarcopeziza* (*Pezizaceae*, Ascomycota), a new monotypic genus for Inzenga's old taxon *Peziza sicula*. Ascomycete.org 10(4):177–186

Alvarado P, Moreno G, Manjón JL, Sánz MA (2011) *Eremiomyces magnisporus* (*Pezizales*), a new species from central Spain. Mycotaxon 118:103–111

Alvarez LV, Groenewald JZ, Crous PW (2016) Revising the *Schizoparmaceae*: *coniella* and its synonyms *Pilidiella* and *Schizoparme*. Stud Mycol 85:1–34

Anastasiou CJ (1967) Two species of *Coprinus* from alkali lakes. Can J Bot 45:2213–2222

Anonymous (2004) The online auction color chart. Online Auction Color Co, Palo Alto

Antonín V, Ryoo R, Shin HD (2010) Two new marasmielloid fungi widely distributed in the Republic of Korea. Mycotaxon 112:189–199

Antonín V, Ryoo R, Shin HD (2012) Marasmioid and gymnopoid fungi of the Republic of Korea. 4. *Marasmius* sect. Sicci. Mycol Prog 11:615–638

Aptroot A (1998) A world revision of *Massarina* (Ascomycota). Nova Hedwigia 66(1):89–162

Ariyawansa HA, Tanaka K, Thambugala KM, Phookamsak R, Tian Q, Camporesi E, Hongsanan S, Monkai J, Wanasinghe DN, Mapook A, Chukeatirote E (2014) A molecular phylogenetic reappraisal of the *Didymosphaeriaceae* (= *Montagnulaceae*). Fungal Divers 68:69–104

Ariyawansa HA, Hyde KD, Jayasiri SC, Buyck B, Chethana KWT, Dai DQ, Dai YC, Daranagama DA, Jayawardena RS, Lücking R, Ghobad-Nejhad M, Niskanen T, Thambugala KM, Voigt K, Zhao RL, Li GJ, Doilom M, Boonmee S, Yang ZL, Cai Q, Cui YY, Bahkali AH, Chen J, Cui BK, Chen JJ, Dayarathne MC, Dissanayake AJ, Ekanayaka AH, Hashimoto A, Hongsanan S, Jones EBG, Larsson E, Li WJ, Li QR, Liu JK, Luo ZL, Maharachchikumbura SSN, Mapook A, McKenzie EHC, Norphanphoun C, Konta S, Pang KL, Perera RH, Phookamsak R, Phukhamsakda C, Pinruan U, Randrianjohany E, Singtripop C, Tanaka K, Tian CM, Tibpromma S, Abdel-Wahab MA, Wanasinghe DN, Wijayawardene NN, Zhang JF, Zhang H, Abdel-Aziz FA, Wedin M, Westberg M, Ammirati JF, Bulgakov TS, Lima DX, Callaghan TM, Callac P, Chang CH, Coca LF, Dal Forno M, Dollhofer V, Fliegerová K, Greiner K, Griffith GW, Ho HM, Hofstetter V, Jeewon R, Kang JC, Wen TC, Kirk PM, Kytövuori I, Lawrey JD, Xing J, Li H, Liu ZY, Liu XZ, Liimatainen K, Lumbsch HT, Matsumura M, Moncada B, Nuankaew S, Parnmen S, de Azevedo Santiago ALCM, Sommai S, Song Y, de Souza CAF, de Souza-Motta CM, Su HY, Suetrong S, Wang Y, Wei SF, Wen TC, Yuan HS, Zhou LW, Réblová M, Fournier J, Camporesi E, Luangsa-ard JJ, Tasanathai K, Khonsanit A, Thanakitpipattana D, Somrithipol S, Diederich P, Millanes AM, Common RS, Stadler M, Yan JY, Li XH, Lee HW, Nguyen TTT, Lee HB, Battistin E, Marsico O, Vizzini A, Vila J, Ercole E, Eberhardt U, Simonini G, Wen HA, Chen XH (2015a) Fungal Diversity Notes 111–252 taxonomic and phylogenetic contributions to fungal taxa. Fungal Divers 75:1–248

Ariyawansa HA, Phukhamsakda C, Thambugala KM, Bulgakov TS, Wanasinghe DN, Perera RH, Mapook A, Camporesi E, Kang JC, Jones EG, Bahkali AH (2015b) Revision and phylogeny of *Leptosphaeriaceae*. Fungal Divers 74(1):19–51

Ariyawansa HA, Phillips AJ, Chuang WY, Tsai I (2018) *Tzeananiaceae*, a new pleosporalean family associated with *Ophiocordyceps macroacicularis* fruiting bodies in Taiwan. MycoKeys 37:1–17

Babos M, Halász K, Zagyva T, Zöld-Balogh Á, Szegő D, Bratek Z (2011) Preliminary notes on dual relevance of ITS sequences and pigments in *Hygrocybe* taxonomy. Persoonia 26:99–107

Bakhshi M, Arzanlou M, Groenewald JZ, Quaedvlieg W, Crous PW (2019) *Parastagonosporella fallopiae* gen. et sp. nov. (*Phaeosphaeriaceae*) on *Fallopia convolvulus* from Iran. Mycol Prog 18:203–214

Baral HO (1992) Vital versus herbarium taxonomy: morphological differences between living and dead cells of ascomycetes, and their taxonomic implications. Mycotaxon 44:333–390

Barbosa FR, Silva SS, Fiuza PO, Gusmão LFP (2011) Conidial fungi from the semi-arid Caatinga biome of Brazil. New species and records for *Thozetella*. Mycotaxon 115:327–334

Barbosa FR, Gusmão LF, Raja HA, Shearer CA (2013) New species and new records of freshwater ascomycetes from Brazil and Costa Rica. Mycologia 105(2):335–343

Barge EG, Cripps CL (2016) New reports, phylogenetic analysis, and a key to *Lactarius* Pers. in the Greater Yellowstone Ecosystem informed by molecular data. Mycokeys 15:1–58

Barge EG, Cripps CL, Osmundson TW (2016) Systematics of the ectomycorrhizal genus *Lactarius* in the Rocky Mountain alpine zone. Mycologia 108(2):414–440

Barr ME (1976) Perspectives in the Ascomycotina. Mem N Y Bot Gard 28:1–8

Barr ME (1978) The *Diaporthales* in North America: with emphasis on *Gnomonia* and its segregates. Mycol Mem 7:1–232. https://doi.org/10.1002/fedr.19800910313

Barr ME (1979) A classification of Loculoascomycetes. Mycologia 71:935–957

Barr ME (1987) New taxa and combinations in the Loculoascomycetes. Mycotaxon 29:501–505

Barr ME (1990) Prodomus to nonlichenized, pyrenomycetous members of class Hymenoascomycetes. Mycotaxon 39:43–184

Bas C (2000) A broader view on Amanita. Boll Gruppo Micol G Bresadola 43:9–12

Benny GL (2008) Methods used by Dr. R. K. Benjamin, and other mycologists, to isolate Zygomycetes. Aliso 26:37–61

Benny GL, Humber RA, Voigt K (2014) Zygomycetous fungi: Phylum Entomophthoromycota and subphyla Kickxellomycotina, Mortierellomycotina, Mucoromycotina, and Zoopagomycotina. In: McLaughlin DJ, Spatafora JW (eds) Mycota VII, part A, Systematics and evolution. Springer, New York, pp 209–250

Berkeley MJ, Broome CE (1871) The fungi of Ceylon. (Hymenomycetes, from *Agaricus* to *Cantharellus*). Bot J Linn Soc 11:494–567

Berlese AN (1902) Icones Fungorum omnium hucusque cognitorum ad usum Sylloges Saccardianae Adcommodatae. Abellini 3(3–4):58

Beyma JFH (1940) Beschreibung einiger neuer Pilzarten aus dem Centraalbureau voor Schimmelcultures, Baarn (Nederland). VI. Mitteilung. Antonie van Leeuwenhoek. 6:263–290

Bhatt RP, Tulloss RE, Semwal KC, Bhatt VK, Moncalvo JM, Stephenson SL (2003) *Amanitaceae* from India. A critically annotated checklist. Mycotaxon 88:249–270

Bi ZS, Li TH (1986) A preliminary note on *Russula* species from Guangdong, with a new species and a new variety. Guihaia 6(3):193–199

Binder M, Hibbett DS, Larsson KH, Larsson E, Langer E, Langer G (2005) The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (Homobasidiomycetes). Syst Biodivers 3:1–45

Bissett J, Gams W, Jaklitsch W, Samuels GJ (2015) Accepted *Trichoderma* names in the year 2015. IMA Fungus 6(2):263–295

Blanco-Dios JB (2015) *Agaricales* of the dunes of Galicia (IV): *Marasmiellus ciesanus* (*Omphalotaceae*), a new species found in the National Maritime-Terrestrial Park of the Atlantic Islands of Galicia (Spain). Mycosphere 6(5):585–592

Boerema GH, Kesteren HAV (1964) The nomenclature of two fungi parasitizing *brassica*. Persoonia 3(1):17–28

Boertmann D (1995) The fungi of northern Europe. The genus *Hygrocybe*, vol 1. Greve, Denmark

Bondartsev A, Singer R (1941) Zur Systematik der Polyporaceae. Ann Mycol 39:43–65

Boonmee S, D'souza MJ, Luo Z, Pinruan U, Tanaka K, Su H, Bhat JD, McKenzie EHC, Jones EBG, Taylor JE, Phillips AJL, Hirayama K, Eungwanichayapant PD, Hyde KD (2016) Dictyosporiaceae fam. nov. Fungal Divers 80:457–482

Borse BD, Borse KN, Patil SY, Pawara CM, Nemade LC, Patil VR (2016) Freshwater higher fungi of India. Lulu, Com

Both EE (1998) New taxa of boletes and two boletes with identity problems. Bull Buffalo Soc Nat Sci 36:215–232

Bourdot H, Galzin A (1912) Hyménomycètes de France: IV. Corticiés: Aleurodiscus. Bull Soc Mycol Fr 28:349–354

Bourdot H, Galzin A (1928) Contribution à la flore mycologique de la France I. Hyménomycètes de France, Paris

Brahmanage RS, Lu YZ, Bhat DJ, Wanasinghe DN, Yan JY, Hyde KD, Boonmee S (2017) Phylogenetic investigations on freshwater fungi in *Tubeufiaceae* (*Tubeufiales*) reveals the new genus *Dictyospora* and new species *Chlamydotubeufia aquatica* and *Helicosporium flavum*. Mycosphere 8(7):917–933

Braun U, Nakashima C, Crous PW, Groenewald JZ, Moreno-Rico O, Rooney-Latham S, Blomquist CL, Haas J, Marmolejo J (2018) Phylogeny and taxonomy of the genus *Tubakia* s. lat. FUSE 1:41–99

Brazee NJ, Lindner DL, Fraver S, D'Amato AW, D'Amato AM (2012) Wood-inhabiting fungi in aspen-dominated forests managed for biomass in the U.S. Lake States. Fungal Ecol 5(5):600–609

Brazee NJ, Lindner DL, D'Amato AW, Fraver S, Forrester JA, Mladenoff DJ (2014) Disturbance and diversity of woo-inhabiting fungi: effects of canopy gaps and downed debris. Biodivers Conserv 23:2155–2172

Breitenbach J, Kränzlin F (1995) Pilze der Schweiz, vol 4. Verlag Mycologia, Luzern

Bulliard JBF (1788) Herbier de la France. Tome 8:337–384

Burdsall HH (1985) A contribution to the taxonomy of the genus *Phanerochaete*. Mycol Mem 10:1–165

Burdsall HH Jr, Laursen GA (2004) Fungi of New Zealand's subantartic islands I: Two new species of *Dacrymyces* (Basidiomycotina). In: Miller OK, Crips CL (eds) Fungi in forest ecosystems: systematic, diversity and ecology. New York Botanical Garden, Bronx, pp 107–111

Burt EA (1918) The *helephoraceae* of North America: IX. *Aleurodiscus*. Ann Mo Bot Gard 5:177–203

Buyck B, Thoen D, Watling R (1996) Ectomycorrhizal fungi of the Guinea-Congo Region. Proc R Soc Edinb 104:313–333

Buyck B, Hofstetter V, Eberhardt U, Verbeken A, Kauff F (2008) Walking the thin line between *Lactarius* and *Russula*: the dilemma of *Russula* sect. *Ochricompactae*. Fungal Divers 28:15–40

Buyck B, Hofstetter V, Verbeken A, Walleyn R (2010) Proposal 1919: to conserve *Lactarius* nom. cons. (Basidiomycota) with a conserved type. Mycotaxon 111:504–508

Cacialli G, Caroti V, Doveri F (1999) Contributio ad cognitionem coprinorum. A.M.B, Trento

Cai L, Jeewon R, Hyde KD (2005) Phylogenetic evaluation and taxonomic revision of *Schizothecium* based on ribosomal DNA and protein coding genes. Fungal Divers 19:1–21

Cai L, Jeewon R, Hyde KD (2006a) Phylogenetic investigations of *Sordariaceae* based on multiple gene sequences and morphology. Mycol Res 110:137–150

Cai L, Jeewon R, Hyde KD (2006b) Molecular systematics of *Zopfiella* and allied genera: evidence from multi-gene sequence analyses. Mycol Res 110:359–368

Cai Q, Tulloss RE, Tang LP, Tolgor B, Zhang P, Chen ZH, Yang ZL (2014) Multi-locus phylogeny of lethal amanitas: implications for species diversity and historical biogeography. BMC Evol Biol 14:143. https://doi.org/10.1186/1471-2148-14-143

Campbell J, Volkmann-Kohlmeyer B, Gräfenhan T, Spatafora JW, Kohlmeyer J (2005) A re-evaluation of *Lulworthiales*: relationships based on 18S and 18S rDNA. Mycol Res 109:556–568

Cannon PF (1991) A revision of *Phyllachora* and some similar genera on the host family *Leguminosae*. Mycol Pap 163:1–302

Cannon PF, Kirk PM (eds) (2007) Fungal families of the world. CABI, Wallingford

Cantrell SA, Hanlin RT (1997) Phylogenetic relationships in the family *Hyaloscyphaceae* inferred from sequences of ITS regions, 5.8S ribosomal DNA and morphological characters. Mycologia 89(5):745–755

Cantrell SA, Lodge DJ (2001) *Hygrophoraceae* (*Agaricales*) of the Greater Antilles: *Hygrocybe* subgenus *Pseudohygrocybe* section *Firmae*. Mycol Res 105:215–224

Carbone I, Kohn LM (1999) A method for designing primer sets for speciation studies in filamentous ascomycetes. Mycologia 91:553–556

Carlucci A, Raimondo ML, Santos J, Phillips AJ (2012) *Plectosphaerella* species associated with root and collar rots of horticultural crops in southern Italy. Persoonia Mol Phylogeny Evol Fungi 28:34–48

Carmarán CC, Romero AI, Giussani LM (2006) An approach towards a new phylogenetic classification in *Diatrypaceae*. Fungal Divers 23:67–87

Castañeda-Ruiz RF, Arnold GRW (1985) Deuteromycotina de Cuba. I. Hyphomycetes. Revista del Jardín Botánico Nacional Universidad de la Habana 6(1):47–67

Castañeda-Ruiz RF, Guarro J, Vel asquez-Noa S, Gene J (2003) A new species of *Minimelanolocus* and some hyphomycete records from rain forests in Brazil. Mycotaxon 85:231–239

Castlebury LA, Rossman AY, Jaklitsch WJ, Vasilyeva LN (2002) A preliminary overview of *Diaporthales* based on large subunit nuclear ribosomal DNA sequences. Mycologia 94:1017–1031. https://doi.org/10.1080/15572536.2003.11833157

Cesati V, De Notaris G (1863) Schema di classificazione degle sferiacei italici aschigeri piu' o meno appartenenti al genere Sphaerianell'antico significato attribuitoglide Persono. Commentario della Soc Crittogamol Ital 1:177–420

Chaiwan N, Lu YZ, Tibpromma S, Bhat DJ, Hyde KD, Boonmee S (2017) *Neotubeufia* gen. nov. and *Tubeufia guangxiensis* sp. nov. (Tubeufiaceae) from freshwater habitats. Mycosphere 8(9):1443–1456

Chang JW, Kao HW, Wang YZ (2010) Molecular Phylogeny of *Cercophora*, *Podospora*, and *Schizothecium* (*Lasiosphaeriaceae*, Pyrenomycetes). Taiwania 55:110–116

Cheewangkoon R, Groenewald JZ, Verkley GJ, Hyde KD, Wingfield MJ, Gryzenhout M, Summerell BA, Denman S, Toanun C, Crous PW (2010) Re-evaluation of *Cryptosporiopsis eucalypti* and Cryptosporiopsis-like species occurring on *Eucalyptus* leaves. Fungal Divers 44(1):89–105

Chen J, Parra LA, Kesel AD, Khalid AN, Qasim T, Ashraf A, Bahkali AH, Hyde KD, Zhao RL, Callac P (2016) Inter- and intraspecific diversity in *Agaricus endoxanthus* and allied species reveals a new taxon, *A. punjabensis*. Phytotaxa 252(1):1–16

Chethana KWT, Zhou Y, Zhang W, Liu M, Xing QK, Hyde KD, Yan JY, Li XH (2017) *Coniella vitis* sp. nov. is the common pathogen of white rot in Chinese vineyards. Plant Dis 101:2123–2136

Chou WN, Wang YZ (2005) Nine Species of *Russula* (Basidiomycotina) New to Taiwan. Taiwania 50(2):93–100

Cibula WG, Weber NS (1996) *Hygrocybe andersonii* a new psammophilus *Hygrocybe* from Horn Island, a Mississippi barrier island. Mycologia 88:514–516

Clements FE, Shear CL (1931) Genera of fungi, 2 vol. H.W. Wilson, New York, pp i–vii

Cochrane G, Karsch-Mizrachi I, Nakamura Y (2011) The international nucleotide sequence database collaboration. Nucleic Acids Res 39:D15–D18

Cochrane G, Karsch-Mizrachi I, Takagi T (2015) Sequence Database Collaboration IN. The international nucleotide sequence database collaboration. Nucleic Acids Res 44(D1):D48–D50

Cooke WB (1953) The genera of Homobasidiomycetes (exclusive of the Gasteromycetes). USDA:1–100

Corner EJH (1950) A monograph of *Clavaria* and allied genera. Oxford University Press, London

Corner EJH (1970) Supplement to "A monograph of *Clavaria* and allied genera". Beih Nova Hedwig 33:1–299

Corner EJH, Bas C (1962) The genus *Amanita* in Singapore and Malaya. Persoonia 2:241–304

Corner EJ, Thind KS, Dev S (1958) The *Clavariaceae* of the Mussoorie Hills (India). IX. Trans Br Mycol Soc 41(2):203–206

Crous PW, Braun U, Groenewald JZ (2007a) *Mycosphaerella* is polyphyletic. Stud Mycol 58:1–32

Crous PW, Schubert K, Braun U, De Hoog GS, Hocking AD, Shin HD, Groenewald JZ (2007b) Opportunistic, human-pathogenic species in the *Herpotrichiellaceae* are phenotypically similar to saprobic or phytopathogenic species in the *Venturiaceae*. Stud Mycol 58:185–217

Crous PW, Summerell BA, Shivas RG, Burgess TI, Decock CA, Dreyer LL, Granke LL, Guest DI, Hardy GS, Hausbeck MK, Hüberli D, Jung T, Koukol O, Lennox CL, Liew ECY, Lombard L, McTaggart AR, Pryke JS, Roets F, Saude C, Shuttleworth LA, Stukely MJC, Vánky K, Webster BJ, Windstam ST, Groenewald JZ (2012) Fungal Planet description sheets: 107–127. Persoonia 28:138–182

