



## Mycosphere notes 345–386

**Manawasinghe IS<sup>1</sup>, Calabon MS<sup>2,3</sup>, Jones EBG<sup>4</sup>, Zhang YX<sup>1</sup>, Liao CF<sup>1,2,3</sup>, Xiong YR<sup>1,2,3</sup>, Chaiwan N<sup>2</sup>, Kularathnage ND<sup>1,2,3</sup>, Liu NG<sup>2,3</sup>, Tang SM<sup>2,3,5</sup>, Sysouphanthong P<sup>2,3,6</sup>, Du TY<sup>2,3,7,8</sup>, Luo M<sup>1</sup>, Pasouvang P<sup>2,3,9</sup>, Pem D<sup>2,3</sup>, Phonemany M<sup>2,3</sup>, Ishaq M<sup>10</sup>, Chen JW<sup>1</sup>, Karunarathna SC<sup>7</sup>, Mai ZL<sup>1</sup>, Rathnayaka AR<sup>2,3,11</sup>, Samarakoon MC<sup>12,13</sup>, Tennakoon DS<sup>2,18,19</sup>, Wijesinghe SN<sup>2,3</sup>, Yang YH<sup>1,2,3</sup>, Zhao HJ<sup>1,2,3</sup>, Fiaz M<sup>10</sup>, Doilom M<sup>1</sup>, Dutta AK<sup>14</sup>, Khalid AN<sup>15</sup>, Liu JW<sup>1</sup>, Thongklang N<sup>2,3</sup>, Senanayake IC<sup>1,3</sup>, Tibpromma S<sup>7</sup>, You LQ<sup>1</sup>, Camporesi E<sup>16</sup>, Gafforov YS<sup>17</sup> and Hyde KD<sup>1,2,18,19</sup>**

<sup>1</sup>Innovative Institute for Plant Health, Zhongkai University of Agriculture and Engineering, Guangzhou 510225, PR of China

<sup>2</sup>Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand

<sup>3</sup>School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand

<sup>4</sup>Department of Botany and Microbiology, College of Science, King Saud University, P.O Box 2455, Riyadh 11451, Saudi Arabia

<sup>5</sup>Biotechnology and Germplasm Resources Institute, Yunnan Academy of Agricultural Sciences, Kunming 650205, China

<sup>6</sup>Ecology Division, Biotechnology and Ecology Institute, Ministry of Science and Technology, P.O. Box: 2279, Vientiane Capital, Lao PDR

<sup>7</sup>Center for Yunnan Plateau Biological Resources Protection and Utilization, College of Biological Resource and Food Engineering, Qujing Normal University, Qujing, Yunnan 655011, P.R. China

<sup>8</sup>CIFOR-ICRAF China Program, World Agroforestry (ICRAF), Kunming 650201, China

<sup>9</sup>Plant Protection Unit, Department of Agronomy, Faculty of Agriculture, National University of Laos NUOL, P.O. Box: 7322, Dongdok, Vientiane, Lao PDR

<sup>10</sup>Department of Botany, Hazara University, Mansehra, Khyber Pakhtunkhwa, Pakistan

<sup>11</sup>Department of Plant Medicine, National Chiayi University, 300 Syuefu Road, Chiayi City 60004, Taiwan

<sup>12</sup>Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand

<sup>13</sup>Innovative Agriculture Research Centre, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand

<sup>14</sup>Department of Botany, Gauhati University, Gopinath Bordoloi Nagar, Jalukbari, Guwahati - 781014, Assam, India

<sup>15</sup>University of the Punjab, Department of Botany, Quaid-e-Azam Campus-54590, Lahore, Pakistan

<sup>16</sup>A.M.B. Gruppo, Micologico Forlivese "Antonio Cicognani", Via Roma 18, Forlì, Italy

<sup>17</sup>Laboratory of Mycology, Institute of Botany, Academy of Sciences of the Republic of Uzbekistan, 32 Durmon Yuli Street, Tashkent, 100125, Uzbekistan

<sup>18</sup>Research Center of Microbial Diversity and Sustainable Utilization, Faculty of Science, Chiang Mai University 50200, Chiang Mai, Thailand

<sup>19</sup>Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand

Manawasinghe IS, Calabon MS, Jones EBG, Zhang YX, Liao CF, Xiong Y, Chaiwan N, Kularathnage ND, Liu NG, Tang SM, Sysouphanthong P, Du TY, Luo M, Pasouvang P, Pem D, Phonemany M, Ishaq M, Chen JW, Karunarathna SC, Mai ZL, Rathnayaka AR, Samarakoon MC, Tennakoon DS, Wijesinghe SN, Yang YH, Zhao HJ, Fiaz M, Doilom M, Dutta AK, Khalid AN, Liu JW, Thongklang N, Senanayake IC, Tibpromma S, You LQ, Camporesi E, Gafforov YS, Hyde KD 2022 – Mycosphere notes 345–386. Mycosphere 13(1), 454–557, Doi 10.5943/mycosphere/13/1/3

## Abstract

This is the seventh in a series of Mycosphere notes in which we provide notes on the collection of fungi isolated from various hosts. In this set of notes, we introduce *Pseudophialocephala* as a new genus, nine new species, 27 new host or country records and five new combinations. The new species are *Ceratosphaeria yunnanensis*, *Cytospora salicis-albae*, *Gymnopus bunerensis*, *Kalmusia cordylines*, *Leucoagaricus croceus*, *Leucoagaricus laosensis*, *Neopyrenochaeta shaoguanica*, *Pseudophialocephala cuneata* and *Robillarda aquatica*. *Pseudophialocephala humicola*, *Pseudophialocephala aquatica*, *Pseudophialocephala salinicola*, *Pseudophialocephala terricola* and *Pseudophialocephala xalapensis* are introduced as new combinations. We provide new molecular data for 43 species belonging to two phyla, three classes and 15 orders. Updated phylogenetic trees for 22 families (*Agaricaceae*, *Botryosphaeriaceae*, *Chaetosphaeriaceae*, *Coniochaetaceae*, *Didymosphaeriaceae*, *Gloeophyllaceae*, *Glomerellaceae*, *Hysteriaceae*, *Lophiostomataceae*, *Magnaporthaceae*, *Neopyrenochaetaceae*, *Omphalotaceae*, *Phaeosphaeriaceae*, *Phyllostictaceae*, *Pleosporaceae*, *Sacotheciaceae*, *Savoryellaceae*, *Sporocadaceae*, *Stachybotryaceae*, *Torulaceae*, *Valsaceae*, *Physalacriaceae*) and 32 genera (*Alfaria*, *Aureobasidium*, *Ceratosphaeria*, *Collybiopsis*, *Colletotrichum*, *Comoclathris*, *Coniochaeta*, *Cytospora*, *Dothiorella*, *Gymnopus*, *Gymnopus*, *Heliocybe*, *Hysterium*, *Hysterobrevium*, *Kalmusia*, *Leptospora*, *Letendreaa*, *Leucoagaricus*, *Mucidula*, *Neoleptospora*, *Neopyrenochaeta*, *Paraleptospora*, *Phyllosticta*, *Pseudophialocephala*, *Rhytidhysterion*, *Robillarda*, *Savoryella*, *Sporocadus*, *Thozetella*, *Torula* and *Vaginatispora*) are given.

**Keywords** – 9 new taxa – 27 new records – 5 new combinations – Agaricomycetes – Ascomycota – Basidiomycota – Dothideomycetes – Molecular phylogeny – New hosts – New species – Sordariomycetes – Taxonomy

## Table of Contents

The numbers of taxa in this study are a continuation of Hyde et al. (2021) Mycosphere notes 325-344 – Novel species and records of fungal taxa from around the world.

## Phylum Ascomycota

### Class Dothideomycetes

#### Botryosphaeriales C.L. Schoch, Crous & Shoemaker (2007)

##### *Botryosphaeriaceae* Theiss. & Syd. 1918

345. *Dothiorella sarmentorum* (Fr.) A.J.L. Phillips, A. Alves & J. Luque (2005), new geographical record

##### *Phyllostictaceae* Fr. 1849

346. *Phyllosticta capitalensis* Henn., Hedwigia 48: 13 (1908), new host record on *Synsepalum dulcificum*

#### Dothideales Lindau (1897)

##### *Sacotheciaceae* Bonord. [as ‘Sacotheciei’] (1864)

347. *Aureobasidium melanogenum* (Herm-Nijh.) Zalar, Gostinčar & Gunde-Cim. (2014), new host record on *Khaya senegalensis*

#### Hysteriales Lindau (1897)

##### *Hysteriaceae* Chevall (1826)

348. *Hysterium angustatum* Alb. & Schwein (1805), new host record on *Debregeasia* sp.

399. *Hysterobrevium constrictum* (N. Amano) E. Boehm & C.L. Schoch (2009), new host record on *Alnus cremastogyne*

350. *Rhytidhysterium bruguierae* Dayarathne (2020), new host record on *Nauclea orientalis*

**Pleosporales** Luttr. ex M.E. Barr (1987)

**Didymosphaeriaceae** Munk (1953)

351. *Letendraea cordylinicola* Phook., Ariyaw. & K.D. Hyde (2014), new host record on *Synsepalum dulcificum*

352. *Kalmusia cordylinae* Kular., Senan., & K. D. Hyde, sp. nov.

**Lophiostomataceae** Luerss. (1877)

353. *Vaginatipora amygdali* A. Hashim., K. Hiray. & Kaz. Tanaka (2018), new host record on *Smilax china*

**Neopyrenochaetaceae** Valenz-Lopez, Crous, Stchigel, Guarro & Cano., (2017)

354. *Neopyrenochaeta shaoguanica* YR. Xiong, B. Xu, Manawas & K.D. Hyde, sp. nov.

**Phaeosphaeriaceae** M.E. Barr (1979)

355. *Leptospora thailandica* Phukhams. & K.D. Hyde (2016), new host record on *Sphagneticola trilobata*

356. *Paraleptospora chromolaenae* Mapook & K.D. Hyde (2020), new host record on *Tithonia diversifolia*

**Pleosporaceae** Nitschke (1869)

357. *Comoclathris lonicerae* Brahmanage, Camporesi & K.D. Hyde (2020), new host record on *Colutea arborescens*

**Torulaceae** Corda

358. *Torula fici* Crous (2015), new host record on *Hedychium coronarium*

## **Class Sordariomycetes**

**Amphisphaeriales** D. Hawksw. & O.E. Erikss. (1986)

**Sporocadaceae** Corda (1842)

359. *Robillarda aquatica* M.S. Calabon, E.B.G. Jones & K.D. Hyde, sp. nov.

360. *Sporocadus sorbi* (Wijayaw., Camporesi & K.D. Hyde) F. Liu, L. Cai & Crous (2018), new geographical record

**Chaetosphaeriales** Huhndorf, A.N. Mill. & F.A. Fernández (2004)

**incertae sedis**

361. *Neoleptospora camporesiana* R.H. Perera & K.D. Hyde (2020), new host record on *Heteropanax fragrans*

**Chaetosphaeriaceae** Réblová, M.E. Barr & Samuels (1999)

362. *Pseudophialocephala* M.S. Calabon, E.B.G. Jones & K.D. Hyde, gen. nov.

363. *Pseudophialocephala cuneata* N.G. Liu, M.S. Calabon, E.B.G. Jones & K.D. Hyde, sp. nov.

364. *Pseudophialocephala humicola* (S.C. Jong & E.E. Davis) M.S. Calabon, E.B.G. Jones & K.D. Hyde, comb. nov.

365. *Pseudophialocephala aquatica* (M.J. Wei & H. Zhang) M.S. Calabon, E.B.G. Jones & K.D. Hyde, comb. nov.

366. *Pseudophialocephala salinicola* (Dayarathne & E.B.G. Jones) M.S. Calabon, E.B.G. Jones & K.D. Hyde, comb. nov.

367. *Pseudophialocephala terricola* (Yong Wang bis, Jie & K.D. Hyde) M.S. Calabon, E.B.G. Jones & K.D. Hyde, comb. nov.

368. *Pseudophialocephala xalapensis* (Persiani & Maggi) M.S. Calabon, E.B.G. Jones & K.D. Hyde, comb. nov.

369. *Thozetella nivea* (Berk.) Kuntze (1891), new molecular data

**Coniochaetales** Huhndorf, A.N. Mill. & F.A. Fernández (2004)

**Coniochaetaceae** Malloch & Cain (1971)

370. *Coniochaeta velutina* (Fuckel) Cooke (1887), new host record on *Phyllostachys viridis*

**Diaporthales** Nannf. (1932)

**Valsaceae** Tul. & C. Tul. (1861)

371. *Cytospora salicis-albae* Chaiwan, Bulgakov & K.D. Hyde, sp. nov.

**Glomerellales** Chadeff. ex Réblová, W. Gams & Seifert (2011)

**Glomerellaceae** Locq. 1984

372. *Colletotrichum endophytica* Manamgoda, Udayanga, L. Cai & K.D. Hyde (2013), new host record on *Acacia confusa*

373. *Colletotrichum fruticicola* Prihast., L. Cai & K.D. Hyde (2009), new host record on *Zamia furfuracea* and *Bougainvillea* sp.

374. *Colletotrichum pandanicola* Tibpromma & K.D. Hyde (2018) new host record on *Reineckia carnea*

375. *Colletotrichum syzygicola* B.S. Weir & P.R. Johnst (2012), new host record on *Cymbidium* sp.

**Hypocreales** Lindau (1897)

**Stachybotryaceae** L. Lombard & Crous (2014)

376. *Alfaria cyperi-esculenti* Crous, Montañó-Mata & García-Jim. (2014), new host record on *Galium* sp. and *Cytisus* sp.

**Magnaporthales** P.F. Cannon (1994)

**Magnaporthaceae** P.F. Cannon (1994)

377. *Ceratospaeria yunnanensis* C.F. Liao & Doilom, sp. nov.

**Savoryellales** Boonyuen, Suetrong, Sivichai, K.L. Pang & E.B.G. Jones (2011)

**Savoryellaceae** Jaklitsch & Réblová (2015)

378. *Savoryella nypae* (K.D. Hyde & Goh) S.N. Zhang, K.D. Hyde & J.K. Liu, new host record

## Phylum Basidiomycota

### Class Agaricomycetes

**Agaricales** Underw. (1899)

**Agaricaceae** Chevall. (1826)

379. *Leucoagaricus croceus* S.M. Tang & K.D. Hyde, sp. nov.

380. *Leucoagaricus laosensis* Sysouph., sp. nov.

**Physalacriaceae** Corner (1970)

381. *Mucidula mucida* var. *venosolamellata* (Imazeki & Toki) R.H. Petersen (2010), new geographical record

**Omphalotaceae** Bresinsky (1985)

382. *Collybiopsis biformis* (Peck) Halling (1997), new geographical record

383. *Collybiopsis subnuda* (Ellis ex Peck) R.H. Petersen (2021), new geographical record

384. *Gymnopus bunerensis* Ishaq, M, Fiaz, M & Khalid, sp. nov.

385. *Gymnopus ocior* (Pers.) Antonín and Noordel. (1997), new geographical record

**Gloeophyllales** Thorn (2007)

**Gloeophyllaceae** Jülich (1982)

386. *Heliocybe villosa* Ming Zhang & T.H. Li (2018), new geographical record

## Introduction

In the last two decades, contributions to fungal taxonomy have increased rapidly (Hyde et al. 2019, 2020b, Phookamsak et al. 2019, Hyde et al. 2020b, 2020c, Cheek et al. 2020, Phukhamsakda et al. 2020, Yuan et al. 2020, Boonmee et al. 2021). The application of molecular techniques in fungal taxonomy has facilitated resolving species complexes, and the discovery of unculturable taxa from specialized environments (Thambugala et al. 2017, Hyde et al. 2020b, 2020c, Boonmee et al. 2021). However, publishing a single new species, new host record is challenging. Thus, the question pops up: where to publish these single entries? During past years publications series including Fungal Diversity notes, Fungal Biodiversity Profiles, Fungal Systematics and Evolution—New and Interesting Fungi, Mycosphere notes, and Fungal Planet has facilitated the publication of over 2000 single entries.

The Mycosphere note series publishes notes on new fungal taxa, new host records and new geographical records with molecular data (Thambugala et al. 2017, Boonmee et al. 2017, Jayawardena et al. 2018, Hyde et al. 2018, Pem et al. 2019, Hyde et al. 2021). In addition, several papers in this series focused on specialized research topics such as grass (*Poaceae*) inhabiting Dothideomycetes (Thambugala et al. 2017) and saprotrophic fungi on *Vitis* (Jayawardena et al. 2018). To date, over 100 species have been introduced in this series. This is the seventh paper in the Mycosphere note series with 43 taxa from contributions worldwide.

## Materials & Methods

For species isolation and morphological characterizations, Senanayake et al. (2020) was followed. For molecular identification and phylogenetic analyses, Dissanayake et al. (2020) was followed. Furthermore, phylogenetic relationships were inferred using maximum parsimony (MP) implemented in PAUP (v4.0) (Swofford & Sullivan 2003), maximum likelihood (ML) in RAxML (Silvestro & Michalak 2016) and Bayesian posterior probability analysis (BYPP) in MrBayes (v3.0b4) (Ronquist & Huelsenbeck 2003). Species delineations were based on Cao et al. (2021), Chethana et al. (2021), Jayawardena et al. (2021), Maharachchikumbura et al. (2021), Manawasinghe et al. (2021), and Pem et al. (2021). Taxonomic novelties were submitted to the Faces of Fungi database (Jayasiri et al. 2015) and Index Fungorum (2021). Sequences generated in this study were deposited in GenBank and accession numbers are given under each entry. Order of classes, family and genus is organized as in Wijayawardene et al. (2020, 2022). Species descriptions, phylogenetic analysis and notes for taxa identified in this study are provided. The Greater Mekong Subregion records are added to the GMS MICROFUNGI database (Chaiwan et al. 2021).

## Taxonomy

### Dothideomycetes

For treatments of Dothideomycetes, we follow Hongsanan et al. (2020a, b).

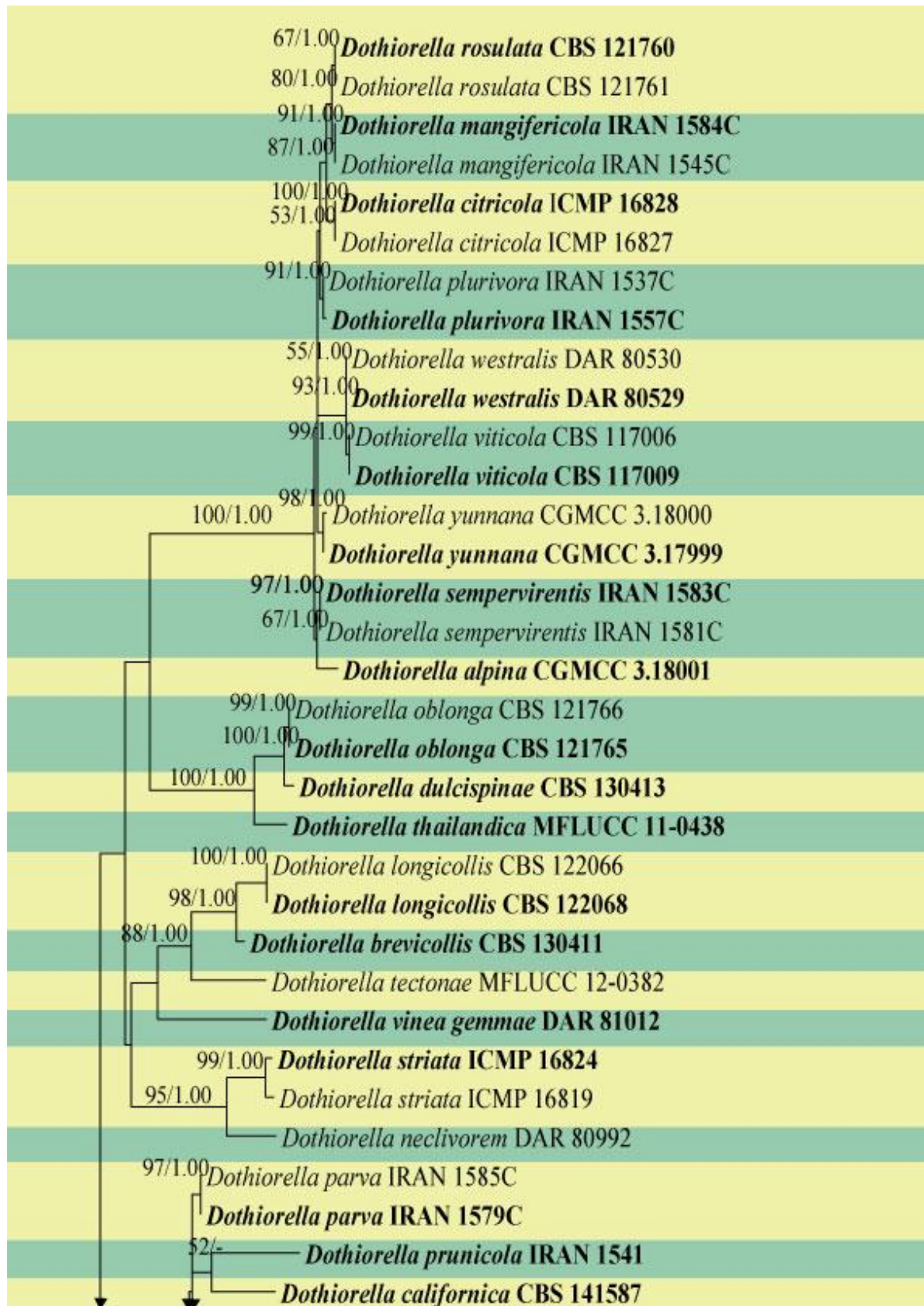
### *Botryosphaeriaceae*

*Botryosphaeriaceae* encompasses endophytes, pathogens and saprobes on a wide range of hosts worldwide (Hongsanan et al. 2020b). They are opportunistic pathogens on many economically important crops (Chethana et al. 2016, Manawasinghe et al. 2016). For taxonomic treatments of this family, we follow Phillips et al. (2019), Hongsanan et al. (2020b), Zhang et al. (2020) and Wu et al (2021).

### *Dothiorella* Sacc., *Michelia* 2(no. 6): 5 (1880)

*Dothiorella* was introduced by Saccardo (1880) with *D. pyrenophora* as the type species. The asexual morph of *Dothiorella* species is more prevalent and characterized by brown and 1-septate conidia. Sexual morphs of *Dothiorella* are characterised by pigmented, septate ascospores. There are

257 morphological species of *Dothiorella* but only 44 species have molecular data (Hongsanan et al. 2020b). *Dothiorella* species are endophytes, pathogens and saprobes on a wide variety of woody hosts (Crous et al. 2006, Hyde et al. 2013, Liu et al. 2012, Phillips et al. 2013).



**Figure 1** – Phylogenetic tree generated by ML analysis of combined ITS and *tef1-α* sequence data of 66 species. The analyses included 65 strains and the tree is rooted with *Neofusicoccum parvum*

(CMW 9081). The tree topology of the ML analysis was similar to the MP and BYPP. The best scoring RAxML tree with a final likelihood value of -5745.297124 is presented. The matrix had 451 distinct alignment patterns, with 19.92% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.213010, C = 0.286649, G = 0.252833, T = 0.247507; substitution rates AC = 1.439556, AG = 2.497377, AT = 1.290192, CG = 1.356569, CT = 5.095700, GT = 1.000000; gamma distribution shape parameter  $\alpha = 0.575367$ . RAxML bootstrap support values  $\geq 50\%$  and maximum parsimony bootstrap support values  $\geq 50\%$  are shown near the nodes. Nodes with  $\geq 0.95$  (BYPP) Bayesian posterior probabilities are indicated with thickened lines. The scale bar indicates 0.04 changes per site. Ex-type/ ex-epitype strains are in bold. New isolates recovered in this study are in red.

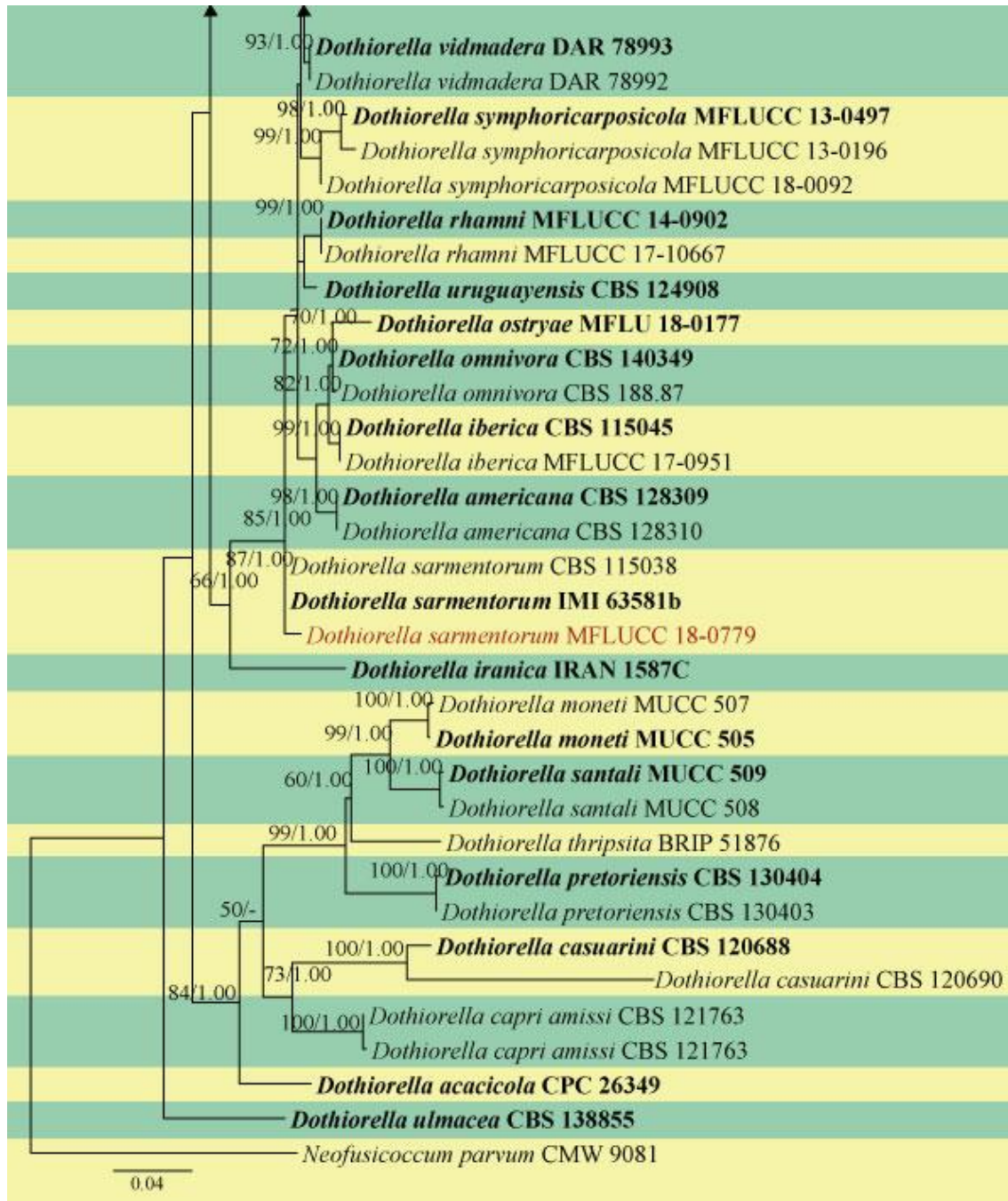


Figure 1 – Continued.

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

Fig. 2

Index Fungorum number: IF 501403; Facesoffungi number: FoF 02148

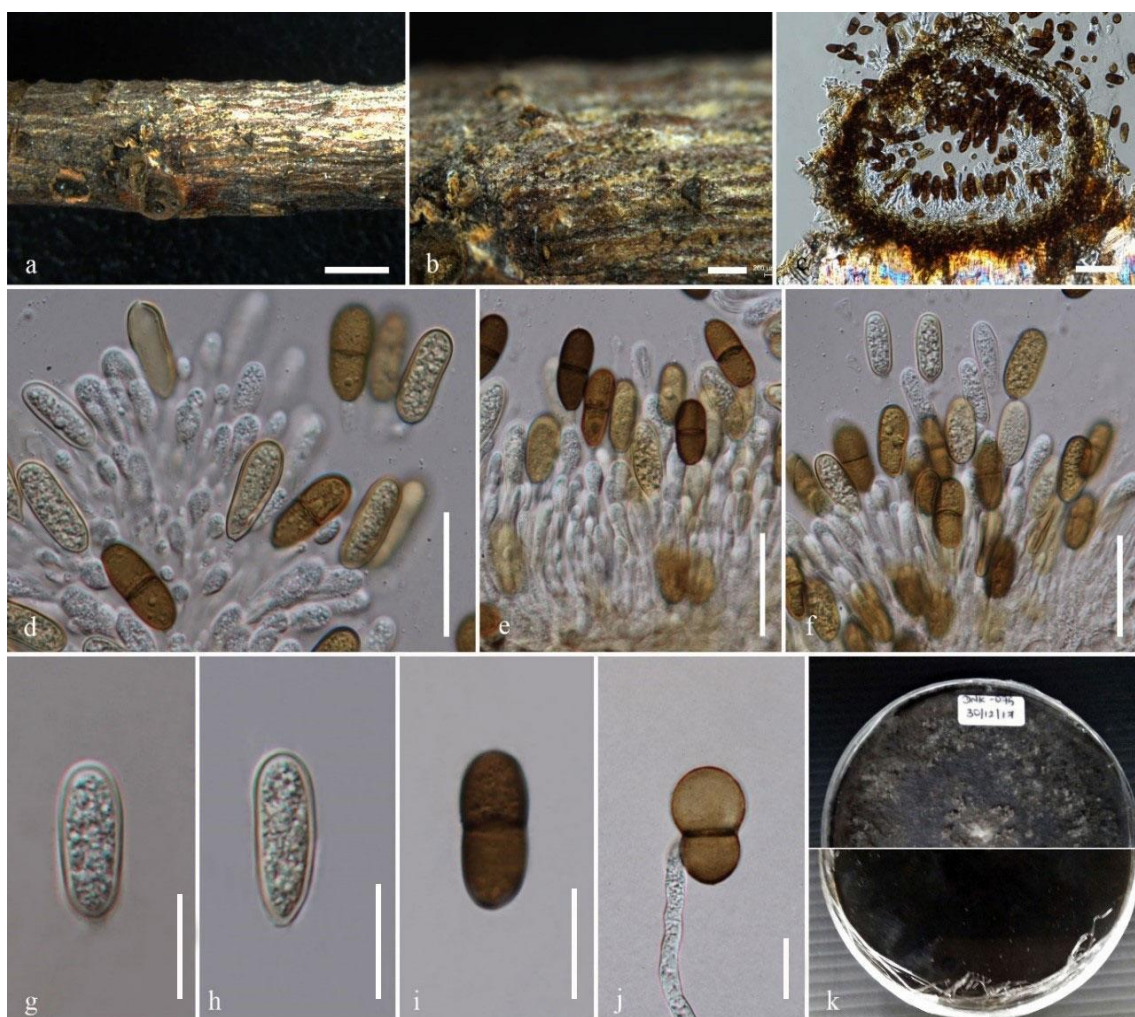
≡ *Sphaeria sarmentorum* Fr., K. svenska Vetensk-Akad. Handl., ser. 3 40: 107 (1819)

*Saprobic* on a dead twigs and branches of *Ulmus minor*. Sexual morph: Not observed. Asexual morph: Ceolomycetous. *Conidiomata* 320–450  $\mu\text{m}$  high  $\times$  220–350  $\mu\text{m}$  diam., semi-immersed, solitary, stromatic, globose. *Conidiomatal wall* 19–30  $\mu\text{m}$  composed of dark brown, thick-walled cells of *textura angularis*, becoming thin-walled and hyaline toward the inner region. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 10–15  $\times$  5–10  $\mu\text{m}$  ( $\bar{x}$  = 9.2  $\times$  5.2  $\mu\text{m}$ , n = 10), lining the pycnidial cavity, holoblastic, hyaline, subcylindrical, developing at the same level giving rise to periclinal thickenings or rarely proliferating per currently to form one or two close, indistinct annellations. *Conidia* 14–16  $\times$  4–6  $\mu\text{m}$  ( $\bar{x}$  = 15.3  $\times$  5.7  $\mu\text{m}$ , n = 10), brown walled, 1-septate, slightly constricted at the septum, rod-shaped to ovoid with a broadly rounded apex and truncate base.

Culture characteristics – Colonies on MEA, reaching 20–30 mm diam. after 4 weeks at 25°C, circular, surface rough, entire edge with dense mycelium, above and reverse black, whitish at the center, form small black stromatic flakes on the colony surface.

Material examined – Ukraine, Donetsk Region, Donetsk City, Shakhtarsk District, Donetsk, Regional Landscape Park «Donetsk ridge» (Rus. Donetsk kryazh), old artificial forest, on dead twigs and branches of *Ulmus minor* Mill. (*Ulmaceae*), 19 May 2017, T.S. Bulgakov (MFLU 17-2497, new geographical record), living culture MFLUCC 18-0779.

GenBank accession numbers – ITS: OK642280, *tefl- $\alpha$* : OL829928.



**Figure 2** – *Dothiorella sarmentorum* (MFLU 17-2497, new geographical record). a, b Appearance of conidiomata on the host surface. c Vertical section through conidioma. d–f Conidia developing on



conidiogenous cells. g–i Conidia. j Germinating conidium. k Culture characteristics on MEA. Scale bars: a = 1000  $\mu\text{m}$ , b = 500  $\mu\text{m}$ , c = 10  $\mu\text{m}$ , d–f = 20  $\mu\text{m}$ , g–j = 10  $\mu\text{m}$ .

Notes – Our taxon MFLUCC 18-0779 is morphologically similar and phylogenetically related to *Dothiorella sarmentorum* (Fig. 1). *Dothiorella sarmentorum* on *Ulmus minor* was reported from England, Italy while this collection is from Ukraine collected on *Ulmus minor* from a different geographical location (Farr & Rossaman 2022).

**Phyllostictaceae** Fr. [as ‘Phyllostictici’], Summa veg. Scand., Sectio Post. (Stockholm): 420 (1849).

For taxonomic treatments of this family, we follow Phillips et al. (2019), Hongsanan et al. (2020b) and Zhang et al. (2020).

**Phyllosticta** Pers., Traité champ. Comest. (Paris): 55, 147 (1818)

*Phyllosticta* was previously placed in *Botryosphaeriaceae*, as following phylogenetic analysis by Wikee et al. (2013) placed this genus in *Phyllostictaceae*.

**Phyllosticta capitalensis** Henn., Hedwigia 48: 13 (1908) [1909]

Fig. 4

Index Fungorum number: IF 168326; Facesoffunginumber: FoF 06888

Associated with *Synsepalum dulcificum* leaf spots. Sexual morph: Not observed. Asexual morph: *Conidia* hyaline, transparent, single-celled, smooth wall, mostly pear-shaped, or long pear-shaped, with a size of 10–15  $\mu\text{m}$   $\times$  5–10  $\mu\text{m}$  ( $\bar{x}$  = 11 $\pm$ 0.9  $\times$  6 $\pm$ 0.6  $\mu\text{m}$ , n = 50), wrapped by a layer of transparent mucus, with a transparent accessory filament at the distal end of the conidia, 3–15  $\mu\text{m}$  long.

Culture characteristics – Colonies on PDA, reaching 4 cm diam. after 7 days at 25°C, white from above, dark green or dark brown, dark green from below, with raised elevation, margin undulate. Colonies on MEA and OA reach 3 cm and 2 cm diam. after 7 days at 25°C, respectively.

Material examined – China, Guangzhou, Guangdong Province, on *Synsepalum dulcificum* (Schumach. & Thonn.) Daniell., (*Sapotaceae*), March 2021, Y.H. Huang & L.Q. You (new host record), living culture ZHKUCC 21-0107.

GenBank accession numbers – LSU: OL687398, ITS: OL687395; *tef1- $\alpha$* : OL828267; *act*: OL828268.

Notes – In the phylogenetic analysis, our taxon clustered with *P. capitalensis* (CBS 101228), with 87% ML and 97% MP (Fig. 3) support. When comparing the morphology of *Phyllosticta capitalensis* with other presentative strains our isolate shares similar conidial morphology and culture characters (Wikee et al. 2013). *Phyllosticta capitalensis* has a very wide host range and may be a species complex (Bhunjun et al. 2022). Based on both morphological and molecular data, we introduce *Phyllosticta capitalensis* (ZHKUCC 21-0107) as a new host record for *Synsepalum dulcificum*.