Crous PW, Giraldo A, Hawksworth DL, Vincent R, Paul K, Josep G, Barbara R, Conrad S, Ulrike D, Thippawan T, Johannes G (2014a) The genera of fungi: fixing the application of type species of generic names. IMA Fungus 5:141–160

Crous PW, Wingfield MJ, Schumacher RK, Summerell BA, Giraldo A, Gené J, Guarro J, Wanasinghe DN, Hyde KD, Camporesi E, Garethjones EB, Thambugala KM, Malysheva EF, Malysheva VF, Acharya K, Álvarez J, Alvarado P, Assefa A, Barnes CW, Bartlett JS, Blanchette RA, Burgess TI, Carlavilla JR, Coetzee MPA, Damm U, Decock CA, Denbreeÿen A, Devries B, Dutta AK, Holdom DG, Rooney-Latham S, Manjón JL, Marincowitz S, Mirabolfathy M, Moreno G, Nakashima C, Papizadeh M, Shahzadehfazeli SA, Amoozegar MA, Romberg MK, Shivas RG, Stalpers JA, Stielow B, Stukely MJC, Swart WJ, Tan YP, Vanderbank M, Wood AR, Zhang Y, Groenewald JZ (2014b) Fungal Planet description sheets: 281–319. Persoonia 33:212–289

Crous PW, Carris LM, Giraldo A, Groenewald JZ, Hawksworth DL, Hernández-Restrepo M, Jaklitsch WM, Lebrun MH, Schumacher RK, Stielow JB, Van der Linde EJ (2015a) The genera of fungi-fixing the application of the type species of generic names—G 2: *Allantophomopsis*, *Latorua*, *Macrodiplodiopsis*, *Macrohilum*, *Milospium*, *Protostegia*, *Pyricularia*, *Robillarda*, *Rotula*, *Septoriella*, *Torula,* and *Wojnowicia*. IMA Fungus 6(1):163–198

Crous PW, Wingfield MJ, Guarro J, Hernández-Restrepo M, Sutton DA, Acharya K, Barber PA, Boekhout T, Dimitrov RA, Duenas M, Dutta AK (2015b) Fungal planet description sheets: 320–370. Persoonia 34:167–266

Crous PW, Wingfield MJ, Burgess TI, Hardy GSJ, Crane C, Barrett S, Cano-Lira JF, Le Roux JJ, Thangavel R, Guarro J, Stchigel AM, Martín MP, Alfredo DS, Barber PA, Barreto RW, Baseia IG, Cano-Canals J, Cheewangkoon R, Ferreira RJ, Gené J, Lechat C, Moreno G, Roets F, Shivas RG, Sousa JO, Tan YP, Wiederhold NP, Abell SE, Accioly T, Albizu JL, Alves JL, Antoniolli ZI, Aplin N, Araújo J, Arzanlou M, Bezerra JDP, Bouchara JP, Carlavilla JR, Castillo A, Castroagudín VL, P.C. Ceresini PC, Claridge GF, Coelho G, Coimbra VRM, Costa LA, da Cunha KC, Silva SS, Daniel R, de Beer ZW, Dueñas M, Edwards J, Enwistle P, Fiuza PO, Fournier J, García D, Gibertoni TB, Giraud S, Guevara-Suarez M, Gusmão LFP, Haituk S, Heykoop M, Hirooka Y, Hofmann TA, Houbraken J, Hughes DP, Kautmanová I, Koppel O, Koukol O, Larsson E, Latha KPD, Lee DH, Lisboa DO, Lisboa WS, López-Villalba Á, Maciel JLN, Manimohan P, Manjón JL, Marincowitz S, Marney TS, Meijer M, Miller AN, Olariaga I, Paiva LM, Piepenbring M, Poveda-Molero JC, Raj KNA, Raja HA, Rougeron A, Salcedo I, Samadi R, Santos TAB, Scarlett K, Seifert KA, Shuttleworth LA, Silva GA, Silva M, Siqueira JPZ, Souza-Motta CM, Stephenson SL, Sutton DA, Tamakeaw N, Telleria MT, Valenzuela-Lopez N, Viljoen A, Visagie CM, Vizzini A, Wartchow F, Wingfield BD, Yurchenko E, Zamora JC, Groenewald JZ (2016a) Fungal Planet description sheets: 469–557 Persoonia 37:218–403

Crous PW, Wingfield MJ, Richardson DM, Le Roux JJ, Strasberg D, Edwards J, Roets F, Hubka V, Taylor PWJ, Heykoop M, Martín MP, Moreno G, Sutton DA, Wiederhold NP, Barnes CW, Carlavilla JR, Gené J, Giraldo A, Guarnaccia V, Guarro J, Hernández-Restrepo M, Kolařík M, Manjón JL, Pascoe IG, Popov ES, Sandoval-Denis M, Woudenberg JHC, Acharya K, Alexandrova AV, Alvarado P, Barbosa RN, Baseia IG, Blanchette RA, Boekhout T, Burgess TI, Cano-Lira JF, Čmoková A, Dimitrov RA, Dyakov MY, Dueñas M, Dutta AK, Esteve-Raventós F, Fedosova AG, Fournier J, Gamboa P, Gouliamova DE, Grebenc T, Groenewald M, Hanse B, Hardy GESJ, Held BW, Jurjević Ž, Kaewgrajang T, Latha KPD, Lombard L, Luangsa-ard JJ, Lysková P, Mallátová N, Manimohan P, Miller AN, Mirabolfathy M, Morozova OV, Obodai M, Oliveira NT, Ordóñez ME, Otto EC, Paloi S, Peterson SW, Phosri C, Roux J, Salazar WA, Sánchez A, Sarria GA, Shin HD, Silva BDB, Silva GA, Smith MT, Souza-Motta CM, Stchigel AM, Stoilova-Disheva MM, Sulzbacher MA, Telleria MT, Toapanta C, Traba JM, Valenzuela-Lopez N, Watling R, Groenewald JZ (2016b) Fungal Planet description sheets: 400–468. Persoonia 36:316–458

Crous PW, Wingfield MJ, Burgess TI, Hardy GEStJ, Barber PA, Alvarado P, Barnes CW, Buchanan PK, Heykoop M, Moreno G (2017) Fungal Planet description sheets: 558–624. Persoonia 38:240–384

Crous PW, Schumacher RK, Wingfield MJ, Akulov A, Denman S, Roux J, Braun U, Burgess TI, Carnegie AJ, Váczy KZ, Guatimosim E (2018) New and interesting FUNGI. 1. FUSE 1(1):169–215

Cui YY, Cai Q, Tang LP, Yang ZL, Liu JW (2018) The family *Amanitaceae*: molecular phylogeny, higher-rank taxonomy and the species in China. Fungal Divers 91:5–230

Dai LD, He SH (2016) New species and new records of *Aleurodiscus s.l.* (Basidiomycota) in China. Mycol Prog 15:717–730

Dai DQ, Phookamsak R, Wijayawardene NN, Li WJ, Bhat DJ, Xu JC, Taylor JE, Hyde KD, Chukeatirote E (2017a) Bambusicolous fungi. Fungal Divers 82:1–105

Dai LD, Wu SH, Karen N, Burdsall HH Jr, He SH (2017b) Two new species of *Aleurodiscus s.l.* (*Russulales*, Basidiomycota) on bamboo from tropics. Mycoscience 58:213–220

Dai LD, Zhao Y, Wu SH (2017c) Three new species of *Aleurodiscus s.l.* (*Russulales*, Basidiomycota) on bamboos from East Asia. Cryptogam Mycol 38:227–239

Damm U, Fourie PH, Crous PW (2010) *Coniochaeta* (Lecythophora), *Collophora* gen. nov. and *Phaeomoniella* species associated with wood necroses of *Prunus* trees. Persoonia 24:60–80

Daranagama DA, Hyde KD, Sir EB, Thambugala KM, Tian Q, Samarakoon MC, McKenzie EHC, Jayasiri SC, Tibpromma S, Bhat JD, Liu XZ, Stadler M, Liu X (2018) Towards a natural classification and backbone tree for *Graphostromataceae*, *Hypoxylaceae*, *Lopadostomataceae* and *Xylariaceae*. Fungal Divers 88:1–65

Das K (2013) *Lactarius fennoscandicus* (*Russulaceae*) A new record for India. Nelumbo 55:214–218

Das K, Sharma JR (2005) *Russulaceae* of Kumaon Himalaya. Botanical Survey of India, Kolkata, p 255

Das K, Verbeken A (2011) Three new species of *Lactarius* (*Russulaceae*) from Sikkim, India. Cryptogam Mycol 32(4):365–381

Das K, Miller SL, Sharma JR (2006a) *Russula* in Himalaya 2: four new taxa. Mycotaxon 95:205–215

Das K, Sharma JR, Atri NS (2006b) *Russula* in Himalaya 3: a new species of subgenus Ingratula. Mycotaxon 95:271–275

Das K, Van de Putte K, Buyck B (2010) New or interesting *Russula* from Sikkim Himalaya (India). Cryptogam Mycol 31(4):373–387

Das K, Atri NS, Buyck B (2013) Three new species of *Russula* (*Russulales*) from India. Mycosphere 4(4):707–717

Das K, Dowie NJ, Li GJ, Miller SL (2014) Two new species of *Russula* (Russulales) from India. Mycosphere 5(5):612–622

Das K, Verbeken A, Nuytinck J (2015) Morphology and phylogeny of four new *Lactarius* species from Himalayan India. Mycotaxon 130:105–130

Das K, Ghosh A, Bhatt RP, Chakraborty D, Hofstetter V, Buyck B (2017a) Fungal biodiversity profiles 41–50. Cryptogam Mycol 38(4):527–547

Das K, Ghosh A, Chakraborty D, Li J, Qiu L, Baghela A, Halama M, Hembrom ME, Mehmood T, Parihar A, Pencakowski B, Bielecka M, Reczynska K, Sasiela D, Singh U, Song Y, Swierkosz K, Szczesniak K, Uniyal P, Zhang J, Buyck B (2017b) Fungal biodiversity profiles 31–40. Cryptogam Mycol 38(3):1–56

Dayarathne MC, Phookamsak R, Ariyawansa HA, Jones EBG, Camporesi E and Hyde KD (2015) Phylogenetic and morphological appraisal of *Leptosphaeria italica* sp. nov. (*Leptosphaeriaceae*, *Pleosporales*) from Italy. Mycosphere 6(5): 634–642

Dayarathne MC, Maharachchikumbura SSN, Jones EBG, Goonasekara ID, Bulgakov TS, Al-Sadi AM, Hyde KD, Lumyong S, McKenzie EHC (2017) *Neophyllachora* gen nov. (*Phyllachorales*), three new species of *Phyllachora* from *Poaceae* and resurrection of *Polystigmataceae* (*Xylariales*). Mycosphere 8(10):1598– 1625

Dayarathne MC, Wanasinghe DN, Jones EG, Chomnunti P, Hyde KD (2018) A novel marine genus, *Halobyssothecium* (*Lentitheciaceae*) and epitypification of *Halobyssothecium obiones* comb. nov. Mycol Prog 17(10):1161–1171

De Almeida DAC, Gusmão LFP, Miller AN (2016) Taxonomy and molecular phylogeny of *Diatrypaceae* (Ascomycota, *Xylariales*) species from the Brazilian semi-arid region, including four new species. Mycol Prog 15:1–27

De Crop E, Nuytinck J, Van de Putte K, Wisitrassameewong K, Hackel J, Stubbe D, Hyde KD, Roy M, Halling RE, Moreau PA, Eberhardt E, Verbeken A (2017) A multi-gene phylogeny of *Lactifluus* (Basidiomycota, *Russulales*) translated into a new infrageneric classification of the genus. Persoonia 38:58–80

De Gruyter JD, Woudenberg JHC, Aveskamp AA, Verkley GJM, Groenewald JZ, Crous PW (2013) Redisposition of phoma-like anamorphs in *Pleosporales*. Stud Mycol 75:1–36

De Koker TH, Nakasone KK, Haarhof J, Burdsall HH Jr, Janse BJ (2003) Phylogenetic relationships of the genus *Phanerochaete* inferred from the internal transcribed spacer region. Mycol Res 107:1032–1040

De Notaris G (1844) Osservazione su alcuni generi e specie della tribu dei Pirenomiceti sferiacei. G Bot Ital 2:38–55

De Souza PM, Bittencourt MLA, Caprara CC, Freitas M, Almeida RPC, Silveira D, Fonseca YM, Ferreira Filho EX, Pessoa Junior A, Magalhães PO (2015) A biotechnology perspective of fungal proteases. Braz J Microbiol 46:337–346

Dennis RWG (1949) A revision of the British *Hyaloscyphaceae*, with notes on related European species. Mycol Papers 32:1–97

Desjardin DE, Retnowati A, Horak E (2000) *Agaricales* of Indonesia: 2. A preliminary monograph of *Marasmius* from Java and Bali. Sydowia 52:92–193

Devadatha B, Sarma VV, Jeewon R, Wanasinghe DN, Hyde KD, Jones EG (2018) *Thyridariella*, a novel marine fungal genus from India: morphological characterization and phylogeny inferred from multigene DNA sequence analyses. Mycol Prog 17(7):791–804

Dharne CG (1965) Taxonomic investigations on the discomycetous genus Lachnellula Karst. Phytopathol Z 53(2):101–144

Dissanayake AJ, Phillips AJL, Li XH, Hyde KD (2016) *Botryosphaeriaceae*: current status of genera and species. Mycosphere 7(7):1001–1073

Dissanayake AJ, Camporesi E, Hyde KD, Yan JY, Li XH (2017) Saprobic *Botryosphaeriaceae*, including *Dothiorella italica* sp nov., associated with urban and forest trees in Italy. Mycosphere 8(2):1157–1176

Doilom M, Shuttleworth LA, Roux J, Chukeatirote E, Hyde KD (2015) *Botryosphaeriaceae* associated with *Tectona grandis* (teak) in Northern Thailand. Phytotaxa 233(1):1–26

Doilom M, Dissanayake AJ, Wanasinghe DN, Boonmee S, Liu JK, Bhat DJ, Taylor JE, Bahkali AH, McKenzie EHC, Hyde KD (2017) Microfungi on *Tectona grandis* (teak) in Northern Thailand. Fungal Divers 82:107–182

Donk MA (1933) Revis. niederl. Homob.-Aph. 2. Proefschr., Utrecht (& Meded. bot. Mus. Herb. Utrecht No. 9, & Meded. Nederl. mycol. Ver. 22)

Donk MA (1957) The generic names proposed for Hymenomycetes–VII. “*Thelephoraceae*” (conclusion). Taxon 6:106–123

Donk MA (1961) Four new families of Hymenomycetes. Persoonia 1(4):405–407

Donk MA (1962) Notes on resupinate Hymenomycetes–VI. Persoonia 2:217–238

Douanla-Meli C (2007) Fungi of Cameroon. Ecological diversity with emphasis on the taxonomy of non-gilled Hymenomycetes from Mbalmayo forest reserve. Biblioth Mycol 202:1–410

Drinkwater LE, Schipanski M, Snapp S, Jackson LE (2017) Ecologically based nutrient management. In: Agricultural systems, 2nd edn. Elsevier, Amsterdam, pp 203–257

Du Z, Hyde KD, Yang Q, Liang YM, Tian CM (2017) *Melansporellaceae*: a novel family of *Diaporthales* (Ascomycota). Phytotaxa 305(3):191–200

Duhem B, Buyck B (2007) Edible mushrooms from Madagascar 2. *Clavulina albiramea* comb. nov. (Cantharellales), an edible clavarioid fungus shared between African miombo and Malagasy Uapaca woodland. Nova Hedwig 85:317–330

Dumortier BC (1829) Analyse des familles des plantes, avec l’indication des principaux genres qui s’y rattachent. J. Casterman, Tornay

Dutta AK, Chandra S, Pradhan P, Acharya K (2014) A new species of *Marasmius* sect. *Sicci* from India. Mycotaxon 128:117–125

Ehrenberg CG (1818) Sylvae Mycologicae Berolinenses. Formis Theophili Bruschcke, Berlin **(In Latin)**

Ekanayaka AH, Hyde KD, Jones EBG, Zhao Q (2018) Taxonomy and phylogeny of operculate discomycetes: Pezizomycetes. Fungal Divers 90(1):161–243

Ellis MB (1971) Dematiaceous hyphomycetes. Key Surrey, England

Ellis MB (1976) More dematiaceous hyphomycetes. Key Surrey, England

Eriksson OE (1981) The families of bitunicate ascomycetes. Opera Bot 60:1–220

Eriksson OE (2001) Outline of Ascomycota. Myconet 6:1–27

Eriksson OE, Hawksworth DL (1993) Notes on ascomycete systematics—Nos 1418–1529. Syst Ascom 11:163–194

Eriksson J, Hjortstam K, Ryvarden L (1978a) The *Corticiaceae* of North Europe, vol 5. *Mycoaciella—Phanerochaete*. Fungiflora, Oslo

Eriksson J, Weresub LK, Burdsall HH (1978b) *Phanerochaete* vs *Grandiniella* (Corticiaceae, *Aphyllophorales*). Taxon 27:51–52

Farook VA, Manimohan P (2015) *Marasmius odoratus*—a new jasmine-scented species of *Marasmius* section *Globulares* from India. Phytotaxa 227(3):275–281

Farr DF, Rossman AY (2018) Fungal databases. U.S. National Fungus Collections, ARS, USDA. https://nt.ars-grin.gov/fungaldatabases/. Retrieved May–Nov 2018

Fatto RM (1998) A study of selected Murrill's Russulas. Mycotaxon 69:487–502

Feng PY, de Hoog GS, Najafzadeh MJ, van den Ende AG, Stielow JB, Badali H, Boeger WA, Vicente VA (2014) *Cladophialophora abundans*, a novel species of *Chaetothyriales* isolated from the natural environment. Mycol prog 13(2):381–391

Ferdman Y, Aviram S, Roth-Bejerano N, Trappe JM, Kagan-Zur V (2005) Phylogenetic studies of *Terfezia pfeilii* and *Choiromyces echinulatus* (*Pezizales*) support new genera for southern African truffles: Kalaharituber and Eremiomyces. Myol Res 109(2):237–245

Finlay RD (2008) Ecological aspects of mycorrhizal symbiosis: with special emphasis on the functional diversity of interactions involving the extraradical mycelium. J Exp Bot 59(5):1115–1126

Firmino AL, Pereira OL (2014) *Lembosia bezerrae*, a new asterinaceous fungus associated with a terrestrial orchid from Bahia, Brazil. Mycotaxon 127:199–205

Fischer E (1897) *Plectacineae*. In: Engler A, Prantl K (eds) Die natürlichen Pflanzenfamilien, vol I. Engelmann, Leipzig

Floudas D, Hibbett DS (2015) Revisiting the taxonomy of *Phanerochaete* (*Polyporales*, Basidiomycota) using a four gene dataset and extensive ITS sampling. Fungal Biol 119:679–719

Fresenius G (1850) Beiträge zur Mykologie 1:1–38

Friebes G (2012) A key to the non-lichenicolous species of the genus *Capronia* (*Herpotrichiellaceae*). Ascomycete.org 4(3):55–64

Fries EM (1825) as 'Cytisporei'. Syst. orb. veg. (Lundae) 1:118

Frisvad JC, Samson RA (2004) Polyphasic taxonomy of *Penicillium* subgenus *Penicillium*. A guide to identification of food and air-borne terverticillate Penicillia and their mycotoxins. Stud Mycol 49:1–174

Galli R (1996) Le Russule. Edinatura, Milano

Gao L, Ma Y, Zhao W, Wei Z, Gleason ML, Chen H, Hao L, Sun G, Zhang R (2015) Three new species of *Cyphellophora* (*Chaetothyriales*) associated with sooty blotch and flyspeck. PLoS ONE 10(9):e0136857

Geiser DM, LoBuglio KF, Gueidan C (2015) 5. Pezizomycotina: Eurotiomycetes. In: Systematics and evolution. Springer, Berlin, pp 121–141

Ghimire SR, Hyde KD (2008) Fungal endophytes. In: Plant surface microbiology. Springer, Berlin, pp 281–292

Ghobad-Nejhad M, Liu SL, Langer E, Dai YC (2015) Molecular and morphological evidence reveal a new species in the core *Phanerochaete* clade (*Polyporales*). Mycol Prog 14:1–7

Ghosh A, Das K (2017) *Russula* (*Russulaceae*) in western Himalaya 1: two new species from subg. *Russula*. Phytotaxa 323(3):237–252

Ghosh A, Das K, Adhikari S, Bhatt RP (2016) A novel species of *Russula* (*Russulaceae*) from Indian Himalaya. Mycosphere 7(6):778–785

Ghosh A, Das K, Bhatt RP (2017) *Russula sarnarii* sp. nov. (*Russulaceae*, Basidiomycota) from Indian Himalaya. Curr Res Environ Appl Mycol J 7(1):64–72

Gierczyk B, Kujawa A, Pachlewski T, Szczepkowski A, Wójtowski M (2011) Rare species of the genus *Coprinus* Pers. *s. lato*. Acta Mycol 46(1):27–73

Gilbert EJ (1940) Amanitaceae. Icon Mycol 27:1–199

Glass NL, Donaldson GC (1995) Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. Appl Environ Microbiol 61(4):1323–1330

Glez-Peña D, Gòmez-Blanco D, Reboiro-Jato M, Fdez-Riverola F, Posada D (2010) ALTER: program-oriented conversion of DNA and protein alignments. Nucleic Acids Res 38:W14–W18

Gnavi G, Garzoli L, Poli A, Prigione V, Burgaud G, Varese GC (2017) The culturable mycobiota of *Flabellia petiolata*: first survey of marine fungi associated to a Mediterranean green alga. PLoS ONE 12(4):e0175941

Goh TK, Ho WH, Hyde KD, Whitton SR, Umali TE (1998) New records and species of *Canalisporium* (Hyphomycetes), with a revision of the genus. Can J Bot 76:142–152

Gomes RR, Glienke C, Videira CIR, Lombard L, Groenewald JZ, Crous PW (2013) *Diaporthe*: a genus of endophytic, saprobic and plant pathogenic fungi. Persoonia 31:1–41

Goos RD (1985) The anamorph genus *Zalerion*. Mycotaxon 23:445–449

Greslebin AL, Rajchenberg M (2003) Diversity of *Corticiaceae sens. lat*. in Patagonia, Southern Argentina. N Z J Bot 41:437–446

Griffith GW, Easton GL, Jones AW (2002) Ecology and diversity of waxcap (*Hygrocybe* spp.) fungi. Bot J Scotl 54:7–22

Grum-Grzhimaylo AA, Debets AJM, van Diepeningen AD, Georgieva ML, Bilanenko EN (2013) *Sodiomyces alkalinus*, a new holomorphic alkaliphilic ascomycete within the *Plectosphaerellaceae*. Persoonia 31:147–158

Guarro J, Cannon PF, van der Aa HA (1991) A synopsis of the genus *Zopfiella* (Ascomycetes, *Lasiosphaeriaceae*). Syst Ascom 10:79–112

Guatimosim E, Firmino AL, Bezerra JL, Pereira OL, Barreto RW, Crous PW (2015) Towards a phylogenetic reappraisal of *Parmulariaceae* and *Asterinaceae* (Dothideomycetes). Persoonia 35:230–241

Gueidan C, Aptroot A, da Silva Cáceres ME, Badali H, Stenroos S (2014) A reappraisal of orders and families within the subclass Chaetothyriomycetidae (Eurotiomycetes, Ascomycota). Mycol Prog 13(4):990. https://doi.org/10.1007/s11557-014-0990-2

Guindon S, Gascuel O (2003) A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. Syst Biol 52:696–704

Haelewaters D, Page RA, Pfister DH, Balboa P (2018) *Hyperparasites*: Morphological and molecular diversity of *Laboulbeniales* fungi associated with ectoparasitic bat flies (*Diptera: Nycteribiidae, Streblidae*). Studies of the laboulbeniomycetes: diversity, evolution, and patterns of speciation 179

Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp Ser 41:95–98

Hall BG (2004) Phylogenetic trees made easy: a how-to manual, 2nd edn. Sinauer Associates, Sunderland

Halling RE, Nuhn M, Fechner NA, Osmundson TW, Soytong K, Arora D, Hibbett DS, Binder M (2012) Sutorius: a new genus for *Boletus eximius*. Mycologia 104:951–961

Han JG, Hosoya T, Sung GH, Shin HD (2014) Phylogenetic reassessment of *Hyaloscyphaceae sensu lato* (*Helotiales*, Leotiomycetes) based on multigene analyses. Fungal Biol 118(2):150–167

Hansen K, Læssøe T, Pfister DH (2001) Phylogenetics of the *Pezizaceae*, with an emphasis on *Peziza*. Mycologia 93(5):958–990

Hansen K, Læssøe T, Pfister DH (2002) Phylogenetic diversity in the core group of *Peziza* inferred from ITS sequences and morphology. Mycol Res 106(8):879–902

Hansen K, LoBuglio KF, Pfister DH (2005) Evolutionary relationships of the cup-fungus genus *Peziza* and *Pezizaceae* inferred from multiple nuclear genes: RPB2, β-tubulin, and LSUrDNA. Mol Phylogenet Evol 36(1):1–23

Hansford CG (1946) The foliicolous Ascomycetes, their parasites and associated fungi. Mycol Pap 15:1–240

Hashimoto A, Matsumura M, Hirayama K, Tanaka K (2017) Revision of *Lophiotremataceae* (*Pleosporales*, Dothideomycetes): *Aquasubmersaceae*, *Cryptocoryneaceae*, and *Hermatomycetaceae* fam. nov. Persoonia 39(1):51–73

Hawksworth DL (1991) The fungal dimension of biodiversity: magnitude, significance, and conservation. Mycol Res 95(6):641–655

Hawksworth DL (2001) The magnitude of fungal diversity: the 1.5 million species estimate revisited. Mycol Res 105(12):1422–1432

Hawksworth DL, Lücking R (2017) Fungal diversity revisited: 2.2 to 3.8 million species. Microbiol Spectrum. https://doi.org/10.1128/microbiolspec.FUNK-0052-2016

Hawksworth DL, Kirk PM, Sutton BC, Pegler DN (1995) Ainsworth and Bisby 's dictionary of the fungi, 8th edn. CAB International, Wallingford

He G, Chen SL, Yan SZ (2016) Morphological and molecular evidence for a new species in *Clavulina* from southwestern China. Mycoscience 57:255–263

Heilmann-Clausen J, Verbeken A, Vesterholt J (1998) The genus *Lactarius*, vol 2—fungi of northern Europe. Svampetryk, Danish Mycological Society, Denmark

Henkel TW, Meszaros R, Aime MC, Kennedy A (2005) New *Clavulina* species from the Pakaraima Mountains of Guyana. Mycol Prog 4:343–350

Henkel TW, Aime MC, Uehling JK, Smith ME (2011) New species and distribution records of *Clavulina* (Cantharellales, Basidiomycota) from the Guyana Shield. Mycologia 103:883–894

Henkel TW, Obase K, Husbands D, Uehling JK, Bonito G, Aime MC, Smith ME (2016) New *Boletaceae* taxa from Guyana: *Binderoboletus segoi* gen. and sp. nov., *Guyanaporus albipodus* gen. and sp. nov., *Singerocomus rubriflavus* gen. and sp. nov., and a new combination for *Xerocomus inundabilis*. Mycologia 108:157–173

Hennebert GL (1968) New species of *Spirosphaera*. Trans Br Mycol SOC 51:13–24

Hernandez-Restrepo M, Schumacher RK, Wingfield MJ, Ishtiaq A, Cai L, Duong TA, Edwards J, Gene J, Groenewald JZ, Sana J, Khalid AN (2016) FUSE: FUSE 2. Sydowia 68:193–230

Hesler LR (1960) A study of *Russula* types. Memoirs of the Torrey Botanical Club 21(2):1–59

Hibbett DS, Bauer R, Binder M, Giachini AJ, Hosaka K, Justo A, Larsson E, Larsson KH, Lawrey JD, Miettinen O, Nagy LG, Nilsson RH, Weiss M, Thorn RG (2014) 14 Agaricomycetes. In: McLaughlin D., Spatafora J. (eds) Systematics and evolution. The Mycota (A comprehensive treatise on fungi as experimental systems for basic and applied research), vol 7A. Springer, Berlin, pp 373–429

Hirayama K, Hashimoto A, Tanaka K (2014) A new species, *Lophiostoma versicolor*, from Japan (*Pleosporales*, Dothideomycetes). Mycosphere 5(3):411–417

Hirayama K, Tanaka K (2011) Taxonomic revision of *Lophiostoma* and *Lophiotrema* based on reevaluation of morphological characters and molecular analyses. Mycoscience 52:401–412

Hjortstam K, Ryvarden L (2007) Checklist of corticioid fungi (Basidiomycotina) from the tropics, subtropics and the southern hemisphere. Syn Fung 22:27–146

Hjortstam K, Roberts P, Spooner B (2009) Corticoid fungi from the Kimberley Region, Western Australia. Kew Bull 64:353–368

Holmskjold T (1790) Beata ruris otia fungis danicis, vol. 1. Copenhagen, Denmark

Honan AH, Desjardin DE, Perry BA, Horak E, Baroni TJ (2015) Towards a better understanding of *Tetrapyrgos* (Basidiomycota, *Agaricales*): new species, type studies, and phylogenetic inferences. Phytotaxa 231(2):101–132

Hong SB, Cho HS, Shin HD, Frisvad JC, Samson RA (2006) Novel *Neosartorya* species isolated from soil in Korea. Int J Syst Evol Microbiol 56:477–486

Hongsanan S, Hyde KD (2017) Phylogenetic placement of *Micropeltidaceae*. Mycosphere 8(10):1930–1942

Hongsanan S, Li YM, Liu JK, Hofmann T, Piepenbring M, Bhat JD, Boonmee S, Doilom M, Singtripop C, Tian Q, Mapook A (2014) Revision of genera in *Asterinales*. Fungal divers 68(1):1–68

Hongsanan S, Hyde KD, Bahkali AH, Camporesi E, Chomnunti P, Ekanayaka H, Gomes AAM, Hofstetter V, Jones EBG, Pinho DB, Pereira OL, Tian Q, Wanasinghe DN, Xu JC, Buyck B (2015) Fungal biodiversity profiles 11–20. Cryptogam Mycol 36(3):355–380

Hongsanan S, Sánchez-Ramírez S, Crous PW, Ariyawansa HA, Zhao RL, Hyde KD (2016) The evolution of fungal epiphytes. Mycosphere 7(11):1690–1712

Hongsanan S, Maharachchikumbura SS, Hyde KD, Samarakoon MC, Jeewon R, Zhao Q, Al-Sadi AM, Bahkali AH (2017) An updated phylogeny of *Sordariomycetes* based on phylogenetic and molecular clock evidence. Fungal Divers 84(1):25–41

Horne WT (1905) A new species of *Lembosia*. Bull Torrey Bot Club 32:69–71

Horwath WR (2017) The role of the soil microbial biomass in cycling nutrients. A Paradigm Shift in Terrestrial Biogeochemistry, In Microbial Biomass, pp 41–66

Hosagoudar VB, Archana GR, Dan M (2009) *Maheshwaramyces*, a new genus of the family *Lembosiaceae*. Indian J Sci Technol 2:12–13

Hosen MI, Feng B, Wu G, Zhu XT, Li YC, Yang ZL (2013) *Borofutus*, a new genus of *Boletaceae* from tropical Asia: phylogeny, morphology and taxonomy. Fungal Divers 58:215–226

Hosen MI, Li TH, Aminuzzaman FM, Islam MR (2016) *Hygrocybe umbilicata* sp. nov., with first generic report for Bangladesh and its phylogenetic placement. Phytotaxa 280:70–76

Hosoya T, Sasagawa R, Hosaka K, Sung GH, Hirayama Y, Yamaguchi K, Toyama K, Kakishima M (2010) Molecular phylogenetic studies of *Lachnum* and its allies based on the Japanese material. Mycoscience 51(3):170–181

Houbraken J, Samson RA (2011) Phylogeny of *Penicillium* and the segregation of *Trichocomaceae* into three families. Stud Mycol 70:1–51

Houbraken J, Frisvad JC, Samson RA (2011) Taxonomy of *Penicillium* section *Citrina*. Stud Mycol 70:53–138

Huang S, Maharachchikumbura SSN, Jeewon R, Bhat DJ, Phookamsak R, Hyde KD, Al-Sadi AM, Kang J (2018) *Lecanicillium* *subprimulinum* (*Cordycipitaceae*, *Hypocreales*), a novel species from Baoshan, Yunnan. Phytotaxa 348(2):99–108

Huhndorf SM, Fernández FA (2005) Teleomorph-anamorph connections: *Chaetosphaeria raciborskii* and related species, and their Craspedodidymum-like anamorphs. Fungal Divers 19:23–49

Huhndorf SM, Miller AN, Fernández FA (2004) Molecular systematics of the *Sordariales*: the order and the family *Lasiosphaeriaceae* redefined. Mycologia 96(2):368–387

Hyde KD, Soytong K (2008) The fungal endophyte dilemma. Fungal Divers 33(163173):2

Hyde KD, Kang JC, Kong RYC (1996) Fungi from palms. XXX. Notes on *Amphisphaeria* species described from palms and a description of A. umbrina. Nova Hedwig 63:101–108

Hyde KD, Goh TK, Taylor JE, Fröhlich J (1999) *Byssosphaeria*, *Chaetosphaeria*, *Niesslia* and *Ornatispora* gen. nov., from palms. Mycol Res 103:1423–1439

Hyde KD, Bussaban B, Paulus B, Crous PW, Lee S, Mckenzie EH, Photita W, Lumyong S (2007) Diversity of saprobic microfungi. Biodivers Conserv 16(1):7–35

Hyde KD, Jones EBG, Liu JK, Ariyawansa HA, Boehm E, Boonmee S, Braun U, Chomnunti P, Crous PW, Dai DQ, Diederich P, Dissanayake A, Doilom M, Doveri F, Hongsanan S, Jayawardena R, Lawrey JD, Li YM, Liu YX, Lücking R, Monkai J, Muggia L, Nelsen MP, Pang KL, Phookamsak R, Senanayake IC, Shearer CA, Suetrong S, Tanaka K, Thambugala KM, Wijayawardene NN, Wikee S, Wu HX, Zhang Y, Aguirre-Hudson B, Alias SA, Aptroot A, Bahkali AH, Bezerra JL, Bhat DJ, Camporesi E, Chukeatirote E, Gueidan C, Hawksworth DL, Hirayama K, De Hoog S, Kang JC, Knudsen K, Li WJ, Li XH, Liu ZY, Mapook A, McKenzie EHC, Miller AN, Mortimer PE, Phillips AJL, Raja HA, Scheuer C, Schumm F, Taylor JE, Tian Q, Tibpromma S, Wanasinghe DN, Wang Y, Xu JC, Yacharoen S, Yan JY, Zhang M (2013) Families of Dothideomycetes. Fungal Divers 63:1–313

Hyde KD, Hongsanan S, Jeewon R, Bhat DJ, McKenzie EHC, Jones EBG, Phookamsak R, Ariyawansa HA, Boonmee S, Zhao Q, Abdel-Aziz FA, Abdel-Wahab MA, Banmai S, Chomnunti P, Cui BK, Daranagama DA, Das K, Dayarathne MC, de Silva NI, Dissanayake AJ, Doilom M, Ekanayaka AH, Gibertoni TB, Góes-Neto A, Huang SK, Jayasiri SC, Jayawardena RS, Konta S, Lee HB, Li WJ, Lin CG, Liu JK, Lu YZ, Luo ZL, Manawasinghe IS, Manimohan P, Mapook A, Niskanen T, Norphanphoun C, Papizadeh M, Perera RH, Phukhamsakda C, Richter C, de Santiago ALCMA, Drechsler-Santos ER, Senanayake IC, Tanaka K, Tennakoon TMDS, Thambugala KM, Tian Q, Tibpromma S, Thongbai B, Vizzini A, Wanasinghe DN, Wijayawardene NN, Wu HX, Yang J, Zeng XY, Zhang H, Zhang JF, Bulgakov TS, Camporesi E, Bahkali AH, Amoozegar AM, Araujo-Neta LS, Ammirati JF, Baghela A, Bhatt RP, Bojantchev S, Buyck B, da Silva GA, de Lima CLF, de Oliveira RJV, de Souza CAF, Dai YC, Dima B, Duong TT, Ercole E, Mafalda-Freire F, Ghosh A, Hashimoto A, Kamolhan S, Kang JC, Karunarathna SC, Kirk PM, Kytövuori I, Lantieri A, Liimatainen K, Liu ZY, Liu XZ, Lücking R, Medardi G, Mortimer PE, Nguyen TTT, Promputtha I, Raj KNA, Reck MA, Lumyong S, Shahzadeh-Fazeli SA, Stadler M, Soudi MR, Su HY, Takahashi T, Tangthirasunun N, Uniyal P, Wang Y, Wen TC, Xu JC, Zhang ZK, Zhao YC, Zhou JZ, Zhu L (2016) Fungal diversity notes 367–490: taxonomic and phylogenetic contributions to fungal taxa. Fungal Divers 80:1–270

Hyde KD, Norphanphoun C, Abreu VP, Bazzicalupo A, Chethana KWT, Clericuzio M, Dayarathne MC, Dissanayake AJ, Ekanayaka AH, He MQ, Hongsanan S, Huang SK, Jayasiri SC, Jayawardena RS, Karunarathna A, Konta S, Kušan I, Lee H, Li J, Lin CG, Liu NG, Lu YZ, Luo ZL, Manawasinghe IS, Mapook A, Perera RH, Phookamsak R, Phukhamsakda C, Siedlecki I, Soares AM, Tennakoon DS, Tian Q, Tibpromma S, Wanasinghe DN, Xiao YP, Yang J, Zeng XY, Abdel-Aziz FA, Li WJ, Senanayake IC, Shang QJ, Daranagama DA, De Silva NI, Thambugala KM, Abdel-Wahab MA, Bahkali AH, Berbee ML, Boonmee S, Bhat DJ, Bulgakov TS, Buyck B, Camporesi E, Castañeda-Ruiz RF, Chomnunti P, Doilom M, Dovana F, Gibertoni TB, Jadan M, Jeewon R, Jones GEB, Kang JC, Karunarathna SC, Lim YW, Liu JK, Liu ZY, Plautz HL Jr, Lumyong S, Maharachchikumbura SSN, Matočec N, Mckenzie EHC, Mešič A, Miller D, Pawłowska J, Pereira OL, Promputtha I, Romero AI, Ryvarden L, Su HY, Suetrong S, Tkalčec Z, Vizzini A, Wen TC, Wisitrassameewong K, Wrzosek M, Xu JC, Zhao Q, Zhao RL, Mortimer PE (2017) Fungal diversity notes 603–708: taxonomic and phylogenetic notes on genera and species. Fungal Divers 87:1–235

Hyde KD, Al-Hatmi AM, Andersen B, Boekhout T, Buzina W, Dawson TL, Eastwood DC, Jones EG, de Hoog S, Kang Y, Longcore JE (2018a) The world's ten most feared fungi. Fungal Divers 85:1–34