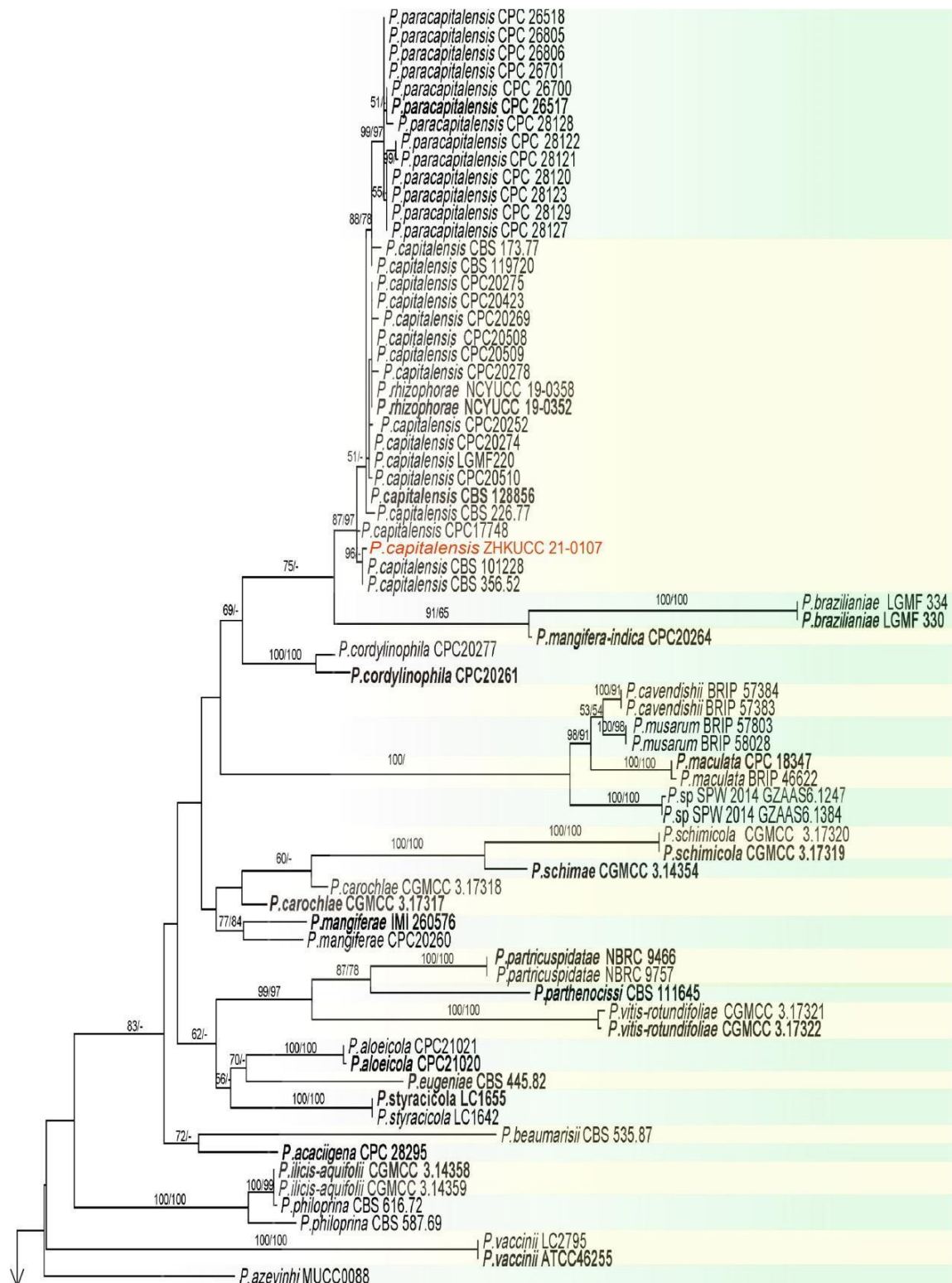
**Dothideales** Lindau

**Sacotheciaceae** Bonord. [as ‘Sacotheciei’], Abh. naturforsch. Ges. Halle 8: 82 (1864)

Species belonging to this family are parasitic or saprobic on twigs, wood and leaves on a wide range of hosts and human skin (Thambugala et al. 2014, Hongsanan et al. 2020b). Seven genera are accepted in this family. For taxonomic treatments we follow Hongsanan et al. (2020b).

**Aureobasidium** Viala & G. Boyer, Rev. gén. Bot. 3: 371(1891)

*Aureobasidium* is typified by *A. pullulans* (Schoch et al. 2006, Thambugala et al. 2014). The genus typically forms aseptate, dark and also sometimes hyaline conidia. Members of this genus are parasitic or saprobic on a wide range of plants, fruits and cause human skin diseases (Thambugala et al. 2014a, van Nieuwenhuijzen et al. 2016).



**Figure 3** – Phylogenetic tree generated by ML analysis of combined ITS, LSU, *gapdh*, *tef1-α* and *act* sequence data set for *Phyllosticta* species. The analyses consisted with 156 strains and the tree is rooted with *Botryosphaeria stevensii* (CBS 112553). The tree topology of the ML analysis was similar to the MP. The best scoring RAxML tree with a final likelihood value of -21744.764919 is presented. The matrix had 1131 distinct alignment patterns, with 39.71% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.217255, C = 0.283299, G = 0.278942, T = 0.220504; substitution rates AC = 1.300430, AG = 3.840652, AT = 1.687481, CG = 1.452310, CT = 9.334606, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.667828. Maximum parsimony analysis of 2100 constant characters and 719 informative characters resulted in 100 equally most

parsimonious trees (CI = 0.413, RI = 0.816, RC = 0.338, HI = 0.587). RAxML bootstrap support values and maximum parsimony bootstrap support values  $\geq 50\%$  are shown near the nodes. The scale bar indicates 0.04 changes per site. Ex-type/ex-epitype strains are in bold. New isolates recovered in this study are in red.

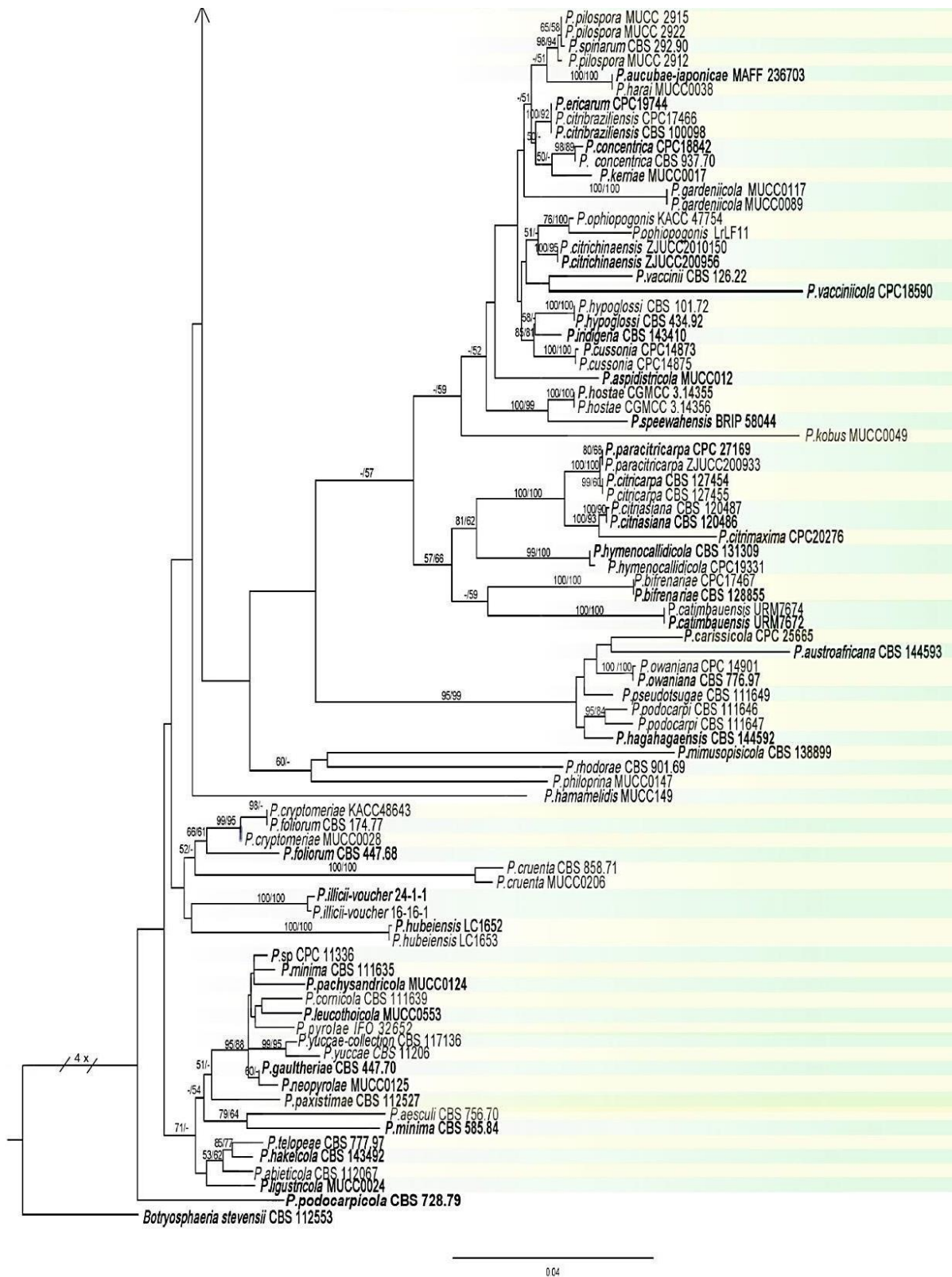
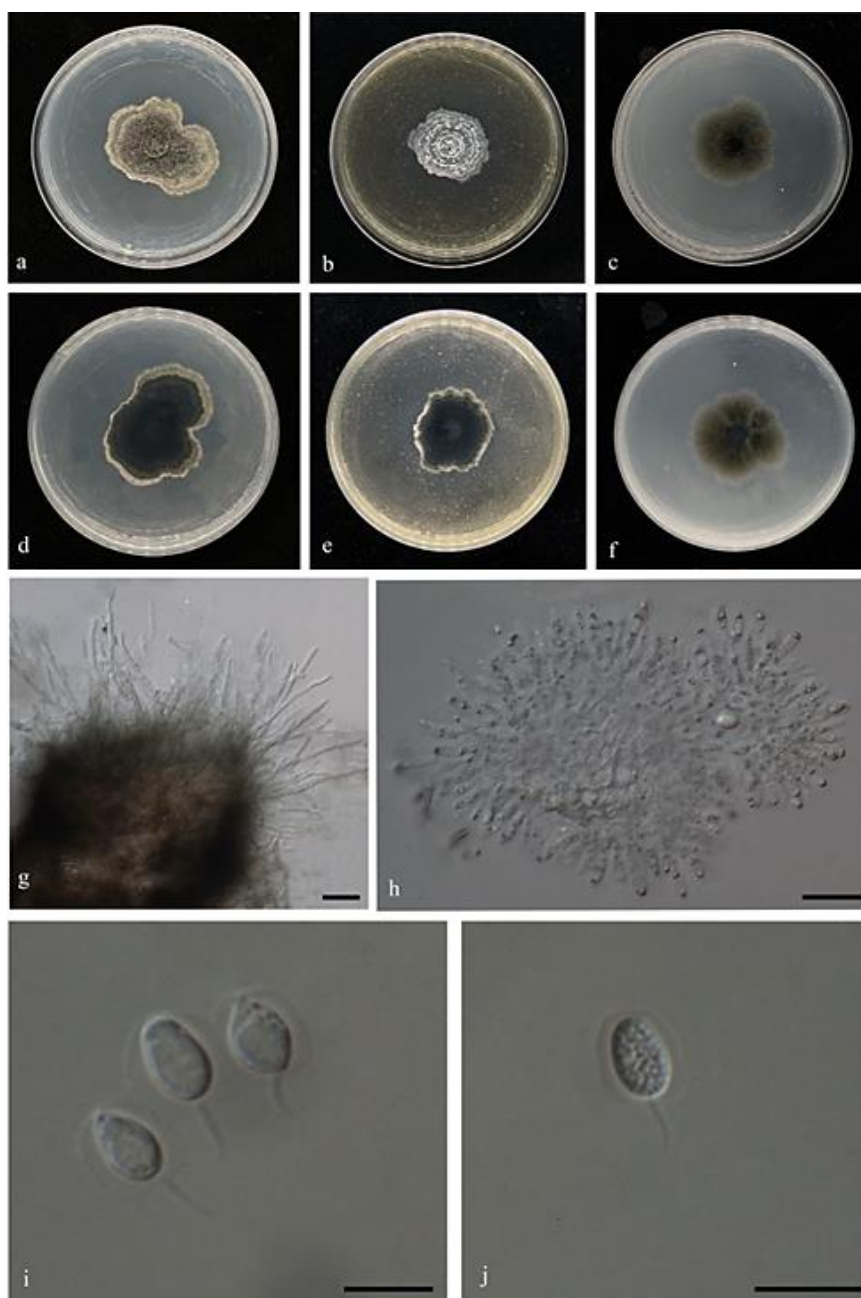


Figure 3 – Continued.



**Figure 4** – *Phyllosticta capitalensis* (ZHKUCC 21-0107, new host record). a Upper view of colony characteristics on PDA. b Reverse view of colony characteristics on MEA. c Upper view of colony characteristics on OA. d Reverse view of colony characteristics on PDA. e Upper view of colony characteristics on MEA. f Reverse view of colony characteristics on OA. g Hypha. h Conidiogenous cells. i–j Conidia. Scale bars: g–h = 25  $\mu$ m, i–j = 10  $\mu$ m.

*Aureobasidium melanogenum* (Herm-Nijh.) Zalar, Gostinčar & Gunde-Cim., in Gostinčar, Ohm, Kogej, Sonjak et al. BMC Genomics 15(1): 16 (2014) Fig. 6

Index Fungorum number: IF 807698; Facesoffunginumber: FoF 00098

Saprobic on *Khaya senegalensis*. Sexual morph: *Ascstromata* 600–800  $\mu$ m high  $\times$  500–800  $\mu$ m diam ( $\bar{x}$  = 710  $\times$  662  $\mu$ m, n = 10), dark brown to black, semi-immersed on host tissue, solitary, scattered, globose to subglobose, carbonaceous. *Peridium* 40–170  $\mu$ m diam ( $\bar{x}$  = 115  $\mu$ m, n = 30)  $\mu$ m, thick-walled, comprised of an inner layer of hyaline cells and an outer layer of brown cells of *textura angularis*. *Hamathecium* unbranched 1–4  $\mu$ m diam ( $\bar{x}$  = 3  $\mu$ m, n = 30), longer than asci. *Asci* 150–200  $\times$  5–10  $\mu$ m ( $\bar{x}$  = 180  $\times$  10  $\mu$ m, n = 30), 8-spored, unitunicate, cylindrical, rounded at the apex, with an ocular chamber. *Ascospores* 20–40  $\times$  5–10  $\mu$ m ( $\bar{x}$  = 30  $\times$  7  $\mu$ m, n = 30), overlapping uniseriate,

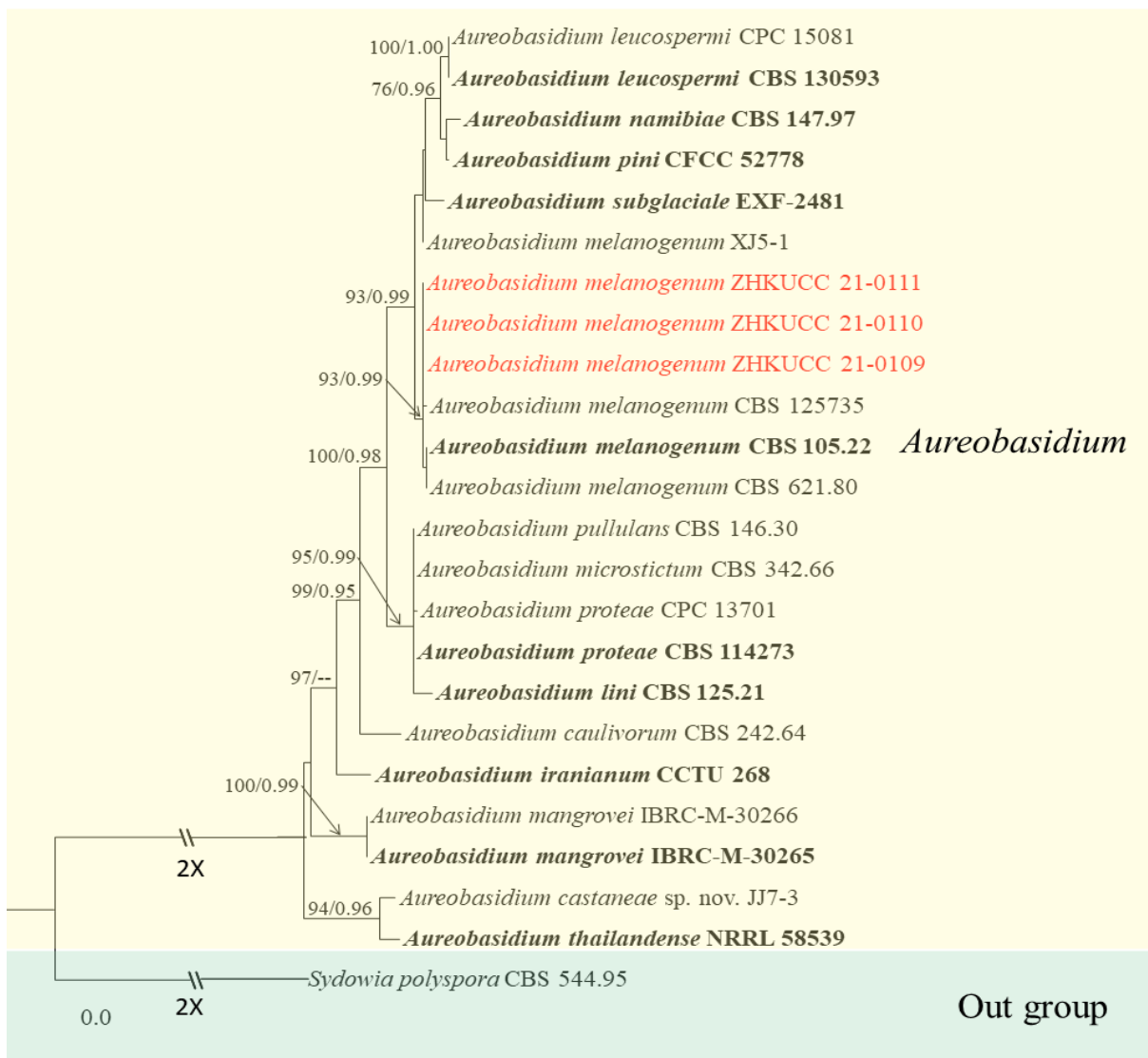
1–3 septate, constricted at the septum, fusiform to ellipsoid, gradually tapering towards the apex, containing up to four refractive oil globules. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching up to 80 mm in 14 days at 25°C, smooth, flat, cream-colored from above and below, rounded margins.

Material examined – China, Guangdong Province, Guangzhou City, Haizhu District, Zhongkai University of Agriculture Engineering, 23°6'32" N, 113°16'37" E, alt. 20 m, on the bark of *Khaya senegalensis* (Desr.) A. Juss. (*Meliaceae*), 27 July 2021, YH. Yang & CF. Liao (ZHKU 21-0099, new host record), living culture ZHKUCC 21-0109, ZHKUCC 21-0110, ZHKUCC 21-0111.

GenBank accession numbers – LSU: OL621897, OL621898, OL621899; ITS: OL584325, OL584327, OL584326.

Notes – In the phylogenetic tree, our new collection is closely affiliated with *Aureobasidium melanogenum* (CBS 125735) with 93% ML bootstrap and 1.00 BYPP values (Fig. 5). Most of the species in this genus are recorded as asexual morphs and we account for a sexual morph herein. Our species was first discovered on *Khaya senegalensis*. Hence, we illustrated a new record on *Khaya senegalensis*.



**Figure 5** – Phylogram generated from RAxML analysis based on combined ITS and LSU sequence data of *Aureobasidium* isolates. The tree is rooted to *Sydowia polyspora* (CBS 544.95). The tree topology of the ML analysis was similar to the MP and BYPP. The best scoring RAxML tree with a final likelihood value of -1518.634967 is presented. The matrix had 105 distinct alignment patterns, with 4.07% of undetermined characters or gaps. Estimated base frequencies were as follows: A =

0.249151, C = 0.241978, G = 0.249245, T = 0.259626; substitution rates AC = 1.413344, AG = 1.754716, AT = 3.122952, CG = 0.888557, CT = 8.423714, GT = 1.000000; gamma distribution shape parameter  $\alpha = 0.167616$ . RAxML bootstrap support values  $\geq 50\%$  and maximum parsimony bootstrap support values  $\geq 50\%$  are shown near the nodes. Nodes with  $\geq 0.95$  Bayesian posterior probabilities (BYPP) are indicated with thickened lines. The scale bar indicates 0.04 changes per site. Ex-type/ ex-epitype strains are in bold. New isolates recovered in this study are in red.



**Figure 6** – *Aureobasidium melanogenum* (ZHKU 21-0099, new host record). a–c Appearance of ascomata on dead wood. d Section through an ascoma. e Peridium. f Hamathecium. g–j Asci. k–p Ascospores. Scale bars: d–j = 50  $\mu\text{m}$ , k–p = 20  $\mu\text{m}$ .

***Hysteriaceae*** Chevall. [as ‘Hysterineae’], Fl. gén. env. Paris (Paris) 1: 432 (1826)

*Hysteriaceae* was introduced by Chevallier (1826) which has been traditionally defined as specialized ascocarp termed the hysterothecium (Clements 1909). There are 13 genera in this family viz; *Actidiographium*, *Gloniella*, *Gloniopsis*, *Hystero brevium*, *Hystero carina*, *Hystero diffractum*, *Hystero glonium*, *Oedo hystero*, *Ostroichnion*, *Pseudo scypha*, *Psilo glonium*, *Rhytid hystero* and *Hystero* as the type genus (Hongsanan et al. 2020b).

***Hysterium*** Pers., Tent. disp. meth. fung. (Lipsiae): 5 (1797)

*Hysterium* was introduced by Persoon (1797), with *Hysterium pulicare* as the type species. There are 224 records listed in Species Fungorum (2021), while only 16 species have molecular data (Hongsanan et al. 2020b). This genus is characterised by three or more transversely septate, pigmented, versicolorous or concolorous asymmetric phragmospores, borne in hysterothecia (Boehm et al. 2009).

***Hysterium angustatum*** Alb. & Schwein., Consp. fung. (Leipzig): 55 (1805)

Fig. 8

Index Fungorum number: IF 221405; Facesoffungi number: FoF 04579

*Saprobic* on dead stems of *Debregeasia* sp. Sexual morph: *Ascomata* 500–700 × 200–280 × 200–230 µm ( $\bar{x}$  = 625 × 237 × 209 µm, n = 10), elongate and depressed conchate, scattered or aggregated, semi-immersed to superficial, base immersed in substrate, surface black, shiny, longitudinally striate, apex compressed, opening by a longitudinal slit. *Peridium* 40–60 µm wide ( $\bar{x}$  = 53 µm, n = 10), carbonaceous, brittle, heavily pigmented, consists of brown to black prosenchymatous cells of *textura globulosa* to *textura angularis*. *Hamathecium* 1–2 µm wide, septate, branched, pseudoparaphyses, borne in a gel matrix. *Asci* 60–80 × 10–15 µm ( $\bar{x}$  = 68 × 12 µm, n = 20), 8-spored, bitunicate, oblong to clavate, with a short narrow pedicel, apically thickened. *Ascospores* 15–20 × 5–10 µm ( $\bar{x}$  = 16 × 5.5 µm, n = 20), uniseriate to biseriate, fusiform, hyaline when young and becoming brown at maturity, 3-septate, smooth-walled, 1–6 different sized and prominent guttules, without mucilaginous sheath. Asexual morph: not observed.

Culture characteristics – Colonies on PDA, slow-growing, reaching 2 cm diam. after 14 days at 25°C under natural light conditions, white to light brown from above, middle brown and edge light brown from below, produce yellow secretion, with dense mycelium, flat and circular margin.

Material examined – China, Guizhou Province, Guiyang City, Yunyan District, Zaoshan Road Qianling Mountain Park, on dead stems of *Debregeasia* sp. (*Urticaceae*), 10 February 2021, T.Y. Du, (HKAS 121128, new geographical and host record); living culture, KUMCC 21-0213.

GenBank accession numbers – ITS: OK482567; LSU: OK482568; SSU: OK442653; *tef1-α*: OK398120; *rpb2*: OK506219.

Notes – In phylogenetic analyses (Fig. 7), our taxon (KUMCC 21-0213) grouped with the *Hysterium angustatum* clade. Our collection from *Debregeasia* sp. from China is morphologically similar to *Hysterium angustatum* in having 3-septate, brown, fusiform ascospores (Jayasiri et al. 2018). *Hysterium angustatum*, was isolated from unidentified hosts in Kenya, New Zealand, North America (Boehm et al. 2009, Jayasiri et al. 2018). To our knowledge, this is a new geographical and a new host record of *Hysterium angustatum* on *Debregeasia* sp. from China.

***Hysterobrevium*** E. Boehm & C.L. Schoch, in Boehm, Mugambi, Miller, Huhndorf, et al. Stud. Mycol. 64, 62 (2009)

*Hysterobrevium* was introduced by Boehm et al. (2009) with three new combinations (*Hysterobrevium constrictum*, *H. mori* and *H. smilacis*) and *H. mori* as the type species. There are seven records in Index Fungorum (2021) with molecular data. This genus is characterized by hyaline or pigmented dictyospores, usually less than 25 µm long, and constricted at least at the median septum (Boehm et al. 2009).

***Hysterobrevium constrictum*** (N. Amano) E. Boehm & C.L. Schoch, in Boehm et al., Stud. Mycol. 64, 64 (2009)

Fig. 9

Index Fungorum number: IF 515337; Facesoffungi number: FoF 06461

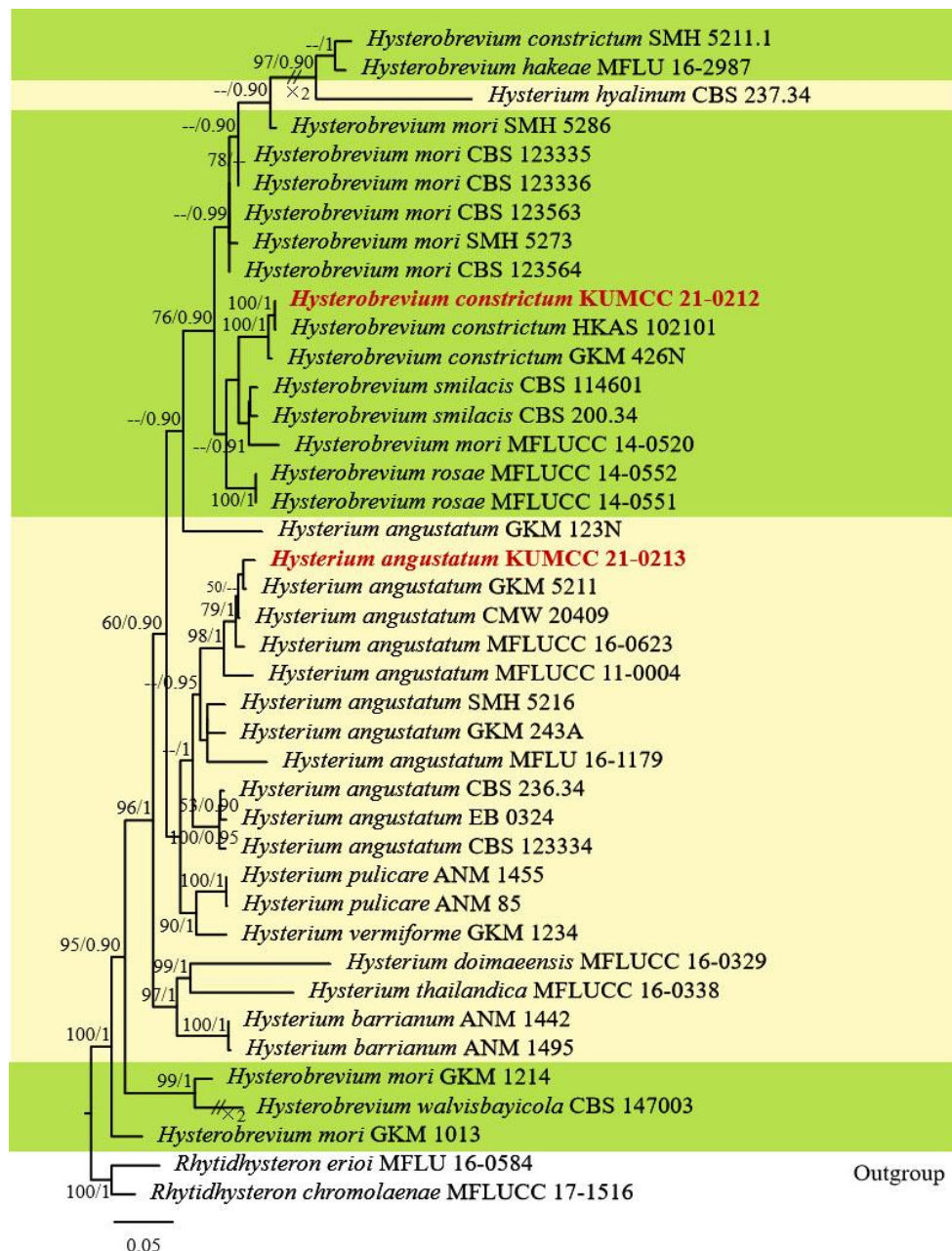
≡ *Gloniopsis constricta* N. Amano, Trans. Mycol. Soc. Japan 24(3): 289 (1983)

*Saprobic* on dead twigs of *Alnus cremastogyne*. Sexual morph: *Ascomata* 600–1000 × 350–500 × 250–350 µm ( $\bar{x}$  = 900 × 430 × 285 µm, n = 10), elongate and depressed conchate, sometimes bent or deformed, scattered or aggregation, semi-immersed to superficial, base immersed in substrate, surface black, shiny, longitudinally striate. *Peridium* 30–60 µm ( $\bar{x}$  = 38 µm, n = 10) wide, carbonaceous, thick-walled, brown to black cells of *textura globulosa* to *textura angularis*.

*Hamathecium* 1–2 µm wide, hyaline, numerous, branched, pseudoparaphyses. *Asci* 90–120 × 20–30 µm ( $\bar{x}$  = 102 × 23 µm, n = 20), 8-spored, short pedicellate, rounded at the apex. *Ascospores* 20–30 × 10–15 µm ( $\bar{x}$  = 25 × 10 µm, n = 20), uniseriate, muriform, ellipsoid to fusoid, hyaline, smooth-walled, guttules, without mucilaginous sheath. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA, slow-growing, reaching one cm diam. after 14 days at 25°C under natural light conditions, grey from above, dark grey from below, mycelium was dense, the surface was raised, and black secretion was produced, margin flat and circular.

Material examined – China, Guizhou Province, Guiyang City, Yunyan District, Zaoshan Road Qianling Mountain Park, on dead twigs of *Alnus cremastogyne* Burkill (*Betulaceae*), 10 February 2021, T.Y. Du, (HKAS 121127, new host record), living culture KUMCC 21-0212.



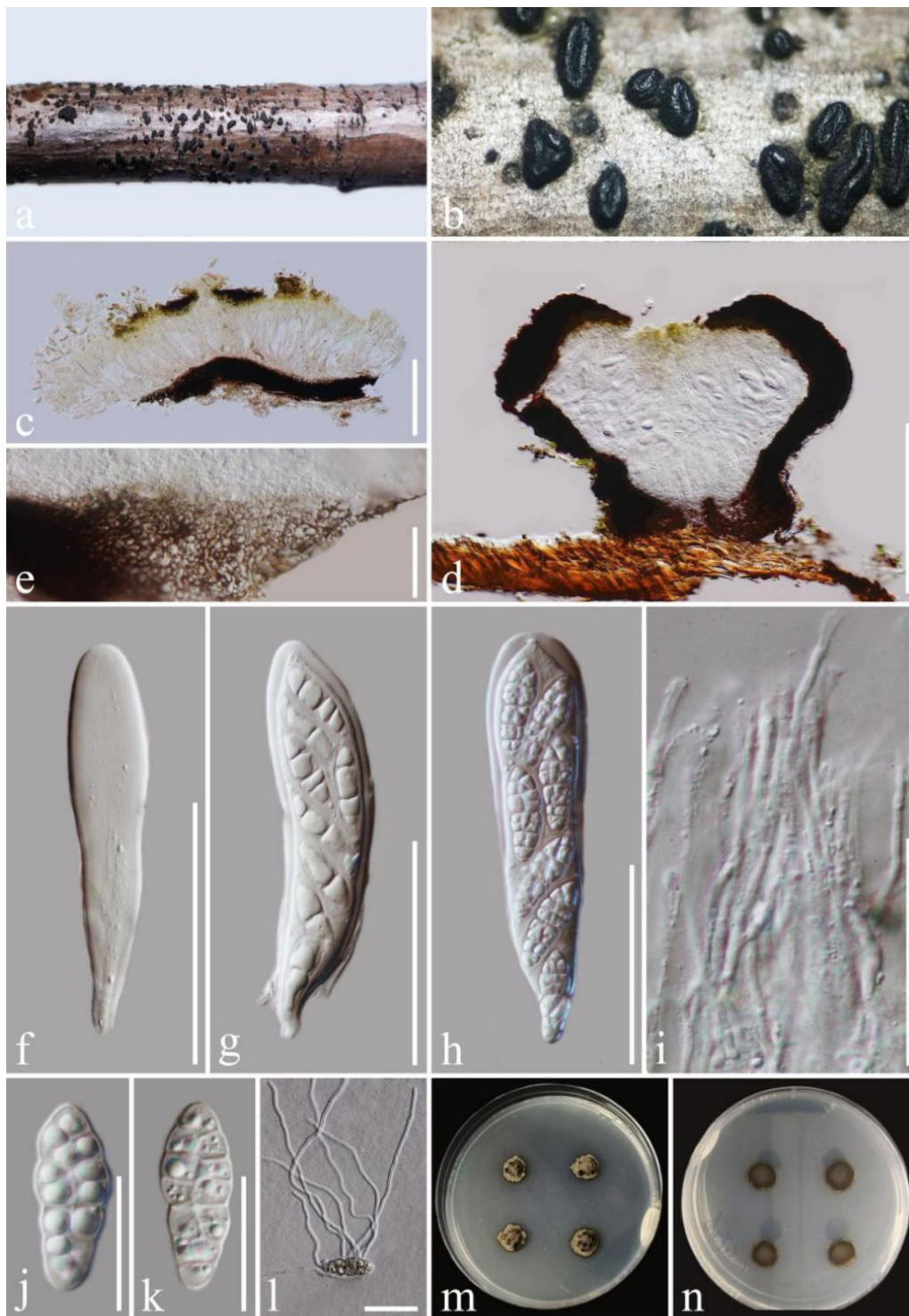
**Figure 7** – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, SSU, *tef1-α* and *rpb2* sequence data. In total, 41 taxa were included in the combined analyses, which comprised 4628 characters (LSU = 1386 bp, ITS = 664 bp, SSU = 880 bp, *tef1-α* = 994 bp, *rpb2* = 704 bp) after alignment. The tree is rooted to *Rhytidhysterion chromolaenae* (MFLUCC 17-1516) and *Rhytidhysterion erioi* (MFLU 16-0584). The best scoring RAxML tree with a final likelihood value



of -19641.984840 is presented. The matrix had 1350 distinct alignment patterns, with 53.90% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.251586, C = 0.240303, G = 0.279133, T = 0.228978; substitution rates: AC = 1.365345, AG = 2.881005, AT = 1.129130, CG = 0.890143, CT = 6.883958, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.453286. Bootstrap support values for ML equal to or greater than 50% and clade credibility values greater than 0.90 (the rounding of values to two decimal proportions) from Bayesian inference analysis are labelled at each node. Ex-type strains are in black bold and isolates from this study are red bold.



**Figure 8** – *Hysterium angustatum* (HKAS 121128, new host record). a, b Appearance of hysterothecia on dead stems of *Debregeasia* sp. c Section through hysterothecium. d Peridium. e Hamathecium. f-j Asci. k-o Ascospores. p. Germinating ascospore. q, r Culture characters on PDA (q: Above view; r: Reverse view). Scale bars: c = 100  $\mu$ m, d, f-j = 50  $\mu$ m, e, k-o = 10  $\mu$ m, p = 30  $\mu$ m.



**Figure 9** – *Hysterobrevium constrictum* (HKAS 121127, new host record). a, b Appearance of hysterothecia on dead twigs of *Alnus cremastogyne*. c, d Section through hysterothecium. e Peridium. f-h Asci. i Hamathecium. j, k Ascospores. l Germinating ascospore. Culture characters on PDA (m: Above view; n: Reverse view). Scale bars: c, d = 200  $\mu$ m, e, j, k = 20  $\mu$ m, f-h = 50  $\mu$ m, i, l = 30  $\mu$ m.