Hyde KD, Chaiwan N, Norphanphoun C, Boonmee S, Camporesi E, Chethana KWT, Dayarathne MC, de Silva NI, Dissanayake AJ, Ekanayaka AH, Hongsanan S, Huang SK, Jayasiri SC, Jayawardena RS, Jiang HB, Karunarathna A, Lin CG, Liu JK, Liu NG, Lu YZ, Luo ZL, Maharachchimbura SSN, Manawasinghe IS, Pem D, Perera RH, Phukhamsakda C, Samarakoon MC, Senwanna C, Shang Q, Tennakoon DS, Thambugala KM, Tibpromma S, Wanasinghe DN, Xiao YP, Yang J, Zeng XY, Zhang JF, Zhang SN, Bulgakov TS, Bhat DJ, Cheewangkoon R, Goh TK, Jones EBG, Kang JC, Jeewon R, Liu ZY, Lumyong S, Kuo CH, McKenzie EHC, Wen TC, Yan JY, Zhao Q (2018b) Mycosphere notes 169–224. Mycosphere 9:271–430

Index Fungorum (2019) Index Fungorum. http://www.indexfungorum.org/names/Names.asp

Inzenga G (1869) Funghi Siciliani. Centuria seconda. Stabilimento F. Lao, Palermo

Jaklitsch WM (2015) *Savoryellaceae* Jaklitsch & Réblová. Index Fungorum 209:1

Jaklitsch WM, Voglmayr H (2016) Hidden diversity in *Thyridaria* and a new circumscription of the *Thyridariaceae*. Stud Mycol 85:35–64

Jaklitsch WM, Baral HO, Lücking R, Lumbsch HT (2016a) Ascomycota. In: Frey W (ed) Syllabus of plant families-Adolf Engler's Syllabus der Pflanzenfamilien, 13th edn. Borntraeger, Stuttgart

Jaklitsch WM, Gardiennet A, Voglmayr H (2016b) Resolution of morphology-based taxonomic delusions: *Acrocordiella, Basiseptospora, Blogiascospora, Clypeosphaeria, Hymenopleella, Lepteutypa, Pseudapiospora, Requienella*, *Seiridium* and *Strickeria*. Persoonia 37:82–105

Jayasiri SC, Hyde KD, Jones EBG, McKenzie EHC, Jeewon R, Phillips AJL, Bhat DJ, Wanasinghe DN, Liu JK (Jack), Lu YZ, Kang JC, Xu JC, Karunarathna SC (2019) Diversity, morphology and molecular phylogeny of Dothideomycetes on decaying wild seed pods and fruits. Mycosphere 10(1):1–186

Jayawardena RS, Purahong W, Zhang W, Wubet T, Li X, Liu M, Zhao W, Hyde KD, Liu J, Yan J (2018) Biodiversity of fungi on *Vitis vinifera* L. revealed by traditional and high-resolution culture-independent approaches. Fungal Divers 90(1):1–84

Jayawardena RS, Hyde KD, Jeewon R, Ghobad-Nejhad M, Wanasinghe DN, Liu NG, Phillips AJL, Oliveira-Filho JRC, da Silva GA, Gibertoni TB, Abeywikrama P, Carris LM, Chethana KWT, Dissanayake AJ, Hongsanan S, Jayasiri SC, McTaggart AR, Perera RH, Phutthacharoen K, Savchenko KG, Shivas RG, Thongklang N, Dong W, Wei DP, Wijayawardena NN, Kang JC (2019) One stops shop II: taxonomic update with molecular phylogeny for important phytopathogenic genera: 26–50 (2019) Fungal Divers 94(1):41–129

Jeewon R, Hyde KD (2016) Establishing species boundaries and new taxa among fungi: recommendations to resolve taxonomic ambiguities. Mycosphere 7:1669–1677

Jeewon R, Yeung SY, Hyde KD (2009) A novel phylogenetic group within *Thozetella Chaetosphaeriaceae*): a new taxon based on morphology and DNA sequence analyses. Can J Microbiol 55(6):680–687

Jiang HB, Hyde KD, Jayawardena RS, Doilom M, Xu JC, Phookamsak R (2019) Taxonomic and phylogenetic characterizations reveal two new species and two new records of *Roussoella* (*Roussoellaceae*, *Pleosporales*) from Yunnan. China, Mycol Prog (proof)

Jones EBG, Suetrong S, Sakayaroj J, Bahkali AH, Abdel-Wahab MA, Boekhout T, Pang KL (2015) Classification of marine Ascomycota, Basidiomycota, Blastocladiomycota and Chytridiomycota. Fungal Divers 73:1–72

Jülich W (1981) Higher taxa of Basidiomycetes. Biblioth Mycol 85:1–185

Justo A, Miettinen O, Floudas D, Ortiz-Santana B, Sjökvist E, Lindner DL, Nakasone K, Niemelä T, Larsson KH, Ryvarden L, Hibbett DS (2017) A revised family-level classification of the the *Polyporales* (Basidiomycota). Fungal Biol 121(9):798–824

Kämmerer A, Besl H, Bresinsky A (1985) *Omphalotaceae* fam. nov. und *Paxillaceae*, ein chemotaxonomischer Vergleich zweier Pilzfamilien der *Boletales*. Plant Syst Evol 150:101–117

Karsten PA (1873) Mycologia fennica. Pars secunda. Pyrenomycetes. Bidrag till Kännedom av Finlands Natur och Folk 23:1–252

Karsten PA (1889) Kritsk öfvergit af Finlands Basidswampar (Basidiomycetes, Gastero- & Hymenomycetes). Bidr Känn Finl Nat Folk 48:1–470

Karsten PA (1890) Fragmenta mycologica XXIX. Hedwigia 29:147–149

Karunarathna SC, Chen J, Mortimer PE, Xu JC, Zhao RL, Callac P, Hyde KD (2016) Mycosphere Essay 8: a review of genus *Agaricus* in tropical and humid subtropical regions of Asia. Mycosphere 7(4):417–439

Karunarathna A, Papizadeh M, Senanayake IC, Jeewon R, Phookamsak R, Goonasekara ID, Wanasinghe DN, Wijayawardene NN, Amoozegar MA, Shahzadeh Fazeli SA, Camporesi E (2017) Novel fungal species of *Phaeosphaeriaceae* with an asexual/sexual morph connection. Mycosphere 8:1818–1834

Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol 30:772–780

Kelly KL, Judd DB (1976) COLOR. Universal language and dictionary of names. National Bureau of Standards, Special Publications 440

Kendrick B (2000) The fifth kingdom. Hackett Publishing, Indianapolis

Kepler R, Ban S, Nakagiri A, Bischoff J, Hywel-Jones N, Owensby CA, Spatafora JW (2013) The phylogenetic placement of hypocrealean insect pathogens in the genus *Polycephalomyces*: an application of One Fungus One Name. Fungal Biol 117:611–622

Kepler RM, Luangsa-Ard JJ, Hywel-Jones NL, Quandt CA, Sung GH, Rehner SA, Aime MC, Henkel TW, Sanjuan T, Zare R, Chen M, Li Z, Rossman AY, Spatafora JW, Shrestha B (2017) A phylogenetically-based nomenclature for *Cordycipitaceae* (*Hypocreales*). IMA Fungus 8(2):335–353

Kerrigan RW (2016) *Agaricus* of North America. Mem N Y Bot Gard 114:1–574

Khan ZU, Gené J, Ahmad S, Cano J, Al-Sweih N, Joseph L, Chandy R, Guarro J (2013) *Coniochaeta polymorpha*, a new species from endotracheal aspirate of a preterm neonate, and transfer of *Lecythophora* species to *Coniochaeta*. Antonie Van Leeuwenhoek 104(2):243–252

Kibby G (2014) The genus *Russula* in Great Britain: with synoptic keys to species. Published by the Author

Kibby G, Fatto RM (1990) Key to the species of *Russula* in northeastern North America, 3rd edn. Kibby-Fatto Enterprises, Somerville

Kirk PM (2017) Species Fungorum (version January 2016). In: Roskov Y, Abucay L, Orrell T, Nicolson D, Bailly N, Kirk PM, Bourgoin T, DeWalt RE, Decock W, De Wever A, Nieukerken E van, Zarucchi J, Penev L (eds) Species 2000 & ITIS Catalogue of Life, 30 June 2017. Digital Resource. www.catalogueoflife.org/col. Species 2000: Naturalis, Leiden. ISSN 2405-8858

Kirk PM (continuously updated) Index Fungorum. www.indexfungorum.org. Accessed 19 Apr 2018

Kirk PM, Cannon PF, Minter DW, Stalpers JA (2008) Ainsworth & Bisby's dictionary of the fungi, 10th edn. CABI, Wallingford

Knapp DG, Kovács GM, Zajta E, Groenewald JZ, Crous PW (2015) Dark septate endophytic pleosporalean genera from semiarid areas. Persoonia 35:87–100

Knudsen H, Borgen T (1982) *Russulaceae* in Greenland. In: G. Laursen & J.F. Ammirati (eds) Arct Alp Mycol 1:216–238

Knudsen H, Ruotsalainen J, Vauras J (2012) Russula Pers. In: Knudsen H, Vesterholt J (eds) Funga Nordica. Nordsvamp, Copenhagen, pp 144–186

Kobayasi Y (1939) On the Dacrymyces-group (Fungorum ordinis *Tremellalium* strudia monographica III). Sci Rep Tokyo Bunrika Daigaku Sect B 4:105–128

Kõljalg U, Nilsson RH, Abarenkov K, Tedersoo L, Taylor AF, Bahram M, Bates ST, Bruns TD, Bengtsson-Palme J, Callaghan TM, Douglas B, Drenkhan T, Eberhardt U, Dueñas M, Grebenc T, Griffith GW, Hartmann M, Kirk PM, Kohout P, Larsson E, Lindahl BD, Lücking R, Martín MP, Matheny PB, Nguyen NH, Niskanen T, Oja J, Peay KG, Peintner U, Peterson M, Põldmaa K, Saag L, Saar I, Schüßler A, Scott JA, Senés C, Smith ME, Suija A, Taylor DL, Telleria MT, Weiss M, Larsson K-H (2013) Towards a unified paradigm for sequence-based identification of Fungi. Mol Ecol 22:5271–5277

Komura DL, De Oliveira JJ, Moncalvo JM, Margaritescu S, Zartman CE (2016) *Marasmius calvocystidiatus* sp. nov. and *M. horridulus* (*Marasmiaceae*): characterization of two unusual species from central Amazonia. Phytotaxa 280(3):222–240

Kornerup A, Wanscher JH (1963) Methuen handbook of colour. Eyre Methuen Ltd., London

Kornerup A, Wanscher JH (1978) Methuen handbook of colour, 3rd edn. Eyre Methuen Ltd., London

Kraichak E, Huang JP, Nelsen M, Leavitt SD, Lumbsch HT (2018) A revised classification of orders and families in the two major subclasses of Lecanoromycetes (Ascomycota) based on a temporal approach. Bot J Linn Soc 188(3):233–249

Kränzlin F (2005) Fungi of Switzerland: *Russulaceae*, vol 6. Verlag Mycologia, Luzern, Switzerland

Krause C, Garnica S, Bauer R, Nebel M (2011) *Aneuraceae* (*Metzgeriales*) and tulasnelloid fungi (Basidiomycota): a model for early steps in fungal simbiosis. Fungal Biol 115:839–851

Krug JC, Jeng RS (1984) *Hapsidomyces*, a new genus of the *Pezizaceae* with ornamented ascospores. Mycologia 76(4):748–751

Kruys A, Huhndorf SM, Miller AN (2015) Coprophilous contributions to the phylogeny of *Lasiosphaeriaceae* and allied taxa within *Sordariales* (Ascomycota, Fungi). Fungal Divers 70:101–113

Kuhnert R, Oberkofler I, Peintner U (2012) Fungal growth and biomass development is boosted by plants in snow-covered soil. Microb Ecol 64(1):79–90

Kuhnert E, Fournier J, Persoh D, Luangsa-ard JJD, Stadler M (2014) New *Hypoxylon* species from Martinique and new evidence on the molecular phylogeny of *Hypoxylon* based on ITS rDNA and b-tubulin data. Fungal Divers 64:181–203

Kuhnert E, Surup F, Sir EB, Lambert C, Hyde KD, Hladki AI, Romero AI, Stadler M (2015) Lenormandins A–G, new azaphilones from *Hypoxylon lenormandii* and *Hypoxylon jaklitschii* sp. nov., recognised by chemotaxonomic data. Fungal Divers 71:165–184

Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Mol Biol Evol 33:1870–1874

Larget B, Simon DL (1999) Markov chain Monte Carlo algorithms for the Bayesian analysis of phylogenetic trees. Mol Biol Evol 16:750–759

Larsson KH (1994) Poroid species in *Trechispora* and use of calcium oxalate crystals for species identification. Mycol Res 98:1153–1172

Larsson A (2014) AliView: a fast and lightweight alignment viewer and editor for large datasets. Bioinformatics 30(22):3276–3278

Larsson KH (1995a) Taxonomy of *Trechispora farinacea* and proposed synonyms I. Species with grandinioid or hydnoid hymenophore. Symb Bot Upsal 30:101–118

Larsson KH (1995b) Taxonomy of *Trechispora farinacea* and proposed synonyms II. Species with smooth hymenophore. Nordic J Bot 16:73–82

Larsson KH (1996) New species and combinations in *Trechispora* (*Corticiaceae*, Basidiomycotina). Nordic J Bot 16:83–98

Larsson KH (2007) Re-thinking the classification of corticioid fungi. Mycol Res 111:1040–1063

Larsson E, Larsson KH (2003) Phylogenetic relationships of russuloid basidiomycetes with emphasis on aphyllophoralean taxa. Mycologia 95:1037–1065

Larsson KH, Larsson E, Kõljalg U (2004) High phylogenetic diversity among corticioid homobasidiomycetes. Mycol Res 108:983–1002

Le HT, Nuytinck J, Verbeken A, Saisamorn L, Desjardin DE (2007) *Lactarius* in Northern Thailand: 1. *Lactarius* subgenus *Piperites*. Fungal Divers 24:173–224

Leelavathy KM, Manimohan P, Arnolds EJM (2006) *Hygrocybe* in Kerala State, India. Persoonia 19:101–151

Lemke PA (1964a) The genus *Aleurodiscus* (*sensu stricto*) in North America. Can J Bot 42:213–282

Lemke PA (1964b) The genus *Aleurodiscus* (*sensu lato*) in North America. Can J Bot 42:723–768

Letourneau A, Seena S, Marvanová L, Bärlocher F (2010) Potential use of barcoding to identify aquatic hyphomycetes. Fungal Divers 40(1):51–64

Léveillé JH (1845) Champignons exotiques. Ann Sci Nat Bot 3:8–71

Li GJ, Li SF, Wen HA (2011) *Russula zhejiangensis* sp. nov. from East China. Cryptogam Mycol 32:127–133

Li GJ, Zhao Q, Zhao D, Yue SF, Li SF, Wen HA, Liu XZ (2013) *Russula atroaeruginea* and *R. sichuanensis* spp. nov. from southwest China. Mycotaxon 124:137–188

Li GJ, Zhao D, Li SF, Wen HA (2015) *Russula chiui* and *R. pseudopectinatoides*, two new species from southwestern China supported by morphological and molecular evidence. Mycol Prog 14:33

Li GJ, Hyde KD, Zhao RN, Hongsanan S, Abdel-Aziz FA, Abdel-Wahab MA, Alvarado P, Alves-Silva G, Ammirati JF, Ariyawansa HA, Baghela A, Bahkali AH, Beug M, Bhat DJ, Bojantchev D, Boonpratuang T, Bulgakov TS, Camporesi E, Boro MC, Ceska O, Chakraborty D, Chen JJ, Chethana KWT, Chomnunti P, Consiglio G, Cui BK, Dai DQ, Dai YC, Daranagama DA, Das K, Dayarathne MC, Crop ED, De Oliveira RJV, de Souza CAF, de Souza JI, Dentinger BTM, Dissanayake AJ, Doilom M, Drechsler-Santos ER, Ghobad-Nejhad M, Gilmore SP, Góes-Neto A, Gorczak M, Haitjema GH, Hapuarachchi KK, Hashimoto A, He MQ, Henske JK, Hirayama K, Iribarren MJ, Jayasiri SC, Jayawardena RS, Jeon SJ, Jerônimo GH, Jesus AL, Jones EBG, Kang JC, Karunarathna SC, Kirk PM, Konta S, Kuhnert E, Langer E, Lee HS, Lee HB, Li WJ, Li XH, Liimatainen K, Lima DX, Lin CG, Liu JK, Liu XZ, Liu ZY, Luangsa-ard JJ, Lücking R, Lumbsch HT, Lumyong S, Leaño EM, Marano AV, Matsumura M, McKenzie EHC, Mongkolsamrit S, Mortimer PE, Nguyen TTT, Niskanen T, Norphanphoun C, O'Malley MA, Parnmen S, Pawłowska J, Perera RH, Phookamsak R, Phukhamsakda C, Pires-Zottarelli CLA, Raspé O, Reck MA, Rocha SCO, de Santiago ALCMA, Senanayake IC, Setti L, Shang QJ, Singh SK, Sir EB, Solomon KV, Song J, Srikitikulchai P, Stadler M, Suetrong S, Takahashi H, Takahashi T, Tanaka K, Tang LP, Thambugala KM, Thanakitpipattana D, Theodorou MK, Thongbai B, Thummarukcharoen T, Tian Q, Tibpromma S, Verbeken A, Vizzini A, Vlasák J, Voigt K, Wanasinghe DN, Wang Y, Weerakoon G, Wen HA, Wen TC, Wijayawardene NN, Wongkanoun S, Wrzosek M, Xiao YP, Xu JC, Yan JY, Yang J, Yang SD, Hu Y, Zhang JF, Zhao J, Zhou LW, Peršoh D, Phillips AJL, Maharachchikumbura SSN (2016) Fungal Diversity notes 253–366: taxonomic and phylogenetic contributions to fungal taxa. Fungal Divers 78:1–237

Liberta AE (1966) On *Trechispora*. Taxon 15:317–319

Liberta AE (1973) The genus *Trechispora* (Basidiomycetes, *Corticiaceae*). Can J Bot 51:1871–1892

Liew EC, Aptroot A, Hyde KD (2000) Phylogenetic significance of the pseudoparaphyses in Loculoascomycete taxonomy. Mol Phylogenetics Evol 16(3):392–402

Link JHF (1809) Observationes in ordines plantarum naturales. Dissertatio I. Magazin der Gesellschaft Naturforschenden Freunde Berlin (in Latin) 3:3–42

Liu SL, He SH (2016) *Phanerochaete porostereoides*, a new species in the core clade with brown generative hyphae from China. Mycosphere 7:648–655

Liu YJ, Whelen S, Hall BD (1999) Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. Mol Biol Evol 16:1799–1808

Liu F, Hu DM, Cai L (2012a) *Canlarium duplumascospora* gen. et. sp nov and *Jobellisia guangdongensis* sp. nov. from freshwater habitats in China. Mycologia 104:1178–1186

Liu JK, Phookamsak R, Doilom M, Wikee S, Li YM, Ariyawansha H, Boonmee S, Chomnunti P, Dai DQ, Bhat JD, Romero AI (2012b) Towards a natural classification of *Botryosphaeriales*. Fungal Divers 57(1):149–210

Liu JK, Phookamsak R, Dai DQ, Tanaka K, Jones EBG, Xu JC, Chukeatirote E, Hyde KD (2014) *Roussoellaceae*, a new pleosporalean family to accommodate the genera *Neoroussoella* gen. nov., *Roussoella* and *Roussoellopsis*. Phytotaxa 181:1–33

Liu JK, Hyde KD, Jones EBG, Ariyawansa HA, Bhat DJ, Boonmee S, Maharachchikumbura SSN, McKenzie EHC, Phookamsak R, Phukhamsakda C, Shenoy BD, Abdel-Wahab MA, Buyck B, Chen J, Chethana KWT, Singtripop C, Dai DQ, Dai YC, Daranagama DA, Dissanayake AJ, Doilom M, D'souza MJ, Fan XL, Goonasekara ID, Hirayama K, Hongsanan S, Jayasiri SC, Jayawardena RS, Karunarathna SC, Li WJ, Mapook A, Norphanphoun C, Pang KL, Perera RH, Peršoh D, Pinruan U, Senanayake IC, Somrithipol S, Suetrong S, Tanaka K, Thambugala KM, Tian Q, Tibpromma S, Udayanga D, Wijayawardene NN, Wanasinghe DN, Wisitrassameewong K, Zeng XY, Abdel-Aziz FA, Adamčík S, Bahkali AH, Boonyuen N, Bulgakov T, Callac P, Chomnunti P, Greiner K, Hashimoto A, Hofstetter V, Kang JC, Lewis D, Li XH, Liu XZ, Liu ZY, Matsumura M, Mortimer PE, Rambold G, Randrianjohany E, Sato G, Sri-Indrasutdhi V, Tian CM, Verbeken A, von Brackel W, Wang Y, Wen TC, Xu JC, Yan JY, Zhao RL, Camporesi E (2015a) Fungal diversity notes 1–110: taxonomic and phylogenetic contributions to fungal species. Fungal Divers 72:1–197

Liu XY, Udayanga D, Luo ZL, Chen LJ, Zhou DQ, Su HY, Hyde KD (2015b) Backbone tree for *Chaetothyriales* with four new species of *Minimelanolocus* from aquatic habitats. Fungal Biol 119:1046–1062

Liu JK, Hyde KD, Jeewon R, Phillips AJ, Maharachchikumbura SS, Ryberg M, Liu ZY, Zhao Q (2017a) Ranking higher taxa using divergence times: a case study in Dothideomycetes. Fungal Divers 84(1):75–99

Liu N, Hongsanan S, Yang J, Bhat DJ, Liu J, Jumpathong J, Liu Z (2017b) *Periconia thailandica* (*Periconiaceae*), a new species from Thailand. Phytotaxa 323(3):253–263

Liu JK, Lu YZ, Cheewangkoon R, To-Anun C (2018) Phylogeny and morphology of *Helicotubeufia* gen. nov., with three new species in *Tubeufiaceae* from aquatic habitats. Mycosphere 9(3):495–509

Liyanage KK, Khan S, Brooks S, Mortimer PE, Karunarathna SC, Xu J, Hyde KD (2018) Morpho-molecular characterization of two *Ampelomyces* spp. (*Pleosporales*) strains mycoparasites of powdery mildew of *Hevea brasiliensis*. Front Microbiol 9:12

Locquin M (1984) Mycologie générale et structural 1–551

Lodge DJ, Ovrebo CL (2008) First records of *Hygrophoraceae* from Panama including a new species of *Camarophyllus* and a new veiled species in *Hygrocybe* section *Firmae*. Fungal Divers 32:69–80

Lodge DJ, Pegler DN (1990) *Hygrophoraceae* of the Luquillo Mountains of Puerto Rico. Mycol Res 94:443–456

Lodge DJ, Matheny PB, Cantrell SA, Moncalvo JM, Vilgalys R, Redhead S (2006) Delineating the *Hygrophoraceae*: character myths vs. gene trees (poster). Inoculum 57(4):27

Lodge DJ, Padamsee M, Matheny PB, Aime MC, Cantrell SA, Boertmann D, Kovalenko A, Vizzini A, Dentinger BTM, Kirk PM, Ainsworth AM, Moncalvo J-M, Vilgalys R, Larsson E, Lücking R, Griffith GW, Smith ME, Norvell LL, Desjardin DE, Redhead SA, Ovrebo CL, Lickey EB, Ercole E, Hughes KW, Courtecuisse R, Young A, Binder M, Minnis AM, Lindner DL, Ortiz-Santana B, Haight J, Læssøe T, Baroni TJ, Geml J, Hattori T (2014) Molecular phylogeny, morphology, pigment chemistry and ecology in *Hygrophoraceae* (*Agaricales*). Fungal Divers 64:1–99

Lofgren LA, LeBlanc NR, Certano AK, Nachtigall J, LaBine KM, Riddle J, Broz K, Dong Y, Bethan B, Kafer CW, Kistler HC (2018) *Fusarium graminearum*: pathogen or endophyte of North American grasses? New Phytol 217(3):1203–1212

Lowy B (1957) A new *Exidia*. Mycologia 49(6):899–902

Lowy B (1971) Tremellales. Flora Neotrop 6:1–153

Lowy B (1976) New Tremellales from Panama. Mycologia 68:1103–1108

Lu YZ, Boonmee S, Liu KJ, Hyde KD, McKenzie EH, Eungwanichayapant PD, Kang JC (2018a) Multi-gene phylogenetic analyses reveals *Neohelicosporium* gen. nov. and five new species of helicosporous hyphomycetes from aquatic habitats. Mycol Prog 17(5):631–646

Lu YZ, Liu JK, Hyde KD, Jeewon R, Kang JC, Fan C, Boonmee S, Bhat DJ, Luo ZL, Lin CG, Eungwanichayapant PD (2018b) A taxonomic reassessment of *Tubeufiales* based on multi-locus phylogeny and morphology. Fungal Divers 92(1):131–344

Lumbsch HT, Huhndorf SM (eds) (2007) Outline of Ascomycota–2007. Myconet 13:1–58

Lumbsch HT, Huhndorf SM (2010) Myconet Volume 14. Part One. Outline of Ascomycota—2009. Part Two. Notes on Ascomycete Systematics. Nos. 4751–5113. Fieldiana Life Earth Sci 1:1–64

Luo ZL, Hyde KD, Liu JK, Bhat DJ, Bao DF, Li WL, Su HY (2018) Lignicolous freshwater fungi from China II: novel *Distoseptispora* (*Distoseptisporaceae*) species from northwestern Yunnan Province and a suggested unified method for studying lignicolous freshwater fungi. Mycosphere 9(3):444–461

Luttrell ES (1951) Taxonomy of the Pyrenomycetes. Univ Mo Stud 24(3):1–120

Lutzoni F, Kauff F, Cox CJ, McLaughlin D, Celio G, Dentinger B, Padamsee M, Hibbett D, James TY, Baloch E, Grube M, Reeb V, Hofstetter V, Schoch C, Arnold AE, Miadlikowska J, Spatafora J, Johnson D, Hambleton S, Crockett M, Shoemaker R, Sung GH, Lücking R, Lumbsch T, O'Donnell K, Binder M, Diederich P, Ertz D, Gueidan C, Hansen K, Harris RC, Hosaka K, Lim YW, Matheny B, Nishida H, Pfister D, Rogers J, Rossman A, Schmitt I, Sipman H, Stone J, Sugiyama J, Yahr R, Vilgalys R (2004) Assembling the fungal tree of life: progress, classification, and evolution of subcellular traits. Am J Bot 91:1446–1480

Maharachchikumbura SSN, Hyde KD, Jones EBG, McKenzie EHC, Huang SK, Abdel-Wahab MA, Daranagama DA, Dayarathne M, Dsouza MJ, Goonasekara ID, Hongsanan S, Jayawardena RS, Kirk PM, Konta S, Liu JK, Liu Z-Y, Norphanphoun C, Pang KL, Perera RH, Senanayake IC, Shang Q, Shenoy BD, Xiao Y, Bahkali AH, Kang J, Somrothipol S, Suetrong S, Wen T, Xu J (2015) Towards a natural classification and backbone tree for Sordariomycetes. Fungal Divers 72:199–301

Maharachchikumbura SSN, Hyde KD, Jones EBG, McKenzie EHC, Bhat JD, Dayarathne MC, Huang SK, Norphanphoun C, Senanayake IC, Perera RH, Shang QJ, Xiao Y, D'souza MJ, Hongsanan S, Jayawardena RS, Daranagama DA, Konta S, Goonasekara ID, Zhuang WY, Jeewon R, Phillips AJL, Abdel-Wahab MA, Al-Sadi AM, Bahkali AH, Boonmee S, Boonyuen N, Cheewangkoon R, Dissanayake AJ, Kang J, Li QR, Liu JK, Liu XZ, Liu ZY, Luangsa-ard JJ, Pang KL, Phookamsak R, Promputtha I, Suetrong S, Stadler M, Wen T, Wijayawardene NN (2016) Families of Sordariomycetes. Fungal Divers 79:1–317

Maharachchikumbura SSN, Larignon P, Al-Sadi AM, Li Z-Y (2017) Characterization of *Neopestalotiopsis*, *Pestalotiopsis* and *Truncatella* species associated with grapevine trunk diseases in France. Phytopathol Mediterr 55(3):380–390

Maharachchikumbura SSN, Ariyawansa HA, Wanasinghe DN, Dayarathne MC, Al-Saady NA, Al-Sadi AM (2019) Phylogenetic classification and generic delineation of *Hydeomyces desertipleosporoides* gen. et sp. nov. (*Phaeosphaeriaceae*) from Jebel Akhdar Mountain in Oman. Phytotaxa 391(1):28–38

Mahdizadeh V, Safaie N, Goltapeh EM, Asef MR, Hosseini SM, Callac P (2016) *Agaricus* section *Xanthodermatei* in Iran. Phytotaxa 247(3):181–196

Malloch D, Cain RF (1971) New cleistothecial *Sordariaceae* and a new family, *Coniochaetaceae*. Can J Bot 49:869–880

Malysheva V, Spirin V (2017) Taxonomy and phylogeny of the *Auriculariales* (Agaricomycetes, Basidiomycota) with stereoid basidiocarps. Fungal Biol 121:689–715

Mapook A, Hyde KD, Dai DQ, Li J, Jones EG, Bahkali AH, Boonmee S (2016) *Muyocopronales*, ord. nov. (Dothideomycetes, Ascomycota) and a reappraisal of *Muyocopron* species from northern Thailand. Phytotaxa 265(3):225–237

Mardones M, Trampe-Jaschik T, Oster S, Elliott M, Urbina H, Schmitt I, Piepenbring M (2017) Phylogeny of the order *Phyllachorales* (Ascomycota, Sordariomycetes): among and within order relationships based on five molecular loci. Persoonia 39:74–90

Mardones M, Trampe-Jaschik T, Hofmann TA, Piepenbring M (2018) Contribution to the phylogeny and a new species of *Coccodiella* (*Phyllachorales*). Mycol Prog 17(1–2):205–213

Marin-Felix Y, Groenewald JZ, Cai L, Chen Q, Marincowitz S, Barnes I, Bensch K, Braun U, Camporesi E, Damm U, De Beer

ZW (2017) Genera of phytopathogenic fungi: GOPHY 1. Stud Mycol 86:99–216

Martin GW (1952) Revision of the North Central *Tremellales*. State Univ Iowa Stud Nat Hist 19(3):1–122

Massee GE (1914) Fungi exotici, XVII. Bulletin of Miscellaneous Information of the Royal Botanical Gardens Kew: 72–76

Matheny PB (2005) Improving phylogenetic inference of mushrooms with RPB1 and RPB2 nucleotide sequences (*Inocybe*; *Agaricales*). Mol Phylogenet Evol 35:1–20

Matheny PB, Curtis JM, Hofstetter V, Aime MC, Moncalvo JM, Ge Z-W, Yang Z-L, Slot JC, Ammirati JF, Baroni TJ, Bougher NL, Hughes KW, Lodge DJ, Kerrigan RW, Seidl MT, Aanen DK, DeNitis M, Daniele GM, Desjardin DE, Kropp BR, Norvell LR, Hibbett DS (2006) Majorclades of *Agaricales*: a multi-locus phylogenetic over view. Mycologia 98(6):984–997

Matssura K, Yashiro T (2010) Parallel evolution of termite-egg mimicry by sclerotium-forming fungi in distant termite groups. Biol J. Linnean Soc 100:531–537

McKenzie EHC, Buchanan PK, Johnston PR (2000) Checklist of fungi on *Nothofagus* species in New Zealand. N Z J Bot 38:635–720

McNabb RFR (1973) Taxonomic studies in the *Dacrymycetaceae* VIII. *Dacrymyces* Nees ex Fries. N Z J Bot 11:461–524

Melo I, Cardoso J, Dueñas M, Salcedo I, Telleria MT (2012) *Peniophora aluticolor* (Fungi, Basidiomycota), an orphaned species restudied. Nova Hedwigia 94:437–440

Miadlikowska J, Kauff F, Högnabba F, Oliver JC, Molnár K, Fraker E, Gaya E, Hafellner J, Hofstetter V, Gueidan C, Otálora MA (2014) A multigene phylogenetic synthesis for the class Lecanoromycetes (Ascomycota): 1307 fungi representing 1139 infrageneric taxa, 317 genera and 66 families. Mol Phylogenet Evol 79:132–168

Miettinen O, Spirin V, Vlasák J, Rivoire B, Stenroos S, Hibbett D (2016) *Polypores* and genus concepts in *Phanerochaetaceae* (*Polyporales*, Basidiomycota). Mycokeys 17:1–46

Miller JH (1933) Some new species of *Hypoxylon*. Mycologia 25:321–329

Miller AN, Huhndorf SM (2005) Multi-gene phylogenies indicate ascomal wall morphology is a better predictor of phylogenetic relationships than ascospore morphology in the *Sordariales* (Ascomycota, Fungi). Mol Phylogenet Evol 35:60–75

Miller SL, Larsson E, Larsson KH, Verbeken A, Nuytinck J (2006) Perspectives in the new *Russulales*. Mycologia 98:960–970

Miller SL, Aime MC, Henkel TW (2012) *Russulaceae* of Pakaraima Mountain of Guyana 2. New species of *Russula* and *Lactifluus*. Mycotaxon 121:233–253

Milne I, Wright F, Rowe G, Marshal DF, Husmeier D, McGuire G (2004) TOPALi: software for automatic identification of recombinant sequences within DNA multiple alignments. Bioinformatics 20:806–1807

Moncalvo JM, Vilgalys R, Redhead SA, Johnson JE, James TY, Aime MC, Hofstetter V, Verduin SJ, Larsson E, Baroni TJ, Thorn RG, Jacobssong S, Clémençond H, Miller OK Jr (2002) One hundred and seventeen clades of euagarics. Mol Phylogenet Evol 23(3):357–400

Monteiro JS, Castañeda-Ruiz RF, Gusmão LFP (2016) *Thozetella coronata* and *T. ypsiloidea* spp. nov. from the Brazilian Amazon forest. Mycotaxon 131(3):605–611

Moreno G, Heykoop M (1998) Type studies in the genus *Coprinus* (*Coprinaceae*, *Agaricales*)–*Coprinus xerophilus* a new record in Europe. Persoonia 17(1):97–111

Morin L, Shivas RG, Piper MC, Tan YP (2010) *Austropleospora osteospermi* gen. et sp. nov. and its host specificity and distribution on *Chrysanthemoides monilifera* ssp. rotundata in Australia. Fungal Divers 40(1):65–74

Müller E, Petrini O, Fisher PJ, Samuels GJ, Rossman AY (1987) Taxonomy and anamorphs of the *Herpotrichiellaceae* with notes on generic synonymy. Trans Br Mycol Soc 88(1):63–74

Munk A (1953) The system of the Pyrenomycetes. Dansk Bot Arkiv 15(2):1–163

Munk A (1957a) Danish Pyrenomycetes. A preliminary flora. Dansk Bot Arkiv 17:1–491

Munk A (1957b) On relations between ecologic and taxonomic aspects in pyrenomycetes. Beih Sydowia 1:9–13

Murrill WA (1945) More fungi from Florida. Lloydia 8:263–290

MycoBank (2019) http://www.mycobank.org/Biolomics.aspx?Table=Mycobank&Page=200

Nag Raj TR (1976) Miscellaneous microfungi. I. Can J Bot 54(12):1370–1376

Nagy L (2007) Notes on taxa of *Coprinus* subsection Alachuani from Hungary. Osterr Z Pilzkd 16:167–180

Nakasone KK (2008) Type studies of corticioid Hymenomycetes described by Bresadola. Cryptog Mycol 29:231–257

Nannfeldt JA (1932) Studien über die Morphologie und Systematik der nicht-lichenisierten inoperculaten Discomyceten. Nova Acta Regiae Soc Sci Ups Ser 4(8):1–368

Nasr S, Bien S, Soudi MR, Alimadadi N, Fazeli SAS, Damm U (2018) Novel *Collophorina* and *Coniochaeta* species from *Euphorbia polycaulis*, an endemic plant in Iran. Mycol Prog 17(6):755–771

Nawawi A, Kuthubutheen AJ (1989) *Canalisporium,* a new genus of lignicolous Hyphomycetes from Malaysia. Mycotaxon 34:475–487

Nepel M, Voglmayr H, Schönenberger J, Mayer VE (2014) High diversity and low specificity of Chaetothyrialean fungi in carton galleries in a Neotropical ant–plant association. PLoS ONE 9(11):e112756

Noordeloos ME (1995) Tribus *Collybieae*. In: Bas C, Kuyper TW, Noordeloos ME, Vellinga EC (eds) Flora Agaricina Neerlandica 3. A.A. Balkema, Rotterdam, pp 123–129

Norphanphoun C, Doilom M, Daranagama DA, Phookamsak R, Wen TC, Bulgakov TS, Hyde KD (2017) Revisiting the genus *Cytospora* and allied species. Mycosphere 8:51–97. https://doi.org/10.5943/mycosphere/8/1/7

Norphanphoun C, Raspé O, Jeewon R, Wen TC, Hyde KD (2018) Morphological and phylogenetic characterisation of novel *Cytospora* species associated with mangroves. MycoKeys 38:93–120

Nuhn ME, Binder M, Taylor AFS, Halling RE, Hibbett D (2013) Phylogenetic overview of the *Boletineae*. Fungal Biol 117:479–511

O'Donnell K (1993) *Fusarium* and its near relatives. CAB International, Wallingford

Oberwinkler F (1993) Genera in a monophyletic group: the *Dacrymycetales*. Mycol Helv 6:35–72

Oberwinkler F (2014) Dacrymycetes. In Esser K, McLaughin DJ, Spataphora JS (eds) The fungi, vol IVB, pp 317–325

Olariaga I, Salcedo I (2012) New combinations and notes in clavarioid fungi. Mycotaxon 121:37–44

Olariaga I, Begoña MJ, Garcıá-Etxerbarria K, Salcedo I (2009) Species delimitation in the European species of *Clavulina* (*Cantharellales*, Basidiomycota) inferred from phylogenetic analyses of ITS region andmorphological data. Mycol Res 113:1261–1270

Ordynets A, Larsson KH, Langer E (2015) Two new *Trechispora* species from La Réunion Island. Mycol Prog 14:1–11

Paloi S, Dutta AK, Acharya K (2015) A new species of *Russula* (*Russulales*) from Eastern Himalaya, India. Phytotaxa 234(3):255–262

Parbery DG (1967) Studies on graminicolous species of *Phyllachora* Nke in Fckl. V. A taxonomic monograph. Aust J Bot 15:271–375

Parmasto E (1968) Conspectus systematis corticiacearum. Inst Zool Bot Acad Scient Estonicae, Tartu

Parra LA (2013) *Agaricus* L. *Allopsalliota*, Nauta & Bas, Fungi Europaei, vol 1A. Candusso Edizioni s.a.s. Alassio

Parra LA, Angelini C, Ortiz-Santana B, Mata G, Billette C, Rojo C, Chen J, Callac P (2018) The genus *Agaricus* in the Caribbean. Nine new taxa mostly based on collections from the Dominican Republic. Phytotaxa 345(3):219–271

Patouillard N (1904) Contribution à l'histoire naturelle de la Tunisie. Notes mycologiques. Bull Soc Hist Nat. Autun. 17:143–156

Pearce CA, Hyde KD (1994) The genus *Phyllachora* from Australia: observations on taxa from Callistemon species. Mycol Res 98:1393–1401

Pearson AA (1950) The Genus *Russula*. The Naturalists Univ. of Leeeds, London

Peck CH (1900) New species of fungi. Bull Torrey Bot Club 27:14–21

Pegler DN (1986) Agaric flora of Sri Lanka. Kew Bull Add Ser XII, Her Majesty's Stationary Office, London