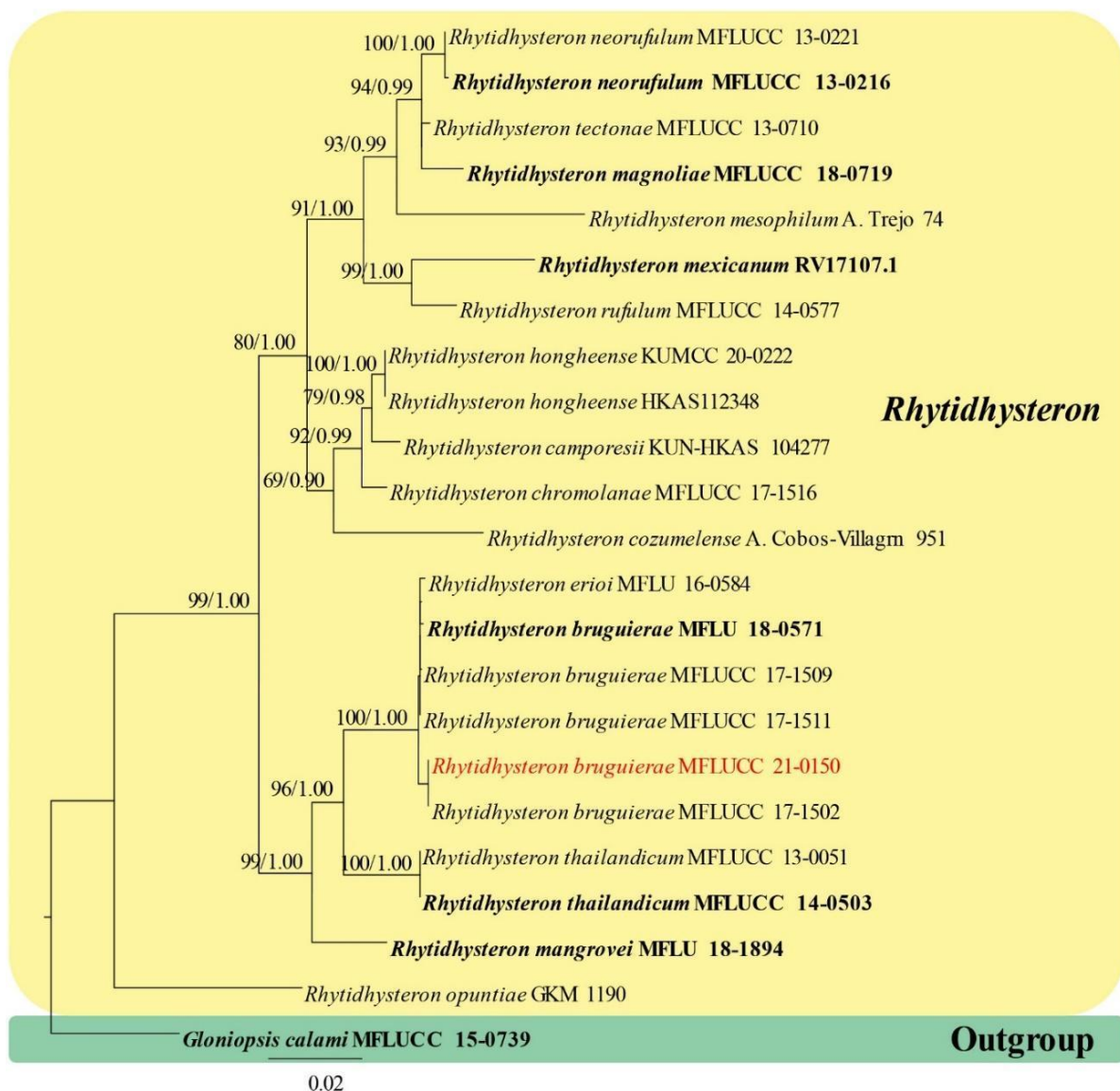
GenBank accession numbers – ITS: OK482565; LSU: OK482566; SSU: OK442652; *tef1- $\alpha$* : OK398119; *rpb2*: OK506220.

Notes – In phylogenetic analyses our taxon clustered with *Hysterobrevium constrictum* with 100% ML bootstrap and 1.0 BYPP support (Fig. 7). Our collection from *Alnus cremastogyne* is morphologically similar to *Hysterobrevium constrictum* with *textura globulosa* to *textura angularis* peridium and muriform, ellipsoid to fusoid, hyaline ascospores (Hyde et al. 2020b). *Hysterobrevium*

*constrictum*, isolated from decorticated wood, in Honshu (Japan), Amano & Boehm et al. (2009) introduced this species from New Zealand. Based on morphology and molecular phylogeny, we introduced our collection as a host record from *Alnus cremastogyne*.

***Rhytidhysterion*** Speg. [as ‘Rhytidhysterion’], Anal. Soc. cient. argent. 12(4): 188 (1881)

*Rhytidhysterion* was introduced by Spegazzini (1881) with *Rhytidhysterion brasiliense* and *R. viride*. Clements & Shear (1931) named *R. brasiliense* as the type species (Dayarathne et al. 2020b) and consists of 21 species (Wijayawardene et al. 2020). Previously, this genus was listed under *Patellariaceae* (Lumbsch & Huhndorf 2010). *Rhytidhysterion* is placed within *Hysteriaceae* based on multi-gene phylogenetic analyses (Thambugala et al. 2016, Dayarathne et al. 2020b). This genus is characterized by closed and navicular, irregularly apothecioid ascomata. Ascospores are heavily pigmented and thick-walled (Boehm et al. 2009, Thambugala et al. 2016). For *Rhytidhysterion* “Aposphaeria-like” or “Diplodia-like” asexual morphs have been reported (Samuels & Müller 1979).



**Figure 10** – Phylogenetic tree generated by ML analysis of combined LSU, and ITS sequence data of *Rhytidhysterion* species. The analyses included 23 strains and the tree was rooted with *Gloniopsis calami* (MFLUCC 15-0739). The tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of -6051.577714 is presented. The matrix had 349 distinct alignment patterns, with 17.28% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.229645, C = 0.260727, G = 0.284958, T = 0.224671; substitution

rates AC = 1.838276, AG = 2.745223, AT = 1.542871, CG = 0.745534, CT = 9.350908, GT = 1.000000; gamma distribution shape parameter  $\alpha = 0.096014$ . RAxML bootstrap support values  $\geq 50\%$  and Bayesian posterior probabilities (BYPP)  $\geq 0.95$  are shown near the nodes. Ex-type/ ex-epitype strains are in bold. New isolates recovered in this study are in red.

***Rhytidhysterion bruguierae*** Dayarathne, in Dayarathne, Jones, Maharachchikumbura, Devadatha, Sarma, Khongphinitbunjong, Chomnunti & Hyde, Mycosphere 11(1): 20 (2020) Fig. 11

Index Fungorum number: IF 556574; Facesoffungi number: FoF 06154

*Saprobic* on dead twigs of *Nauclea orientalis*. Sexual morph: *Ascomata* 250–300 × 1000–1250  $\mu\text{m}$  ( $\bar{x} = 290 \times 1120 \mu\text{m}$ ,  $n = 10$ ), hysterothecial, boat-shaped, crowded to aggregated, superficial, brown-black, with exposed, lenticular to irregular, brown-black discs, folded along the margins when dry and forming an elongate slit, perpendicularly striate. *Exciple* 50–60  $\mu\text{m}$  wide ( $n = 10$ ), composed of dark brown to black, thick-walled cells of *textura angularis*. *Hamathecium* comprising 1–3  $\mu\text{m}$  wide, cylindrical to filiform, septate pseudoparaphyses, branched and forming a red epithecium above the asci, fused and slightly swollen at the apex and enclosed in a gelatinous matrix. *Asci* 90–150 × 7–10  $\mu\text{m}$  ( $\bar{x} = 120 \times 10 \mu\text{m}$ ,  $n = 15$ ), 6–8-spored, bitunicate, cylindrical, with short, furcate pedicel, rounded at the apex, with distinct ocular chamber. *Ascospores* 20–25 × 5–10  $\mu\text{m}$  ( $\bar{x} = 21 \times 8 \mu\text{m}$ ,  $n = 20$ ), uniseriate, slightly overlapping, hyaline when immature, becoming yellowish-brown to reddish-brown when mature, ellipsoidal to fusiform, rounded to slightly pointed at both ends, 1–3-septate, slightly constricted at the septa, with smooth wall, guttulate. Asexual morph: Not observed.

Culture characteristics – Ascospores germinating on PDA within 24 h and germ tubes produced from the second cell from the apex. Colonies growing on PDA 5 cm diam. after 1 week at 25°C, flat, circular, initially white becoming greenish to a reddish-brown, smooth surface with undulate edge.

Material examined – Thailand, Chiang Rai Province, Nang Lae Village, on a dead twig of *Nauclea orientalis* (L.) L., (*Rubiaceae*), 4 June 2020, A.R Rathnayaka, MFLU 21-0174, living culture MFLUCC 21-0150.

GenBank accession numbers – LSU: OK605045; ITS: OK605037.

Note – Our strain (MFLUCC 21-0150) grouped with other *Rhytidhysterion bruguierae* strains (MFLU 18-0571, MFLUCC 17-1509, MFLUCC 17-1511 and MFLUCC 17-1502) with 100% ML bootstrap and 1.00 BYPP values (Fig. 10). The strain from the present study shares similar morphological features with the holotype of *Rhytidhysterion bruguierae* (MFLU 18-0571). Dayarathne et al. (2020b) reported *R. bruguierae* on submerged branches of *Bruguiera* sp., while Mapook et al. (2020) reported this species on dead stems of *Chromolaena odorata* (*Asteraceae*). Both records are from Thailand. Our collection is recorded on a dead twig of *Nauclea orientalis* from Thailand. Therefore, we introduce our species of *Rhytidhysterion bruguierae* as a new host record for *Nauclea orientalis*.

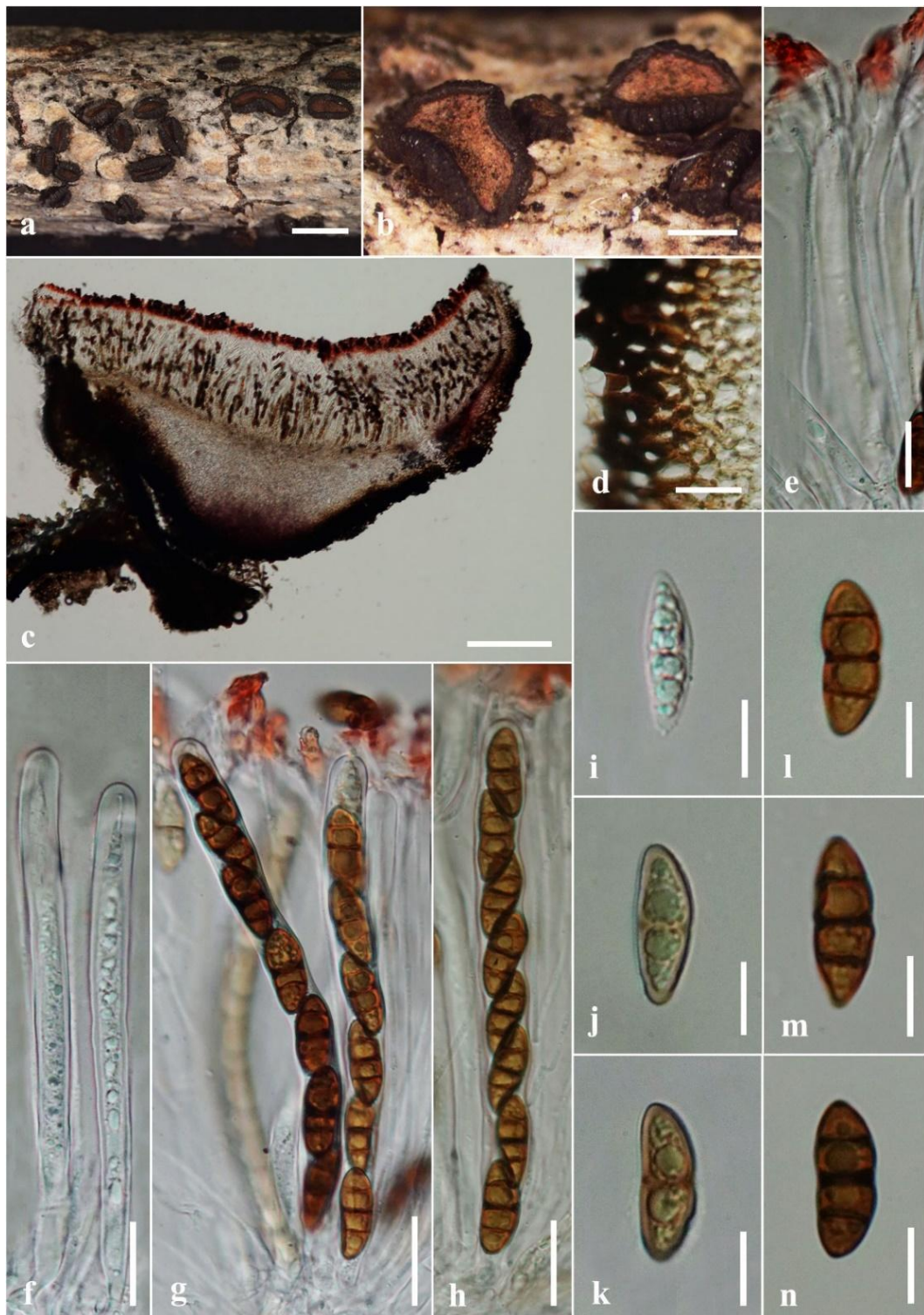
**Pleosporales** Luttr. ex M.E. Barr, Prodr. Cl. Loculoasc. (Amherst): 67 (1987)

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

*Didymosphaeriaceae* is an important family typified by *Didymosphaeria* with *D. epidermidis* as the type species (Munk 1953). Members of this family are characterized by brown, 1-septate ascospores and trabeculate pseudoparaphyses that anastomose mostly above the asci (Hyde et al. 2013, Ariyawansa et al. 2014). *Didymosphaeriaceae* species are saprobes, endophytes and pathogens of a wide range of hosts worldwide (Liu et al. 2015, Wanasinghe et al. 2016).

***Letendraea*** Sacc., Michelia 2(no. 6): 73 (1880)

*Letendraea* was introduced by Michelia (1880). This genus includes astromatic, brown-spored species of *Nectria* and *L. eurotioides* is the type species. Species of *Letendraea* are saprobic in terrestrial habitats, pathogenic associated with leaf spot disease in *Cordyline* sp. (Ariyawansa et al. 2014) and recorded from marine environments (Huang et al. 2019). There are 21 epithets in Index Fungorum (2021) of which five have molecular data (Tennakoon et al. 2021).



**Figure 11** – *Rhytidhysterium bruguierae* (MFLU 21-0174, new host record). a, b Appearance of hysterothecia on *Nauclea orientalis*. c Vertical section through a hysterothecium. d Exciple. e Pseudoparaphyses with branched swollen reddish tips. f–h Young and mature asci. i–m Ascospores. Scale bars: a = 1 mm, b = 500  $\mu$ m, c = 200  $\mu$ m, d–h, m = 20  $\mu$ m, i–n = 10  $\mu$ m.

*Letendraea cordylinicola*, Phook., Ariyaw. & K.D. Hyde, in Ariyawansa, Tanaka, Thambugala, Phookamsak et al. Fungal Diversity 68, 89 (2014) Fig. 13

Index Fungorum number: IF550698; Facesoffunginumber: FoF00046

Associated with *Synsepalum dulcificum* leaf spots. Sexual morph: Asci 8-spored, brown, bitunicate, fissitunicate, cylindric-clavate, short pedicellate, apically rounded with an indistinct

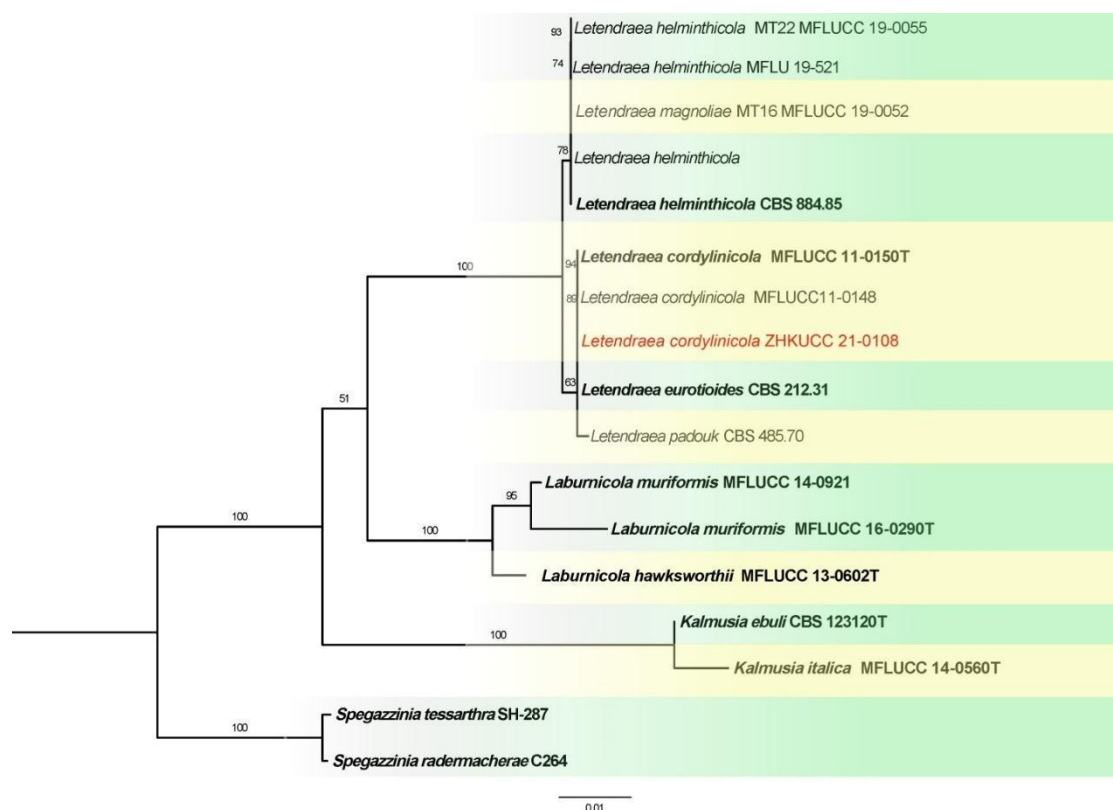
ocular chamber, arising from the base of the ascoma. *Ascospores* 10–15  $\mu\text{m} \times 3\text{--}5 \mu\text{m}$  ( $\bar{x} = 14 \pm 0.9 \times 4 \pm 0.4 \mu\text{m}$ ,  $n = 50$ ), 1–3 seriate, didymosporous, fusiform, pale brown to brown, 1-septate, constricted at the septum, often enlarged near septum in the upper cell, smooth-walled, with distinct appendage at both ends, surrounded by a mucilaginous sheath. Asexual morph: not observed.

Culture characteristics – Colonies on PDA, reach 5 cm diam. after 7 days at 25°C, white then light yellow from above, white to orange-red from the center and some white dot on it; orange-red from below, margin with well-defined to slightly radiating. Colonies on MEA and OA reach 5 cm after 7 days at 25°C.

Material examined – China, Guangzhou, Guangdong Province, on *Synsepalum dulcificum* (Schumach. & Thonn.) Daniell., (*Sapotaceae*), March 2021, Y.H. Huang & L.Q. You. Living culture ZHKUCC 21-0108.

GenBank accession numbers – LSU: OL687397; ITS: OL687396.

Notes – In the phylogenetic analysis, our isolate clustered together with the *L. cordylinicola* (MFLU11-0148/ 0150), *L. eurotioides* (CBS 212.31) and *L. padouk* (CBS 485.70) with 63% ML support (Fig. 12). ZHKUCC 21-0108 isolated and described in this study, is morphologically similar to *L. cordylinicola* (Ariyawansa et al. 2014). In pairwise sequence comparison, ZHKUCC 21-0108 is 100% similar to *L. cordylinicola* strains. In LSU there was one base pair difference with *L. cordylinicola* and *L. eurotioides*. Asci and ascospores of ZHKUCC 21-0108 are similar to *L. cordylinicola*. The ascospores of *L. eurotioides* are 1–2-seriate, ellipsoidal to fusoid with wider upper-cell towards the base narrow and rounded ends (Ariyawansa et al. 2014). Based on morphological and molecular data, we identify ZHKUCC 21-0108 as *L. cordylinicola*, a new host record for *Synsepalum dulcificum* from China.



**Figure 12** – Phylogenetic tree constructed for *Letendraea* species and closely related species in *Didymosphaeriaceae*. Phylogenetic tree generated by ML analysis of combined LSU, SSU and ITS sequence data of 12 species. The analyses included 17 strains and *Spegazzinia tessarhra* (SH-287) and *Spegazzinia rademacheriae* (C264) were used as the outgroup. The best scoring RAXML tree with a final likelihood value of -4825.558703 is presented. The matrix had 226 distinct alignment patterns, with 21.21% of undetermined characters or gaps. Estimated base frequencies were as

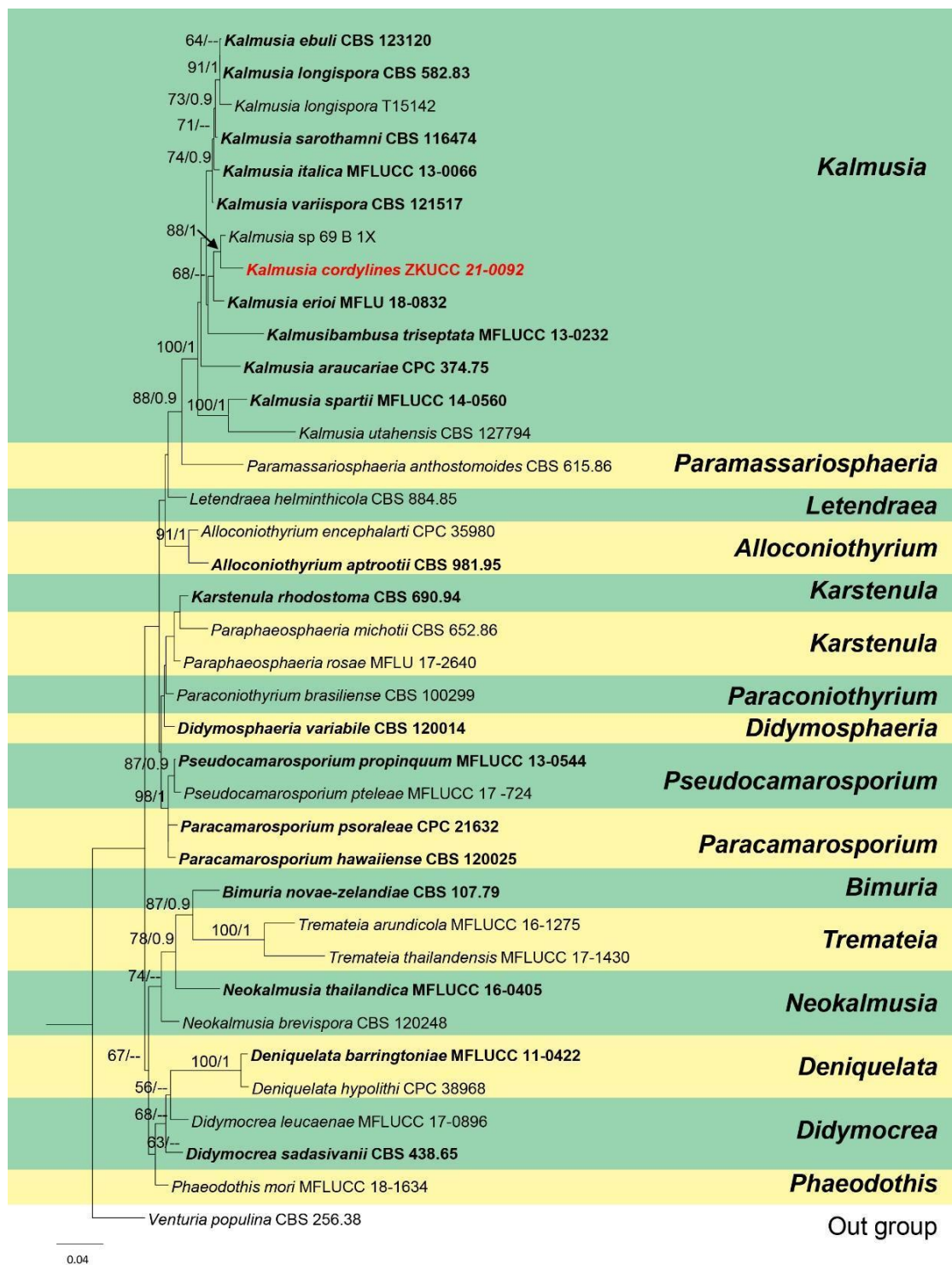
follows: A = 0.249454, C = 0.228095, G = 0.278695, T = 0.243756; substitution rates AC = 1.679795, AG = 1.857857, AT = 1.270173, CG = 0.754688, CT = 5.559118, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.020000. RAxML bootstrap support values  $\geq 50\%$  are shown near the nodes. New isolates recovered in this are in red.

***Kalmusia*** Niessl, Verh. nat. Ver. Brünn 10: 204 (1872)

*Kalmusia* was introduced and typified by *K. ebuli* and there are 42 species in this genus (Species Fungorum 2021). Most species are described by the sexual morph and however, asexual morph was reported from *Kalmusia araucariae*, *K. italica*, *K. longispora*, and *K. spartii* only (Tennakoon et al. 2016).



**Figure 13** – *Letendraea cordylinicola* (ZHKUCC 21-0108, new host record). a–d Colony characters on PDA (a upper view; d reverse view). b–e Colony characters on MEA (b upper view; e reverse view). c–f Colony characters on OA (c upper view; f reverse view); g Mycelium. h–k Asci. l Ascospores. Scale bars: h–i = 25  $\mu$ m, j–l = 10  $\mu$ m.



**Figure 14** – Phylogenetic tree generated by ML analysis of combined ITS, LSU, and SSU sequence data of species in *Didymosphaeriaceae*. The analyses included 37 strains and the tree is rooted with *Venturia populina* (CBS 256.38). The tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of BYPP is presented. The matrix had 783 distinct alignment patterns, with 20.61% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.248187, C = 0.240245, G = 0.281611, T = 0.229956; substitution rates AC = 1.210513, AG = 1.462925, AT = 1.226295, CG = 0.814671, CT = 5.242833, GT = 1.0; gamma distribution shape parameter  $\alpha = 0.196099$ . RAxML bootstrap support values  $\geq 50\%$  and Bayesian posterior probabilities (BYPP)  $\geq 0.95$  are shown at the nodes. The scale bar indicates 0.04 changes per site. Ex-type/ ex-epitype strains are in bold. New isolate recovered in this study is in red bold.



*Kalmusia cordylines* Kular., Senan., & K.D. Hyde sp. nov.

Fig. 15

Index fungorum number: IF 559336; Facesoffungi number: FoF 10618

Etymology – Species epithet derived from the host genus from which the fungus was collected.

Holotype – ZHKU 21-0003

Associated with *Cordyline fruticosa* leaf spots. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 280–350 × 380–440 μm ( $\bar{x}$  = 300 × 400 μm, n = 20), pycnidia, solitary or rarely gregarious, semi-immersed, globose to subglobose, ostiolate, apapillate, brown, coriaceous. *Ostiole* wide, covered with short, filamentous, hyaline, periphyses. *Pycnidial wall* 20–40 μm wide, comprising several layers of brown, thick-walled, cells of *textura angularis*. *Conidiophores* reduce to conidiogenous cells or rarely present as cubic, hyaline, smooth. *Conidiogenous cells* 5–10 × 5–6 μm ( $\bar{x}$  = 8 × 6 μm, n = 20), short, cylindrical to globose, hyaline, smooth, conidiogenesis holoblastic. *Conidia* 3–5 × 5–10 μm ( $\bar{x}$  = 4 × 5 μm, n = 25), oblong to oval, aseptate, hyaline, smooth-walled, with two small polar guttules.



**Figure 15** – *Kalmusia cordylines* (ZHKU 21-0003, holotype). a The host plant *Cordyline fruticosa*. b Holotype material. c Conidiomata on substrate. d Pycnidial wall. e Cross-section of conidioma.

f Ostiole opening. g–j Conidiophores, conidiogenous cells and conidia. k Conidia. Scale bars: d, f = 25  $\mu\text{m}$ , e = 100  $\mu\text{m}$ , g–k = 10  $\mu\text{m}$ .

Culture characters – Colonies on PDA reaching a diameter of 3–4 cm in 14 days, at 25°C dark, flat, margin entire, white, with some aerial mycelia; reverse white to off-white, culture did not sporulate.

Material examined – China, Guangdong Province, Shenzhen City, Nanshan, Nanhai Avenue, Shenzhen University, on *Cordyline fruticosa* (L.) A. Chev. (*Asparagaceae*), 5 August 2020, I.C Senanayake (ZHKU 21-0003; holotype), ex-type culture ZHKUCC 21-0092.

GenBank accession numbers – ITS: OL 352082; SSU: OL 818335; LSU OL 818333.

Notes – Mega blast searches of ITS, LSU and SSU sequences of the isolate showed that our strain is closely related to *Kalmusia* species. The combined gene analysis of ITS, LSU and SSU sequence data (Fig. 14) showed that the present strain is a distinct species from previously known species with 86% ML bootstrap and 1.00 BYPP values in the *Kalmusia sensu stricto* sub-clade. Our species differs from *Kalmusia araucariae* Crous and *K. longispora* (Verkley, Göker & Stielow) Ariyaw. & K.D. Hyde having hyaline, small, and oval to ellipsoidal conidia, while it is different from *K. italica* and *K. spartii* by large, hyaline conidia and cylindrical to globose conidiogenous cells (Zhang et al. 2014). Therefore, our taxon is morphologically not affiliated with any existing species. Based on both morphological and phylogenetic approaches, we introduce *Kalmusia cordyline* as a new species. This is the first *Kalmusia* species reported from *Cordyline fruticosa* (Farr & Rosaman 2022). *Cordyline fruticosa* is widely planted common ornamental plant because of its variously coloured leaves thus it is necessary to study the phytopathogenic taxa associated with this host (Hinkle 2007).

**Lophiostomataceae** Luerss., Handbuch der systematischen Botanik mit besonderer Berücksichtigung der Arzneipflanzen 1: 154 (1877)

Nitschke (1869) was first introduced this family as “*Lophiostomeae*”, but Saccardo (1883) recorded it as “*Lophiostomaceae*” until Mugambi and Huhndorf (2009) accepted this family as “*Lophiostomataceae*” and typified with *Lophiostoma macrostomum*. The main characteristics of this taxa after being recognized are immersed-erumpent ascomata with a distinctly flattened neck and opening by slit-like ostioles, mostly clavate, bitunicate asci and 1-septate, multi septate or muriform, hyaline to dark brown ascospores with terminal appendages or mucilaginous sheaths (Holm et al. 1988, Hyde et al. 2013, Ariyawansa et al. 2015, Liu et al. 2015, Thambugala et al. 2015, Hyde et al. 2017, Hashimoto et al. 2018, Bao et al. 2019). Twenty-eight genera have been accepted in this family (Hongsanan et al. 2020b, Wijayawardene et al. 2020).

**Vaginatispora** K.D. Hyde, Nova Hedwigia 61: 234. 1995.

*Vaginatispora* was introduced by Hyde (1995), to accommodate *V. aquatica* as the type species. *Vaginatispora aquatica* has longer ostiolar necks and ascospores bearing an entire sheath than *Massarina*. However, in the phylogenetic analysis of ITS sequences by Liew et al. (2002), this genus was associated with *Lophiostoma*. Zhang et al. (2014) identified it as synonymous with *Lophiostoma* based on the relatedness of the genus to *Lophiostoma*. This conclusion was rejected by Thambugala et al. (2015), and explicitly retained *Vaginatispora* based on the results of a multigene analysis (LSU, *tefl-a*, SSU & ITS). Subsequently, this was also confirmed by Wanasinghe et al. (2016) with phylogenetic support. This genus includes eight species (Hyde et al. 1992, Hyde 1995, Liew et al. 2002, Wanasinghe et al. 2016, Devadatha et al. 2017, Hashimoto et al. 2018, Zhang et al. 2019; Hongsana et al 2020b; Wijewardene et al. 2021).

**Vaginatispora amygdali** A. Hashim., K. Hiray. & Kaz. Tanaka 2018

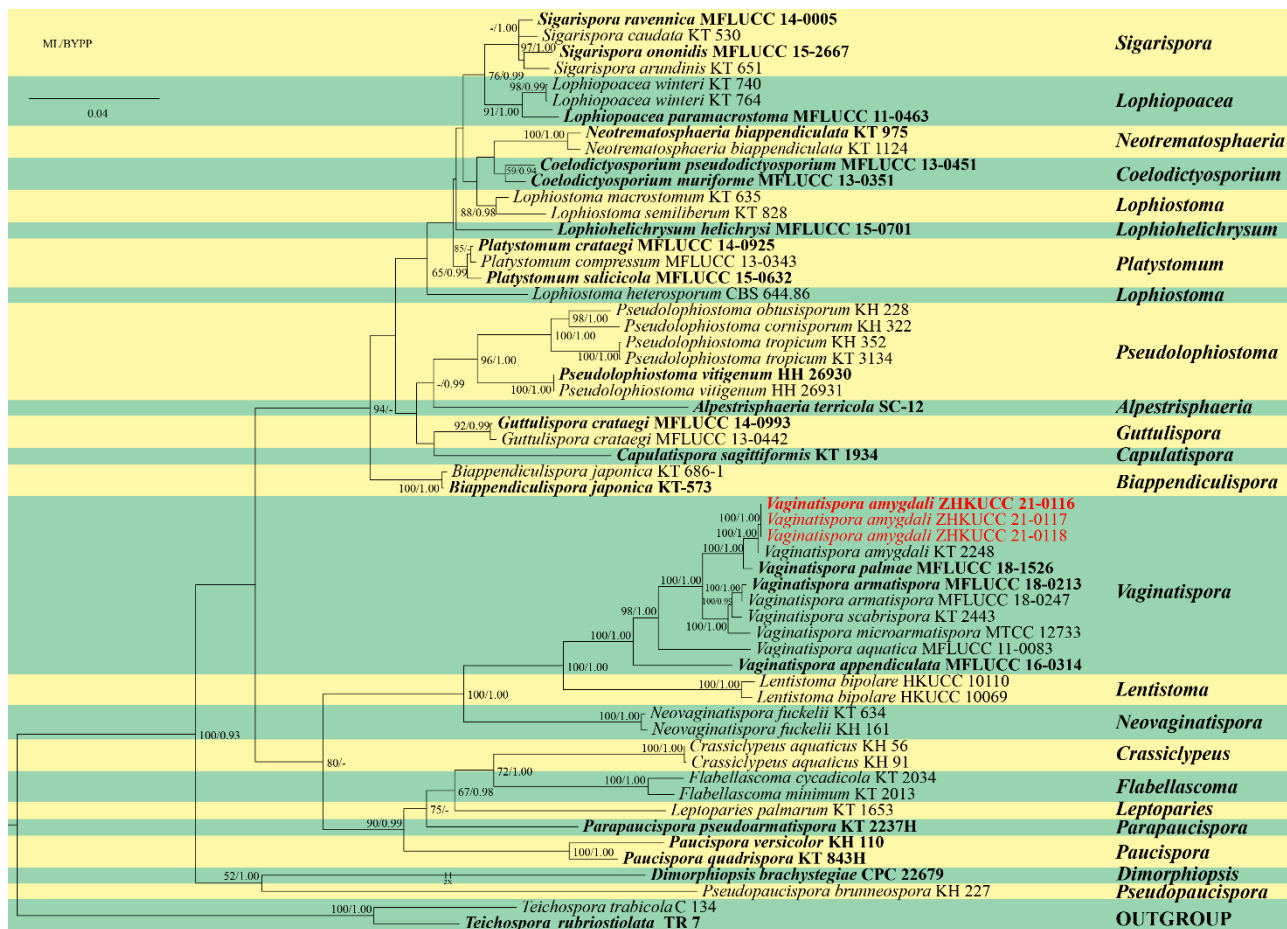
Fig. 17

Index Fungorum number: IF 823145; Facesoffungi number: FoF 05089

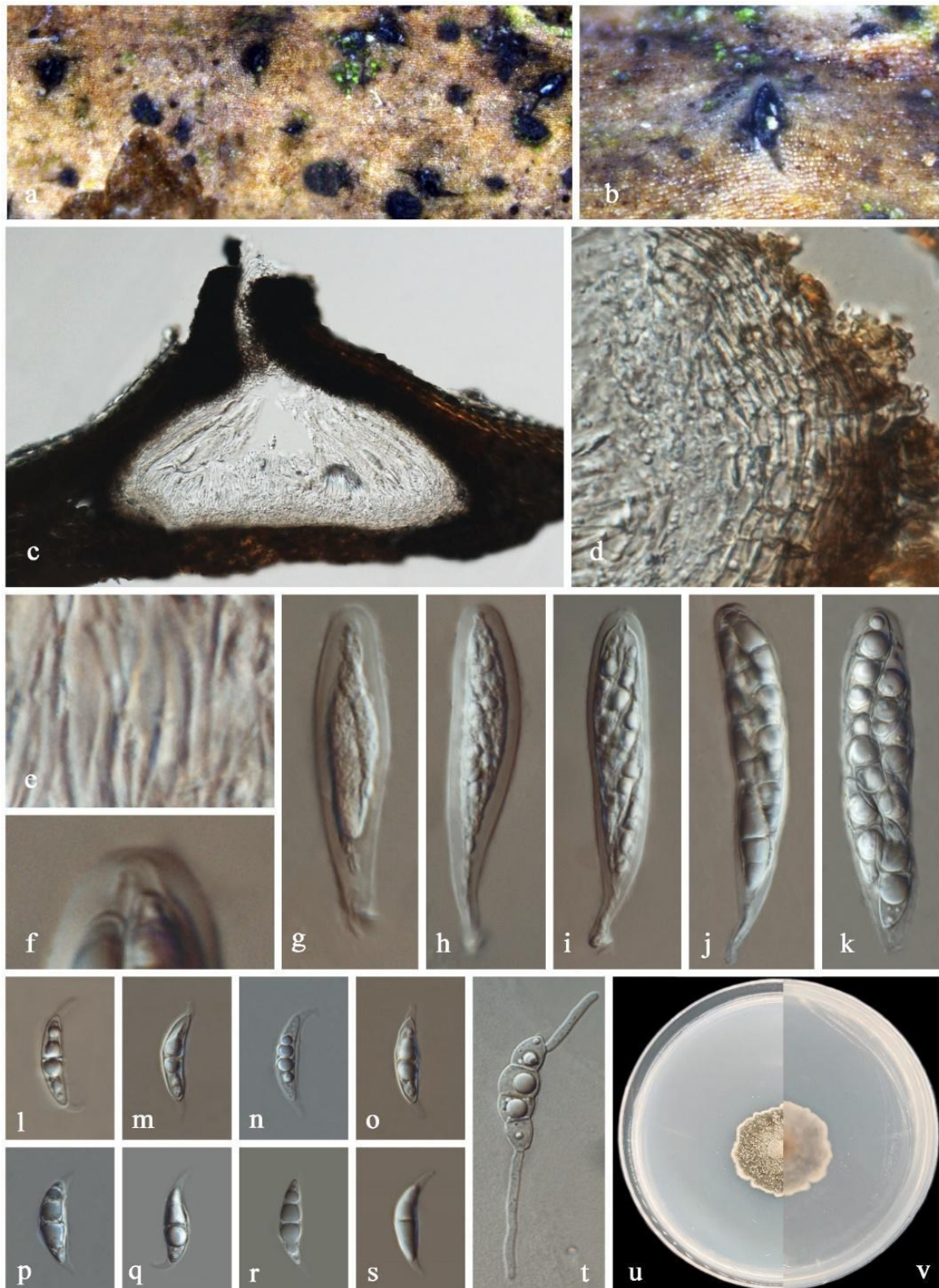
*Saprobic* on dead stems of *Smilax china*. Sexual morph: *Ascomata* 300–400  $\times$  400–500  $\mu\text{m}$  ( $\bar{x}$  = 340  $\times$  435  $\mu\text{m}$ , n = 10), ellipsoidal-fusiform, sparse, immersed, superficial, black, *Ostiolar neck*

100–150 × 100–400 µm wide, central, papillate, elongate, laterally compressed, 15–20 µm diam, globose to elongated, dark brown to black cells in the ostiole. *Peridium* 35–40 µm wide, brown-black, thick side, 5–8 layers of rectangular, 10–15 × 3–5 µm, brown to hyaline cells; light brown, 10–15 µm wide thick base. *Pseudoparaphyses* 1–3 µm wide, numerous, hyphae-like, cellular. *Asci* 80–130 × 15–20 µm ( $\bar{x}$  = 97 × 17 µm, n = 20), bitunicate, fissitunicate, cylindrical-clavate, with a short stipe (10–20 µm, n = 10), apically rounded with a broad ocular chamber, 8-spored. *Ascospores* 25–40 × 5–10 µm ( $\bar{x}$  31 × 8.5 µm, n = 40), hyaline, striate, fusiform, euseptate, verrucose, obtuse ends, slightly constricted at the septa. Sheath drawn out 5–10 µm long at both ends Asexual morph: Not observed.

Culture characteristics – Colonies on PDA, slow-growing, reaching 3 cm diam. after 14 days at 25°C, for above, radial white on the surface then next layer black-brown on down, for the reverse, the centre black, and brown toward the edges, the colour gradually becomes lighter, and the margin is white, irregular, umbonate, rough, undulate and white margin.



**Figure 16** – Phylogenetic tree constructed for *Vaginatispora* species and closely related genera in *Lophiostomataceae*. Phylogenetic tree generated by ML analysis of combined SSU, ITS, LSU, *tef1-α*, *rpb2* and *tub2* sequence data of 45 species. The analyses included 57 strains and the tree is rooted with *Teichospora trabocola* (C134) and *T. rubriostiolata* (TR7). The tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of -28973.713240 is presented. The matrix had 1699 distinct alignment patterns, with 27.5% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.246823, C = 0.247959, G = 0.266751, T = 0.238467; substitution rates AC = 1.572072, AG = 4.164556, AT = 1.198523, CG = 1.437501, CT = 8.297094, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.175352. RAxML bootstrap support values  $\geq 50\%$  and 0.95 (BYPP) Bayesian posterior probabilities are shown near the nodes. The scale bar indicates 0.04 changes per site. Ex-type/ex-type strains are in bold. New isolates recovered in this study are in red.



**Figure 17** – *Vaginatispora amygdali* (ZHKU 21-0008, new host record). a, b Appearance of ascomata on a dead branch. c Longitudinal section of an ascoma. d Peridium. e Pseudoparaphyses. f Ascus apex. g–k Asci. l–s Ascospores. t Germinating ascospore. u, v Culture, characters on PDA (u: Above view; v: Reverse view). Scale bar: c = 200  $\mu$ m, d = 20  $\mu$ m, e, f = 5  $\mu$ m, g–t = 20  $\mu$ m.

Material examined – China, Guangdong Province, Shaoguan City, Danxia Mountain, on *Smilax china* L., (*Smilacaceae*), 11 November 2020, YR. Xiong & B. Xu (ZHKU 21-0008, new host record), living cultures, ZHKUCC 21-0116, ZHKUCC 21-0117 and ZHKUCC 21-0118.

GenBank accession numbers – ITS: OL692367, OL692368, OL692369; LSU: OL692422, OL692423, OL692424; *tef* 1-  $\alpha$ : OL901255, OL901256, OL901257; *tub2*: OL878991, OL878992, OL878993.

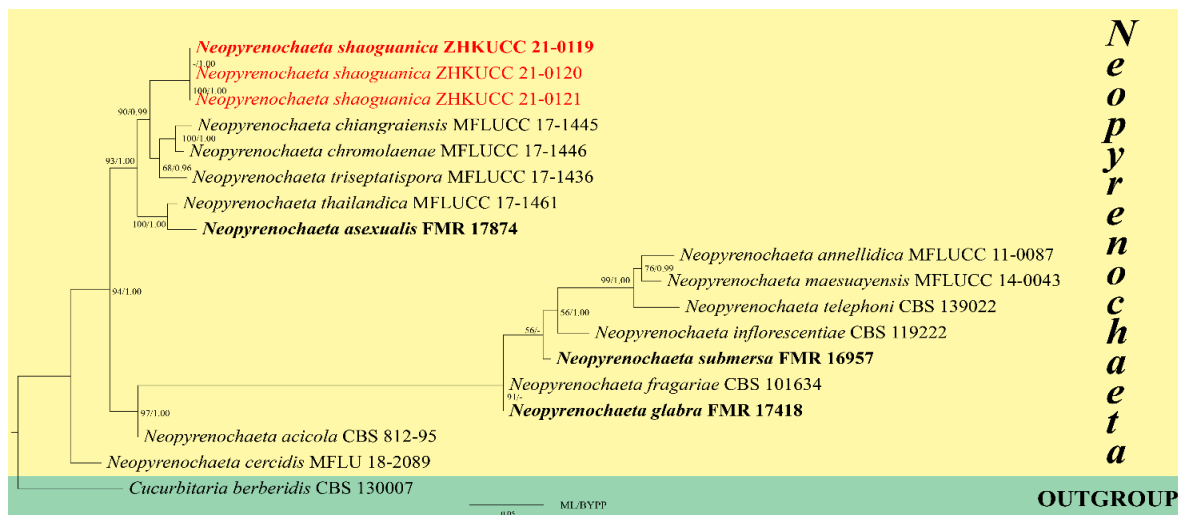
Notes – In the phylogenetic analysis, our strain developed a sister clade to *Vaginatispora amygdali* (CBS 143662) with 100% ML and 1.00 BYPP bootstrap support (Fig. 16). Our isolates were morphologically similar to *Vaginatispora amygdali* (Hashimoto et al. 2018). Asci are fissitunicate, and the ascospores all have a narrow sheath. Moreover, asci and ascospores are similar in size (Hashimoto et al. 2018). The two *Vaginatispora amygdali* strains (ZHKUCC 21-0116 and CBS 143662) did not have any base pair differences in the ITS and LSU regions, and there was one base pair difference in the *tef* 1-  $\alpha$  and *tub2* regions, and only two base pair differences in the *rpb2* region. The two isolates were different only by the internal chamber in the sheath that was not observed in the isolate ZHKUCC 21-0116. Based on these differences in morphology and molecular data, we introduce our isolate (ZHKUCC 21-0116) as a new host record from *Vaginatispora amygdali*.

***Neopyrenochaetaceae*** Valenz-Lopez, Crous, Cano, Guarro & Stchigel, in Valenzuela-Lopez, Cano-Lira, Guarro, Sutton, et al. Stud. Mycol. 90: 54 (2017)

*Neopyrenochaetaceae* was introduced by Valenzuela-Lopez et al. (2018) using combined LSU, ITS, *tub2* and *rpb2* multi-gene phylogeny analysis. *Neopyrenochaetaceae* is a monophyletic family represented by *Neopyrenochaeta* (Jaklitsch et al. 2018, Jayasiri et al. 2019).

***Neopyrenochaeta*** Valenz-Lopez, Crous, Stchigel, Guarro & Cano. in Valenzuela-Lopez, Cano-Lira, Guarro, Sutton, et al. Stud. Mycol. 90: 54 (2017)

*Neopyrenochaeta* proposed by Valenz-Lopez et al. (2017) was based on molecular phylogeny. This genus was morphologically similar to *Pyrenochaeta*, but phylogenetically distinct. *Neopyrenochaeta acicola* is the type species of this genus. *Neopyrenochaeta* species were mainly reported as asexual morphs, however, Mapook et al. (2020) reported sexual morphs and pointed out that this genus has a wide host range. There are 15 accepted species in this genus (Valenz-Lopez et al. 2017, Jayasiri et al. 2019, Mapook et al. 2020, Magaña-Dueñas et al. 2021).



**Figure 18** – Phylogenetic tree generated by ML analysis of combined LSU, ITS, SSU and *rpb2* sequence data of 15 species. The analyses included 18 strains and the tree is rooted with *Cucurbitaria berberidis* (CBS 121124). The tree topology of the ML analysis was similar to the MP and BYPP. The best scoring RAXML tree with a final likelihood value of -11826.712355 is presented. The matrix had 593 distinct alignment patterns, with 27.48% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.253838, C = 0.228967, G = 0.266672, T = 0.250523; substitution rates AC = 1.583824, AG = 3.178114, AT = 1.384426, CG = 1.061232, CT = 7.460270, GT =

1.000000; gamma distribution shape parameter  $\alpha = 0.218880$ . RAxML bootstrap support values  $\geq 50\%$  and  $\geq 0.95$  (BYPP) Bayesian posterior probabilities are shown near the nodes. The scale bar indicates 0.05 changes per site. Ex-type/ ex-epitype strains are in bold. New isolates recovered in this study are in red.

***Neopyrenochaeta shaoguanica*** YR. Xiong, B. Xu, K.D. Hyde & Manawas., sp. nov. Fig. 19

Index Fungorum number: IF559352; Facesoffungi number: FoF 10611

Etymology – Species epithet derived from the location Shaoguan City, Guangdong Province, China, from where the fungus was collected.

Holotype –ZHKU21-0009

*Saprobic* on a dead branch. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiostromata* 350–450  $\mu\text{m}$  long, 500–800  $\mu\text{m}$  wide ( $\bar{x} = 380 \times 600 \mu\text{m}$ ,  $n = 10$ ), gregarious, coriaceous, multilocular, black. *Conidiomata* 200–300  $\times$  150–200  $\mu\text{m}$  ( $\bar{x} = 235 \times 180 \mu\text{m}$ ,  $n=10$ ), loculate; locules arranged in clusters, gregarious, with 3–7 locules forming groups immersed in conidiostroma, globose to subglobose. *Peridium* multi-layered, inner layer 25–45  $\mu\text{m}$  wide, composed of dark-brown, thin-walled cells of *textura angularis*, with outer wall of lighter brown with *textura angularis*. *Conidiophores* with *conidiogenous cells* 25–40  $\times$  2–3  $\mu\text{m}$ , long, cylindrical, branched, hyaline to pale brown, thin-walled, microtubules at the apex, spores are released singularly. *Conidia* 3–4  $\times$  2–3  $\mu\text{m}$  ( $\bar{x} = 3.1 \times 2.2 \mu\text{m}$ ,  $n = 50$ ), one-celled, hyaline, clavate or ellipsoidal to cylindrical, cumulate, straight, smooth- to thin-walled.

Culture characteristics – Colonies on PDA reaching 6 cm diameter after 7 days at 25°C, light brown from above, pale brown from below, filamentous, umbonate, margin entire.

Material examined – China, Guangdong Province, Shaoguan City, isolated from dead wood, 11 November 2020, YR. Xiong & B. Xu (ZHKU21-0009, holotype); living cultures ZHKUCC 21-0120 (ex-holotype), ZHKUCC 21-0119 and ZHKUCC 21-0121.

GenBank accession numbers – ITS: OL692437, OL692438, OL692439; LSU: OL692440, OL692441, OL692442.

Notes – In the phylogenetic analysis isolates obtained in this study clustered together with the other *Neopyrenochaeta* species with 90% ML bootstrap support and 0.99 BYPP support and developed a distinct clade in *Neopyrenochaeta*. *Neopyrenochaeta shaoguanica* is an asexual morph, while sister taxa to our species; *N. chiangraiensis* (MFLUCC 17-1445), *N. chromolaenae* (MFLUCC 17-1446) and *N. triseptatispora* (MFLUCC 17-1436) are sexual morphs. Compared with *N. asexualis* (FMR 17874), *N. shaoguanica* (ZHKUCC 21-0119) has shorter rectangular conidia (*N. asexualis* :4–5  $\times$  1.5–2.5 vs *N. shaoguanica*: 3–3.5  $\times$  2–2.5). However, in the phylogenetic tree, the sexual morph (MFLUCC 17-1445) and asexual morph (MFLUCC 13-0881) of *N. chiangraiensis* are not in the same clade. Considering both morphological and phylogenetic approaches we introduce our species; *Neopyrenochaeta shaoguanica* as a novel taxon in *Neopyrenochaeta*.

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

Barr (1979) introduced *Phaeosphaeriaceae* and designated *Phaeosphaeria* as the generic type in this family. *Phaeosphaeriaceae* species have immersed to superficial, globose to subglobose ascomata, short papilla, bitunicate asci and hyaline to pigmented, fusiform to ellipsoidal, fliform, or muriform ascospores (Hongsanan et al. 2020b, Mapook et al. 2020, Phukhams et al. 2020, Tenakoon et al. 2021). The asexual morphs of *Phaeosphaeriaceae* are commonly known as coelomycetous but there are some hyphomycetous taxa (Phookamsak et al. 2014, Maharachchikumbura et al. 2019, Hongsanan et al. 2020). Wijayawardene et al. (2020) accepted 82 genera in this family.

***Leptospora*** Rabenh., Hedwigia 1: 116 (1857)

*Leptospora* was introduced by Rabenhorst (1857) with *L. rubella* as the type species. *Leptospora* species have large, flask-shaped ascomata with long cylindrical asci and thin, filiform, multi-septate ascospores, and members of this genus also had been reported to produce a reddish-purple pigmentation to stain the host tissue around the ostiole (Walker 1980; Hyde et al. 2016; Zhang

et al. 2019a). There are 40 species listed in Index Fungorum (2021), 15 species are listed in Species Fungorum (2021).



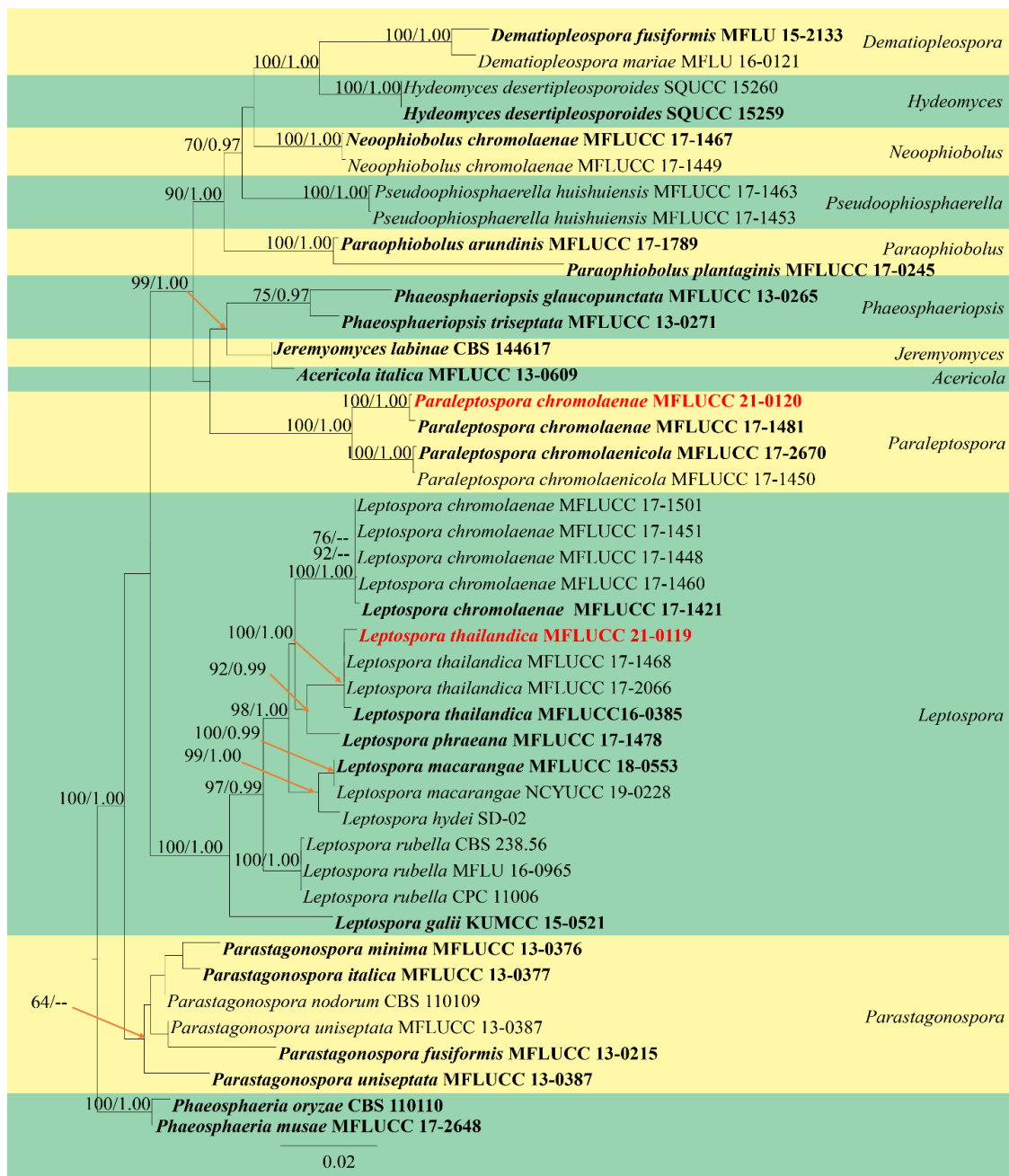
**Figure 19** – *Neopyrenochaeta shaoguanica* (ZHKU21-0009, holotype). a–c Appearance of Conidiostromata on dead wood. d Section through a Conidiostromata. e Locule. f Peridium. g–h Conidiogenous cells and Conidiogenesis. i–m Conidia. n Germinating conidium. o, p Culture characters on PDA (o: Above view; p: Reverse view). Scale bar: d, e = 100  $\mu$ m, f = 50  $\mu$ m, g = 20  $\mu$ m, h, i = 10  $\mu$ m, j–m = 5  $\mu$ m, n = 20  $\mu$ m.

*Leptospora thailandica* Phukhams. & K.D. Hyde, in Hyde et al., Fungal Divers. 80: 100 (2016)

Fig. 21

Index Fungorum number: IF 552239; Facesofungi number: FoF 02381

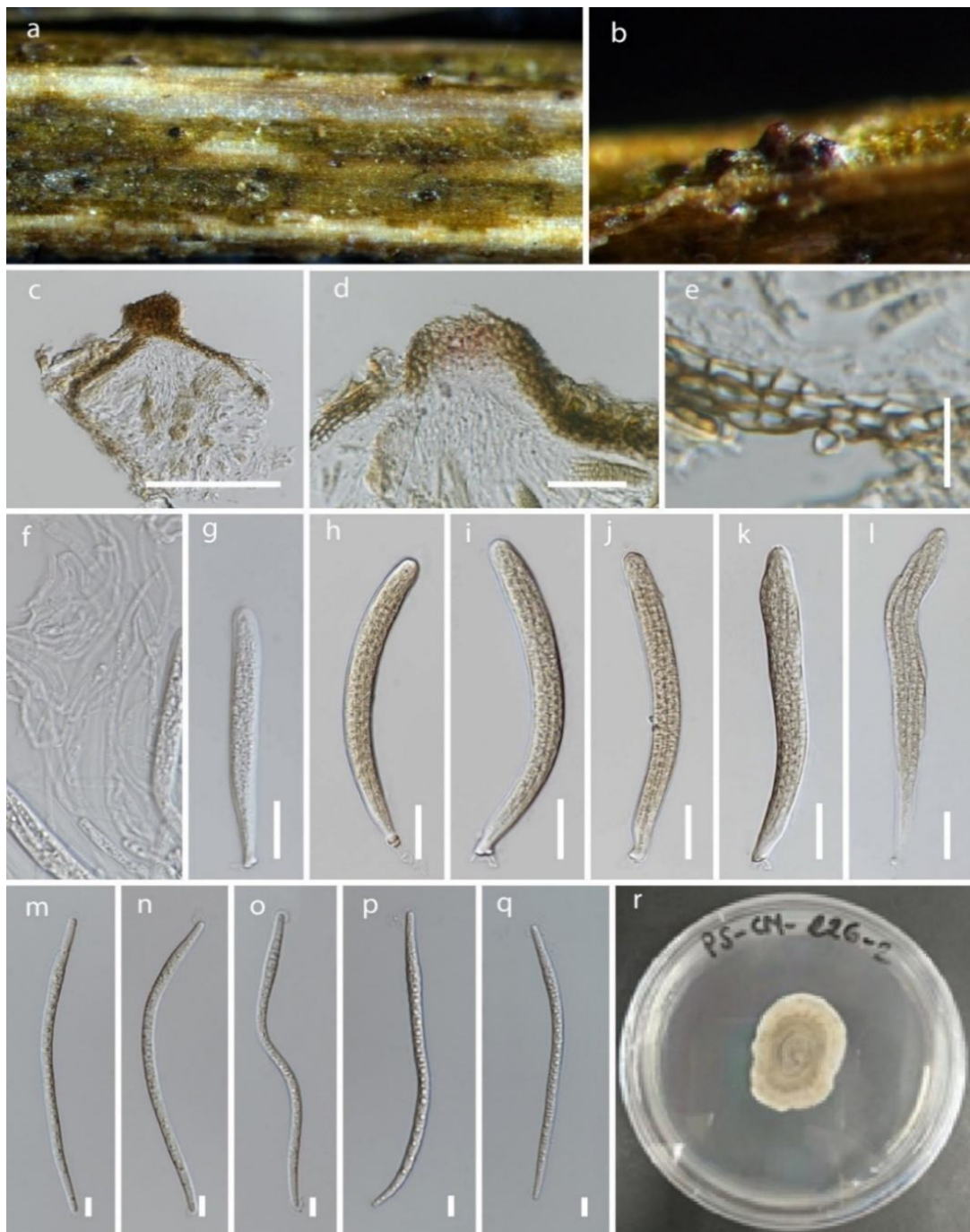
*Saprobic* on dead stems of *Sphagneticola trilobata*. Sexual morph: *Ascomata* 150–170 × 130–170 μm ( $\bar{x}$  = 153 × 162 μm, n = 4), immersed to semi-immersed, solitary or scattered, giving the impression as dark spots, coriaceous, globose to obpyriform, reddish-brown to dark brown. *Ostiolar neck* protruding. *Peridium* 5–10 μm wide, 2 layers, inner layers comprising hyaline cells of *textura prismatica*, outer layers comprising light brown to brown cells of *textura angularis*. *Hamathecium* comprising 2–3 μm wide, cylindrical, septate, branching pseudoparaphyses, anastomosing above the asci. *Asci* 60–100 × 5–10 μm ( $\bar{x}$  = 76 × 7 μm, n = 11), overlapping, 8-spored, bitunicate, fissitunicate, cylindric-clavate, straight or slightly curved, apically rounded, with a short, bulbous pedicel, ocular chamber visible when immature. *Ascospores* 90–100 × 3–4 μm ( $\bar{x}$  = 92 × 3.2 μm, n = 6), fasciculate, in parallel, scolecosporous, pale brown, cylindrical to broadly filiform, 13–15-septate when mature, minute guttule in each cell, straight or slightly curved, with polar appendages. Asexual morph: Not observed.



**Figure 20** – Maximum likelihood tree based on a combined dataset of LSU, SSU, ITS and *tef1-α* sequence data. The tree is rooted with *Phaeosphaeria musae* (MFLUCC 17–2648) and *P. oryzae*



(CBS 110110). This consisted of 43 taxa including our strains. The best scoring RAxML tree with a final likelihood value of  $-11451.082297$  is presented. The matrix had 696 distinct alignment patterns, with 20.79% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.247625, C = 0.235731, G = 0.265323, T = 0.251321; substitution rates: AC = 0.976620, AG = 2.680596, AT = 2.054625, CG = 0.707516, CT = 7.235653, GT = 1.000000; gamma distribution shape parameter  $\alpha = 0.572169$ . Bootstrap support values for ML equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.98 are displayed on the nodes, respectively. Type and ex-type strains are in black bold. New isolates recovered in this study are in red.



**Figure 21** – *Leptospora thailandica* (MFLU 21-0257, new host record). a, b Appearance of ascomata on dead branches. c Section through an ascoma. d Close up of ostiole. e Peridium. f Pseudoparaphyses. g–l Asci. m–q Ascospores with globose polar appendages. r Colonies on PDA after 15 days. Scale bars: a, b = 500  $\mu\text{m}$ , c = 100  $\mu\text{m}$ , d = 50  $\mu\text{m}$ , e–l = 20  $\mu\text{m}$ , m–q = 10  $\mu\text{m}$ .

Culture characteristics – Ascospores germinating on PDA within 24 h and colonies on PDA reaching 5 mm diam after 3 weeks at room temperature. Irregular in shape, at the surface gray in the center and yellowish at the margin in reverse.

Material examined – Thailand, Chiang Mai Province, Mae Taeng, Mushroom Research Centre, on dead stem of *Sphagneticola trilobata* (L.) Pruski (*Asteraceae*). 10 September 2020, P. Pahoua (MFLU 21-0257), living culture MFLUCC 21-0119.

GenBank accession numbers – OL824732; SSU: OL872251; ITS: OL824725, *tef1-α*: OL957090.

Notes – In the phylogenetic analysis, our new strain (MFLU 21-0257) clustered with *Leptospora thailandica* as a monophyletic lineage with 100% ML and 1.00 BYPP statistical support (Fig. 20). The characters of our new collection (MFLU 21-0257) similar to those are in *L. thailandica* Hyde et al. (2016). Therefore, we confirm our new isolate as *Leptospora thailandica* based on phylogenetic analyses with morphological comparison. This is the first record of *L. thailandica* on *Sphagneticola trilobata* from Thailand.

***Paraleptospora*** Mapook & K.D. Hyde in Mapook, Hyde, McKenzie, Jones et al. Fungal Diversity 101: 75 (2020)

*Paraleptospora* belongs to *Phaeosphaeriaceae* and *Paraleptospora* was estimated as a new genus by Mapook et al. (2020). Members of *Paraleptospora* are characterized by immersed to semi-immersed, solitary or scattered ascomata which are globose or subglobose to ampulliform, brown to dark brown, appearing as a dark spot with red area on host surface. Asci are 8-spored, bitunicate, fissitunicate, cylindrical to cylindrical-subclavate, straight or slightly curved, pedicellate, apically rounded, with an ocular chamber (Mapook et al. 2020).

***Paraleptospora chromolaenae*** Mapook & K.D. Hyde, in Mapook, Hyde, McKenzie, Jones, et al. Fungal Diversity 101: 76 (2020) Fig. 22

Index Fungorum number: IF557348; Facesofungi number: FoF07811

*Saprobic* on dead stems of *Tithonia diversifolia*. Sexual morph: *Ascomata* 240–280 × 280–320 μm ( $\bar{x}$  = 250 × 295 μm, n=4), immersed or semi-immersed to superficial, solitary or scattered, gregarious, globose to subglobose, coriaceous, gregarious, dark brown to black. *Ostiole* neck protruding. *Peridium* 20–25 μm wide, several layers, comprising dense, thick-walled, reddish, yellow or brown to dark brown, pseudoparenchymatous cells, arranged in *textura angularis*. *Hamathecium* comprising 2 μm wide, oblong to cylindrical, septate, branching pseudoparaphyses, anastomosing above the asci. *Asci* 80–100 × 5–15 μm ( $\bar{x}$  = 95 × 7 μm, n = 5), 8-spored, bitunicate, cylindrical to cylindrical-subclavate, straight, slightly curved to apically rounded, pale brown with an ocular chamber. *Ascospores* 50–60 × 5–10 μm ( $\bar{x}$  = 54 × 6.6 μm, n = 5), overlapping, 1–2-seriate, pale yellow, cylindrical-fusiform, tapering towards the narrow the rounded ends, 5–7-septate, broader at the center and slightly constricted at septa, straight to slightly curved, guttulate, without polar appendages. Asexual morph: Not observed.

Material examined – Thailand, Chiang Rai Province, Doi Mae Salong, on a dead stem of *Tithonia diversifolia* (Hemsl.) A. Gray (*Asteraceae*), 11 November 2020, P. Pahoua (MFLU 21-0258), living culture MFLUCC 21-0120.

Culture characteristics: the ascospore germinating on PDA within 24 h. at room temperature and colonies on PDA reaching 6 mm diam after 3 weeks. A circular, mycelium umbonate, cultures white at the surface, creamy-white in reverse.

GenBank accession numbers – LSU: OM004048; ITS: OL824726; *tef1-α*: OL957091.

Notes – In a BLASTn search of GenBank, the closest match with the ITS, *tef1-α* and LSU sequence of MFLUCC 21-0120 were similar with *Paraleptospora chromolaenae* (strain MFLUCC 17-1481). The closest sequence with 100% (MN994586), 99.43% (MN998167) and 99.75% (MN994563) respectively. The morphology of *Paraleptospora chromolaenae* (MFLU 21-0258) was similar with *Paraleptospora chromolaenae* (MFLUCC 17-1481) immersed or semi-immersed to superficial solitary or scattered, appearing as dark spot with reddish-brown on the host surface, while

our strain differs from *Paraleptospora chromolaenae* in having a bigger ascospore  $50 \times 6 \mu\text{m}$  vs  $35 \times 3.5 \mu\text{m}$ . However, in the phylogenetic tree our new isolate cluster with *Paraleptospora chromolaenae* (MFLUCC 17-1481) (Fig. 22). Hence, we introduced our new strain as a new host record for *Tithonia diversifolia* from Thailand.



**Figure 22** – *Paraleptospora chromolaenae* (MFLU 21-0258, new host record). a–c Appearance of superficial ascomata on *Tithonia diversifolia* substrate. d Section through an ascoma. e Ostiole. f Peridium. g Pseudoparaphyses. h–j Asci. k–o Ascospores. p Germinated spore on PDA. Scale bars: a–c = 200  $\mu\text{m}$ , d = 100  $\mu\text{m}$ , e = 50  $\mu\text{m}$ , f–j = 20  $\mu\text{m}$ , k–o = 10  $\mu\text{m}$ , p = 5  $\mu\text{m}$ .

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

*Pleosporaceae* consists of pathogenic and saprobic taxa on a wide range of hosts (Valenzuela-Lopez et al. 2018). Twenty-three genera are accepted and for taxonomic treatments, we follow Hongsanan et al. (2020b).

**Comoclathris** Clem., Gen. fung. (Minneapolis): 37 (1909)

*Comoclathris* was described by Clements (1909), and it was typified by *C. lanata* (Clements 1909, Zhang et al. 2012, Ariyawansa et al. 2014, 2015, Brahmanage et al. 2020, Crous et al. 2021). The genus is characterized by operculate perithecia and asymmetrical, muriform ascospores (Shoemaker & Babcock 1992, Ariyawansa et al. 2014, Wanasinghe et al. 2018, Crous et al. 2021). Ariyawansa et al. (2015) placed *Comoclathris* in Pleosporales. Forty-three *Comoclathris* species are listed in Species Fungorum (2021), and 18 species have DNA sequence data in GenBank (Brahmanage et al. 2020, Crous et al. 2021).

**Comoclathris lonicerae** Brahmanage, Camporesi & K.D. Hyde, in Brahmanage, Dayarathne, Wanasinghe et al. Mycosphere 11, 2525 (2020) Fig. 24

Index Fungorum number: IF557586; Facesoffungi number: FoF 08016

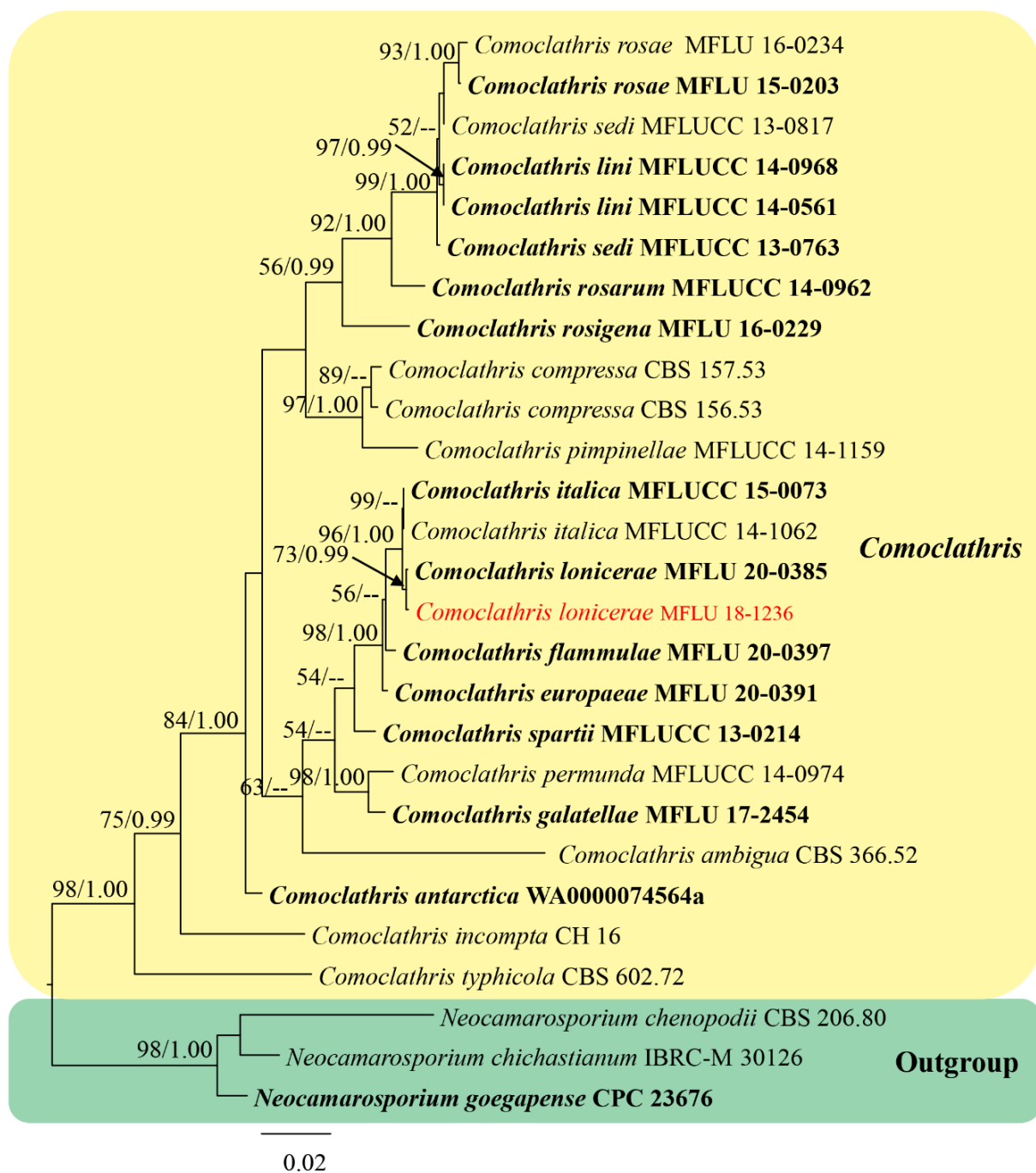
*Saprobic* on a dead hanging branch of *Colutea arborescens*. Sexual morph: *Ascomata* 300–350 × 100–300 µm ( $\bar{x}$  = 310.16 × 185.49 µm, n = 10), solitary, sessile, semi-immersed, erumpent through host surface, globose to subglobose, dark brown to black, uniloculate. *Ostiole* inconspicuous. *Peridium* 20–40 µm ( $\bar{x}$  = 28.14 µm, n = 15) wide at the sides, comprising of 3–5 cell layers, outermost layer composed dark brown loosely packed cells of *textura angularis*, inner layer composed light brown to hyaline flattened cells of *textura angularis*. *Hamathecium* comprising numerous, 2–4 µm wide ( $\bar{x}$  = 3.24 µm, n = 20), filamentous, septate, pseudoparaphyses, branching and anastomosing between, below and above the asci. *Asci* 150–200 × 40–50 µm ( $\bar{x}$  = 150.32 × 45.0 µm, n = 10), 8-spored, bitunicate, fissitunicate, broadly cylindrical to cylindrical-clavate, short pedicellate, rounded at the apex, with a shallow ocular chamber. *Ascospores* 30–45 × 10–20 µm ( $\bar{x}$  = 35 × 15 µm, n = 30), overlapping, biserial, narrowly fusiform, transversely septate or muriform, with 3–5 transverse septa, one longitudinal septum in the central cells, constricted at the septa, upper part is slightly wider than the lower part, hyaline at the beginning, becoming brown at maturity, rounded to acute at the apices, rough-walled. Asexual morph: Not observed.