Pegler DN, Fiard JP (1978) *Hygrocybe* sect. *Firmae* (*Agaricales*) in tropical America. Kew Bull 32:297–312

Perdomo H, García D, Gené J, Cano J, Sutton DA, Summerbell Guarro J (2013) *Phialemoniopsis*, a new genus of Sordariomycetes, and new species of *Phialemonium* and *Lecythophora*. Mycologia 105(2):398–421

Perera RH, Maharachchikumbura SSN, Bhat JD, Al-Sadi AM, Liu JK, Hyde KD, Liu ZY (2016) New species of *Thozetella* and *Chaetosphaeria* and new records of *Chaetosphaeria* and *Tainosphaeria* from Thailand. Mycosphere 7:1301–1321

Pérez-De-Gregorio MA, Vizzini A, Contu M, Roqué C, Ercole E (2011) *Marasmiellus celebanticus* (*Agaricales*, *Omphalotaceae*), a new species of *Marasmiellus* sect. *Candidi* collected in the Mediterranean area. Phytotaxa 25:49–59

Petersen RH (1967) Notes of clavarioid fungi VI. Two new species and notes on the origin of *Clavulina*. Mycologia 59:39–47

Petersen RH (1983) Notes on clavarioid fungi XVIII. A preliminary outline of *Clavulina* in Southeastern Australia. Nova Hedwigia 37:19–35

Petersen RH (1985) Notes on clavarioid fungi XX. New taxa and distributional records in *Clavulina* and *Ramaria*. Mycologia 77:903–919

Petersen RH (1988a) The clavarioid fungi of New Zealand. DSIR Science Information Publishing, Wellington

Petersen RH (1988b) Notes on clavarioid fungi XXII. Three interesting South American collections. Mycologia 80:571–576

Petrak F (1923) Beiträge zur Pilzflora von Sternberg in Mähren. Ann Mycol 21:107–132

Pfister DH, Matočec N, Kušan I (2009) Integrated studies in the classification of the *Pezizaceae*. Re-evaluation of the genus *Pachyella* with a new segregate genus *Adelphella*. Mycol Monten 11:7–17

Phillips R (1990) Der Kosmos-Pilzatlas. Franckh-Kosmos Verlag, Stuttgart, p 288

Phillips AJL, Alves A, Correia A, Luque J (2005) Two new species of *Botryosphaeria* with brown, 1-septate ascospores and *Dothiorella* anamorphs. Mycologia 97:513–529

Phillips AJL, Alves A, Pennycook SR, Johnston PR, Ramaley A, Akulov A, Crous PW (2008) Resolving the phylogenetic and taxonomic status of dark-spored teleomorph genera in the *Botryosphaeriaceae*. Persoonia 21:29

Phillips AJL, Alves A, Abdollahzadeh J, Slippers B, Wingfield MJ, Groenewald JZ, Crous PW (2013) The *Botryosphaeriaceae*: genera and species known from culture. Stud Mycol 76:51–167

Phillips AJL, Hyde KD, Alves A, Liu JKJ (2018) Families in *Botryosphaeriales*: a phylogenetic, morphological and evolutionary perspective. Fungal Divers 94: 1–22

Phookamsak R, Liu JK, Manamgoda DS, Wanasinghe DN, Ariyawansa H, Mortimer PE, Chukeatirote E, McKenzie EH, Hyde KD (2014a) Epitypification of two bambusicolous fungi from Thailand. Cryptogam Mycol 35(3):239–256

Phookamsak R, Liu JK, McKenzie EHC, Manamgoda DS, Ariyawansa HA, Thambugala KM, Dai DQ, Camporesi E, Chukeatirote E, Wijayawardene NN, Bahkali AH, Mortimer PE, Xu JC, Hyde KD (2014b) Revision of Phaeosphaeriaceae. Fungal Divers. 68:159–238

Phookamsak R, Manamgoda DS, Li WJ, Dai DQ, Singtripop C, Hyde KD (2015a) *Poaceascoma helicoides* gen et sp. nov., a new genus with scolecospores in *Lentitheciaceae*. Cryptogam Mycol 36(2):213–224

Phookamsak R, Norphanphoun C, Tanaka K, Dai DQ, Luo ZL, Liu JK, Su HY, Bhat DJ, Bahkali AH, Mortimer PE, Xu JC, Hyde KD (2015b) Towards a natural classification of Astrosphaeriella-like species; introducing *Astrosphaeriellaceae* and *Pseudoastrosphaeriellaceae* fam. nov and *Astrosphaeriellopsis,* gen. nov. Fungal Divers 74:143–197

Phookamsak R, Wanasinghe DN, Hongsanan S, Phukhamsakda C, Huang SK, Tennakoon DS, Norphanphoun C, Camporesi E, Bulgakov TS, Promputtha I, Mortimer PE, Xu JC, Hyde KD (2017) Towards a natural classification of *Ophiobolus* and ophiobolus-like taxa; introducing three novel genera *Ophiobolopsis, Paraophiobolus* and *Pseudoophiobolus* in *Phaeoshaeriaceae* (*Pleosporales*). Fungal Divers 87:299–339

Phookamsak R, Lu YZ, Hyde KD, Jeewon R, Li J, Doilom M, Boonmee S, Promputtha I (2018) Phylogenetic characterization of two novel *Kamalomyces* species in *Tubeufiaceae* (*Tubeufiales*). Mycol Prog 17(5):647–660

Phukhamsakda C, Ariyawansa HA, Phookamsak R, Chomnunti P, Bulgakov TS, Yange JB, Bhat DJ, Bahkalih AH, Hyde KD (2015) *Muriphaeosphaeria galatellae* gen. et sp. nov. in *Phaeosphaeriaceae* (*Pleosporales*). Phytotaxa 227(1):55–65

Phukhamsakda C, Hongsanan S, Ryberg M, Ariyawansa HA, Chomnunti P, Bahkali AH, Hyde KD (2016) The evolution of *Massarineae* with *Longipedicellataceae* fam. nov. Mycosphere 7(11):1713–1731

Phukhamsakda C, Bhat DJ, Hongsanan S, Tibpromma S, Yang JB, Promputtha I (2017) *Magnicamarosporium diospyricola* sp. nov (*Sulcatisporaceae*) from Thailand. Mycosphere 8(4):512–520

Phukhamsakda C, Bhat DJ, Hongsanan S, Xu JC, Stadler M, Hyde KD (2018) Two novel species of *Neoaquastroma* (*Parabambusicolaceae*, *Pleosporales*) with their phoma-like asexual morphs. MycoKeys 34:47

Pilát A (1926) Monographie der mitteleuropeischen Aleurodisineen. Ann Mycol 24:203–230

Pilát A (1930) Monographie der europaischen Stereaceen. Hedwigia 70:10–132

Pitt JI (1979) The genus *Penicillium* and its teleomorphic states *Eupenicillium* and *Talaromyces*. Academic Press, London

Pitt JI, Hocking AD (2009) Fungi and food spoilage, 3rd edn. Springer, New York

Posada D, Crandall KA (1998) MODELTEST: testing the model of DNA substitution. Bioinformatics 14(9):817–818

Preuss CGT (1851) Übersicht untersuchter Pilze, besonders aus der Umgegend von Hoyerswerda. Linnaea 24:99–153

Promputtha I, Lumyong S, Dhanasekaran V, McKenzie EH, Hyde KD, Jeewon R (2007) A phylogenetic evaluation of whether endophytes become saprotrophs at host senescence. Microb Ecol 53(4):579–590

Promputtha I, Hyde KD, McKenzie EH, Peberdy JF, Lumyong S (2010) Can leaf degrading enzymes provide evidence that endophytic fungi becoming saprobes? Fungal Divers 41(1):89–99

Quaedvlieg W, Binder M, Groenewald JZ, Summerell BA, Carnegie AJ, Burgess TI, Crous PW (2014) Introducing the Consolidated Species Concept to resolve species in the *Teratosphaeriaceae*. Persoonia 33:1

R Core Team (2015) R: a language and environment for statistical computing. R Foundation for Statistical Computing, Vienna

Rabenhorst, GL (1874) Fungi europaea exsiccate. Cent. XIX, No. 1824. Hedwigia 13:184

Raitviír A (1964) Izv. Akad Nauk Estonsk SSR 13:29

Raitviir A (2002) A revision of the genus *Dasyscyphella* (*Hyaloscyphaceae*, *Helotiales*). Polish Bot J 47(2):227–241

Raitviir A (2004) Revised Synopsis of the *Hyaloscyphaceae*. Scripta Mycol 20:1–133

Rambaut A, Suchard M, Drummond A (2013) Tracer, v1.6. http://tree.bio.ed.ac.uk/software/tracer/

Rappaz F (1992) *Phomatospora berkeleyi*, *P. arenaria* and their *Sporothrix* anamorphs. Mycotaxon 45:323–330

Raspé O, Vadthanarat S, De Kesel A, Degreef J, Hyde KD, Lumyong S (2016) *Pulveroboletus fragrans*, a new Boletaceae species from Northern Thailand, with a remarkable aromatic odor. Mycol Prog 15:38

Rawla GS (2001) Himalayan species of *Russula* Pers. Ex S.F. Gray. In: Pande PC, Samant SS (eds) Plant diversity of the Himalaya. Gyanodaya Prakashan, Nainital, pp 1–48

Rayner RW (1970) A mycological colour chart. Commonwealth Mycological Institute, Kew, p 34

Rayner RW (1985) Keys to the British species of *Russula*, 3rd edn. British Mycological Society, Cambridge, p 99

Réblová M (2000) The genus *Chaetosphaeria* and its anamorphs. Stud Mycol 45:149–168

Réblová M, Barr ME, Samuels GJ (1999) *Chaetosphaeriaceae*, a new family for *Chaetosphaeria* and its relatives. Sydowia 51:49–70

Réblová M, Untereiner WA, Réblová K (2013) Novel Evolutionary Lineages Revealed in the *Chaetothyriales* (Fungi) based on Multigene Phylogenetic Analyses and Comparison of ITS Secondary Structure. PLoS ONE 8(5):e63547

Réblová M, Miller AN, Rossman AY, Seifert KA, Crous PW, Hawksworth DL, Abdel-Wahab MA, Cannon PF, Daranagama DA, De Beer ZW, Huang SK, Hyde KD, Jayawardena RS, Jaklitsch W, Jones EBG, Ju YM, Judith C, Maharachchikumbura SSN, Pang KL, Petrini LE, Raja HA, Romero AI, Shearer C, Senanayake IC, Voglmayr H, Weir BS, Wijayawardene NN (2016) Recommendations for competing sexual-asexually typified generic names in *Sordariomycetes* (except *Diaporthales*, *Hypocreales*, and *Magnaporthales*). IMA Fungus 7(1):131–153

Redhead SA, Vilgalys R, Moncalvo JM, Johnson J, Hopple JS Jr (2001) *Coprinus* Pers. and the disposition of *Coprinus* species *sensu lato*. Taxon 50:203–241

Rehner SA (2001) Primers for elongation factor 1-alpha (EF1-alpha). http://www.aftol.org/pdfs/EF1primer.pdf

Reid DA (1955) New or interesting records of Australasian basidiomycetes. Kew Bull 10:631–648

Reid DA (1974) A monograph of the British Dacrymycetales. Trans Br Mycol Soc 62(3):404–433

Retnowati A (2012) Taxonomic study of the genus *Marasmiellus* Murrill in Java and Bali. Doctoral Thesis. University of Indonesia

Ribes JA, Vanover-Sams CL, Baker DJ (2000) Zygomycetes in human disease. Clin Microbiol Rev 13:236–301

Roberts P (1999) Clavarioid fungi from Korup National Park, Cameroon. Kew Bull 54:517–539

Roberts P (2006) Caribbean heterobasidiomycetes: 2. Jamaica. Mycotaxon 96:83–107

Rogers DP (1944) The genera *Trechispora* and *Galzinia* (*Thelephoraceae*). Mycologia 36:70–103

Rogers DP (1951) *Trechispora* and *Pellicularia*. Mycologia 43:111

Rogerson CT (1970) The hypocrealean fungi (ascomycetes, *Hypocreales*). Mycologia 62(5):865–910

Romagnesi H (1967) Les Russules d' Europe et d' Afrique du nord. Bordas, Paris, p 998

Ronquist F, Teslenko M, Van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol 61:539–542. https://doi.org/10.1093/sysbio/sys029

Rossman AY, Farr DF, Castlebury LA (2007) A review of the phylogeny and biology of the *Diaporthales*. Mycoscience 48:135–144

Rossman AY, Adams GC, Cannon PF, Castlebury LA, Crous PW, Gryzenhout M, Jaklitsch WM, Mejia LC, Stoykov D, Udayanga D, Voglmayr H (2015) Recommendations of generic names in *Diaporthales* competing for protection or use. IMA Fungus 6(1):145–154

Ryvarden L (2002) A note on the genus Hydnodon Banker. Syn Fung 15:31–33

Ryvarden L, Melo I (2014) Poroid fungi of Europe. Synopsis Fung 31:1e455

Saccardo PA (1878) Fungi Italici autographice delineati a Prof. P.A. Saccardo. Patavii 1878. Fascicoli V.-VIII. Michelia 1(3):326–350

Saccardo PA (1880a) Conspectus generum fungorum Italiae inferiorum nempe ad Sphaeropsideas, Melanconieas et Hyphomyceteas pertinentium systemate sporologico dispositorum. Michelia 2(6):1–38

Saccardo PA (1880b) Fungi Gallici lecti a cl. viris P. Brunaud, Abb. Letendre, A. Malbranche, J. Therry, vel editi in Mycotheca Gallica C. Roumeguèri. Series II. Michelia 2(6):39–135

Saccardo PA (1882) Sylloge Fungorum I: 198

Saccardo PA (1883a) Sylloge Fungorum. Omnium hucusque cognitorum 2:658–661

Saccardo PA (1883b) Sylloge Pyrenomycetum, vol. II. Sylloge Fungorum 2:1–813

Saccardo PA (1892) Supplementum Universale, Pars II. Discomyceteae-Hyphomyceteae. Syll Fung 10:1–964

Sádlíková M, Kout J (2017) A new *Phanerochaete* (*Polyporales*, Basidiomycota) with brown subicular hyphae from Thailand. Mycosphere 8:1024–1030

Saini SS, Atri NS (1989) North Indian *Agaricales* XI-section *Russula* Pers. of Genus *Russula* Pers. in India. Indian J Mycol Plant Pathol 19:44–49

Samarakoon MC, Hyde KD, Promputtha I, Hongsanan S, Ariyawansa HA, Maharachchikumbura SSN, Daranagama DA, Stadler M, Mapook A (2016) Evolution of Xylariomycetidae (Ascomycota: Sordariomycetes). Mycosphere 7(11):1746–1761

Samarakoon MC, Gafforov Y, Liu NG, Maharachchikumbura SSN, Bhat JD, Liu JK, Promputtha I, Hyde KD (2018) Combined multi-gene backbone tree for the genus *Coniochaeta* with two new species from Uzbekistan. Phytotaxa 336(1):43–58

Samson RA, Houbraken J, Thrane U (2010) Food and indoor fungi. CBS KNAW Biodiversity Center, Utrecht

Samuels GJ (2006) *Trichoderma*: systematics, the sexual state, and ecology. Phytopathology 96(2):195–206

Samuels GJ, Dodd SL, Gams W, Castlebury LA, Petrini O (2002) *Trichoderma* species associated with the green mold epidemic of commercially grown *Agaricus bisporus*. Mycologia 94(1):146–170

Samuelson DA (1978) Asci of the *Pezizales*. I. The apical apparatus of iodine-positive species. Can J Bot 56(16):1860–1875

Sarnari M (1998) Monografia Iillustrata Del Genere *Russula* in Europa. Tomo Primo, Italy: 799

Sarnari M (2005) Monografia Illustrata Del Genere *Russula* in Europa. Tromo Secondo, Italy, 2:762

Schardl CL, Young CA, Hesse U, Amyotte SG, Andreeva K, Calie PJ, Fleetwood DJ, Haws DC, Moore N, Oeser B, Panaccione DG, Schweri KK, Voisey CR, Farman ML, Jaromczyk JW, Roe BA, O'Sullivan DM, Scott B, Tudzynski P, An Z, Arnaoudova EG, Bullock CT, Charlton ND, Chen L, Cox M, Dinkins RD, Florea S, Glenn AE, Gordon A, Güldener U, Harris DR, Hollin W, Jaromczyk J, Johnson RD, Khan AK, Leistner E, Leuchtmann A, Li C, Liu JG, Liu J, Liu M, Mace W, Machado C, Nagabhyru P, Pan J, Schmid J, Sugawara K, Steiner U, Takach JE, Tanaka E, Webb JS, Wilson EV, Wiseman JL, Yoshida R, Zeng Z (2013) Plant-symbiotic fungi as chemical engineers: multi-genome analysis of the *Clavicipitaceae* reveals dynamics of alkaloid loci. PLoS Genet 9(2):e1003323

Schoch CL, Seifert KA, Huhndorf S, Robert V, Spouge JL, Levesque CA, Chen W and Fungal Barcoding Consortium (2012) Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. PNAS 109(16):6241–6246

Schröter J (1888) Pilze. Erste Hälfe. In: Cohn F (ed) Krypt.-Fl. Schlesien 3. J.U. Kern Verlag (Max Müller), Breslau (1889)

Schröter J (1889) Pilze. Erste Hälfte. In: F. Cohn Kryptogamen-Flora von Schlesien 3 (1), [ii–iv], 1–814. J.U. Kern's Verlag, Germany

Schuster A, Schmoll M (2010) Biology and biotechnology of *Trichoderma*. Appl Microbiol Biotechnol 87(3):787–799

Senanayake IC, Maharachchikumbura SSN, Hyde KD, Bhat JD, Jones EBG, McKenzie EHC, Dai DQ, Daranagama DA, Dayarathne MC, Goonasekara ID, Konta S, Li WJ, Shang QJ, Stadler M, Wijayawardene NN, Xiao YP, Norphanphoun C, Li Q, Liu XZ, Bahkali AH, Kang JC, Wang Y, Wen TC, Wendt L, Xu JC, Camporesi E (2015) Towards unravelling relationships in Xylariomycetidae (Sordariomycetes). Fungal Divers 73:73–144

Senanayake IC, Crous PW, Groenewald JZ, Maharachchikumbura SSN, Jeewon R, Phillips AJL, Bhat JD, Perera RH, Li QR, Li WJ, Tangthirasunun N, Norphanphoun C, Karunarathna SC, Camporesi E, Manawasighe IS, Al-Sadi AM, Hyde KD (2017) Families of *Diaporthales* based on morphological and phylogenetic evidence. Stud Mycol 86:217–296

Senanayake IC, Jeewon R, Chomnunti P, Wanasinghe DN, Norphanphoun C, Karunarathna A, Pem D, Perera RH, Camporesi E, McKenzie EHC, Hyde KD (2018) Taxonomic circumscription of *Diaporthales* based on multigene phylogeny and morphology. Fungal Divers 93(1):241–443

Senthilarasu G, Kumaresan V, Singh SK (2010) A new species of *Hygrocybe* in section *Firmae* from Western Ghats, India. Mycotaxon 111:301–307

Senwanna C, Phookamsak R, Doilom M, Hyde KD, Cheewangkoon R (2017) Novel taxa of *Diatrypaceae* from *Para rubber* (*Hevea brasiliensis*) in northern Thailand; introducing a novel genus *Allocryptovalsa*. Mycosphere 8:1835–1855

Shang QJ, Hyde KD, Phookamsak R, Doilom M, Bhat DJ, Maharachchikumbura SS, Promputtha I (2017) *Diatrypella tectonae* and *Peroneutypa mackenziei* sp. nov. (*Diatrypaceae*) from northern Thailand. Mycol Prog 16:463–476