Material examined – Italy, Forlì-Cesena Province [FC], Converselle - Castrocaro Terme e Terra del Sole, on a dead hanging branch of *Colutea arborescens* L. (*Fabaceae*), 15 August 2018, E. Camporesi, IT2665 (MFLU 18-1236).

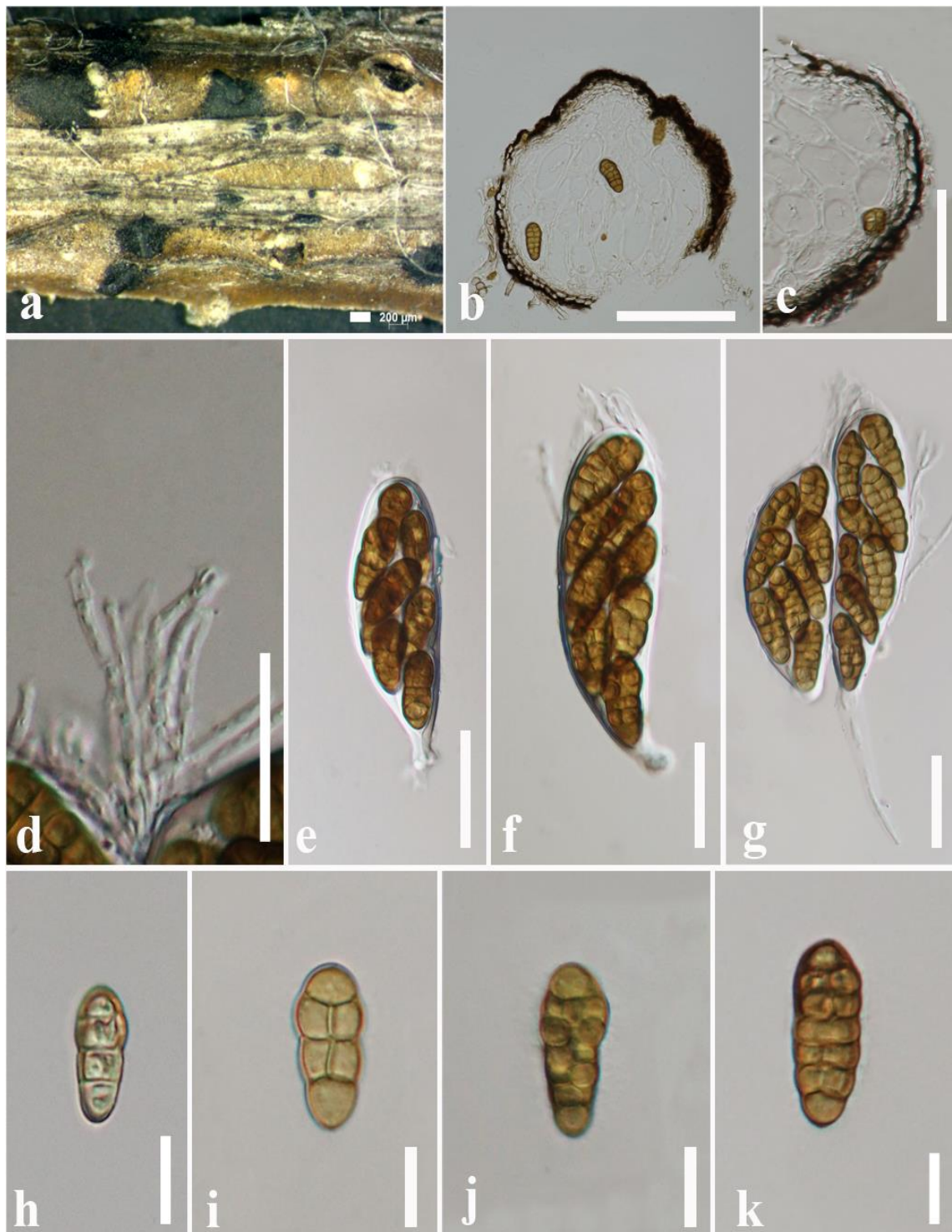
GenBank accession numbers – LSU: OL744433, SSU: OL744435, ITS: OL744429; *rpb2*: OL771441.

Notes – In the multi-gene phylogeny (LSU, SSU, ITS, and *rpb2*) of this study, our strain (MFLU 18-1236) and the holotype strain of *Comoclathris lonicerae* (MFLU 20-0385) clustered together with 73 % ML bootstrap and 0.99 BYPP support (Fig. 23). These strains were collected from different hosts but in the same locality. In the nucleotide comparison, the ITS region (ITS1-5.8S-ITS2, 527 nucleotides), SSU region (1022 nucleotides) and *rpb2* region (865 nucleotides), there are zero bp (0 %) differences between MFLU 18-1236 and MFLUCC 20-0385 strains, while the LSU rDNA region has 854 base pair (0.11 %) differences without gaps.

The characters of our species overlap with the holotype strain described by Brahmanage et al. (2020). Both species are similar with solitary, semi-immersed to erumpent, globose to subglobose, dark brown to black ascomata, a peridium comprising the cells of *textura angularis*, broadly cylindrical to cylindrical-clavate asci with a short pedicellate and rounded apex and shallow ocular chamber and muriform ascospores with 3–5 transverse septa and 1–2 longitudinal septa. However, the ascomata, asci and ascospores of our new collection are comparatively smaller than the ex-type strain. Considering both morpho-molecular data analyses, we conclude that our new collection is a record of *Comoclathris lonicerae* and a new host record on *Colutea arborescens* in Italy.



**Figure 23** – Phylogenetic tree generated by ML analysis of combined LSU, SSU, ITS, and *rpb2* sequence data of 21 species including 18 ingroup species. The analyses included 27 strains and the tree is rooted with *Neocamarosporium chenopodii* (CBS 206.80), *Neocamarosporium chichastinum* (IBRC-M 30126) and *Neocamarosporium goegapense* (CPC 23676). The tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of -9701.581041 is presented. The matrix had 538 distinct alignment patterns, with 13 undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.255332, C = 0.225223, G = 0.267910, T = 0.251535; substitution rates AC = 2.042916, AG = 4.119531, AT = 1.433265, CG = 1.030913, CT = 6.802017, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.020000. RAxML bootstrap support values  $\geq 50\%$  and Bayesian posterior probabilities (BYPP)  $\geq 0.95$  are shown near the nodes. Ex-type/ ex-epitype strains are in bold. New isolates recovered in this study are in red.



**Figure 24** – *Comoclathris loniceriae* (MFLU 18-1236, new host record). a Ascomata on a dead hanging branch of *Colutea arborescens*. b Longitudinal section of ascoma. c Peridium. d Pseudoparaphyses. e–g Asci and arrangement of ascospores. h–k Ascospores. Scale bars: a–c = 200  $\mu$ m, e–g = 50  $\mu$ m, d, h–k = 20  $\mu$ m.

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

*Torulaceae* was introduced by Sturm (1829) and is typified by *Torula*. *Torulaceae* members have erect, micro- or macronematous, straight or flexuous, subcylindrical conidiophores and doliiform to ellipsoid or clavate, brown, smooth to verruculose conidiogenous cells. Conidia are subcylindrical, phragmosporous, acrogenous, brown, dry, and smooth to verrucose, characteristically produced in branched chains (Hyde et al. 2016, Li et al. 2017, Mapook et al. 2020, Tennakoon et al.

2021). Six genera are accepted in *Torulaceae*, namely *Dendryphion*, *Neotorula*, *Rostriconidium*, *Rutola*, *Sporidesmioides* and *Torula* (Hongsanan et al. 2020b).

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

*Torula* was introduced by Persoon (1794) to accommodate *T. herbarum* as the type species. The neotype of *T. herbarum* was designated by Crous et al. (2015). Only asexual morphs are known from this genus and characterized by doliiform to ellipsoid or clavate, cupulate conidiogenous cells, with thick and heavily melanized walls at the base, while thin at the apex. The conidia are subcylindrical, phragmosporous, brown, smooth-walled to verrucose, and appear as branched or unbranched chains (Crane and Miller 2016, Li et al. 2017, Mapook et al. 2020, Tennakoon et al. 2021). There are 54 *Torula* species are listed in Species Fungorum (2021).

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

Fig. 26

Index Fungorum number: IF816154; Facesoffungi number: FoF 02712

*Saprobic* on a dead stem of *Hedygium coronarium*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effuse on host, black, powdery. *Mycelium* superficial on the dead substrate, composed of septate, branched, smooth, hyaline hyphae. *Conidiophores* macronematous, mononematous, solitary, erect, light brown, verruculose, thick-walled, consisting of with 1 or 2 cells, without apical branches, ellipsoid to subglobose, arising from hypha. *Conidiogenous cells* 3–5 × 3–5 μm ( $\bar{x}$  = 4.5 × 3.5 μm, n = 15), polyblastic, terminal, dark brown to black, smooth to minutely verruculose, thick-walled, ellipsoidal. *Conidia* 10–20 × 5–10 μm ( $\bar{x}$  = 15 × 5.2 μm, n = 30), catenate, acrogenous, phragmosporous, light brown to dark brown, smooth to distinctly verrucose, 2–3-septate, rounded and paler at the apex, slightly constricted at some septa, subcylindrical. *Conidial secession* schizolytic.

Culture characteristics – Conidia germinating on PDA within 18 h and reaching 20–23 mm diam. after three weeks, colonies from above: medium dense, circular, flat, slightly raised, surface smooth with crenate edge, with smooth aspects, light brown at the margin, white to cream in the centre; reverse: light yellow at the margin, light brown in the centre.

Material examined – Taiwan, Chiayi, Ali Shan Mountain, Fanlu Township Area, Dahu Forest, dead stem of *Hedygium coronarium* J. Koenig (*Zingiberaceae*), 25 August 2018, D. S. Tennakoon, XP026A (MFLU 18-2520), living culture MFLUCC 19-0143, *ibid.*, 05 September 2018, XP026B (NCYU 19-0157), NCYUCC 19-0179.

GenBank accession numbers – MFLUCC 19-0143: LSU: OL757569; ITS: OL757573; *tef1-α*: OL792172; *rpb2*: OL792170, NCYUCC 19-0179: LSU: OL757570; ITS: OL757574; *tef1-α*: OL792173; *rpb2*: OL792171.

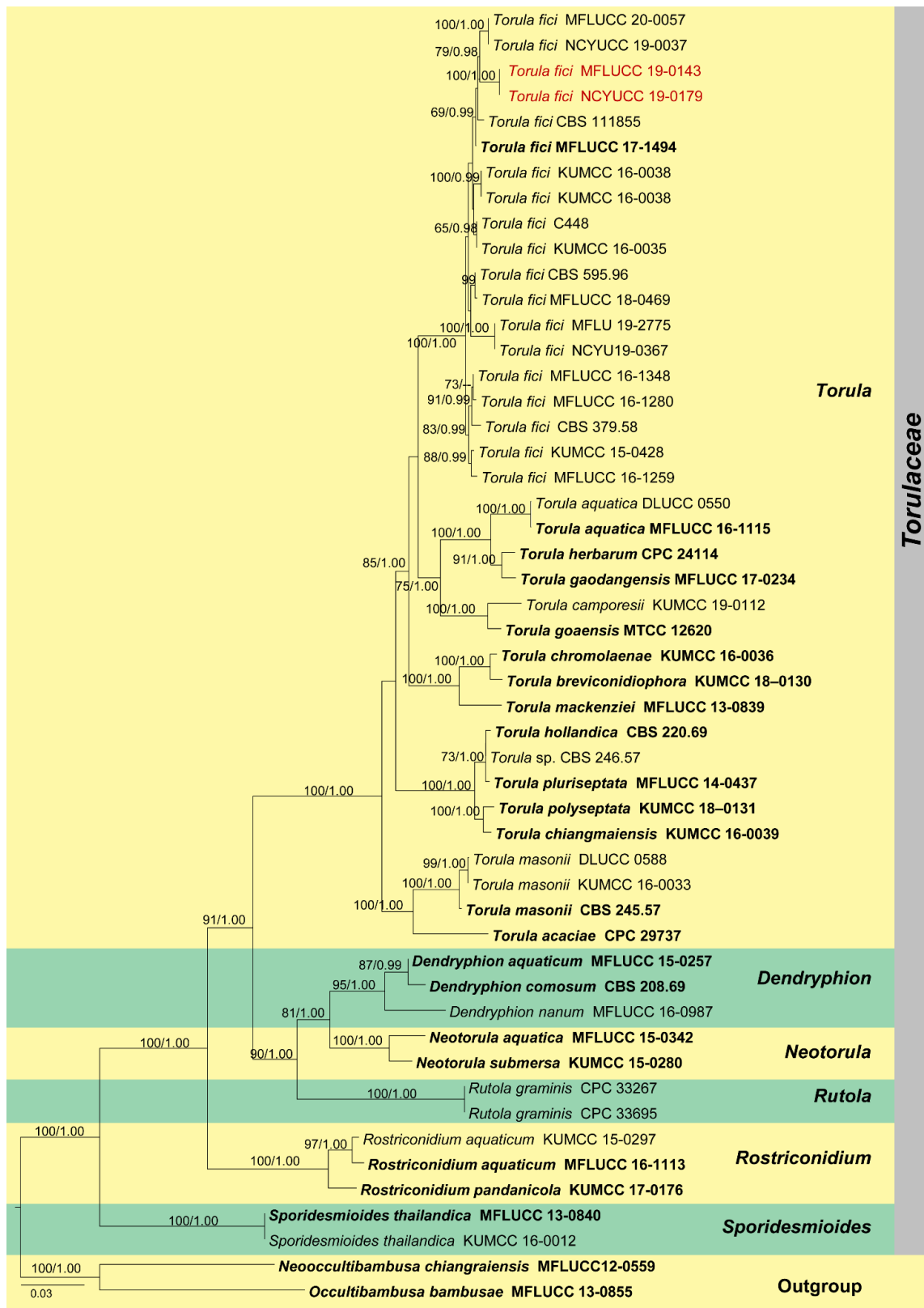
Notes – *Torula fici* was introduced by Crous et al. (2015) from *Ficus religiosa* in Cuba. The characters of our collection (MFLUCC 19-0143 and NCYUCC 19-0179) fit well with *Torula fici* in having dark brown to black, ellipsoidal conidiogenous cells and light brown to dark brown, smooth to distinctly verrucose, 2–3-septate, subcylindrical conidia (Crous et al. 2015, Jayasiri et al. 2019, Tennakoon et al. 2021). Multi-gene phylogeny also indicates that our collection (MFLUCC 19-0143 and NCYUCC 19-0179) nested with other *Torula fici* strains in a 100% ML and 1.00 BYPP supported clade (Fig. 25). Therefore, we conclude that our collection is a new host record of *Torula fici* from *Hedygium coronarium* in Taiwan (Table 1).

## Sordariomycetes

For taxonomic treatments, Hyde et al. (2020a) and Wijayawardene et al. (2020) are followed.

*Sporocadaceae* Corda as ‘Sporocadeae’, Icon. fung. (Prague) 5: 34 (1842)

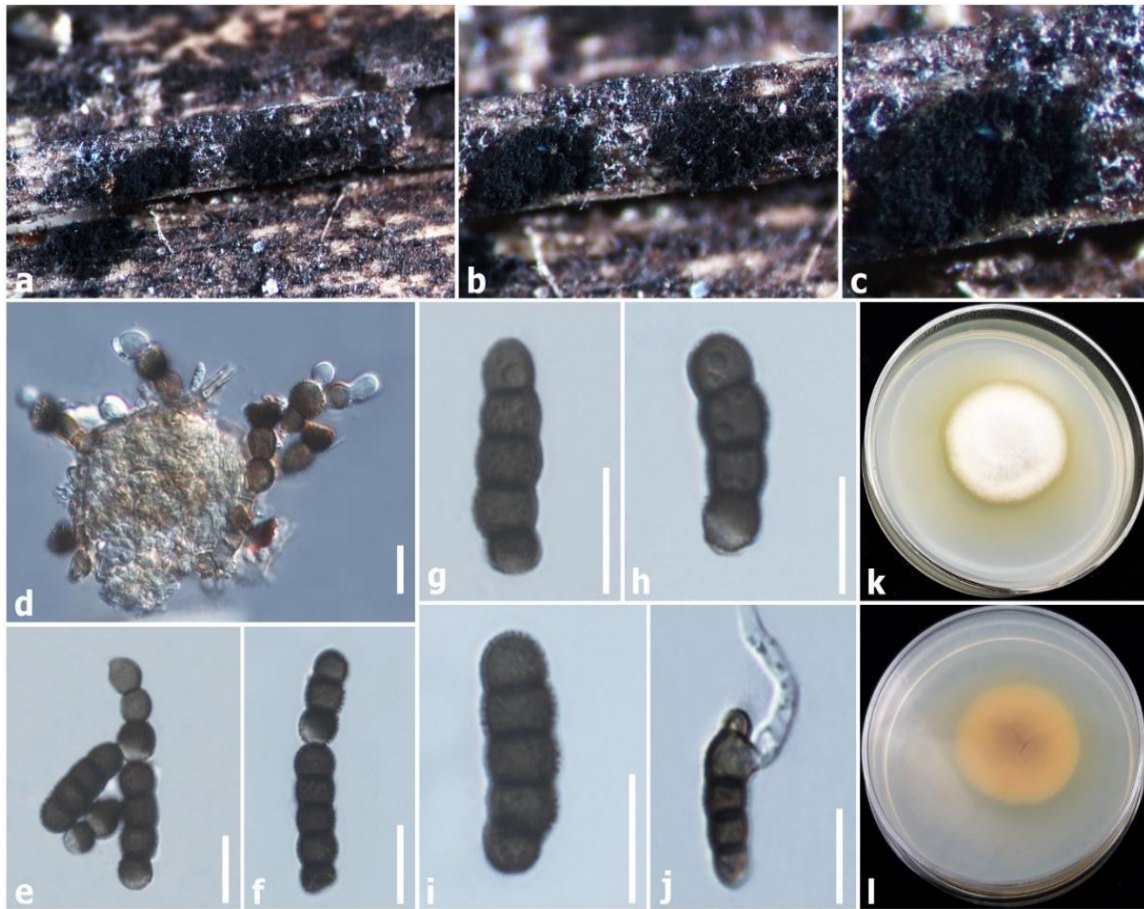
Corda (1842) introduced *Sporocadaceae* with *Sporocadus* as the type genus, and this was re-validated by Jaklitsch et al. (2016). It includes genera that are typically appendaged-bearing coelomycetes with saprobic, endophytic, or foliar pathogenic lifestyles (Nag Raj 1993, Tanaka et al. 2011, Hyde et al. 2020). Wijayawardene et al. (2020) included 33 genera in *Sporocadaceae*.



**Figure 25** – The best scoring RAXML tree with a final likelihood value of - 20084.73 for a combined dataset of LSU, SSU, ITS, *tef1- $\alpha$*  and *rpb2* sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses. The tree is rooted with *Neooccultibambusa chiangraiensis* (MFLUCC 12-0559) and *Occultibambusa bambusae* (MFLUCC 13-0855). The matrix had 1431 distinct alignment patterns with 41.80% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.245421, C = 0.262254, G = 0.270377, T = 0.221948; substitution rates AC = 1.880732, AG = 3.690777, AT = 1.708622, CG = 1.114706, CT =



8.197829, GT = 1.000000; gamma distribution shape parameter  $\alpha = 0.471909$ . Ex-type strains are in bold and newly generated sequences are in red. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes.



**Figure 26** – *Torula fici* (MFLU 18-2520, new host record). a–c Colonies on dead stem of *Hedychium coronarium*. d Conidiophores with conidiogenous cells. e–f Conidial budding. g–i Conidia. j A germinating conidium. k Colonies from above (on PDA). n Colonies from below (on PDA). Scale bars: d–j = 8  $\mu$ m.

***Robillarda*** Sacc., *Michelia* 2(no. 6): 8 (1880)

Saccardo (1880a) introduced *Robillarda* to accommodate the type species *R. sessile*. This genus is characterized by flexuous, narrow tubular, aseptate appendages and holoblastic conidiogenous cells, proliferating sympodially or percurrently near the apex (Crous et al. 2015, Wijayawardene et al. 2016). Tennakoon et al. (2021) is used for the treatment of this genus. In this paper, we introduce one novel *Robillarda* species from a freshwater habitat in Thailand.

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

Fig. 28

Index Fungorum number: IF559337; Facesoffungi number: FoF10600

Etymology– in reference to the habitat where the fungus was collected

Holotype – MFLU 21–0253

*Saprobic* on decaying wood submerged in freshwater. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 170–200  $\times$  170–230  $\mu$ m ( $\bar{x}$  = 181.6  $\times$  192.7  $\mu$ m, n = 10), pycnidial, black, semi-immersed, mostly erumpent, uniloculate, solitary, scattered, irregular in shape, thick-walled, ostiolate. *Conidiomatal wall* 10–15  $\mu$ m wide, thin-walled, slightly thick at the pycnidial upper wall, composed of two layers, dark brown to black, thick-walled cells in outer layer, arranged in *textura angularis*, becoming hyaline towards the inner layer. *Conidiophores* reduced to

conidiogenous cells lining the cavity of the conidiomata. *Conidiogenous cells* 5–15 × 5–10 μm ( $\bar{x}$  = 11.9 × 6.6 μm, n = 20), holoblastic, proliferating sympodially at apex, ampulliform to subcylindrical, hyaline, aseptate, smooth and thin-walled. *Conidia* 15–20 × 3–5 μm ( $\bar{x}$  = 15.9 × 3.7 μm, n = 50), hyaline, oblong to ellipsoidal, narrow towards the basal cell, straight or slightly curved, (0–)1-septate, smooth and thin-walled, slightly constricted at the septum, apical cell modified into a branched appendage; appendages 30–45 × 1–2 μm ( $\bar{x}$  = 37.3 × 1.4 μm, n = 50), dividing into 3–4 divergent branches, devoid of cell contents, flexuous, attenuated toward the apex, slightly swollen at the apex.

Culture characteristics – Conidia germinating on malt extract agar (MEA) within 24 h. Germ tubes produced from the basal and apical cell of conidia. Colonies on MEA reaching 30–35 mm diam. after 2 weeks at 25°C. Mycelia superficial, circular, flat, surface slightly rough, with entire margin, forming small, black pycnidia on colony after two weeks of incubation; from above, grey to light brown; reverse, light brown at the center and becoming dark brown towards margin; not producing pigmentation in agar.

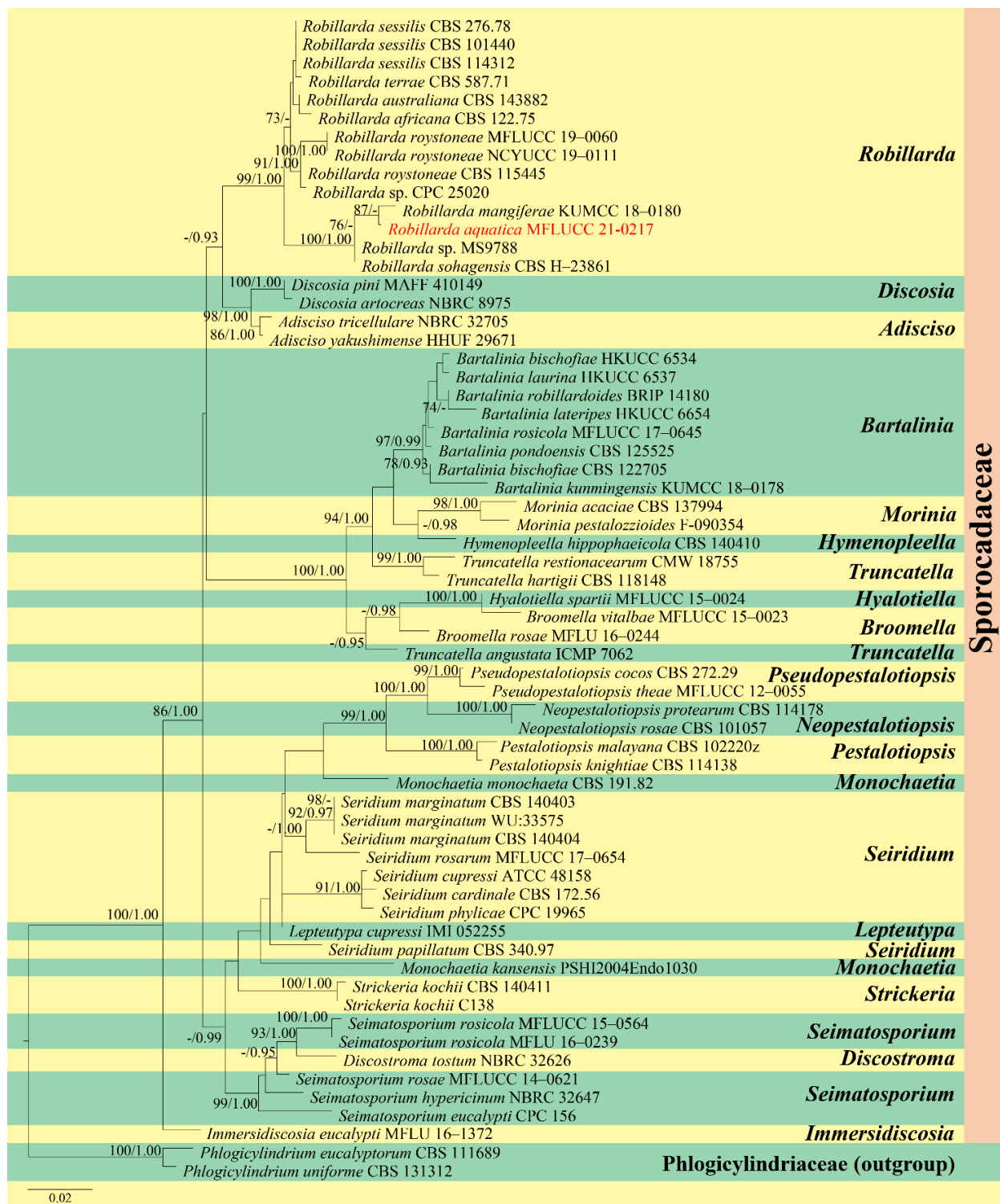
Material examined – Thailand, Tak Province, Tha Sing Yang, Ban Mae Ja Wang, on decaying wood submerged in a river, 17 October 2019, N. Padaruth, CC20 (MFLU 21–0253, holotype), ex-type living culture, MFLUCC 21–0217.

GenBank accession numbers – LSU: OL477390; ITS: OL504777.

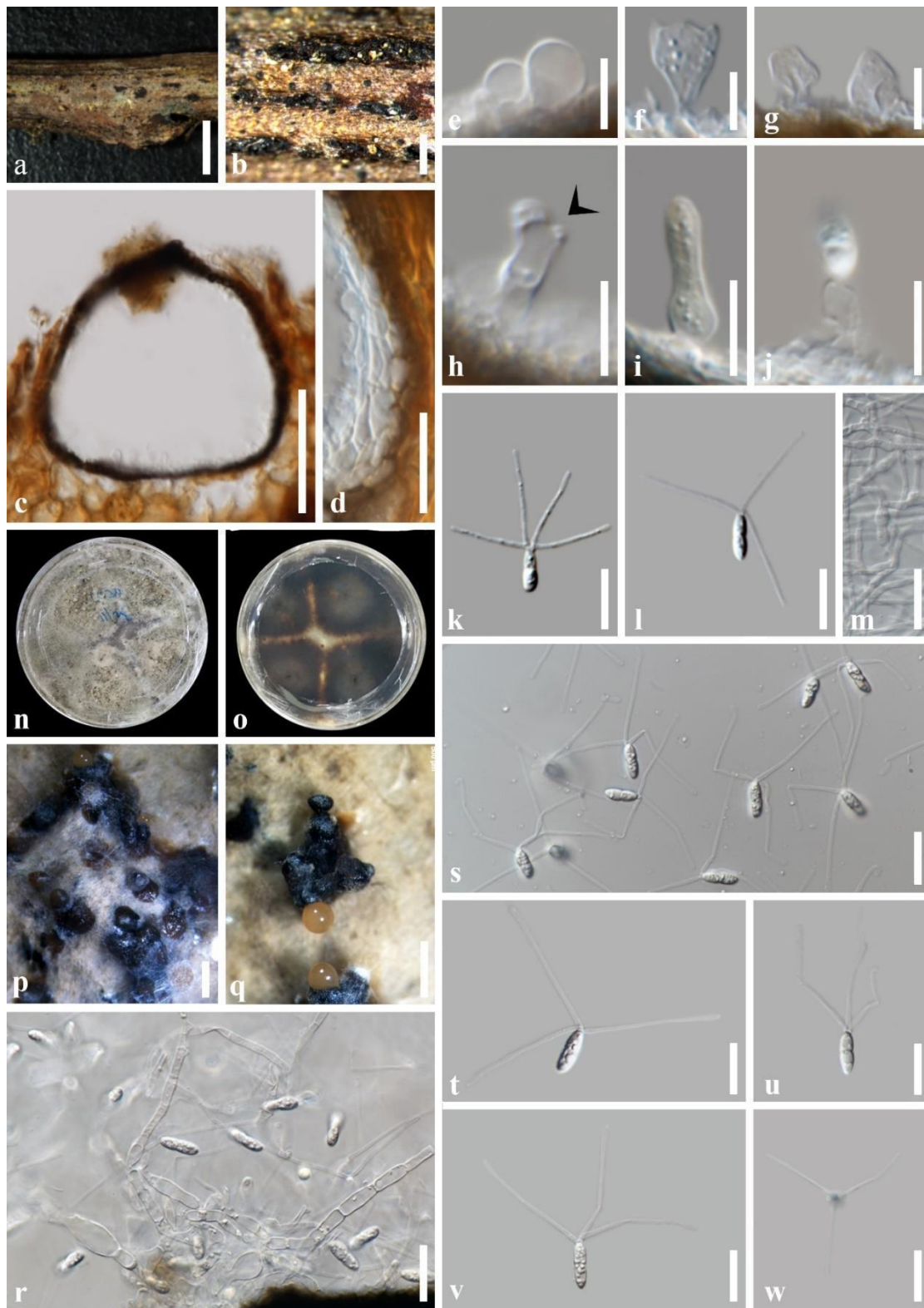
Notes – *Robillarda aquatica* is the third species recorded from freshwater habitats; the other two species, *R. sohagensis* and *R. sessilis*, were recorded from submerged decaying leaves of *Phoenix dactylifera* in a river (Egypt) and unidentified plant litter in a stream (Korea), respectively (Song et al. 2020, Goh et al. 2020). The phylogenetic analyses of a combined LSU and ITS sequence dataset show that *R. aquatica* clusters with other *Robillarda* species and is closely related to *R. mangiferae* (KUMCC 18-0180), *R. sohagensis* (CBS H-23861), and *Robillarda* sp. (MS9788) with 100% MP bootstrap and 1.00 BYPP support (Fig. 27). *Robillarda aquatica* differs from *R. mangiferae* by having longer conidia (15–20 × 3–5 μm vs. (7.5–)10–11(–12) × (2.5–)3–4(–4.5) μm vs.), and longer apical appendages (30–45 × 1–2 μm vs. 25–35 × 1–2.5 μm) (Phookamsak et al. 2019). *Robillarda sohagensis* has larger conidiomata (765–2025 × 270–495 μm vs. 170–200 × 170–230 μm) compared to *R. aquatica* which has shorter appendages (26–41 × 1–1.5 μm vs. 30–45 × 1–2 μm) (Song et al. 2020). The morphological comparison with closely related taxa and two-locus phylogenetic analysis support the introduction of a novel freshwater species, *R. aquatica*.

**Table 1** Synopsis of *Torula* species with similar morphology features discussed in this study. Newly added data are in bold.

<i>Torula</i> species	Conidiogenous cells (μm)	Conidia (μm)	Septation	References
<i>T. brevicongiophora</i> (MFLU 18-1693)	4–7 × 3–7	8–21 × 3.5–7	1–4	Hyde et al. (2019)
<i>T. Chiangmaiensis</i> (MFLU 16-2815)	3.4–6.5 × 4.8–7.6	(5.4–) 25.5–70 (–86.5) × 5.6–7.8	4–12	Li et al. (2017)
<i>T. chromolaenae</i> (MFLUCC 17-1514)	3–6 × 3.5–6	7–18.5 × 4–8	1–3	Mapook et al. (2020)
<i>T. fici</i> (MFLUCC 17-1494)	4–7 × 5.5–7	10–25 × 5.5–8	1–5	Mapook et al. (2020)
<i>T. fici</i> (MFLU 16-2817)	5.4–8.5 × 5–7.4	12–20 × 4.6–6.6	2–4	Li et al. (2017)
<i>T. fici</i> (MFLU 18-0025)	3–5 × 2–3	10–23 × 4–7	1–3	Tibpromma et al. (2018)
<i>T. fici</i> (MFLU 18-1694)	4.5–8.5 × 4.5–8	10–40 × 3.5–7.5	2–8	Hyde et al. (2019)
<b><i>T. fici</i> (MFLU 18-2520)</b>	<b>3.2–5 × 3–5</b>	<b>12–20 × 4–6</b>	<b>2–3</b>	<b>This study</b>
<i>T. polyseptata</i> (MFLUCC 17-1495)	5.5–7.7 × 4.5–8	15–55 × 6.5–9	1–10	Mapook et al. (2020)



**Figure 27** – Phylogenetic tree generated by ML analysis of combined LSU and ITS sequence data of *Sporocadaceae*. The analyses included 63 strains and the tree is rooted with *Phlogicylindrium eucalyptorum* (CBS 111689) and *Phlogicylindrium uniforme* (CBS 131312). The tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of -8243.687976 is presented. The matrix had 594 distinct alignment patterns, with 33.45% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.261909, C = 0.211108, G = 0.259193, T = 0.267790; substitution rates AC = 0.998621, AG = 2.475880, AT = 1.324142, CG = 0.858286, CT = 4.291128, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.182492. RAxML bootstrap support values  $\geq 70\%$  and  $\geq 0.90$  BYPP are shown near the nodes. New isolates recovered in this study are in red.



**Figure 28** – *Robillarda aquatica* (MFLU 21–0253, holotype). a Host. b Appearance of conidiomata on natural substrate. c Vertical section of conidiomata. d Conidiomatal wall. e–j Conidiogenous cells (arrow = sympodial proliferation). k, l Conidia. m Germinated conidium. Colonies on MEA from above (n) and below (o). p, q Conidiomata on MEA. r Conidiogenous cells and conidia. s–w Conidia. Scale bars: a = 5 mm, b = 500  $\mu$ m, c = 100  $\mu$ m, d, k–m, r–w = 20  $\mu$ m, e–j = 10  $\mu$ m, p, q = 1000  $\mu$ m.

*Sporocadus* Corda, Icon. fung. (Prague) 3: 23 (1839)

*Sporocadus* was introduced by Corda (1839) to accommodate four species (*Spo. herbarum*, *Spo. georginae*, *Spo. lichenicola*, and *Spo. maculans*), but no generic type was designated (Corda

1839). Hughes (1958) provided a lectotype based on *Spo. lichenicola*. Sutton (1975) synonymized *Sporocadus* under *Seimatosporium*. Brockman (1976) and Nag Raj (1993) did not agree with Sutton (1975) and treated *Sporocadus* as distinct from *Seimatosporium*. In the phylogenetic analysis of Liu et al. (2019), *Sporocadus* formed a distinct lineage with *Seimatosporium* hence *Sporocadus* was resurrected and epitypified by *Spo. lichenicola*. *Sporocadus* is characterized by 3-septate, fusoid, cylindrical and obovoid conidia lacking appendages. Two species *S. trimorphus* and *Spo. rosarum* are exceptions as they produce both non-appendaged and appendaged conidia. *Sporocadus* can be differentiated from *Seimatosporium* based on DNA sequence data. In this study, we provide a geographical record for *Sporocadus sorbi* from Uzbekistan. The latter was introduced by Wijayawardene et al. (2015) as *Seimatosporium sorbi*. Liu et al. (2019) provided the combination *Sporocadus sorbi*.

***Sporocadus sorbi*** (Wijayaw., Camporesi & K.D. Hyde) F. Liu, L. Cai & Crous, in Liu, Bonthond, Groenewald, Cai & Crous, Stud. Mycol. 92: 404 (2018) [2019] Fig. 30

Index Fungorum number: IF828421; Facesoffungi number: FoF00669

*Saprobic* on dead stems of *Rosa ecae*. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 200–350 µm diam., 170–250 µm high, acervular, subepidermal, unilocular, subglobose, superficial, solitary, dark brown to black, apapillate ostiolate, pycnidial, subepidermal, black, gregarious, unilocular, globose to subglobose, papillate ostiole, central. *Conidiomata wall* multi-layered, outer wall 15–35 µm wide, composed of brown, thin-walled cells of *textura angularis*, with inner layer of hyaline, thin-walled cells of *textura angularis*. *Conidiophores* 5–15 × 2–3 µm ( $\bar{x}$  = 7.1 × 2.7 µm, n = 20), cylindrical, branched, hyaline to sub-hyaline, smooth-walled. *Conidiogenous cells* 2–4 × 5–7 µm ( $\bar{x}$  = 2.9 × 6 µm, n = 20), enteroblastic, phialidic with percurrent proliferation, simple, short, hyaline to pale brown, thin-walled, indeterminate, discrete to integrated. *Conidia* 15–20 × 6–10 µm ( $\bar{x}$  = 17.1 × 6.7 µm, n = 20), brown, clavate or ellipsoid to subcylindrical sometimes with truncate base, straight, with 3-septa, septa brown to dark brown, slightly constricted at the septa, with hyaline to sub-hyaline basal cell, smooth-walled.

Culture characteristics – Colonies on PDA, slow growing, reaching 2 cm diam. after 7 days at 25°C, light brown from above, pale brown from below, with sparse mycelium, flat, margin circular.

Material examined – Uzbekistan, Tashkent Province, Chotqol Biosphere Reserve, Chimyon Mountain, on *Rosa ecae* Aitch. (*Rosaceae*), 21 July 2019, Y. Gafforov (TASM 6165), living culture, MFLUCC 21-0221

GenBank accession numbers – LSU: OK642226; ITS: OK642281.

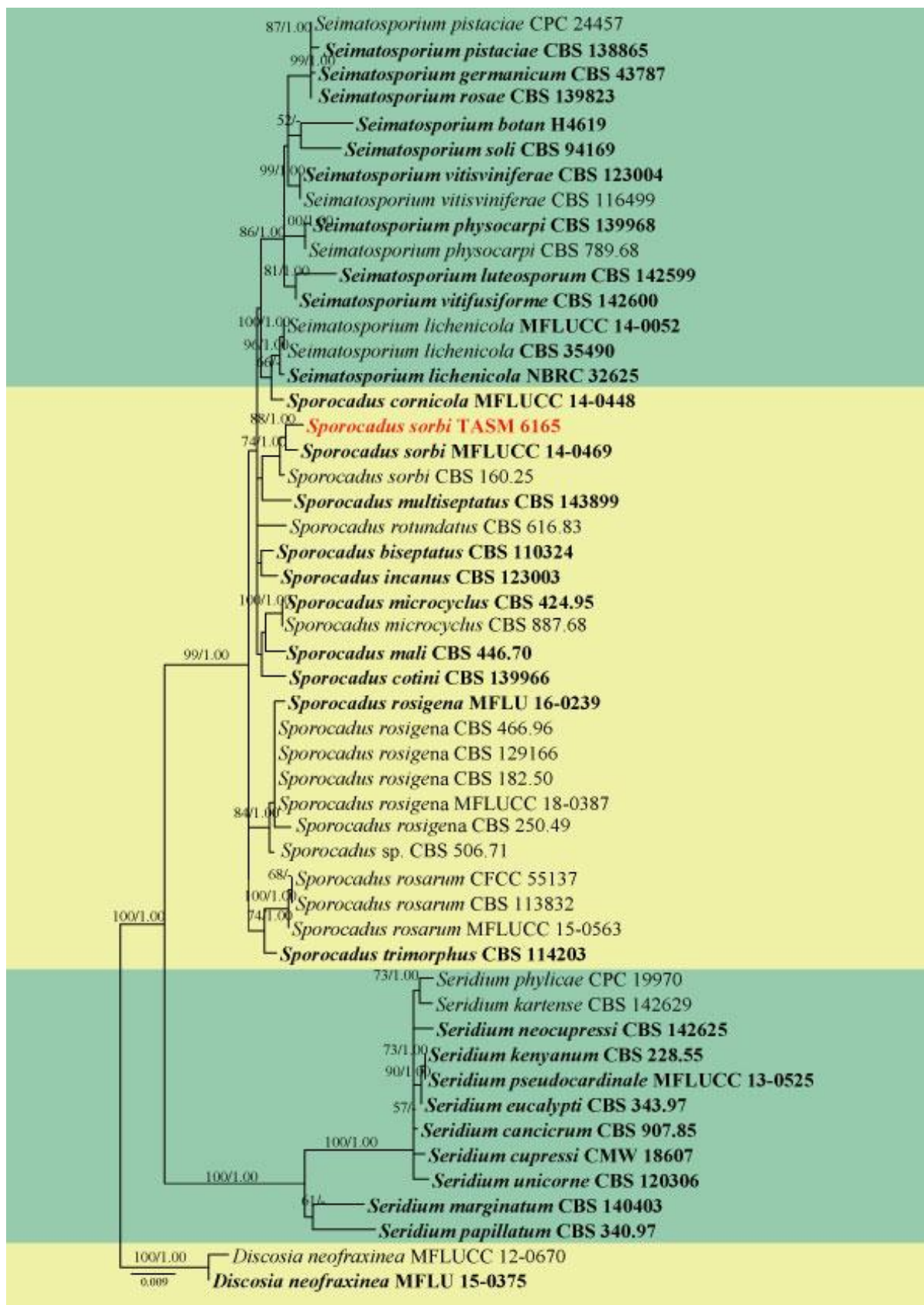
Notes – Our collection from *Rosa ecae* is morphologically similar to *Sporocadus sorbi*, and phylogenetic analyses (Fig. 29) showed that it grouped with *Sporocadus sorbi*. Wijayawardene al. (2015) reported *Sporocadus sorbi* as *Seimatosporium sorbi* on a dead leaf of *Sorbus torminalis* (*Rosaceae*) in Italy. In molecular analyses, our taxon groups with *Sporocadus sorbi* (MFLUCC 14-0469). Comparison of base pairs between our isolate as *Sporocadus sorbi* (MFLUCC 14-0469) and *Sporocadus sorbi* (CBS 16025) reveals two and one base-pair differences respectively. Our taxon is also morphologically similar to *Sporocadus sorbi* and thus is introduced as a new geographical record for Uzbekistan.

**Chaetosphaeriales** Huhndorf, A.N. Mill. & F.A. Fernández, Mycologia 96(2): 378 (2004)

### *Incertae sedis*

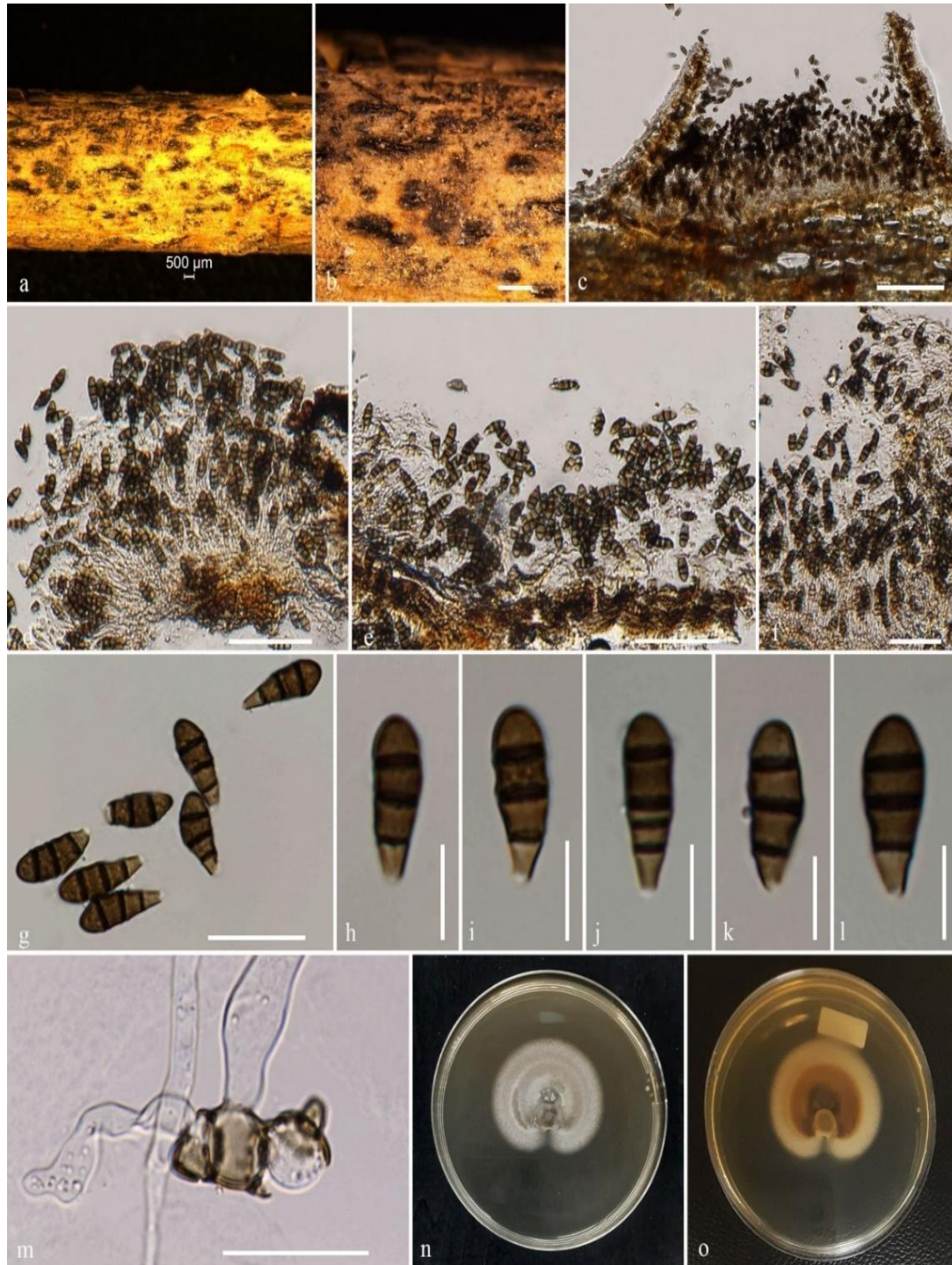
***Neoleptosporella*** Phukhams. & K.D. Hyde, in Phukhamsakda et al., Fungal Diversity 102: 147 (2020)

Phukhamsakda et al. (2018) accepted *Neoleptosporella* in Chaetosphaeriales genera *incertae sedis*. The genus is characterised by immersed ascomata which are partially carbonaceous at the apex, asci with J- apical rings and, fusiform, aseptate ascospores (Hyde et al. 2020a, Phukhamsakda et al. 2020).

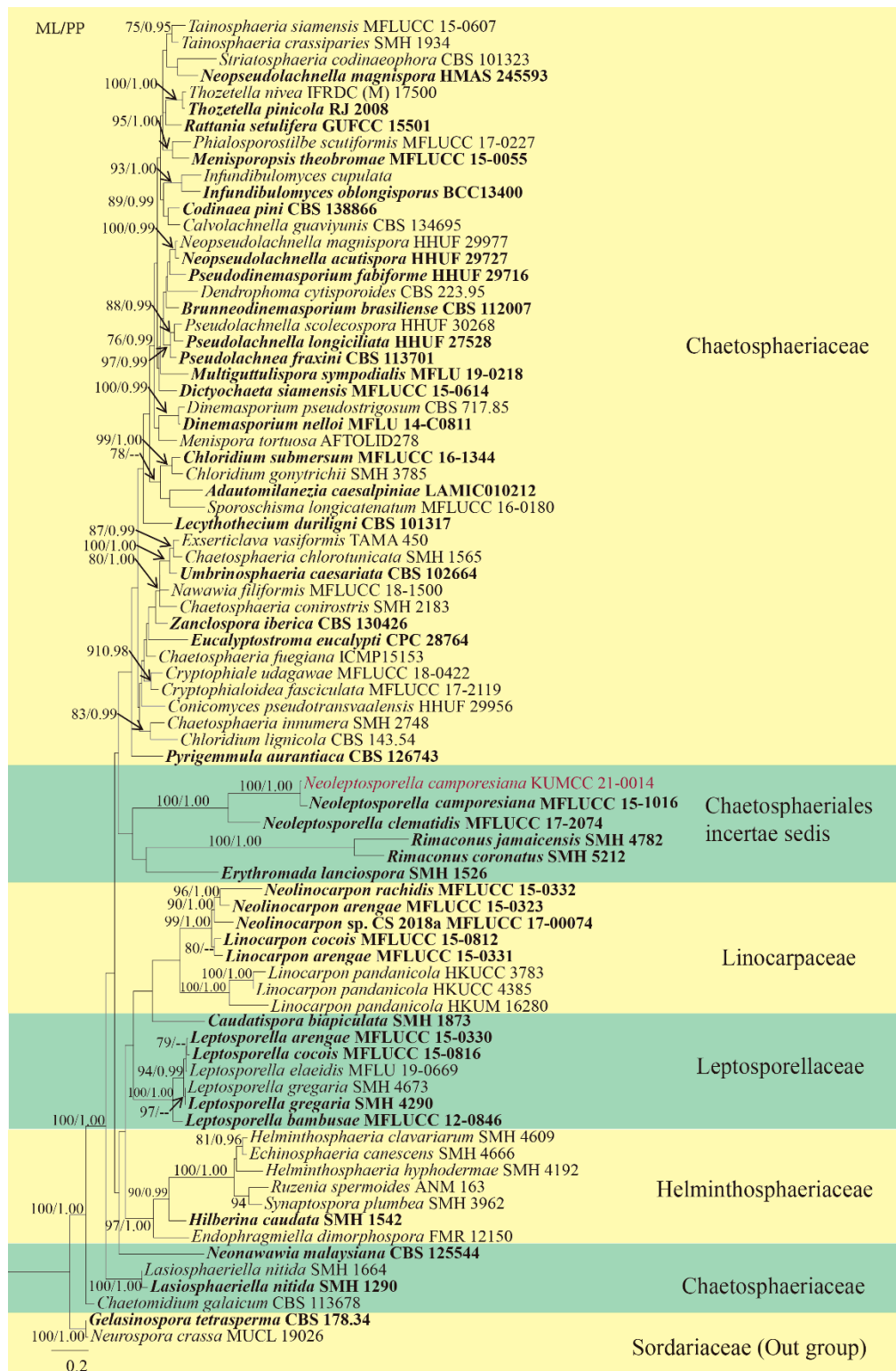


**Figure 29** – Phylogenetic tree generated by ML analysis of combined LSU and ITS sequence data of 51 species. The analyses included 51 strains and the tree was rooted with *Discosia neofraxinea* (MFLU 15-0375) and *Discosia fraxinea* (NTIT469). The tree topology of the ML analysis was similar to the MP and BYPP. The best scoring RAxML tree with a final likelihood value of -3830.828429 is presented. The matrix had 262 distinct alignment patterns, with 9.26% of

undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.252365, C = 0.217671, G = 0.256360, T = 0.273603; substitution rates AC = 0.772616, AG = 3.254856, AT = 1.929542, CG = 0.483348, CT = 6.879926, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.751628. RAxML bootstrap support values  $\geq 50\%$  and maximum parsimony bootstrap support values  $\geq 50\%$  are shown near the nodes. Nodes with  $\geq 0.95$  (BYPP) Bayesian posterior probabilities are indicated with thickened lines. The scale bar indicates 0.009 changes per site. Ex-type/ ex-epitype strains are in bold. New isolates recovered in this study are in red.



**Figure 30** – *Sporocadus sorbi* (TASM 6165, new geographical record). a, b Appearance of pycnidia on a dead branch of *Rosa ecae*. c Section through conidioma. d–f Conidia developing on conidiogenous cells. g–l Conidia. m Germinating conidium. n, o Culture characters on MEA (n: Above view; o: Reverse view).



**Figure 31** – Phylogenetic tree generated by ML analysis of combined LSU and ITS sequence data of 80 species. *Gelasinospora tetrasperma* (CBS 178.34) and *Neurospora crassa* (MUCL 19026) were used as outgroup taxa. The tree topology of the ML analysis was similar to the BYPP. The best scoring RAXML tree with a final likelihood value of -20765.086284 is presented. The matrix had 900 distinct alignment patterns with 30.81% undetermined characters or gaps. Estimated base frequencies were A = 0.221860, C = 0.274373, G = 0.319603, T = 0.184164; substitution rates AC = 1.570428, AG = 2.097555, AT = 1.612952, CG = 1.187456, CT = 7.503192, GT = 1.000000. RAXML bootstrap support values 75% and nodes with  $\geq 0.95$  (BYPP) Bayesian posterior probabilities are shown near



the nodes. The scale bar indicates 0.2 changes per site. Ex-type/ ex-epitype strains are in black bold, the newly generated sequence in this study is in red.

***Neoleptosporella camporesiana*** R.H. Perera & K.D. Hyde, in Hyde et al., Fungal Diversity 100: 219 (2020) Fig. 32

Index Fungorum number: IF 823145, Facesoffungi number: FoF 10584

*Saprobic* on a stem of *Heteropanax fragrans*. Sexual morph: *Ascomata* 200–400 × 150–300 μm ( $\bar{x}$  = 303 × 267 μm, n = 30), solitary, erumpent or immersed, black, coriaceous, uni-loculate, subglobose to depressed globose, flat at the base, ostiole central. *Ostioles* 100–200 × 20–50 μm ( $\bar{x}$  = 125 × 32 μm, n = 30), black, cylindrical. *Peridium* 10–20 μm ( $\bar{x}$  = 12 μm, n = 30) thin, comprised of an inner layer of hyaline cells of *textura angularis* and an outer layer of brown flattened cell, outer cells merging with the host epidermal cells. *Paraphyses* 1–3 μm wide ( $\bar{x}$  = 1.8 μm, n = 30), hyaline, unbranched, septate, border at the base, tapering to the ends, longer than asci. *Asci* 50–150 × 10–15 μm ( $\bar{x}$  = 98 × 12 μm, n = 30), 8-spored, unitunicate, cylindrical, apex rounded with a wedge-shaped, J-shaped, apical ring. *Ascospores* 50–100 × 2–5 μm ( $\bar{x}$  = 70 × 3 μm, n = 30), filiform, straight or curved, hyaline, aseptate, ends rounded, with polar mucilaginous appendage at the apex, guttulate or verrucose. Asexual morph: Not observed.

Material examined – China, Yunnan Province, Kunming, on dead stem of *Heteropanax fragrans* (Roxb.) Seem., (*Araliaceae*), 12 August 2020, C.F. Liao (KUN–HKAS 112879), living culture KUMCC 21-0014.

GenBank accession numbers – LSU: OL473548; ITS: OL352056.

Notes – In the phylogenetic analysis, our strain is related to the *Neoleptosporella camporesiana* (MFLUCC 15-1016) (Fig. 31). In morphology, our strain resembles *Neoleptosporella* having immersed ascomata which are globose to depressed-globose, asci with wedge-shaped, and J-shaped apical rings, with fusiform, aseptate ascospores. However, our collection differs from *Neoleptosporella camporesiana* by its smaller ascomata (303 × 267 μm vs 250 × 800 μm), asci (98 × 12 μm vs 187 × 10 μm) and ascospores (70 × 3 μm vs 126 × 3 μm). In the phylogenetic analysis, our collection grouped *Neoleptosporella camporesiana* (MFLUCC 17-2074) with 100/1.00 ML/BYPP (Fig.31). In pairwise nucleotide comparison, 22 base pairs difference and nine base pairs difference were observed for ITS (474 base pairs) and LSU (849 base pairs) respectively. Based on morphological and phylogenetic evidence, we introduced our collection as a new host record for *Heteropanax fragrans* from China.

***Chaetosphaeriaceae*** Réblová, M.E. Barr & Samuels, Sydowia 51(1): 56 (1999)

We follow Hyde et al. (2020c) the latest treatment of *Chaetosphaeriaceae*. The family comprises 44 genera with *Chaetosphaeria* being the most speciose genus comprising 109 species (Wijayawardene et al. 2020; Species Fungorum 2021).

***Pseudophialocephala*** M.S. Calabon, E.B.G. Jones & K.D. Hyde, gen. nov.

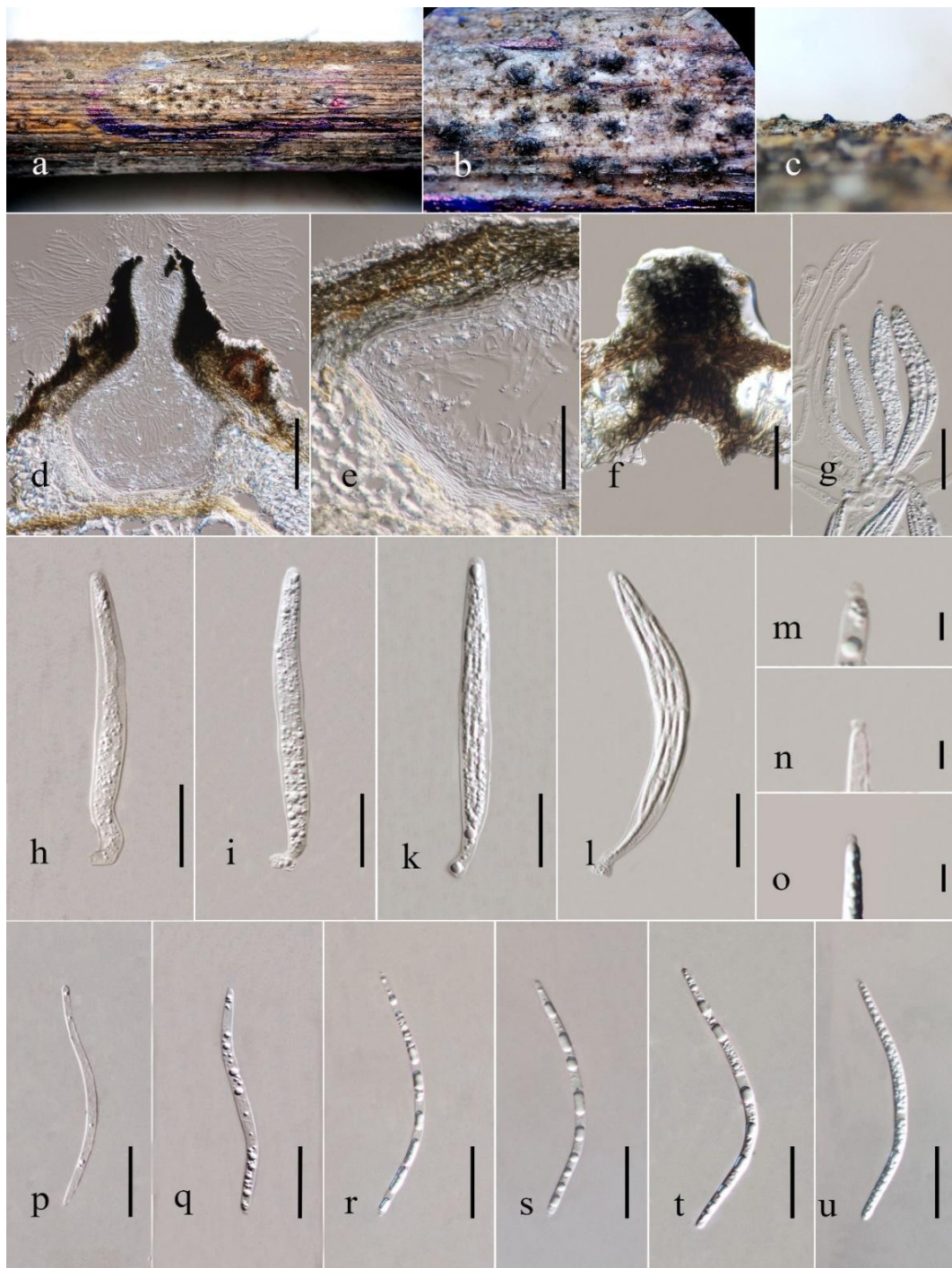
Index Fungorum number: IF559318; Facesoffungi number: FoF 10602

Etymology – Name reflects the morphological similarity to *Phialocephala*

*Saprobic* on decaying wood from terrestrial and aquatic habitats. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, white, brown, velvety. *Mycelium* partly superficial to immersed, composed of hyaline, branched, septate, guttulate hyphae constricted at the septa. *Conidiophores* determinate, macronematous, scattered, solitary, composed of *stipe* and *penicillate heads*. *Stipe* thick-walled, erect, straight, or broadly curved, cylindrical, brown, and wide at base, paler and slightly tapering toward the apex, terminating in a penicillate head. *Penicillate heads* composed of 1–3 series of metulae terminating in groups of conidiogenous cells. *Metulae* thin-walled, light brown to subhyaline. *Conidiogenous cells* monophialidic, integrated, discrete, determinate, terminal, clustered at the apex of secondary metulae, hyaline to pale brown, thin-walled, cylindrical, with inconspicuous openings, with minute collarettes. *Conidia* acrogenous,

aseptate or 1-septate, aggregated in slimy and white masses, solitary to catenate, hyaline, ellipsoidal, cylindrical, rounded at each end, smooth and thin walled, guttulate.

Type species – *Pseudophialocephala cuneata* N.G. Liu, M.S. Calabon, E.B.G. Jones & K.D. Hyde



**Figure 32** – *Neoleptospora camporesiana* (KUN–HKAS 112879, new host record). a, c Appearance of ascomata on substrate. d Section through ascoma. e Peridium. f Ostiole. g Paraphyses with asci. h–l Asci. m–o Polar mucilaginous appendage. p–u Ascospores. Scale bars: d = 500  $\mu$ m, e = 200  $\mu$ m, f, g, l, p, u = 100  $\mu$ m, m–o = 10  $\mu$ m.

Notes – *Phialocephala sensu stricto*, clade containing the type species *Ph. dimorphospora*, are saprotrophs mostly collected in temperate climates (Wijayawardene et al. 2020, Tanney & Seifert 2020). Species under *Phialocephala sensu stricto* include *Ph. aylmerensis*, *Ph. biguttulata*, *Ph.*

*botulispora*, *Ph. catenospora*, *Ph. cladophialophoroides*, *Ph. collarifera*, *Ph. dimorphospora*, *Ph. heterosperma*, *Ph. lagerbergii*, *Ph. lignicola*, *Ph. mallochii*, *Ph. nodosa*, *Ph. oblonga*, and *Ph. repens* which clustered within *Mollisiaceae*. *Phialocephala sensu lato* is polyphyletic and it includes *Ph. fluminis* (Chaetothyriales), *Ph. fusca* (Ophiostomatales), *Ph. hiberna* (*Mollisiaceae*), *Ph. humicola* (Ophiostomatales, Sordariales), *Ph. scopiformis* (*Mollisiaceae*), *Ph. virens* (Ophiostomatales), and *Ph. xalapensis* (Ophiostomatales) (Grünig et al. 2002, Jacobs et al. 2003, Day et al. 2012, Tanney & Seifert 2020). Tanney & Miller (2017) suggested the placement of *Phialocephala fusca* and *Ph. humicola* in Chaetosphaeriales based on the BLASTn result of the ITS sequence data. In the present study, the combined LSU-ITS phylogenetic analyses confirm the placement of *Phialocephala humicola* in *Chaetosphaeriaceae* (Figs 33, 34). *Phialocephala fusca* (CBS 301.85), *Chloridium lignicola* (CBS 143.54) and *Ch. pini* (CPC 36627) formed an independent clade basal to the taxa of *Chaetosphaeriaceae* and is distant to the clade shared by *Ps. humicola* and other taxa of *Chloridium* and *Sporochisma*. Since *Phialocephala humicola* was morphologically different from the generic description of *Chloridium* and *Sporochisma*, we introduce a novel genus *Pseudophialocephala* to accommodate this taxon and also transfer *Ch. aquaticum*, *Ch. salinicola*, *Ch. terricola*, and *Ph. xalapensis*. A novel *Pseudophialocephala* taxon, *Ps. cuneata*, collected from decaying wood in Thailand, was introduced based on morphology and phylogenetic analysis of LSU and ITS sequence data. Three *Pseudophialocephala* species are saprobic from aquatic habitats: freshwater (*Ps. aquatica*) (Wei et al. 2018), marine (*Ps. humicola*, *Ps. salinicola*) (Dayarathne et al. 2020a, this study), and in terrestrial habitats (*Ps. cuneata*, *Ps. humicola*, *Ps. terricola*, *Ps. xalapensis*) (Jong & Davis 1972, Kiyuna et al. 2012, Chunyu et al. 2013).

***Pseudophialocephala cuneata*** N.G. Liu, M.S. Calabon, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 35

Index Fungorum number: IF 559313; Facesoffungi number: FoF 10603

Etymology – wedge-shaped, referring to the shape of the conidia

Holotype – MFLU 19–2852

*Saprobic* on decaying wood in terrestrial habitat. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, white, velvety. *Mycelium* mostly immersed, composed of hyaline, branched, septate, guttulate hyphae and constricted at the septa, 1.5–3 µm wide. *Conidiophores* determinate, macronematous, composed of *stipe* and *penicillate heads*. *Stipe* up to 300 µm long, 5–7 µm wide at base, 3.5–4.5 µm wide at apex, macronematous, mononematous, erect, straight, or broadly curved, subcylindrical, wider at base, septate, median brown, thick-walled, branched at the apex, terminated by a penicillate head. *Penicillate heads* composed of 1–2 series of metulae terminating in groups of conidiogenous cells. *Conidiogenous cells* monophialidic, discrete, determinate, terminal, clustered at the apex of secondary metulae, hyaline, thin-walled, cylindrical, with inconspicuous openings, with minute collarettes. *Conidia* 2.5–4 µm long, 2–3.5 µm at widest ( $\bar{x}$  = 3.5 × 2.5 µm, n = 30), acrogenous, aggregated in slimy and white masses, acrogenous, solitary to catenate, hyaline, cuneate, rhomboid or shield-shaped, aseptate, smooth-walled.

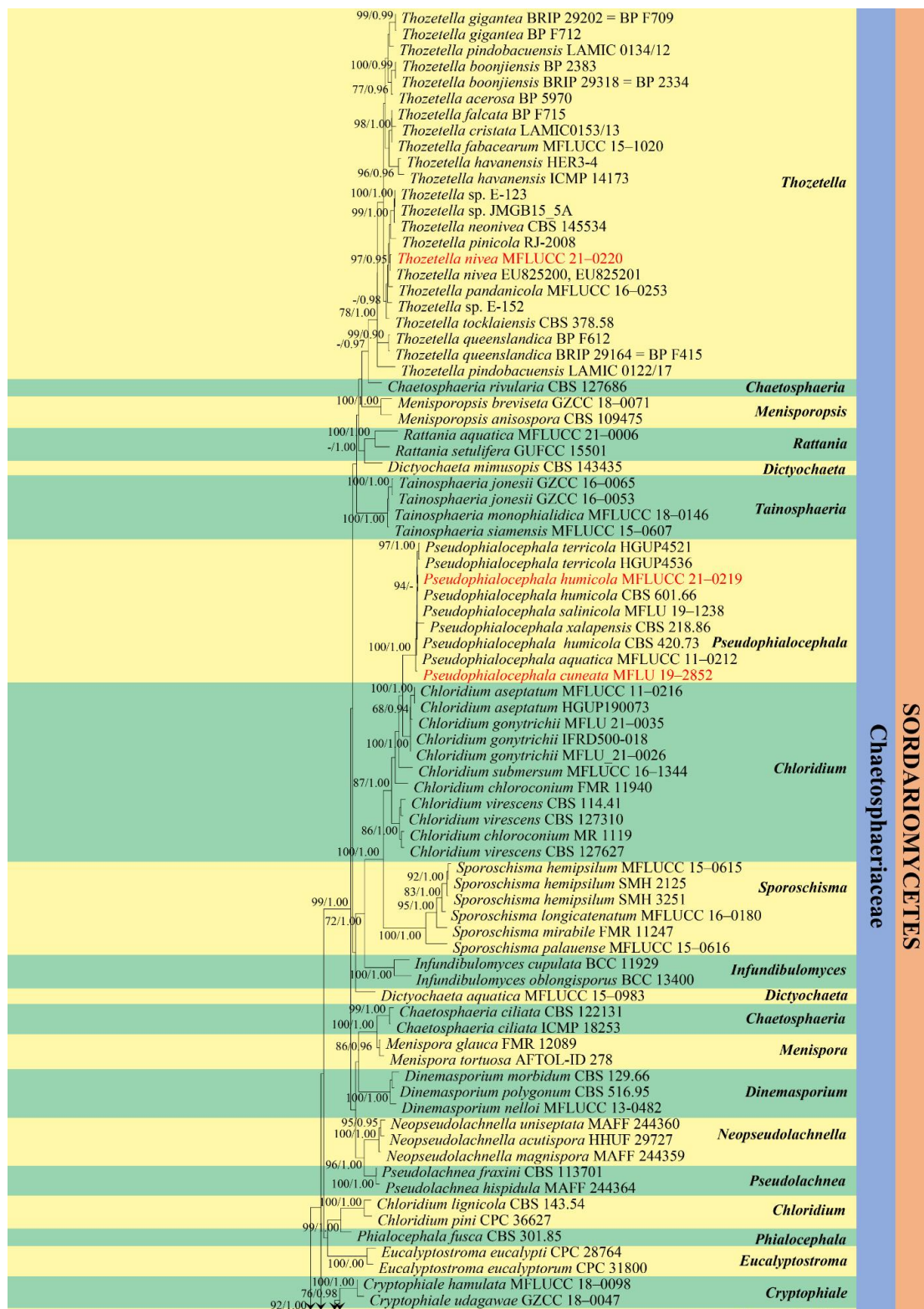
Culture characteristics – Conidia germinated within 48h. Mycelia superficial, decumbent, irregular, with an entire edge, yellowish-brown at center, pale brown at circumference from above.

Material examined – Thailand, Phrae Province, Rong Kwang, on a decaying wood, 10 January 2018, N.G. Liu, N016 (MFLU 19–2852, holotype); ex-type living culture, GZCC 20–0005.

GenBank accession numbers – ITS: MN999924; LSU: MN901120; SSU: MN901150.

Notes – *Pseudophialocephala cuneata* was previously placed in *Vibrissaceae* as *Phialocephala humicola* (GZCC 20-0005) as it clustered with *Ph. humicola* (CBS 601.66) based on the phylogenetic analysis of Hyde et al. (2020a). With the inclusion of other taxa from different classes of Ascomycota, phylogenetic analysis of combined LSU and ITS placed the novel species basal to other *Pseudophialocephala* taxa with low bootstrap support (Figs 33, 34). In addition, the morphology of the isolate supports the inclusion in *Pseudophialocephala* as it resembles the generic description in having conidiophores composed of stipe and penicillate heads (Fig. 35). The conidia of *Ps. cuneata* are cuneate, rhomboid, or shield-shaped and differ from other *Pseudophialocephala* species wherein conidia are cylindrical, ellipsoidal, and oblong. Therefore, based on morphology and

two-locus phylogenetic analysis, the strain GZCC 20-0005 is introduced as *Ps. Cuneata*, a novel taxon from *Pseudophialocephala*. *Pseudophialocephala cuneata* is the second *Pseudophialocephala* species reported from Thailand, while *Ps. humicola* has been observed from decaying *Pinus kesiya* needles (Tokumasu et al. 1990).



**Figure 33** – Phylogenetic tree generated by ML analysis of combined LSU and ITS data of Chaetosphaeriales and closely related taxa. The analyses included 141 strains and the tree is rooted with *Tremella mesenterica* (CBS 6973) and *Trichosporon asahii* (CBS 2479). Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of

-23625.921520 is presented. The matrix had 843 distinct alignment patterns, with 22% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.231971, C = 0.256425, G = 0.298236, T = 0.213368; substitution rates AC = 1.373661, AG = 2.038871, AT = 1.670986, CG = 0.755571, CT = 5.839863, GT = 1.000000; gamma distribution shape parameter  $\alpha = 0.347250$ . RAxML bootstrap support values  $\geq 75\%$  and Bayesian posterior probabilities values  $\geq 0.95$  (BYPP) are shown near the nodes. New isolates recovered in this study are in red.