Shang QJ, Hyde KD, Jeewon R, Khan S, Promputtha I, Phookamsak R (2018) Morpho-molecular characterization of *Peroneutypa* (*Diatrypaceae*, *Xylariales*) with two novel species from Thailand. Phytotaxa 356(1):1–8

Sharma JR, Das K (2003) New and interesting species of *Lactarius* from India. Mycotaxon 88:377–385

Shearer CA, Crane JL, Chandra Reddy KR (1990) Studies in *Leptosphaeria.* Lectotypification of *Sphaeria doliolum*. Mycologia 82:496–500

Shirouzu T, Hosoya T (2017) Type study of Japanese Dacrymycetes described by Yosio Kobayasi: redescriptions of five species and a new name proposal. Mycoscience 58:129–136

Shirouzu T, Hirose D, Tokumasu S (2007) Sequence analyses of the 28S rRNA gene D1/D2 region suggest Dacrymyces (Heterobasidiomycetes, *Dacrymycetales*) is polyphyletic. Mycoscience 48:388–394

Shirouzu T, Hirose D, Tokumasu S (2009) Taxonomic study of Japanese Dacrymycetes. Persoonia 23:16–34

Shirouzu T, Hirose D, Oberwinkler F, Shimomura N, Maekawa N, Tokumasu S (2013) Combined molecular and morphological data for improving phylogenetic hypothesis in Dacrymycetes. Mycologia 105(5):1110–1125

Shirouzu T, Hosaka K, Nam KO, Weir BS, Johnston PR, Hosoya T (2017) Phylogenetic relationships of eight new Dacrymycetes collected from New Zealand. Persoonia 38:156–169

Shivas RG, Marney TS, Tan YP, Abell SE (2016) Fungal planet description sheets: 469–557. Persoonia 37:218–403

Shoemaker RA (1976) Canadian and some extralimital *Ophiobolus* species. Can J Bot 54:2365–2404

Shoemaker RA (1984) Canadian and some extralimital *Leptosphaeria* species. Can J Bot 62:2688–2729

Silva M, Pereira OL (2008) Black mildew disease of the neotropical orchid *Epidendrum secundum* caused by *Lembosia epidendri* sp. nov. from Minas Gerais, Brazil. Mycotaxon 104:385–390

Silvestro D, Michalak I (2012) raxmlGUI: a graphical front-end for RAxML. Org Divers Evol 12:335–337

Singer R (1973) The genera *Marasmiellus*, Crepidotus and Simocybe in the Neotropics. Nova Hedwig Beih 44:1–517

Singer R (1976) *Marasmieae* (Basidiomycetes-*Tricholomataceae*). Flora Neotrop Monogr 17:1–347

Singer R (1986) The *Agaricales* in Modern Taxonomy. Bishen Singh Mahendra Pal Singh, Dehradun

Sjökvist E, Larsson E, Eberhardt U, Ryvarden L, Larsson KH (2012) Stipitate steroid basidiocarps have evolved multiple times. Mycologia 104:1046–1055

Slippers B, Wingfield MJ (2007) *Botryosphaeriaceae* as endophytes and latent pathogens of woody plants: diversity, ecology and impact. Fungal Biol Rev 21:90–106

Slippers B, Boissin E, Phillips AJL, Groenewald JZ, Lombard L, Wingfield MJ, Postma A, Burgess T, Crous PW (2013) Phylogenetic lineages in the *Botryosphaeriales*: a systematic and evolutionary framework. Stud Mycol 76:31–49

Sogonov MV, Castlebury LA, Rossman AY, Mejía LC, White JF (2008) Leaf-inhabiting genera of the *Gnomoniaceae*, *Diaporthales*. Stud Mycol 62:1–79

Spatafora JW, Chang Y, Benny GL, Lazarus K, Smith ME, Berbee ML, Bonito G, Corradi N, Grigoriev I, Gryganskyi A, James TY, O'Donnell K, Roberson RW, Taylor TN, Uehling J, Vilgalys R, White MM, Stajich JE (2016) A phylum-level phylogenetic classification of zygomycete fungi based on genome-scale data. Mycologia 108:1028–1046

Spegazzini C (1908) Fungi aliquot paulistani. Revista del Museo de La Plata 15:7–48

Spirin V, Volobuev S, Okun M, Miettinen O, Larsson KH (2017) What is the type of *Phanerochaete* (*Polyporales*, Basidiomycota)? Mycol Prog 16:171–183

Sri-Indrasutdhi V, Boonyuen N, Suetrong S, Chuaseeharonnachai C, Sivichai S, Jones EG (2010) Wood-inhabiting freshwater fungi from Thailand: *Ascothailandia grenadoidia* gen. et sp. nov., *Canalisporium grenadoidia* sp. nov. with a key to *Canalisporium* species (Sordariomycetes, Ascomycota). Mycoscience 51(6):411–420

Staden R, Beal KF, Bonfield JK (1998) The Staden Package. Comput Methods Mol Biol 132: 115–130. In: Misener S, Krawetz SA (eds) Bioinformatics methods and protocols. The Humana Press, Totowa

Stöver BC, Müller KF (2010) TreeGraph 2: combining and visualizing evidence from different phylogenetic analyses. BMC Bioinformatics 11:7

Stubbe D, Nuytinck J, Verbeken A (2010) Critical assessment of the *Lactarius gerardii* species complex (*Russulales*). Fungal Biol 114(2–3):271–283

Stubbe D, Le HT, Wang XH, Nuytinck J, Van de Putte K, Verbeken A (2012a) The Australasian species of *Lactarius* subgenus *Gerardii* (*Russulales*). Fungal Divers 52(1):141–167

Stubbe D, Wang XH, Verbeken A (2012b) New combinations in *Lactifluus*. 2. *L.* subgenus *Gerardii*. Mycotaxon 119:483–485

Su H, Hyde KD, Maharachchikumbura SSN, Ariyawansa HA, Luo Z, Promputtha I, Tian Q, Lin C, Shang QJ, Zhao YC, Chai HM, Liu XY, Bahkali AH, Bhat DJ, McKenzie EHC, Zhou DQ (2016) The families *Distoseptisporaceae* fam. nov., *Kirschsteiniotheliaceae*, *Sporormiaceae* and *Torulaceae,* with new species from freshwater in Yunnan Province, China. Fungal divers 80:375–409

Su L, Deng H, Niu YC (2017) Phylogenetic analysis of *Plectosphaerella* species based on multi-locus DNA sequences and description. Mycol Prog 16:823–829

Sun JZ, Liu XZ, McKenzie EHC, Jeewon R, Liu JK, Zhang XL, Zhao Q, Hyde KD (2019) Fungicolous fungi: terminology, diversity, distribution, evolution and species checklist. Fungal Divers. https://doi.org/10.1007/s13225-019-00422-9

Sung GH, Hywel-Jones NL, Sung JM, Luangsa-ard JJ, Shrestha B, Spatafora JW (2007) Phylogenetic classification of *Cordyceps* and the clavicipitaceous fungi. Stud Mycol 57:5–59

Sutton BC (1977) Coelomycetes VI. Nomenclature of generic names proposed for coelomycetes. Mycol Pap 141:1–253

Suwannarach N, Kumla J, Lumyong S (2016) *Pseudoplagiostoma dipterocarpi* sp. nov., a new endophytic fungus from Thailand. Mycoscience 57(2):118–122

Sydow H (1939) Fungi Aequatorienses (series prima). Ann Mycol 37:275–438

Tamura K, Nei M (1993) Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. Mol Biol Evol 10:512–526

Tamura K, Stecher G, Peterson D, Filipski A, Kumar S (2013) MEGA6: molecular Evolutionary Genetics Analysis Version 6.0. Mol Biol Evol 30:2725–2729

Tan YS, Desjardin DE, Perry BA, Vikineswary S, Noorlidah A (2009) *Marasmius sensu stricto* in Peninsular Malaysia. Fungal Divers 37:9–100

Tanaka K, Harada Y (2003a) *Pleosporales* in Japan (2): the genus *Lophiotrema*. Mycoscience 44(2):115–121

Tanaka K, Harada Y (2003b) *Pleosporales* in Japan (3). The genus *Massarina*. Mycoscience 44:173–185

Tanaka K, Hirayama K, Yonezawa H, Sato G, Toriyabe A, Kudo H, Hashimoto A, Matsumura M, Harada Y, Kurihara Y, Shirouzu T (2015) Revision of the *Massarineae* (*Pleosporales*, Dothideomycetes). Stud Mycol 82:75–136

Tang LP, Cai Q, Lee SS, Buyck B, Zhang P, Yang ZL (2015) Taxonomy and phylogenetic position of species of *Amanita* sect. *Vaginatae s.l.* from tropical Africa. Mycol Prog 39:1–15

Tedersoo L, Sánchez-Ramírez S, Kõljalg U, Bahram M, Döring M, Schigel D, May T, Ryberg M, Abarenkov K (2018) High-level classification of the Fungi and a tool for evolutionary ecological analyses. Fungal Divers 90(1):135–159

Telleria MT, Melo I, Dueñas M, Larsson K-H, Martín MP (2013) Molecular analyses confirm *Brevicellicium* in *Techisporales*. IMA Fungus 4:21–28

Tennakoon DS, Hyde KD, Phookamsak R, Wanasinghe DN, Camporesi E, Promputtha I (2016) Taxonomy and phylogeny of *Juncaceicola* gen. nov. *Phaeosphaeriaceae*, *Pleosporinae*, *Pleosporales*. Cryptogam Mycol 37(2):135–156

Tennakoon DS, Phookamsak R, Wanasinghe DN, Yang JB, Lumyong S, Hyde KD (2017) Morphological and phylogenetic insights resolve *Plenodomus sinensis* (*Leptosphaeriaceae*) as a new species. Phytotaxa 324(1):73–82

Thacker JR, Henkel TW (2004) New species of *Clavulina* from Guyana. Mycologia 96:650–657

Thambugala KM, Singtripop C, Chunfang Y, Mckenzie EHC, Liu ZY, Chukeatirote E, Hyde KD (2014) Towards a natural classification of Dothideomycetes 7: the genera *Allosoma*, *Austropleospora*, *Dangeardiella*, *Griggsia* and *Karschia* (Dothideomycetes genera *incertae sedis*). Phytotaxa 181(1):34–46

Thambugala KM, Hyde KD, Tanaka K, Tian Q, Wanasinghe DN, Ariyawansa HA, Jayasiri SC, Boonmee S, Camporesi E, Hashimoto A, Hirayama K, Schumacher RK, Promputtha I, Liu ZY (2015) Towards a natural classification and backbone tree for *Lophiostomataceae*, *Floricolaceae*, and *Amorosiaceae* fam. nov. Fungal Divers 74:199–266

Thambugala KM, Wanasinghe DN, Phillips AJL, Camporesi E, Bulgakov TS, Phukhamsakda C, Ariyawansa HA, Goonasekara ID, Phookamsak R, Dissanayake A, Tennakoon DS, Tibpromma S, Chen YY, Liu ZY, Hyde KD (2017) Mycosphere notes 1-50: grass (Poaceae) inhabiting Dothideomycetes. Mycosphere 8(4):697–796

Thiers HD, Ammirati JF (1982) New species of *Amanita* from western North America. Mycotaxon 15:155–166

Thind KS (1961) The *Clavariaceae* of India. Indian Council of Agricultural Research, New Delhi

Thind KS, Sharda RM (1984) Three new species of clavarioid fungi from Himalayas. Indian Phytopathol 37:234–240

Thongklang N, Nawaz R, Khalid AN, Chen J, Hyde KD, Zhao R, Parra LA, Hanif M, Moinard M, Callac P (2014) Morphological and molecular characterization of three *Agaricus* species from tropical Asia (Pakistan, Thailand) reveals a new group in section *Xanthodermatei*. Mycologia 106(6):1220–1232

Tibpromma S, McKenzie EHC, Karunarathna SC, Mortimer PE, Xu J, Hyde KD, Hu DM (2016) *Muyocopron garethjonesii* sp. nov. (*Muyocopronales*, Dothideomycetes) on *Pandanus* sp. Mycosphere 7:1480–1489

Tibpromma S, Hyde KD, Jeewon R, Maharachchikumbura SSN, Liu JK, Bhat DJ, Jones EBG, McKenzie EHC, Camporesi E, Bulgakov TS, Doilom M, de Azevedo Santiago ALCM, Das K, Manimohan P, Gibertoni TB, Lim YW, Ekanayaka AH, Thongbai B, Lee HB, Yang JB, Kirk PM, Sysouphanthong P, Singh SK, Boonmee S, Dong W, Raj KNA, Latha KPD, Phookamsak R, Phukhamsakda C, Konta S, Jayasiri SC, Norphanphoun C, Tennakoon DS, Li JF, Dayarathne MC, Perera RH, Xiao Y, Wanasinghe DN, Senanayake IC, Goonasekara ID, de Silva NI, Mapook A, Jayawardena RS, Dissanayake AJ, Manawasinghe IS, Chethana KWT, Luo ZL, Hapuarachchi KK, Baghela A, Soares AM, Vizzini A, Meiras-Ottoni A, Mešič A, Dutta AK, de Souza CAF, Richter C, Lin CG, Chakrabarty D, Daranagama DA, Lima DX, Chakraborty D, Ercole E, Wu F, Simonini G, Vasquez G, da Silva GA, Plautz HL Jr, Ariyawansa HA, Lee H, Kuśan I, Song J, Sun J, Karmakar J, Hu K, Semwal KC, Thambugala KM, Voigt K, Acharya K, Rajeshkumar KC, Ryvarden L, Jadan M, Hosen MI, Mikŝik M, Samarakoon MC, Wijayawardene NN, Kim NK, Matocčec N, Singh PN, Tian Q, Bhatt RP, de Oliveira RJV, Tulloss RE, Aamir S, Kaewchai S, Svetasheva STY, Nguyen TTT, Antonìn V, Li WJ, Wang Y, Indoliya Y, Tkalčec Z, Elgorban AM, Bahkali AH, Tang AMC, Su HY, Zhang H, Promputtha I, Luangsa-ard J, Xu JC, Yan J, Chuan KJ, Stadler M, Mortimer PE, Chomnunti P, Zhao Q, Phillips AJL, Nontachaiyapoom S, Wen TC, Karunarathna SC (2017) Fungal diversity notes 491–602: taxonomic and phylogenetic contributions to fungal taxa. Fungal Divers 83:1–261

Tibpromma S, Hyde KD, McKenzie EHC, Bhat DJ, Phillips AJL, Wanasinghe DN, Samarakoon MC, Jayawardena RS, Dissanayake AJ, Tennakoon DS, Doilom M, Phookamsak R, Tang

AMC, Xu JC, Mortimer PE, Promputtha I, Maharachchikumbura SSN, Khan S, Karunarathna SCK (2018) Fungal diversity notes 840–928: micro-fungi associated with *Pandanaceae*. Fungal Divers 92:1–160

Tode HJ (1791) Fungi Mecklenburgenses selecti. Fasc. II, Generum novorum appendicem, Lüneburg

Trakunyingcharoen T, Lombard L, Groenewald JZ, Cheewangkoon R, To-anun C, Alfenas AC, Crous PW (2014) Mycoparasitic species of *Sphaerellopsis*, and allied lichenicolous and other genera. IMA Fungus 5(2):391–414

Trappe JM, Castellano MA (2007) *Clavulina lilliputiana*, a diminutive new species from Tasmania. Australas Mycol 25:87–89

Troy GC, Panciera DL, Pickett JP, Sutton DA, Gene J, Cano JEF, Guarro J, Thompson EH, Wickes BL (2013) Mixed infection caused by *Lecythophora canina* sp. nov. and *Plectosphaerella cucumerina* in a German shepherd dog. Medical Mycol 51:455–460

Tulasne LR, Tulasne C (1863) Selecta Fungorum Carpologia, Tomus Secundus. Xylariei-Valsei-Sphaeriei 2:1–319

Tulloss RE (2005) *Amanita*-distribution in the Americas, with comparison to eastern and southern Asia and notes on spore character variation with latitude and ecology. Mycotaxon 93:189–231

Tulloss RE, Yang ZL (2016) Studies in the *Amanitaceae*. www.amanitaceae.org. Accessed 2 Dec 2016

Tulloss RE, Ovrebo CL, Halling RE (1992) Studies on *Amanita* (*Amanitaceae*) from Andean Colombia. Mem N Y Bot Gard 66:1–46

Tulloss RE, Kuyper TW, Vellinga EC, Yang ZL, Halling RE, Geml J, Sánchez-Ramírez S, Gonçalves SC, Hess J, Pringle A (2016) The genus *Amanita* should not be split. Amanitaceae 1(3):1–16

Uehling JK, Henkel TW, Aime MC, Vilgalys R, Smith ME (2012a) New species of *Clavulina* (*Cantharellales*, Basidiomycota) with resupinate and effused basidiomata from the Guiana Shield. Mycologia 104:547–556

Uehling JK, Henkel TW, Aime MC, Vilgalys R, Smith ME (2012b) New species and distribution records for *Clavulina* (*Cantharellales*, Basidiomycota) from the Guiana Shield, with a key to the lowland neotropical taxa. Fungal Biol 116:1263–1274

Uljé CB (2005) 1. *Coprinus* Pers. In: Noordeloos ME, Kuyper TW, Vellinga EC (eds) Flora Agaricina Neerlandica 6. Taylor & Francis, Boca Raton, pp 22–109

Uniyal P, Das K, Bhatt RP, Singh U, Mehmood T (2017) *Lactarius kumaonensis*, a novel species in *Russulaceae* from Uttarakhand, India. Nord J Bot 35(6):724–729

Untereiner WA (2000) *Capronia* and its anamorphs: exploring the value of morphological and molecular characters in the systematics of the *Herpotrichiellaceae*. Stud Mycol 45:141–148

Untereiner WA, Gueidan C, Orr MJ, Diederich P (2011) The phylogenetic position of the lichenicolous ascomycete *Capronia peltigerae*. Fungal Divers 49(1):225–233

Vadthanarat S, Raspé O, Lumyong S (2018) Phylogenetic affinities of the sequestrate genus *Rhodactina* (*Boletaceae*), with a new species, *R. rostratispora* from Thailand. MycoKeys 29:63–80

Van Niekerk JM, Groenewald JZE, Verkley GJM, Fourie PH, Wingfield MJ, Crous PW (2004) Systematic reappraisal of *Coniella* and *Pilidiella*, with specific reference to species occurring on *Eucalyptus* and *Vitis* in South Africa. Mycol Res 108:283–303

van de Bogart F (1976) The genus *Coprinus* in Western North America. Part I: Section *Coprinus*. Mycotaxon. Mycotaxon 4(1):233–275

Vellinga EC (2004) Genera in the family *Agaricaceae*: evidence from nrITS and nrLSU sequences. Mycol Res 108(4):354–377

Venturella G (2005) L'iconografia micologica di Giuseppe Inzenga. ISPE Archimede S.r.l, Palermo

Verbeken A, Nuytinck J (2013) Not every milkcap is a *Lactarius*. Scr Bot Belg 51:162–168

Verbeken A, Horak E, Desjardin DE (2001) *Agaricales* in Indonesia. 3. New records of the genus *Lactarius* (Basidiomycota, *Russulales*) from Java. Sydowia 53(2):261–289

Vesterholt J (2012) *Coprinopsis* P. Karst. In: Knudsen H, Vesterholt J (eds) Funga Nordica. Nordsvamp, Copenhagen, pp 672–687

Viégas AP (1945) Alguns Fungos do Brasil VI: *Dacryomycetaceae–Tremellaceae*. Bragantia 5:239–251

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. J Bacteriol 172:4238–4246

Visagie CM, Houbraken J, Frisvad JC, Hong SB, Klaassen CHW, Perrone G, Seifert KA, Varga J, Yaguchi T, Samson RA (2014a) Identification and nomenclature of the genus *Penicillium*. Stud Mycol 78:343–371