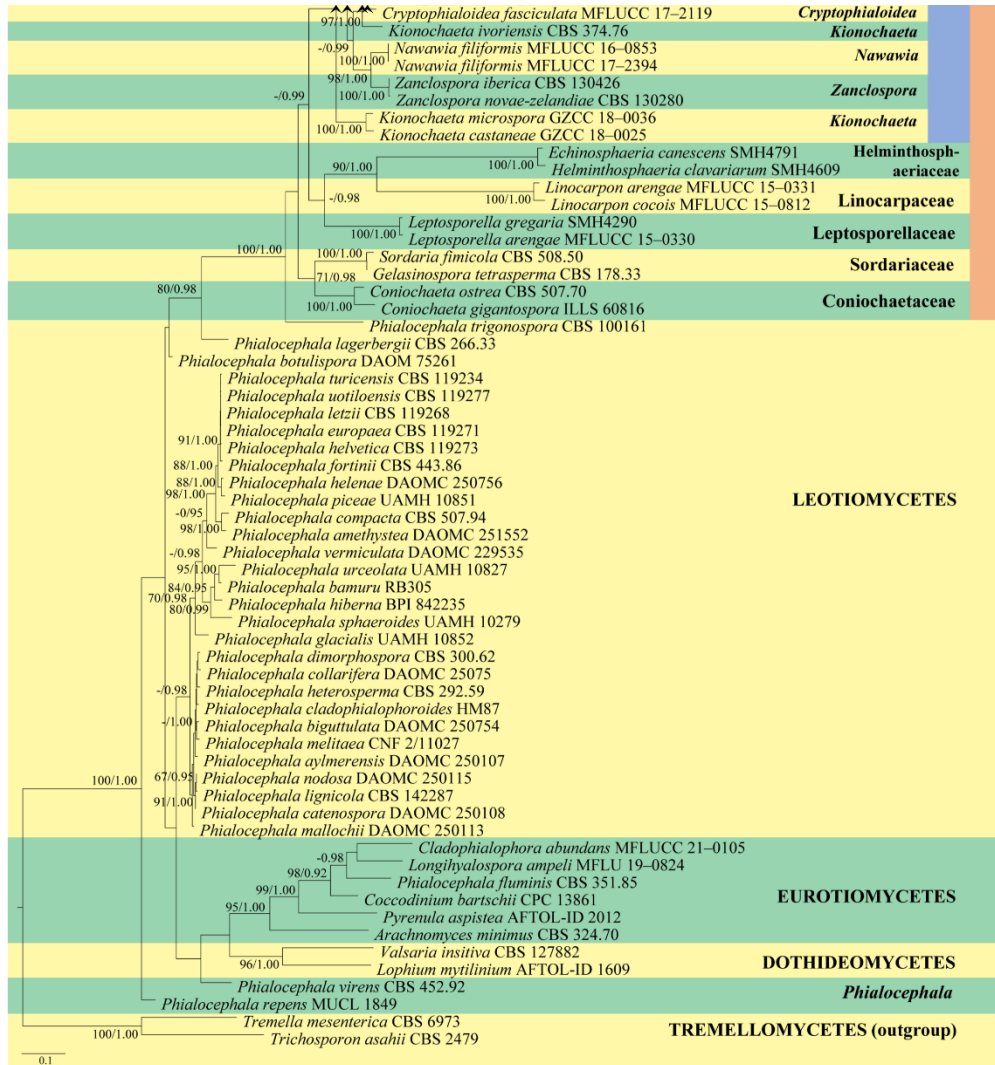


Figure 33 – Continued.

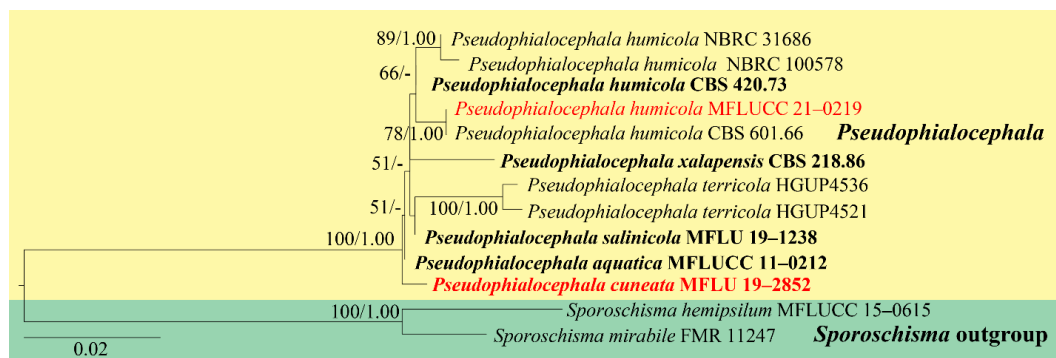


Figure 34 – Phylogenetic tree generated by ML analysis of combined LSU and ITS sequence data of *Pseudophialocephala*. The analyses included 13 strains and the tree is rooted with *Sporoschisma hemipsilum* (MFLUCC 15-0615) and *Sporoschisma mirabile* (FMR 11247). Tree topology of the

ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of -2920.924831 is presented. The matrix had 106 distinct alignment patterns, with 6.78% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.231239, C = 0.266364, G = 0.302672, T = 0.199726; substitution rates AC = 2.586006, AG = 3.386907, AT = 1.676969, CG = 1.508214, CT = 6.123811, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.225772. RAxML bootstrap support values  $\geq 50\%$  and Bayesian posterior probabilities values  $\geq 0.95$  (BYPP) are shown near the nodes. Ex-type/ ex-epitype strains are in bold. New isolates recovered in this study are in red.

***Pseudophialocephala humicola*** (S.C. Jong & E.E. Davis) M.S. Calabon, E.B.G. Jones & K.D. Hyde, comb. nov. Fig. 36

Index Fungorum number: IF 559312; Facesoffungi number: FoF 10604

$\equiv$  *Phialocephala humicola* S.C. Jong & E.E. Davis, Mycologia 64(6): 1352 (1973) [1972]

*Saprobic* on submerged decaying culms from salt marsh habitat. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, white, velvety. *Mycelium* mostly immersed, composed of hyaline, branched, septate, guttulate hyphae, constricted at the septa, 1.5–3  $\mu\text{m}$  wide. *Conidiophore* determinate, macronematous, composed of *stipe* and *penicillate heads*. *Stipe* 350–700  $\mu\text{m}$  long, 5–10  $\mu\text{m}$  wide at base, 3–6  $\mu\text{m}$  wide at tip, mononematous, 9–12 septate, 0.2–0.6  $\mu\text{m}$  thick wall, erect, straight, or broadly curved, cylindrical, brown, and wide at base, paler and slightly tapering toward the apex, terminated by a penicillate head. *Penicillate heads* composed of 1–2 series of metulae terminating in groups of conidiogenous cells. *Metulae* thin-walled, light brown to subhyaline, *primary metulae* 5–10  $\times$  2–3  $\mu\text{m}$  ( $\bar{x}$  = 8.9  $\times$  2.5  $\mu\text{m}$ , n = 20)  $\mu\text{m}$ , *secondary metulae* 5–7  $\times$  2–4  $\mu\text{m}$  ( $\bar{x}$  = 5.5  $\times$  2.7  $\mu\text{m}$ , n = 20). *Conidiogenous cells* 6–10  $\times$  1–5  $\mu\text{m}$  ( $\bar{x}$  = 7.7  $\times$  3  $\mu\text{m}$ , n = 20), monophialidic, discrete, determinate, terminal, clustered at the apex of secondary metulae, hyaline, thin-walled, cylindrical, with inconspicuous openings, with minute collarettes. *Conidia* 2–4  $\times$  1–2  $\mu\text{m}$  ( $\bar{x}$  = 3  $\times$  1.8  $\mu\text{m}$ , n = 50), acrogenous, aseptate, aggregated in slimy and white masses, solitary to catenate, hyaline, ellipsoidal, rounded at each end, smooth and thin-walled, 1–2 guttules.

Culture characteristics – Conidia germinated on saltwater MEA within 24 h. Germ tubes arising from different ends of the conidia. Colonies growing on MEA, reaching 30–40 mm in 4 weeks at 25°C. Mycelia superficial, circular, with entire margin, flat, smooth, grayish-brown to brown, from below dark brown.

Material examined – Thailand, Prachuap Khiri Khan, Pran Buri, on submerged decaying leaf blades of *Spartina* sp. (*Poaceae*), 9 September 2020, M.S. Calabon, SS223 (MFLU 21–0256), living culture (MFLUCC 21–0219).

GenBank accession numbers – LSU: OL477391; ITS: OL504778.

Distribution: USA, soil (Jong & Davis 1972); Japan, decaying tree, paddy field soil (Kiyuna et al. 2012); China, soil (Chunyu et al. 2013); Thailand, submerged decaying *Spartina* culm (this study).

Notes – *Pseudophialocephala humicola* ( $\equiv$  *Phialocephala humicola*) was isolated from soil in the USA (Jong and Davis 1972) and this species was subsequently isolated from the same substrate in other studies in Australia (Matsushima 1989), China (Matsushima 1980), Japan (Matsushima 1975), and the USA (Ellis 1976), and recorded from different plant hosts from China (Matsushima 1980) and Japan (Matsushima 1975). The BLASTn search result of ITS sequence data of *Pseudophialocephala humicola* MFLUCC 21–0219 had 71 hits in Sordariomycetes with 100% similarity with different strains of *Ps. humicola* (32E, NBRC 31686, CBS 420.73, CBS 601.66). LSU BLASTn resulted in 99 hits of Sordariomycetidae with 100% and 99.75% similarities with *Ps. humicola* (CBS 601.66) and *Chloridium salinicola* (MFLU 19-1238), respectively. The preliminary single gene phylogenetic analysis of the top 100 BLASTn hits resulted in a well-defined close association of *Ps. humicola* to *Chaetosphaeriaceae* taxa. The combined ITS-LSU phylogenetic analyses revealed that MFLUCC 21–0219 clustered with the holotype, *Ps. humicola* CBS 420.73, and other strains (CBS 601.66, NBRC 100578) (Fig. 33). Morphological comparison of *Ps. humicola* MFLUCC 21–0219 shows similarity with the description of the holotype except for the presence of

the tertiary metulae that was observed from the holotype. The comparison of the ITS and LSU sequence data of MFLUCC 21–0219 showed no base pair differences with CBS 420.73 and CBS 601.66, respectively. Based on morphology and phylogenetic analysis, this confirms the new host record on *Spartina* sp., new geographical record from Thailand, and new report of *Pseudophialocephala humicola* in marine habitats, and second report of the genus thriving in the marine ecosystems.

***Pseudophialocephala aquatica*** (M.J. Wei & H. Zhang) M.S. Calabon, E.B.G. Jones & K.D. Hyde, comb. nov.

Index Fungorum number: IF 559314; Facesoffungi number: FoF 10605

≡ *Chloridium aquaticum* M.J. Wei & H. Zhang, Phytotaxa 362(2): 192 (2018)

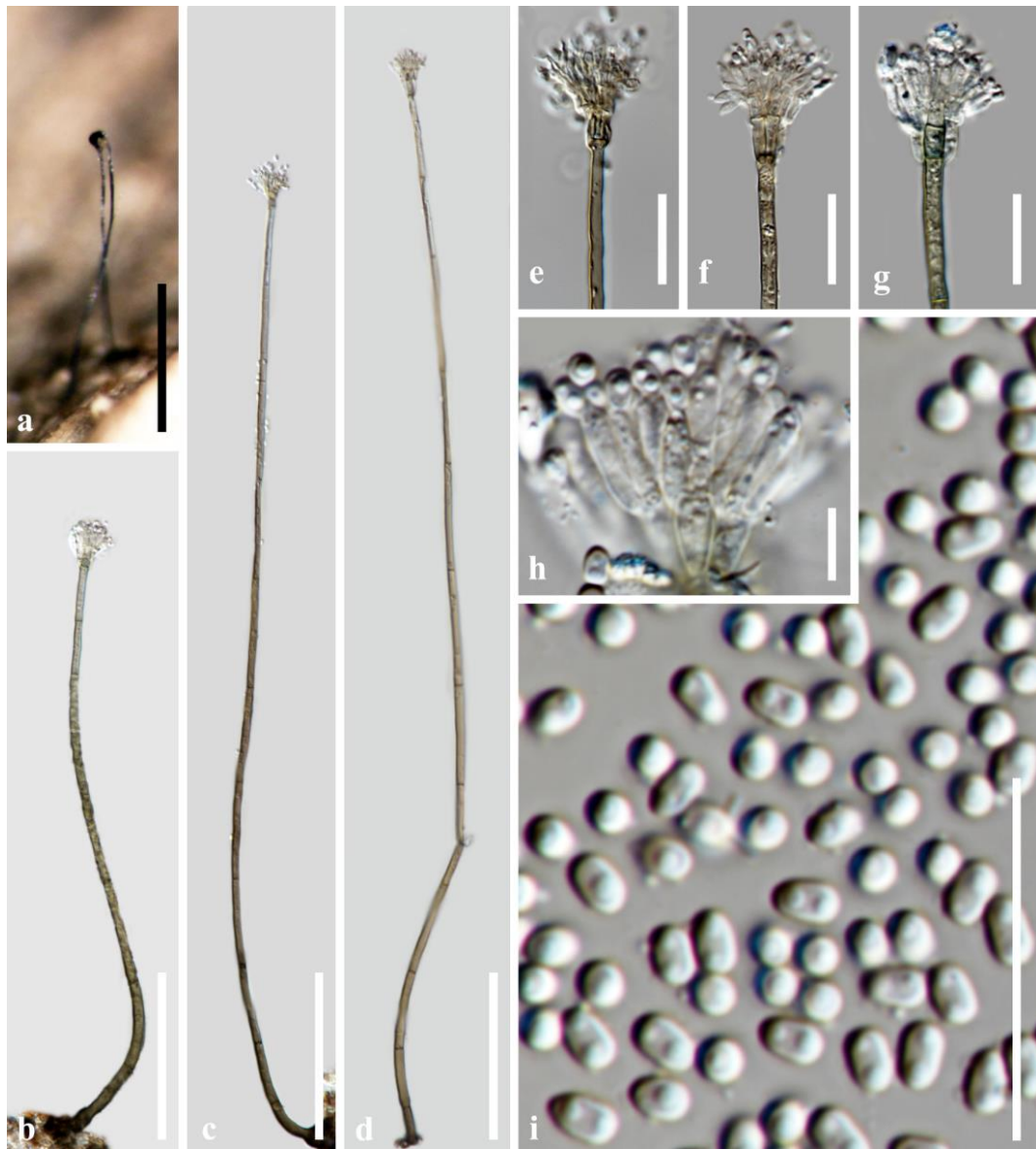
Sexual morph: Not observed. Asexual morph: Descriptions and illustrations refer to Wei et al. (2018)

Distribution – Thailand, Chiang Rai, Khun Korn, on submerged unidentified wood (Wei et al. 2018)

Notes – Holotype MFLU 11–1133. LSU (MH476567), SSU (MH476573), ITS (MH476570) sequence data are available.



**Figure 35** – *Pseudophialocephala cuneata* (MFLU 19–2852, holotype). a–c Conidiophores and conidia. d Conidiogenous cells and conidia. e–j Conidia. Scale bars: a–c = 50  $\mu$ m, d = 10  $\mu$ m, e–j = 3  $\mu$ m.



**Figure 36** – *Pseudophialocephala humicola* (MFLU 21–0256). a Appearance of conidiophore and conidia on natural substrate. b–d Conidiophores, conidiogenous cells, and conidia. e–h Conidiogenous cells and conidia. i Conidia. Scale bars: a = 200  $\mu$ m, b–d = 100  $\mu$ m, e–g, i = 20, h = 5  $\mu$ m.

***Pseudophialocephala salinicola*** (Dayarathne & E.B.G. Jones) M.S. Calabon, E.B.G. Jones & K.D. Hyde, comb. nov.

Index Fungorum number: IF 559315; Facesoffungi number: FoF 10606

≡ *Chloridium salinicola* Dayarathne & E.B.G. Jones, *Mycosphere* 11(1): 122 (2020a)

Sexual morph: Not observed. Asexual morph: Descriptions and illustrations refer to Dayarathne et al. (2020a)

Distribution – UK, Eastney, Hampshire, on unidentified marine wood (Dayarathne et al. 2020a).

Notes – Holotype MFLU 19–1238. LSU (MN017890), SSU (MN017944), ITS (MN047125), TUB2 (MN431494) sequence data are available.

***Pseudophialocephala terricola*** (Yong Wang bis, Jie & K.D. Hyde) M.S. Calabon, E.B.G. Jones & K.D. Hyde, comb. nov.

Index Fungorum number: IF 559316; Facesoffungi number: FoF 10607

≡ *Chloridium terricola* Yong Wang bis, Jie & K.D. Hyde



Sexual morph: Not observed. Asexual morph: Descriptions and illustrations refer to Wang et al. (2017)

Distribution – China, Sichuan Province, on soil (Wang et al. 2017).

Notes – Holotype HGUP 4519. LSU (KM434144, KM434145, KM434146) and ITS (KT893302, KT893303, KT893304) sequence data are available.

***Pseudophialocephala xalapensis*** (Persiani & Maggi) M.S. Calabon, E.B.G. Jones & K.D. Hyde, comb. nov.

Index Fungorum number: IF559317; Facesoffungi number: FoF 10608

≡ *Phialocephala xalapensis* Persiani & Maggi, in Maggi & Persiani, Mycotaxon 20(2): 253 (1984)

Sexual morph: Not observed. Asexual morph: Descriptions and illustrations refer to Maggi and Persiani (1984)

Distribution – India, decaying twig (Kiyuna et al. 2012) and *Coffea arabica* nursery soil (Grünig et al. 2002); Mexico, on nursery soil of *Coffea arabica*; unknown location and substrate (Jacobs et al. 2001).

Notes – Holotype HBR 108S. LSU (MH873636, AF326079, AF269217) and ITS (NR119413) sequence data are available.

### ***Thozetella* Kuntze**

Kuntze (1891) introduced *Thozetella* with *T. nivea* as the type species. Species of *Thozetella* are characterized by conidiophores that are grouped into short or long synnemata, terminated by phialidic conidiogenous cells, aseptate conidia, with unbranched setula at each end and sterile microawns (Paulus et al. 2004, Whitton et al. 2012, Hyde et al. 2020c). Twenty-seven morphological species of *Thozetella* are listed in Index Fungorum (2021), of which 16 have molecular data. We follow Hyde et al. (2020c) for the treatment and updated accounts of *Thozetella*. In this paper, we document *Thozetella nivea* from a freshwater habitat in Thailand. Freshwater *Thozetella* species include *T. canadensis*, *T. coronata*, *T. cristata*, *T. cubensis*, *T. gigantea*, *T. nivea*, *T. pinicola*, *T. queenslandica*, *T. radicata*, *T. submersa*, *T. ypsiloidea* (Sivichai et al. 2002, Pinruan et al. 2007, Barbosa et al. 2011, Barbosa et al. 2013, Pinruan et al. 2014, Monteiro et al. 2016, Fiuza et al. 2018, Calabon et al. 2022).

***Thozetella nivea*** (Berk.) Kuntze, Revis. gen. pl. (Leipzig) 2: 873 (1891)

Fig. 37

Index Fungorum number: IF 144861; Facesoffungi number: FoF 10601

Basionym: *Thozetia nivea* Berk., J. Linn. Soc., Bot. 18: 388 (1881)

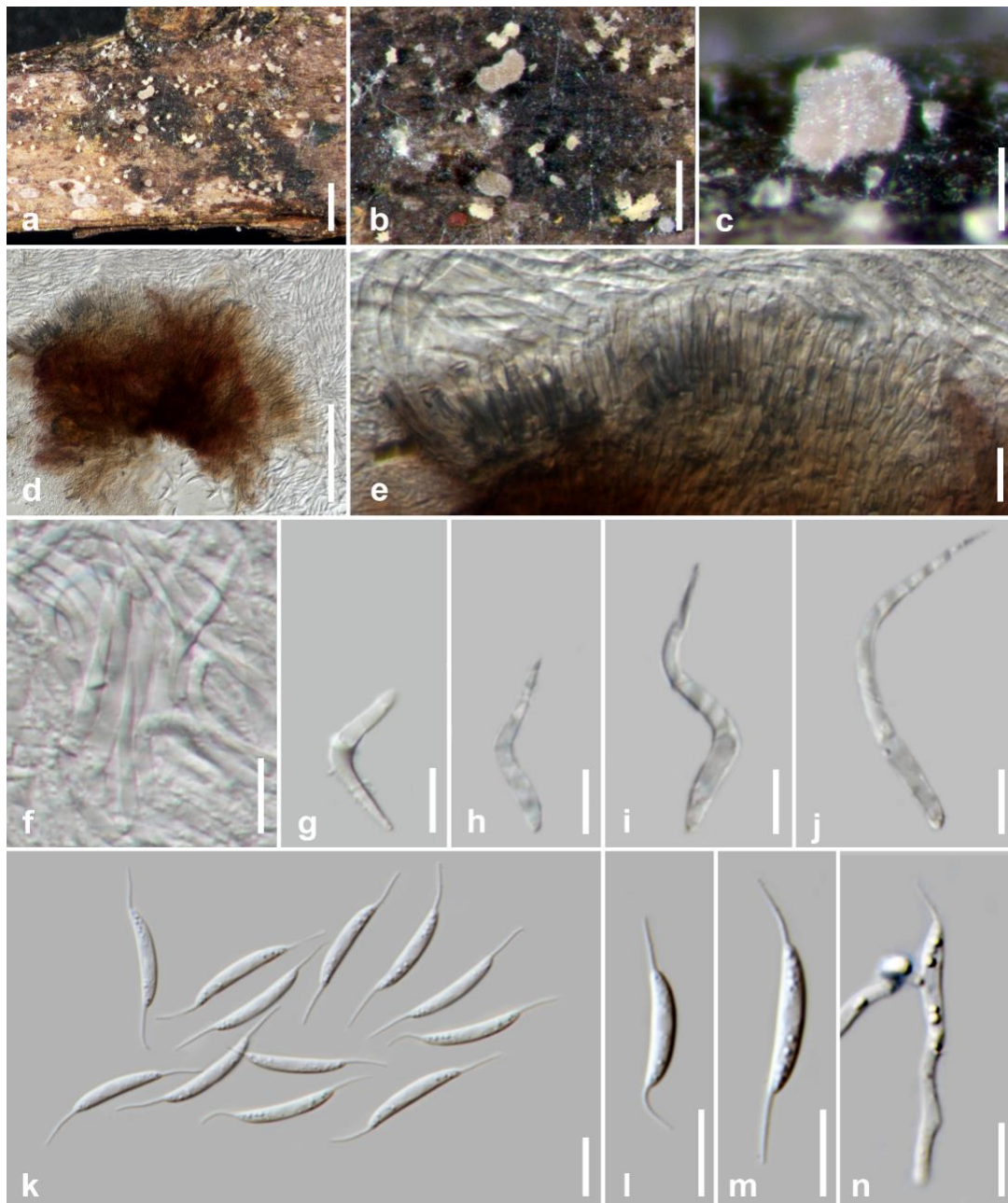
*Saprobic* on submerged decaying wood in freshwater. Sexual morph: Not observed. Asexual morph: Hyphomycetous. Colonies effuse, superficial, sessile sporodochial, cream white. *Sporodochia* 120–220 µm in diam. solitary, scattered, superficial, cylindrical or subulate, cream white to pale yellowish-white, with a white spore mass at the apex. *Microawns* 25–45 µm long, 2–3 µm wide at the widest point ( $\bar{x} = 33.8 \times 2.7$  µm,  $n = 10$ ), visible as small hairs on the sporodochial mass, hyaline, aseptate, smooth-walled, thick-walled, straight, sigmoid, curved. *Conidiophores* macronematous, synnematos, abundant, brown to dark brown, elongated, cylindrical, septate, smooth-walled. *Conidiogenous cells* 10–15 × 2–4 µm ( $\bar{x} = 13.4 \times 2.8$  µm,  $n = 20$ ), phialidic, hyaline, smooth-walled, irregularly subcylindrical, without collarette. *Conidia* 15–20 × 1.5–3.5 µm ( $\bar{x} = 17.2 \times 2.6$  µm,  $n = 50$ ), naviculate to fusiform or ellipsoid, with rounded ends, inequilateral, hyaline, smooth-walled, with a single filiform setula at each end, 6–9 × 0.45–0.75 µm ( $\bar{x} = 7.6 \times 0.6$  µm,  $n = 50$ ).

Culture characteristics – Conidia germinated on MEA within 24 h. Germ tubes arising from terminal ends of the conidia. Mycelia superficial, irregular, with entire edge, pale reddish-brown at the center then becoming yellowish-brown at the margin, tufted colony center elevated, reverse dark brown at the center then becoming light yellowish-brown at the margin.

Material examined – Thailand, Tak Province, Tha Sing Yang, Ban Mae Ja Wang, on decaying wood submerged in a river, 17 October 2019, N. Padaruth, CC60 (MFLU 21– 0254).

GenBank accession numbers – LSU: OL477392; ITS: OL504779.

Notes – The phylogenetic analysis of LSU and ITS sequence data shows that the isolate grouped within the *Thozetella* clade and clustered together with *Thozetella nivea* (GenBank numbers: EU825200, EU825201) (Fig. 33) *Thozetella nivea* MFLUCC 21–0220 has smaller conidiomata (120–220  $\mu\text{m}$  vs. 200–250  $\mu\text{m}$ ), smaller conidia (15–20  $\times$  1.5–3.5  $\mu\text{m}$  vs. 7.5–24  $\times$  3–3.8  $\mu\text{m}$ ), and smaller microawns (25–45  $\times$  2.0–3  $\mu\text{m}$  vs. 50–70  $\times$  1.3–4  $\mu\text{m}$ ) compared to the type description of *T. nivea* (Kuntze 1891). *Thozetella nivea* was previously reported on the biodiversity studies of Sivichai et al. (2002) and Pinruan et al. (2014) from freshwater habitats in Thailand, but complete illustrations and molecular data were not provided, and the present collection add the lacking data of the Thailand strain.



**Figure 37** – *Thozetella nivea* (MFLU 21–0254). a–c Appearance of conidiomata on natural substrate. d Synnemata. e Conidiogenous cells. f–j Microawns. k–n Conidia. Scale bars: a = 1000  $\mu\text{m}$ , b = 500  $\mu\text{m}$ , c = 200  $\mu\text{m}$ , d = 50  $\mu\text{m}$ , e–n = 10  $\mu\text{m}$ .

**Coniochaetaceae** Malloch & Cain, Can. J. Bot. 49: 878 (1971)

*Coniochaetaceae* was erected by Malloch & Cain (1971) to accommodate *Coniochaeta* and *Coniochaetidium*. *Coniochaetidium*, *Ephemeroascus* and *Poroconiochaeta* species transferred into *Coniochaeta* by García et al. (2006) differed from *C. prunicola* by having ornamented or broadly umbonate ascospores, or by lacking *Lecythophora* anamorphs. Species belonging to *Coniochaetaceae* are cosmopolitan in distribution and exhibit different modes of nutrition (Samarakoon et al. 2018, Jones et al. 2019). *Coniochaetaceae* species are saprobic on dung, plant litter and soil, they can be found in strongly acidic water with high heavy metal concentrations and food (Ramaley 1997, Weber et al. 2002, Huhndorf et al. 2004, García et al. 2006, Kirk et al. 2008, Damm et al. 2010, Maharachchikumbura et al. 2015, 2016, Wijayawardene et al. 2017a, Wanasinghe et al. 2018, Jones et al. 2019).

**Coniochaeta** (Sacc.) Cooke, Grevillea 16(no. 77): 16 (1887)

*Coniochaeta*, typified by *Coniochaeta ligniaria*, is characterized by dark brown to black, solitary or aggregated, typically setose, pyriform to globose ascomata, with or without ostioles. The peridium is membranaceous to pseudoparenchymatous, or rarely coriaceous (Damm et al. 2010, Samarakoon et al. 2018, Jones et al. 2019). A paraphysate hamathecium is present or absent. Asci are unitunicate and thin-walled, with a small non-amyloid, apical ring and ascospores are one-celled, usually dark brown and often laterally compressed, with a germ slit (Weber 2002, Asgari et al. 2007). In this study, we introduce *Coniochaeta velutina* from host, *Phyllostachys viridis* to this genus.

**Coniochaeta velutina** (Fuckel) Cooke, Grevillea 16(no. 77): 16 (1887)

Fig. 39

Index Fungorum number: IF 295496; Facesoffungi number: FoF 10626

≡ *Rosellinia velutina* Fuckel, Jb. Nassau. Ver. Naturk. 23-24: 49. 1870.

≡ *Helminthosphaeria velutina* (Fuckel) Kirschst., Trans. Brit. Mycol. Soc. 18: 305. 1934.

*Endophytic* on healthy *Phyllostachys viridis* leaves. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Conidiogenous* cells 1–2 × 1–3 μm ( $\bar{x}$  = 1.5 × 2.5 μm, n = 11) hyaline, flask-shaped or acicular. *Conidia* 3–5 × 2–4 μm ( $\bar{x}$  = 3.8 × 2.8 μm, n = 50), hyaline, smooth-walled, ellipsoidal. *Chlamydospores* 3–5 × 4–5 μm ( $\bar{x}$  = 3.5 × 4 μm, n = 2), solitary or in short chains, hyaline, thick-walled, elongate ellipsoidal or almost globose.

Culture characteristics – Conidia germinated on PDA within 12 hours at 25°C, growing slowly, reaching 4 cm diam. after 14 days at 28°C. Circular, for above, divided into two layers, the top layer is gray and white, and the bottom layer is gray. Reverse, centre dark yellow, toward the edges, gradually becoming lighter, and the margin is white, circular, flat, scattered, partially immersed in the medium; centre of the colony slightly raised.

Material examined – China, Guangdong Province, Guangzhou City, South China Botanical Garden, isolated from healthy leaves of *Phyllostachys viridis* (R. A. Young) McClure (*Poaceae*), 17 June 2020, HJ. Zhao & M. Luo, living cultures, ZHKUCC 21-0112 and ZHKUCC 21-0113.

GenBank accession numbers – ITS: OL763837, OL764359; LSU: OL763831, OL763899.

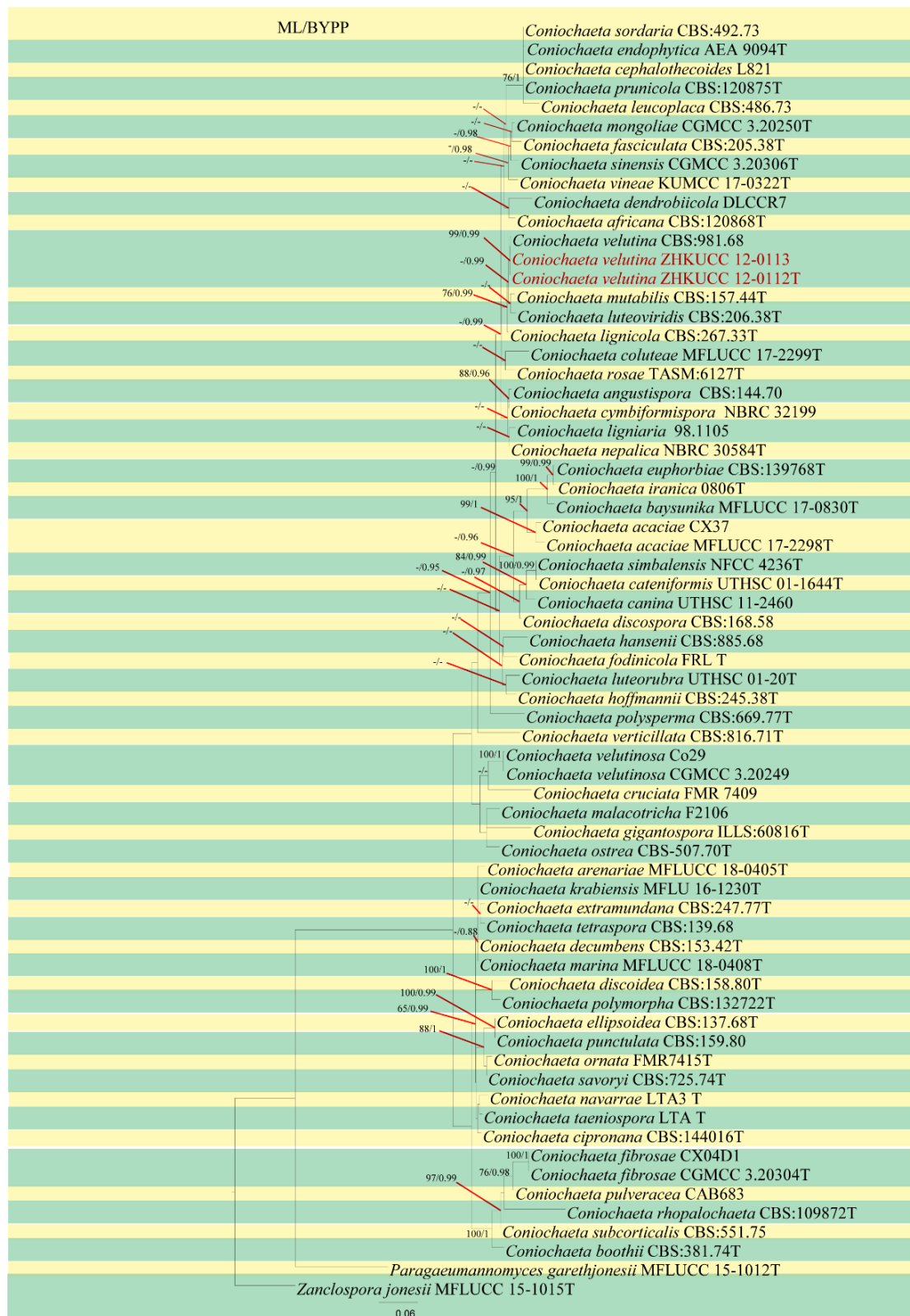
Notes – Two strains (ZHKUCC 21-0112 and ZHKUCC 21-0113) isolated and described in this study, were morphologically similar to *Coniochaeta velutina* (Cooke 1887). In the phylogenetic analysis, our new strains clustered with *Coniochaeta velutina* (CBS 981.68) with 99% ML and 0.99 BYPP support (Fig. 38). The two *Coniochaeta velutina* strains (ZHKUCC 21-0112 and CBS 981.68) had only two base pair differences in the ITS and LSU regions. The two isolates differ in colony colour. Based on morphological and molecular data, we introduced our isolates (ZHKUCC 21-0112 and ZHKUCC 21-0113) as a new host record of *Coniochaeta velutina* for *Phyllostachys viridis*.

**Diaporthales** Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 53 (1932)

**Cytosporaceae** Fr. [as ‘Cytispori’], Syst. orb. veg. (Lundae) 1: 118 (1825)

*Cytosporaceae* was introduced by Fries (1825). Maharachchikumbura et al. (2015) accepted 13 genera in *Cytosporaceae*. Senanayake et al. (2017) accepted five genera *Cytospora*, *Pachytrype*,

*Paravalsa*, *Xenotypa* and *Waydora* in *Cytosporaceae*. We follow the treatments of Wijayawardene et al. (2020) and Hyde et al. (2020a).



**Figure 38** – Phylogenetic tree constructed for *Coniochaeta* species and closely related genera in *Zanclospora*. Phylogenetic tree generated by ML analysis of combined ITS, and LSU sequence data of 60 species. The analyses include 67 strains and the tree is rooted with *Zanclospora jonesii* (MFLUCC15 1015) and *Paragaemannomyces Garethjonesii* (MFLUCC 15 1012). The tree topology of the ML analysis was similar to the BYPP. The best scoring RAXML tree with a final

likelihood value of -9307.861282 is presented. The matrix had 630 distinct alignment patterns, with 27.5% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.243604, C = 0.241116, G = 0.291041, T = 0.224239; substitution rates AC = 1.359772, AG = 1.962490, AT = 1.160058, CG = 1.415261, CT = 6.598688, GT = 1.000000; gamma distribution shape parameter  $\alpha = 0.497031$ . RAxML bootstrap support values  $\geq 75\%$  and nodes with  $\geq 0.95$  (BYPP) values are shown near the nodes. The scale bar indicates 0.06 changes per site. T= Ex-type isolated. New isolates are in red



**Figure 39** – *Coniochaeta velutina* (ZHKUCC 21-0112, new host record). a, b Cultures on PDA from the surface and reverse. c, d Conidiogenous cells. e, f Conidiogenous cell that is producing conidia. g Chlamydospores. h-j Conidia. Scale bars: 10  $\mu\text{m}$ .

### *Cytospora* Ehrenb.

*Cytospora* was introduced by Ehrenberg (1818). This genus is characterized by the fruiting bodies comprised of stromata (conidiomata) with intricate chambers, filamentous, branched conidiophores and hyaline allantoid conidia, exuding from the fruiting bodies as yellow, orange or

red masses. In this paper, we introduce a new species *Cytospora salicis-albae*, based on phylogenetic and morphological evidence (Fig. 40).

*Cytospora salicis-albae* Chaiwan, Bulgakov & K.D. Hyde, sp. nov.

Fig. 41

Index Fungorum number: IF 557812; Facesoffungi number: FoF 06508

Etymology – The specific epithet “*salicis-albae*” refers to the host plant *Salix alba* L.