Visagie CM, Seifert KA, Houbraken J, Samson RA, Jacobs K (2014b) Diversity of *Penicillium* section *Citrina* within the fynbos biome of South Africa, including a new species from a Protea repens infructescence. Mycologia 106:537–552

Voglmayr H, Park MJ, Shin HD (2011) *Spiroplana centripeta* gen. & sp. nov., a leaf parasite of Philadelphus with a remarkable aeroaquatic conidium morphology. Mycotaxon 116:203–216

Volobuev S, Okun M, Ordynets A, Spirin V (2015) The *Phanerochaete sordida* group (*Polyporales*, Basidiomycota) in temperate Eurasia, with a note on *Phanerochaete pallida*. Mycol Prog 14:1–13

von Arx JA, Müller E (1954) Die Gattungen der amerosporen Pyrenomyceten. Beitrage zur Kryptogamenflora der Schweiz 11(1):434

von Arx JA, Müller E (1975) A re-evaluation of the bitunicate ascomycetes with keys to families and genera. Stud Mycol 9:1–159

von Höhnel F (1918) Dritte vorlaufige Mitteilung mycologischer Ergebnisse (Nr. 201–304). Berichte der Deutschen Botanischen Gesellschaft 36:309–317

Wäli PP, Huhtinen S, Pino-Bodas R, Stenroos S (2014) Three common bryophilous fungi with meristematic anamorphs and phylogenetic alliance to *Teratosphaeriaceae,* Capnodiales. Fungal Biol 118(12):956–969

Walther G, Pawlowska J, Alastruey-Izquierdo A, Wrzosek M, Rodriguez-Tudela JL, Dolatabadi S, Chakrabarti A, de Hoog GS (2013) DNA barcoding in *Mucorales*: an inventory of biodiversity. Persoonia 30:11–47

Wanasinghe DN, Jones EBG, Camporesi E, Boonmee S, Ariyawansa HA, Wijayawardene NN, Hyde KD (2014a) An exciting novel member of *Lentitheciaceae* in Italy from *Clematis vitalba*. Cryptogam Mycol 35(4):323–337

Wanasinghe DN, Jones EG, Camporesi E, Boonmee S, Karunarathna SC, Thines M, Mortimer PE, Xu J, Hyde KD (2014b) *Dematiopleospora mariae* gen. sp. nov., from *Ononis spinosa* in Italy. Cryptogam Mycol 35(2):105–171

Wanasinghe DN, Jones EBG, Camporesi E, Dissanayake AJ, Kamolhan S, Mortimer PE, Xu JC, Abd-Elsalam K, Hyde KD (2016) Taxonomy and phylogeny of *Laburnicola* gen. nov. and *Paramassariosphaeria* gen. nov. (*Didymosphaeriaceae*, *Massarineae*, *Pleosporales*. Fungal Biol 120(11):1354–1373

Wanasinghe DN, Hyde KD, Konta S, To-Anun C, Jones EG (2017) Saprobic Dothideomycetes in Thailand: *Neoaquastroma* gen. nov. (*Parabambusicolaceae*) introduced based on morphological and molecular data. Phytotaxa 302(2):133–144

Wanasinghe DN, Phukhamsakda C, Hyde KD, Jeewon R, Lee HB, Jones EBG, Tibpromma S, Tennakoon DS, Dissanayake AJ, Jayasiri SC, Gafforov Y, Camporesi E, Bulgakov TS, Ekanayake AH, Perera RH, Samarakoon MC, Goonasekara ID, Mapook A, Li WJ, Senanayake IC, Li JF, Norphanphoun C, Doilom M, Bahkali AH, Xu JC, Mortimer PE, Tibell L, Tibell S, Karunarathna SC (2018) Fungal diversity notes 709–839: taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on *Rosaceae*. Fungal Divers 89:1–236

Wang M, Jiang X, Wu W, Hao Y, Su Y, Cai L, Xiang M, Liu X (2015) Psychrophilic fungi from the world's roof. Persoonia 34:100–112

Wang RX, Luo ZL, Hyde KD, Bhat DJ, Su XJ, Su HY (2016) New species and records of *Dictyocheirospora* from submerged wood in north-western Yunnan, China. Mycosphere 7(9):1357–1367

Wang X, Cai W, Ende AG, Zhang J, Xie T, Xi L, Li X, Sun J, Hoog S (2018) Indoor wet cells as a habitat for melanized fungi, opportunistic pathogens on humans and other vertebrates. Sci Rep 8(1):7685

Wannathes N, Desjardin DE, Hyde KD, Perry BA, Lumyong S (2009) A monograph of *Marasmius* (Basidiomycota) from Northern Thailand based on morphological and molecular (ITS sequences) data. Fungal Divers 37:209–306

Wartchow F (2012) *Clavulina incrustata*, a new species from Pernambuco, Brazil. Cryptogam Mycol 33:105–113

Wehmeyer LE (1975) The pyrenomycetous fungi. Mycol Mem 6:1–250

Weiß M, Oberwinkler F (2001) Phylogenetic relationships in *Auriculariales* and related groups—hypotheses derived from nuclear ribosomal DNA sequences. Mycol Res 105(4):403–415

Wendt L, Sir EB, Kuhnert E, Heitkämper S, Lambert C, Hladki AI, Romero AI, Luangsa-ard JJ, Srikitikulchai P, Peršoh D, Stadler M (2018) Resurrection and emendation of the *Hypoxylaceae*, recognised from a multigene phylogeny of the *Xylariales*. Mycol Prog 17(1–2):115–154

White TJ, Bruns TD, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (eds) PCR protocols, a guide to methods and applications. Academic, San Diego, pp 315–322

Wijayawardene NN, Hyde KD, Bhat DJ, Goonasekara ID, Nadeeshan D, Camporesi E, Schumacher RK, Wang Y (2015) Additions to Brown Spored Coelomycetous Taxa in *Massarinae*, *Pleosporales*: introducing *Phragmocamarosporium* gen. nov. and *Suttonomyces* gen. nov. Cryptogam Mycol 36:213–224

Wijayawardene NN, Hyde KD, Wanasinghe DN, Papizadeh M, Goonasekara ID, Camporesi E, Bhat DJ, McKenzie EHC, Phillips AJL, Diederich P, Tanaka K, Li WJ, Tangthirasunun N, Phookamsak R, Dai D-Q, Dissanayake AJ, Weerakoon G, Maharachchikumbura SNN, Hashimoto A, Matsumura M, Bahkali AH, Wang Y (2016) Taxonomy and phylogeny of dematiaceous coelomycetes. Fungal Divers 77:1–316

Wijayawardene NN, Hyde KD, Rajeshkumar KC, Hawksworth DL, Madrid H, Kirk PM, Braun U, Singh RV, Crous PW, Kukwa M, Lucking R, Kurtzman CP, Yurkov A, Haelewaters D, Aptroot A, Lumbsch HT, Timdal E, Ertz D, Etayo J, Phillips AJL, Groenewald JZ, Papizadeh M, Selbmann L, Dayarathne MC, Weerakoon G, Jones EBG, Suetrong S, Tian Q, Castanéda-Ruiz RF, Bahkali AH, Pang KL, Tanaka K, Dai DQ, Sakayaroj J, Hujslová M, Lombard L, Shenoy BD, Suija A, Maharachchikumbura SSN, Thambugala KM, Wanasinghe DN, Sharma BO, Gaikwad S, Pandit G, Zucconi L, Onofri S, Egidi E, Raja HA, Kodsueb R, Caceres MES, Perez-Ortega S, Fiuza PO, Monteiro JS, Vasilyeva LN, Shivas RG, Prieto M, Wedin M, Olariaga I, Lateef AA, Agrawal Y, Fazeli SAS, Amoozegar MA, Zhao GZ, Pfliegler WP, Sharma G, Oset M, Abdel MA, Takamatsu S, Bensch K, Silva NI, De Kesel A, Karunarathna A, Boonmee S, Pfister DH, Lu YZ, Luo ZL, Boonyuen N, Daranagama DA, Senanayake IC, Jayasiri SC, Samarakoon MC, Zeng XY, Doilom M, Quijada L, Rampadarath S, Heredia G, Dissanayake AJ, Jayawardana RS, Perera PH, Tang LZ, Phukhamsakda C, Hernández-Restrepo M, Ma XY, Tibpromma S, Gusmao LFP, Weerahewa D, Karunarathna SC (2017a) Notes for genera: Ascomycota. Fungal Divers 86:1–594

Wijayawardene NN, Hyde KD, Tibpromma S, Wanasinghe DN, Thambugala KM, Tian Q, Wang Y (2017b) Towards incorporating asexual fungi in a natural classification: checklist and notes 2012–2016. Mycosphere 8(9):1457–1554

Wijayawardene NN, Hyde KD, Lumbsch HT, Liu JK, Maharachchikumbura SSN, Ekanayaka AH, Tian Q, Phookamsak R (2018a) Outline of Ascomycota: 2017. Fungal Divers 88:167–263

Wijayawardene NN, Pawłowska J, Letcher PM, Kirk PM, Humber RA, Schüßler A, Wrzosek M, Muszewska A, Okrasińska A, Istel Ł, Gęsiorska A, Mungai P, Lateef AA, Rajeshkumar KC, Singh RV, Radek R, Walther G, Wagner L, Walker C, Wijesundara DSA, Papizadeh M, Dolatabadi S, Shenoy BD, Tokarev YS, Lumyong S, Hyde KD (2018b) Notes for genera: basal clades of Fungi (including Aphelidiomycota, Basidiobolomycota, Blastocladiomycota, Calcarisporiellomycota, Caulochytriomycota, Chytridiomycota, Entomophthoromycota, Glomeromycota, Kickxellomycota, Monoblepharomycota, Mortierellomycota, Mucoromycota, Neocallimastigomycota, Olpidiomycota, Rozellomycota and Zoopagomycota). Fungal Divers 92:43–129

Willis KJ (ed) (2018) State of the World's Fungi 2018. Royal Botanic Gardens, Kew

Wilson AW, Desjardin DE (2005) Phylogenetic relationships in the gymnopoid and marasmioid fungi (Basidiomycetes, euagarics clade). Mycologia 97:667–679

Winter G (1884) Rabenhorst's Kryptogamen-Flora. Pilze Ascomyceten 1(2):1–192

Winter G (1887) Pilze, Ascomyceten. In: Rabenhorst's Kryptogamen Flora von Deutschland, Oesterreich und der Schweiz [i–vi] 1:1–928

Wong SW, Hyde KD, Ho WH, Stanley SJ (1998) *Tamsiniella labiosa* gen. et sp.nov., a new freshwater ascomycete from submerged wood. Can J Bot 76:332–337

Wu SH, Boidin J, Chien CY (2000) *Acanthofungus rimosus* gen. et sp. nov., with reevaluation of the related genera. Mycotaxon 76:153–161

Wu SH, Hibbett DS, Binder M (2001) Phylogenetic analyses of *Aleurodiscus s.l.* and allied genera. Mycologia 93:720–731

Wu SH, Nilsson HR, Chen CT, Yu SY, Hallenberg N (2010a) The white-rotting genus *Phanerochaete* is polyphyletic and distributed throughout the phleboid clade of *Polyporales* (Basidiomycota). Fungal Divers 42:107–118

Wu SH, Wang DM, Yu SY (2010b) *Neoaleurodiscus fujii*, a new genus and new species found at the timberline in Japan. Mycologia 102:217–223

Wu X, Schoch CL, Boonmee S, Bahkali AH, Chomnunti P, Hyde KD (2011) A reappraisal of *Microthyriaceae*. Fungal Divers 51:189–248

Wu G, Feng B, Xu J, Zhu XT, Li Y-C, Zeng NK, Hosen MI, Yang ZL (2014) Molecular phylogenetic analyses redefine seven major clades and reveal 22 new generic clades in the fungal family *Boletaceae*. Fungal Divers 69:93–115

Wu G, Zhao K, Li YC, Zeng NK, Feng B, Halling RE, Yang ZL (2015) Four new genera of the fungal family *Boletaceae*. Fungal Divers 81:1–24

Wu G, Li YC, Zhu XT, Zhao K, Hang LH, Cui YY, Li F, Xu JP, Yang ZL (2016) One hundred noteworthy boletes from China. Fungal Divers 81:25–188

Xia JW, Ma YR, Li Z, Zhang XG (2017) Acrodictys-like wood decay fungi from southern China, with two new families *Acrodictyaceae* and *Junewangiaceae*. Sci Rep 7:78–88

Yang ZL (1997) Die *Amanita*-Arten von Südwestchina. Bibl Mycol 170:1–240

Yang ZL (2000) Species diversity of the genus *Amanita* (Basidiomycetes) in China. Acta Bot Yunnanica 22:135–142

Yang ZL (2004) Two new species of *Amanita* (Basidiomycota) from China. In: Agerer R, Piepenbring M, Blanz P (eds) Frontiers in Basidiomycote Mycology. IHW Verlag, Eching, pp 315–324

Yang ZL (2005) Flora fungorum sinicorum, vol 27, *Amanitaceae*. Science Press, Beijing **(in Chinese)**

Yang ZL (2015) Atlas of the Chinese species of *Amanitaceae*. Science Press, Beijing **(in Chinese)**

Yang ZL, Weiss M, Oberwinkler F (2004) New species of *Amanita* from the eastern Himalaya and adjacent regions. Mycologia 96(3):636–646

Yang T, Groenewald JZ, Cheewangkoon R, Jami F, Abdollahzadeh J, Lombard L, Crous PW (2017) Families, genera and species of *Botryosphaeriales*. Fungal Biol 121:322–346

Yang H, Hyde KD, Karunarathna SC, Deng C, Gu CH, Yang SA, Zhang ZC (2018a) New species of *Camptophora* and *Cyphellophora* from China, and first report of sexual morphs for these genera. Phytotaxa 343(2):149–159

Yang J, Liu JK, Hyde KD, Jones EG, Liu ZY (2018b) New species in *Dictyosporium*, new combinations in *Dictyocheirospora* and an updated backbone tree for *Dictyosporiaceae*. MycoKeys 36:83

Yang J, Maharachchikumbura SSN, Liu JK, Hyde KD, Jones EBG, Al-Sadi AM, Liu Z-Y (2018c) *Pseudostanjehughesia aquitropica* gen. et sp. nov. and *Sporidesmium sensu lato* species from freshwater habitats. Mycol Prog 17:591–616

Ying JZ (1991) Studies on the genus *Lactarius* S.F. Gray from China I. New taxa of *Lactarius*. Acta Mycol Sin 10:190–199

Young AM, Mills AK (2002) The Hygrophoraceae of Tasmania. Muelleria 16:3

Yuan ZW, Pei MH, Hunter T, Royle DJ (1998) *Eudarluca caricis*, the teleomorph of the mycoparasite *Sphaerellopsis filum*, on blackberry rust phragmidium violaceum. Mycol Res 102:866–868

Yuan Y, Chen JJ, He SH (2017) *Geliporus exilisporus* gen. et comb. nov., a xanthochroic polypore in *Phanerochaetaceae* from China. Mycoscience 58(3):197–203

Zare R, Gams W (2016) More white Verticillium-like anamorphs with erect conidiophores. Mycol Prog 15:993–1030

Zare R, Gams W, Starink-Willemse M, Summerbell RC (2007) *Gibellulopsis*, a suitable genus for *Verticillium nigrescens*, and *Musicillium*, a new genus for *V. theobromae*. Nova Hedwig 85:463–489

Zechmeister-Boltenstern S, Keiblinger KM, Mooshammer M, Peñuelas J, Richter A, Sardans J, Wanek W (2015) The application of ecological stoichiometry to plant–microbial–soil organic matter transformations. Ecol Monogr 85(2):133–155

Zhan G, Tian Y, Wang F, Chen X, Guo J, Jiao M, Huang L, Kang Z (2016) A novel fungal hyperparasite of *Puccinia striiformis* f. sp. *tritici*, the causal agent of wheat stripe rust. PLoS ONE 9(11):e111484

Zhang N, Wang Z (2015) 3 Pezizomycotina: Sordariomycetes and Leotiomycetes. In: Systematics and evolution. Springer, Berlin, pp 57–88

Zhang Y, Schoch CL, Fournier J, Crous PW, De Gruyter J, Woudenberg JHC, Hirayama K, Tanaka K, Pointing SB, Spatafora JW, Hyde KD (2009a) Multi-locus phylogeny of *Pleosporales*: a taxonomic, ecological and evolutionary re-evaluation. Stud Mycol 64:85–102

Zhang Y, Wang HK, Fournier J, Crous PW, Jeewon R, Pointing SB, Hyde KD (2009b) Towards a phylogenetic clarification of *Lophiostoma/Massarina* and morphologically similar genera in *the Pleosporales*. Fungal Divers 38:225–251

Zhang Y, Crous PW, Schoch CL, Hyde KD (2012) Pleosporales. Fungal Divers 53:1–221

Zhang M, He W, Wu JR, Zhang Y (2016) Two new species of *Spencermartinsia* (*Botryosphaeriaceae*, *Botryosphaeriales*) from China. Mycosphere 7:942–949

Zhang H, Dong W, Hyde KD, Maharachchikumbura SSN, Hongsanan S, Jayarama Bhat D, Al-Sadi AM, Zhang D (2017a) Towards a natural classification of Annulatascaceae-like taxa: introducing *Atractosporales* ord. nov. and six new families. Fungal Divers 85:75–110

Zhang JF, Liu JK, Hyde KD, Yang W, Liu ZY (2017b) Fungi from Asian Karst formations II. Two new species of *Occultibambusa* (*Occultibambusaceae*, Dothideomycetes) from karst landforms of China. Mycosphere 8(4):550–559

Zhang JF, Liu JKJ, Ran HY, Khongphinitbunjong K, Liu ZY (2018) A new species and new record of *Lophiotrema* (*Lophiotremataceae*, Dothideomycetes) from karst landforms in southwest China. Phytotaxa 379(2):169–179

Zhao GZ, Yu P, Liu XZ (2013) *Cancellidium* and *Canalisporium* (hyphomycetes) from China. Nova Hedwig 96(1–2):221–236

Zhao K, Wu G, Feng B, Yang ZL (2014a) Molecular phylogeny of *Caloboletus* (*Boletaceae*) and a new species in East Asia. Mycol Prog 13:1127–1136

Zhao K, Wu G, Yang ZL (2014b) A new genus, *Rubroboletus*, to accommodate *Boletus sinicus* and its allies. Phytotaxa 188:61–77

Zhao RL, Zhou JL, Chen J, Margaritescu S, Sánchez-Ramírez S, Hyde KD, Callac P, Parra LA, Li GJ, Moncalvo JM (2016) Towards standardizing taxonomic ranks using divergence times-a case study for reconstruction of the *Agaricus* taxonomic system. Fungal Divers 78:239–292

Zhao RL, Li GJ, Sánchez-Ramírez S, Stata M, Yang ZL, Wu G, Dai YC, He SH, Cui BK, Zhou JL, Wu F, He MQ, Moncalvo JM, Hyde KD (2017) A six-gene phylogenetic overview of Basidiomycota and allied phyla with estimated divergence times of higher taxa and a phyloproteomics perspective. Fungal Divers 84(1):43–74

Zhou JL, Su SY, Su HY, Wang B, Callac P, Guinberteau J, Hyde KD, Zhao RL (2016) A description of eleven new species of *Agaricus* sections *Xanthodermatei* and *Hondenses* collected from Tibet and the surrounding areas. Phytotaxa 257(2):99–121

Zhu HY, Tian CM, Fan XL (2018) Multigene phylogeny and morphology reveal *Cytospora spiraeae* sp. nov. (*Diaporthales*, Ascomycota) in China. Phytotaxa 338(1):49–62

Zhuang WY (2001) Higher fungi of tropical China. Mycotaxon Limited, Ithaca

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