Holotype – MFLU 17-2391

*Saprobic* on *Salix alba*. Sexual morph: Not observed. Asexual morph: Ceolomycetous. *Pycnidia* immersed on *Salix alba*. *Conidiomata* 200–500 µm high × 250–400 µm diam ( $\bar{x}$  = 350 × 325 µm, n = 10), diameter, scattered, erumpent, multi-loculate, *Locules* composed of numerous interconnecting, chambers arranged radially or irregularly within a continuous, mass of ectostromatic tissue, pycnidial, stromatic, solitary or clustered, immersed in the host when young, semi-erumpent at maturity, dark brown to black, globose, ostiolate. *Ostioles* 90–120 µm. *Peridium* comprising a few to several layers of cells of *textura angularis*, with inner most layer thin, brown, outer later dark brown to black. *Conidiophores* unbranched, reduced to conidiogenous cells. *Conidiogenous cells* blastocytic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. *Conidia* 5–7 × 1–2 µm ( $\bar{x}$  = 6 × 1.5 µm, n = 30), unicellular, elongate-allantoid, slightly curved, hyaline, smooth-walled.

Culture characteristics – *Colonies* growing on PDA, circular, with flat surface, edge entire, were reaching 8 cm in 7 days at 25°C, white to pale brown. Mycelium superficial and partially immersed, branched, septate, hyaline grey to black, smooth.

Material examined – Russia, Krasnosulinsky District, Regional Nature Reserve Area “Gornensky”, trees near Kundryuchya River, on dead branches of *Salix alba* L. (*Salicaceae*) with signs of necroses, 6 July 2017, T.S. Bulgakov (MFLU 17-2391, holotype), ex-type living culture MFLUCC 18-0485

GenBank accession numbers – ITS: MT734820; LSU: MT734819; *act*: OL754585; *rpb2*: OL754584.

Notes – In the multigene analyses *Cytospora salicis-albae* developed a distinct lineage with 79% ML and 64 MP bootstrap support (Fig. 40). In the phylogenetic analysis, *Cytospora salicis-albae* groups with *C. paratranslucens*. These two species differ by *C. paratranslucens* having conidiomata with multi-locules, while *Cytospora salicis-albae* develop smaller conidiomata (450–550 × 270–350 µm diameter) (Norphanphoun et al. 2017). In addition, *Cytospora salicis-albae* has smaller ostioles (90–120 µm) than *C. paratranslucens* (70–150 µm) and conidia are similar in size (Norphanphoun et al. 2017). Our new species was found on dead branches of *Salix alba* with signs of necrosis. The finding of the new species of *Cytospora* on *Salicaceae* plants (*Salix* and *Populus* species) in Southern European Russia can be considered as evidence of the existence of many closely related *Cytospora* associated with *Salicaceae* plants in this region.

### **Glomerellaceae** Locq. 1984

*Glomerellaceae* is a monotypic family belonging to Sordariomycetes. This family produces black, astromatic perithecia with abundant thin-walled paraphyses, clavate asci, and hyaline, curved ascospores (Zhang et al. 2006).

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

*Colletotrichum* is an important genus including a large number of species which are plant pathogens, endophytes and saprobes (Jayawardena et al. 2021). Jayawardena et al (2021) accepted 248 species distributed in 14 species complexes. In the present study, four species belonging to the *Colletotrichum gloeosporioides* complex were identified and are described (Fig. 42).

### **Colletotrichum endophytica** Manamgoda, Udayanga, L. Cai & K.D. Hyde in Manamgoda, Udayanga, Cai, Chukeatirote & Hyde, Fungal Diversity 61: 110 (2013)

Fig. 43

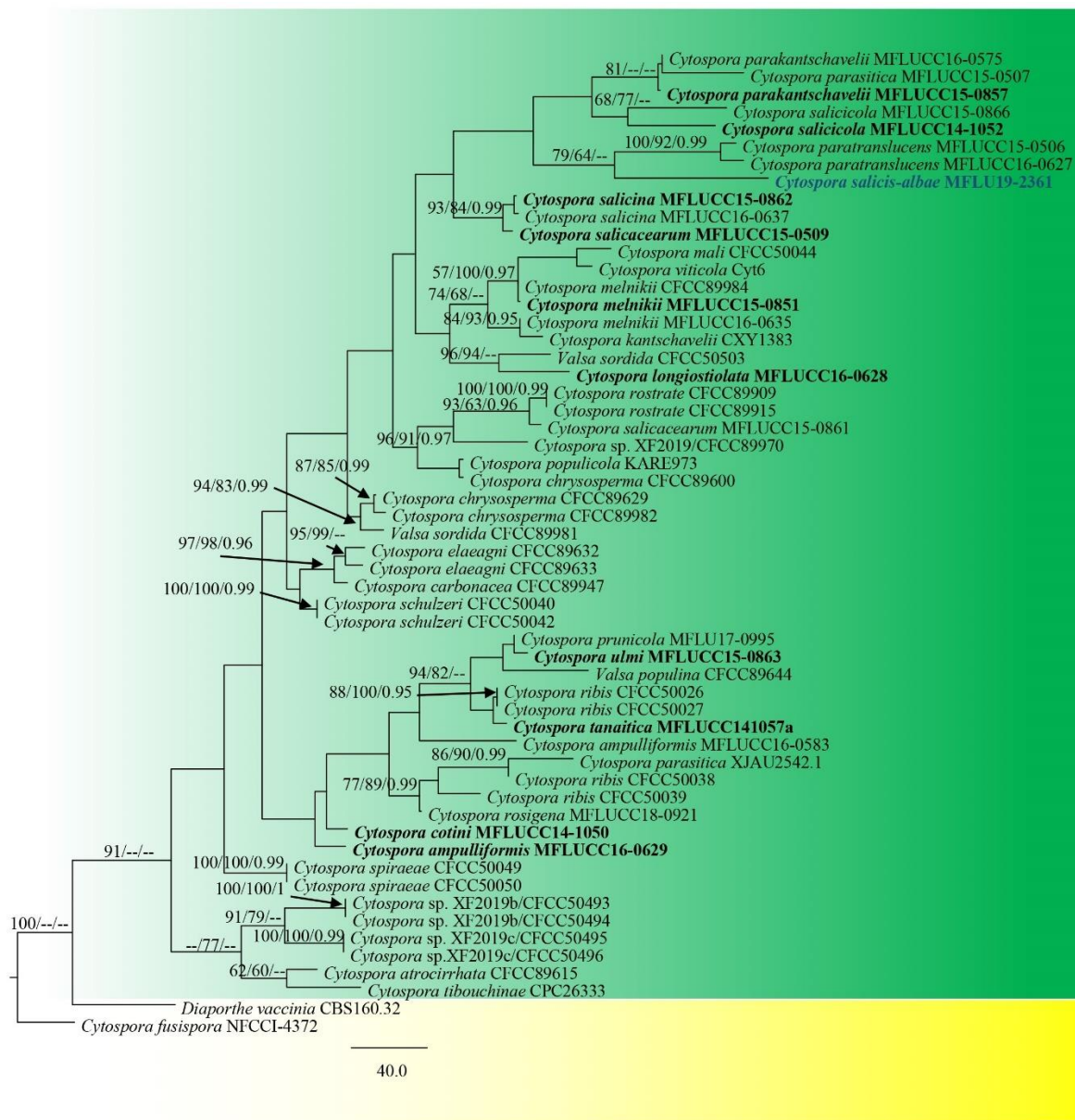
Index Fungorum number: IF 565248; Facesoffungi number: FoF 10611

Associated with leaf spot of *Acacia confusa*. Sexual morph: not observed. Asexual morph: ceolomycetous *Conidiophores* 10–12 × 3–5 μm ( $\bar{x}$  = 10 × 4 μm, n = 30) long, cylindrical or clavate, unbranched. *Conidia* 10–15 × 5–10 μm ( $\bar{x}$  = 12 × 6 μm, n = 50) long, one-celled, cylindrical, appressoria not produced.

Culture characteristics – Colonies on PDA reach 67 mm diam in 7 days at 25°C, growth rate per day 5.00 ± 0.50mm/d, white to grey, reverse dark grey to black at the centre, aerial mycelium dense and raised.

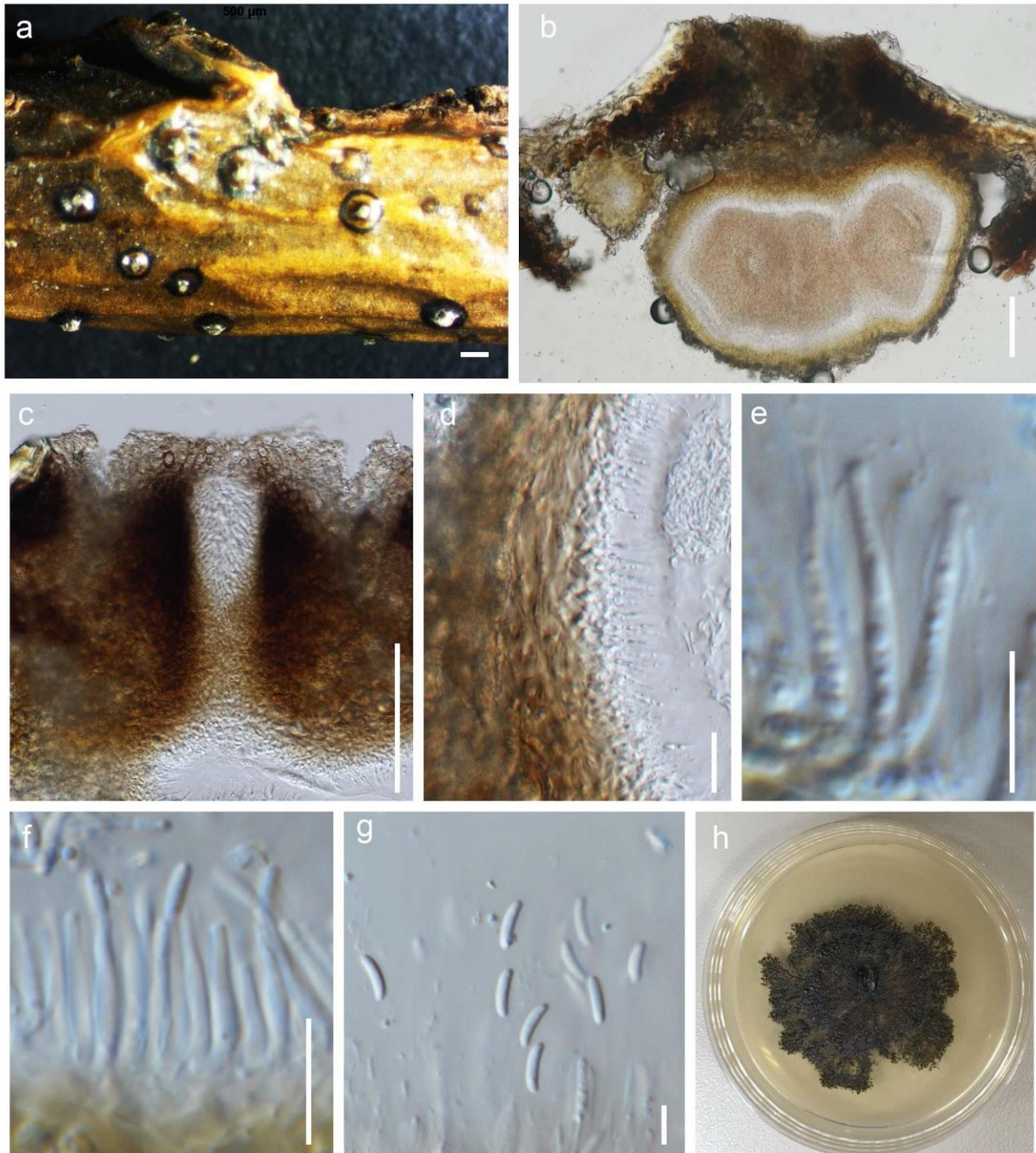
Material examined – China, Guangdong Province, on *Acacia confusa* Merr., (*Fabaceae*) Shenzhen Botanical Garden, 30 November 2020, J.W. Chen, Z.L. Mai and C. Chen (dried cultures ZHKU 21-0070 and ZHKU 21-0071), living culture, ZHKUCC 21-0077, ZHKUCC 21-0078.

GenBank accession numbers – *gapdh*: OL672735, OL672736; *act*: OL672715, OL672716; *chs-1*: OL672725, OL672726; *tub2*: OL739534, OL739533.



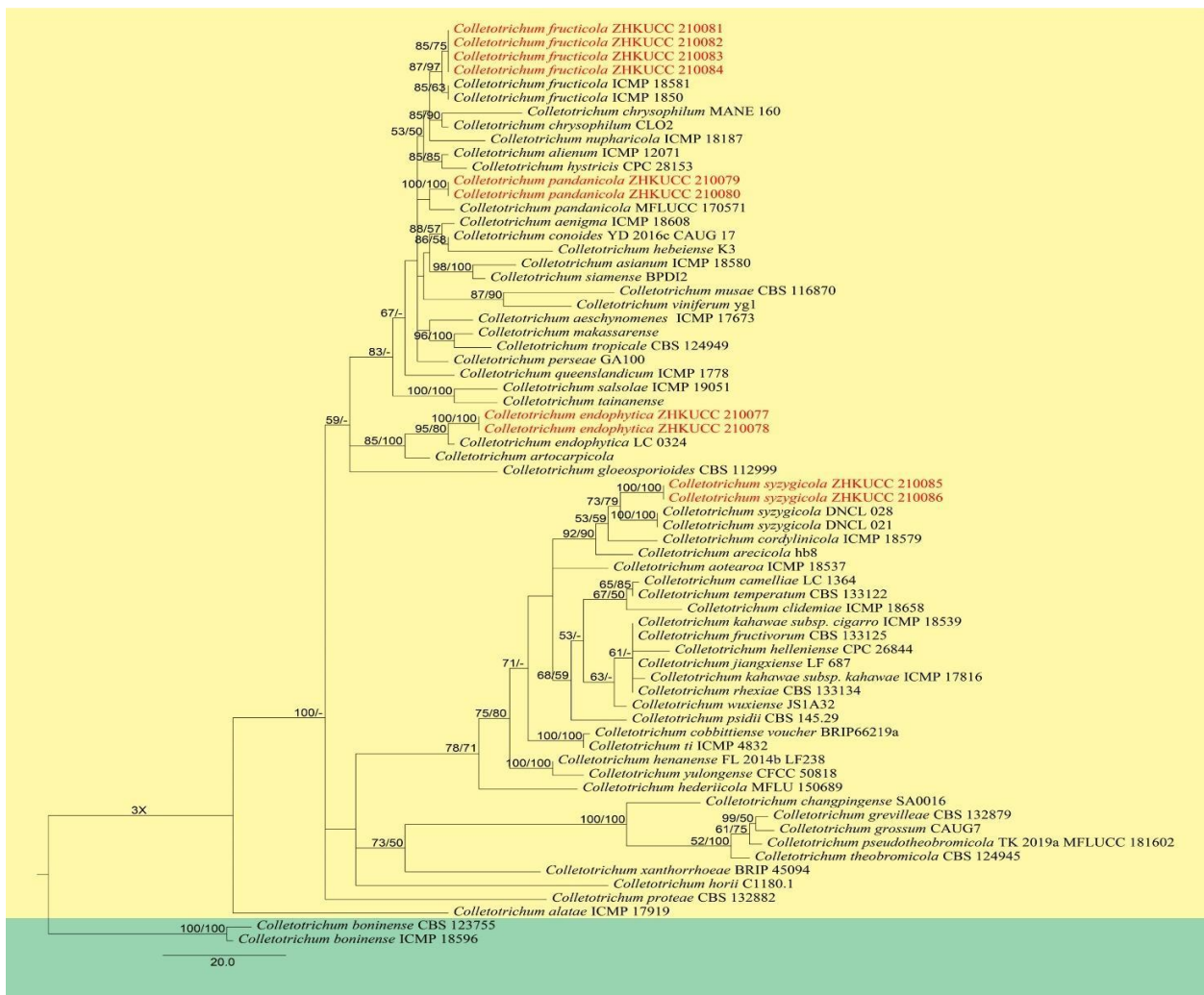
**Figure 40** – Phylogram generated from maximum likelihood analysis based on ITS, LSU, *act* and *rpb2* sequence data representing *Cytospora* species. Related sequences are obtained following Hyde et al. (2020a). Fifty-six strains are included in the combined analyses which comprise 1500 characters for ITS LSU, *act* and *rpb2* after alignment. *Cytospora fusispora* (NFCCI-4372) and *Diaporthe vaccinia* (CBS160.32) were used as the outgroup taxa. Single gene analyses were performed to

compare the topology and clade stability with combined gene analyses. The tree topology of the ML analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -12410.706382 is presented. The matrix had 654 distinct alignment patterns, with 19.27% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.248668, C = 0.264510, G = 0.268463, T = 0.218360; substitution rates AC = 1.704825, AG = 6.919398, AT = 2.518120, CG = 1.871334, CT = 11.836864, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.146256. Bootstrap values for ML equal to or greater than 50% and clade credibility values greater than 0.95 (the rounding of values to 2 decimal proportions) from BYPP analysis labelled on the nodes. The newly generated sequence is indicated in bold and blue.



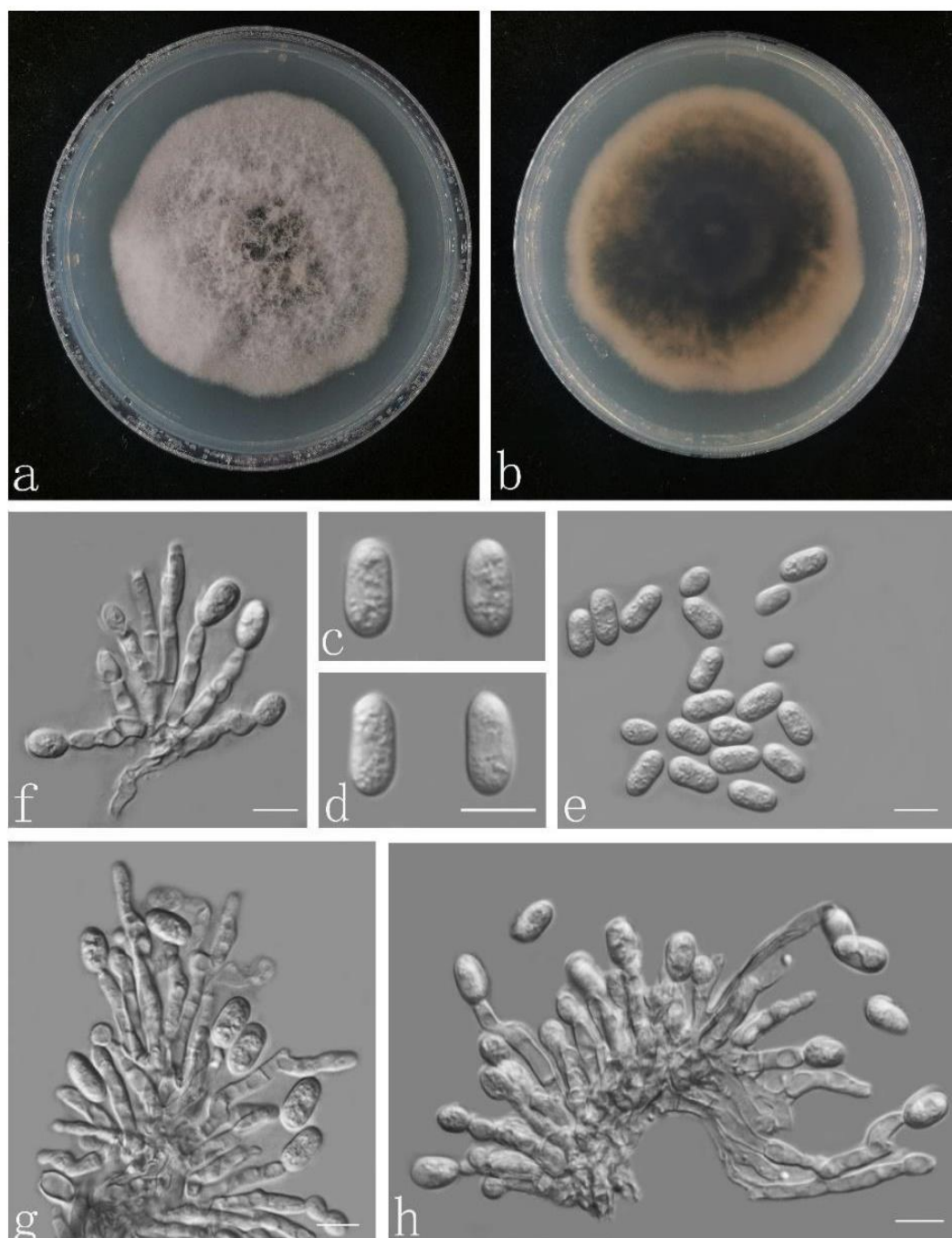
**Figure 41** – *Cytospora salicis-albae* (MFLU 17–2391, holotype). a Appearance of pycnidia on wood. b, c Vertical section through conidiostroma. d Peridium e, f Conidiogenous cells. g Conidia. h Culture. Scale bars: a = 500 µm, b, c = 100 µm, d–f = 10 µm.





**Figure 42** – The ML tree generated for *Colletotrichum* species belonging to *Colletotrichum gloeosporioides* complex using combined data set of ITS, *gapdh*, *act*, *chs-1* and  $\beta$  *tubulin* sequences. In total 69 strains were used including 10 strains from the present study. *Colletotrichum boninense* (CBS123755 and ICMP 18596) was used as an outgroup. Maximum parsimony analysis of 1049 constant characters and 1168 informative characters resulted in 100 equally most parsimonious trees of one step (CI = 0.706, RI = 0.860, RC = 0.608, HI = 0.294). The best scoring RAxML tree had a final likelihood value of -6954.479531. The matrix had 552 distinct alignment patterns, with 10.33 % of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.226235, C = 0.309659, G = 0.241842, T = 0.222264; substitution rates AC = 0.968117, AG = 2.860169, AT = 1.087993, CG = 0.849377, CT = 4.526789, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 1.891799. The MP and ML bootstrap support values  $\geq 50\%$  are indicated at the nodes and branches. The scale bar indicates 20 changes per site. Ex-type/ ex-epitype strains are in bold. New isolates recovered in this study are in red.

Notes – In the present study, two isolates developed a moderate support clade with *C. endophytica* (95% in ML and 80% in MP bootstrap values Fig. 42). The isolates obtained differ from *C. endophytica* in colony characters and conidial size. The colony of *C. endophytica* is white to grey, reverse dark grey to black at the centre, conidia are 13–19 (–21)  $\times$  (4–) 5–6  $\mu\text{m}$  ( $\bar{x}$  = 16  $\times$  5, n = 40) (Manamgoda et al. 2013). The colony of our isolate is white to grey, reverse dark grey at the centre with light yellow at the edge, and the conidia are 10–15  $\times$  5–10  $\mu\text{m}$  ( $\bar{x}$  = 12  $\times$  6  $\mu\text{m}$ , n = 50). However, these variations might be possible with the interspecies diversity of *C. endophytica* as following the data shown in Bhunjun et al. (2019). Therefore, we introduce our two isolates as a new host record of *C. endophytica* from *Acacia confusa* (Farr & Rossman 2022).



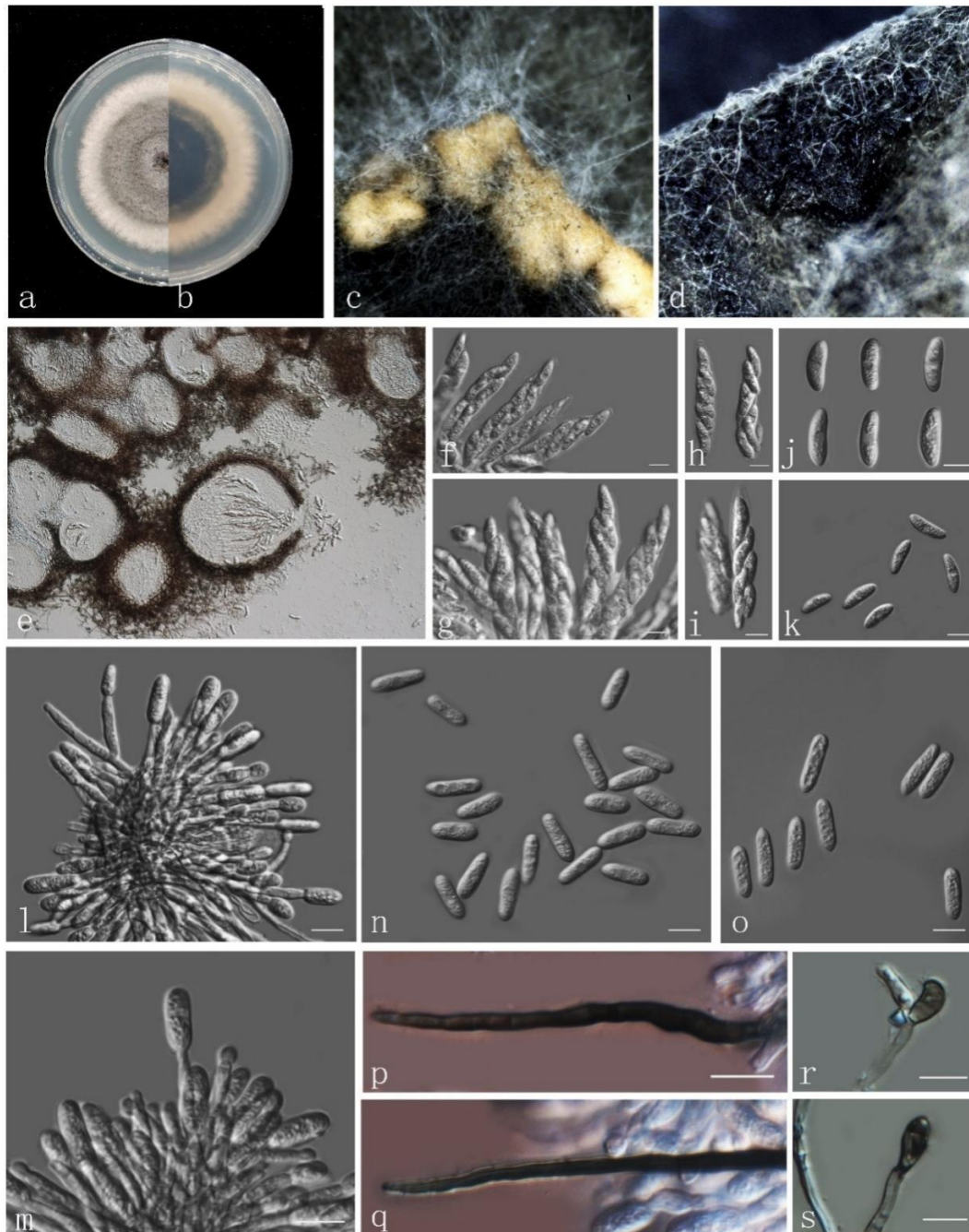
**Figure 43** – *Colletotrichum endophytica* (ZHKUCC 21-0077, new host record). a Upper view on PDA after seven days. b Reverse view on PDA after seven days. c–e Conidia. f–h Conidiophores. Scale bars: f–h = 10  $\mu$ m.

*Colletotrichum fructicola* Prihast., L. Cai & K.D. Hyde, in Prihastuti, Cai, Chen, McKenzie & Hyde, Fungal Diversity 39: 96 (2009) Fig. 44

Index Fungorum number: IF 515409; Facesoffungi number: FoF 06767

Associated with leaf spot of *Zamia furfuracea*. Sexual morph: *Ascomata* greyish-black, globose to subglobose, with hairs, semi-immersed or completely immersed in PDA. *Asci* 50–80  $\times$  10–12  $\mu$ m ( $\bar{x}$  = 60  $\times$  10  $\mu$ m, n = 30) long, thin-walled, 6–8-spored, clavate or cymbiform. *Ascospores* 15–20  $\times$  5–7 ( $\bar{x}$  = 16  $\times$  6  $\mu$ m, n = 50) long, one-celled, with large guttule at the centre, slightly curved to curved with rounded ends. Asexual morph: ceolomycetous, *Setaria* in acervuli on filter paper, abundant, long, dark brown, smooth-walled, with two or more septa, base truncate, apex sharp, 40–60  $\times$  2–5  $\mu$ m ( $\bar{x}$  = 60  $\times$  3  $\mu$ m, n = 10). *Conidiophores* hyaline, smooth-walled to verruculose, aseptate,

unbranched. *Conidia* 15–20 × 5–6 μm ( $\bar{x}$  = 17 × 5 μm, n = 50), formed from the tip of the conidiophore, one-celled, cylindrical with rounded ends, contents appearing, granular, *Appressoria* 8–10 × 5–7 μm ( $\bar{x}$  = 10 × 6 μm, n = 10), in slide cultures formed from branched mycelia, terminal, brown to dark brown, near rhombus to irregular.



**Figure 44** – *Colletotrichum fructicola* (ZHKUCC 21-0081, new host record). a, b Upper and reverse view on PDA after seven days. c Spore masses. d, e Ascomata. f–I Asci. j, k Ascospores. l, m Conidiomata and conidiogenous cells. n, o Conidia. p, q Setae. r, s Appressoria. Scale bars: f–s = 10 μm.

Culture characteristics – Colonies on PDA, reaching 65 mm diam. after 7 days at 25°C, growth rate per day 5 mm/d, grey to green, edge white, regular, reverse dark green, white edge with orange conidial masses.

Material examined – China, Guangdong Province, Shenzhen Botanical Garden, on living *Zamia furfuracea* L.f. ex Aiton (*Zamiaceae*), 30 November 2020, J.W. Chen, Z.L. Mai and C. Chen (dried cultures ZHKU 21-0074 and ZHJU 21-0075, new host record), living cultures ZHKUCC 21-0081 and ZHJUCC 21-0082. Additional material examined – China, Guangdong Province, Shenzhen Botanical Garden, leaf spot of *Bougainvillea* sp. (*Nyctaginaceae*), 30 November 2020, J.W. Chen, Z.L. Mai, C. Chen (dried cultures ZHKU 21-0076 and ZHJU 21-0077, new host record) and living cultures ZHKUCC 21-0083 and ZHJUCC 21-0084.

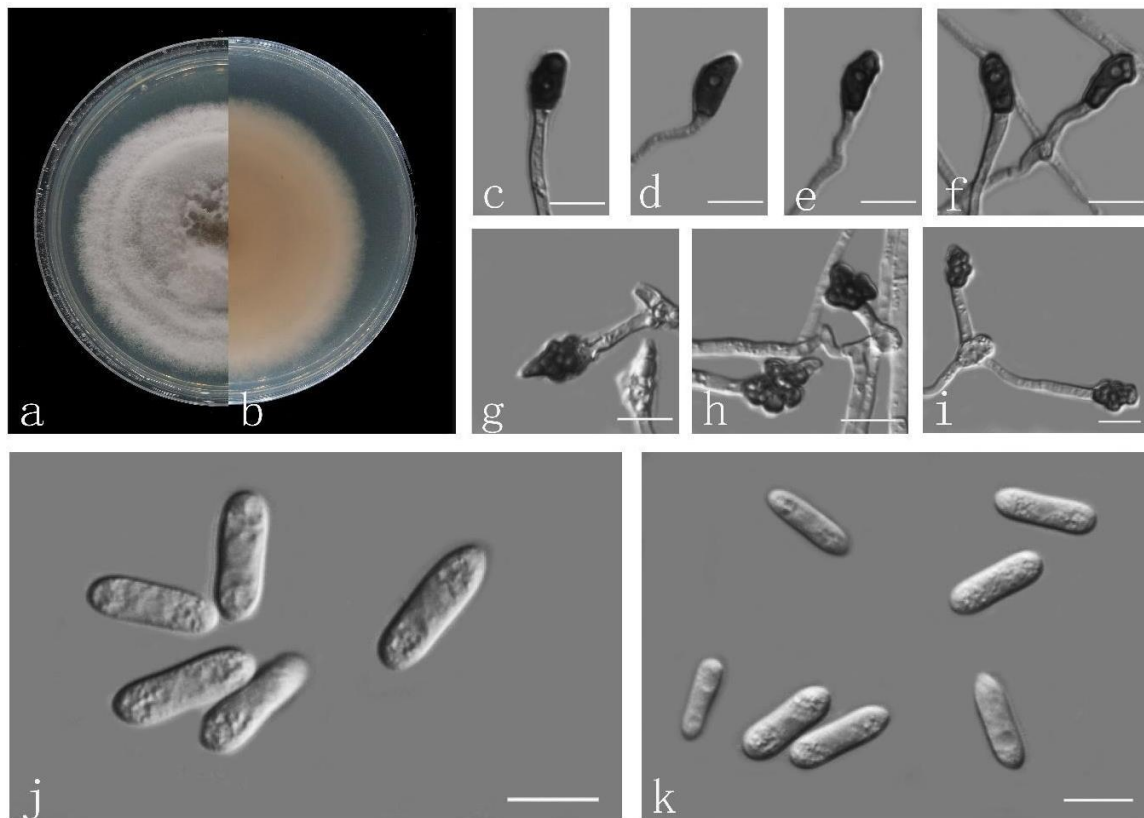
GenBank accession numbers – *gapdh*: OL672731, OL672732, OL672733, OL672733; *act*: OL672710, OL672711, OL672712, OL672713; *chs-1*: OL672721, OL672722, OL672723, OL672724; *tub2*: OL739538, OL739537, OL739536, OL739535.

Notes – The isolates obtained in this study are closely related to *Colletotrichum fructicola* with 87% ML and 97% MP support (Fig. 42). Our isolates are similar in the sexual morph of *C. fructicola* (Prihastuti et al. 2009). They are different in size of conidia as our isolates are  $15\text{--}20 \times 5\text{--}6 \mu\text{m}$  ( $\bar{x} = 17 \times 5 \mu\text{m}$ ,  $n = 50$ ), which are longer and wider than the isolates described by Prihastuti et al (2009);  $9\text{--}14 \times 4.5 \mu\text{m}$  ( $\bar{x} = 12 \times 4 \mu\text{m}$ ,  $n = 18$ ). These strains are isolated from *Zamia furfuracea* and *Bougainvillea* sp from Guangdong Province of China. To our knowledge, these are the first report of *C. fructicola* from *Zamia furfuracea* and *Bougainvillea* sp. (Farr & Rossman 2021).

***Colletotrichum pandanicola*** Tibpromma & K.D. Hyde, in Tibpromma, Hyde, Bhat, Mortimer, Xu, Promputtha, Doilom, Yang, Tang & Karunarathna, MycoKeys 33: 47 (2018) Fig. 45

Index Fungorum number: IF 823841; Facesoffungi number: FoF 10612

Associated with leaf spot of *Reineckia carnea*. Sexual morph: not observed. Asexual morph: ceolomycetous. *Conidia*  $14\text{--}17 \times 4\text{--}6 \mu\text{m}$  ( $\bar{x} = 15 \times 5 \mu\text{m}$ ,  $n = 50$ ), formed with mycelium, one-celled, smooth-walled, most slightly rounded at the ends, slightly curved at one end, some rounded at both ends. *Appressoria* in slide cultures  $10\text{--}16 \times 4\text{--}7$  ( $-8$ )  $\mu\text{m}$  ( $\bar{x} = 12 \times 6 \mu\text{m}$ ,  $n = 50$ ), formed from branched mycelia, brown, some oval to nearly rhombic and often becoming complex with age.



**Figure 45** – *Colletotrichum pandanicola* (ZHKUCC 21-0079, new host record). a, b Upper and reverse view on PDA after seven days. c-i Appressoria. j, k Conidia. Scale bars: c–k = 10  $\mu\text{m}$ .

Culture characteristics – Colonies on PDA attaining 70 mm in diam., in 7 days at 25°C, at first white, becoming light brown, in reverse pale yellowish. Aerial mycelium greyish-white, dense, cottony, without setae and Sclerotium produced.

Material examined – China, Guangdong Province, Shenzhen Botanical Garden, associated with leaf spot on *Reineckia carnea* (Andr.) Kunth., (*Convallariaceae*). 30 November 2020, J.W. Chen, Z.L. Mai, C. Chen (new host record), living cultures ZHKUCC 21-0079 and ZHKUCC 21-0080.

GenBank accession numbers – *gapdh*: OL672737, OL672738; *act*: OL672717, OL672718; *chs-1*: OL672727, OL672728; *tub2*: OL739542, OL739543.

Notes – *Colletotrichum reineckiae* is introduced as a new species based on morphology and phylogenetic evidence. Isolates obtained in this study developed a sister clade with *C. pandanicola* (Fig. 42) with 100% ML and 100% MP bootstrap support. Morphologically, *C. pandanicola* is different from our isolates by the colony and conidial characters. Colonies of *C. pandanicola* are white in the beginning and later become dark grey, while our isolates are white and becomes light brown later, pale yellow in reverse. Conidia develop by our isolates are longer than ( $\bar{x} = 15 \times 5 \mu\text{m}$ ) *C. pandanicola* ( $\bar{x} = 13 \times 5 \mu\text{m}$ ,  $n = 20$ ). However, these variations might be due to the different growth conditions. Based on both morphology and phylogenetic support we introduce novel host record of *C. pandanicola* from *Reineckia carnea* (Farr & Rosaman 2022).

***Colletotrichum syzygicola*** B.S. Weir & P.R. Johnst., in Weir, Johnston & Damm, Stud. Mycol. 73: 139 (2012) Fig. 46

Index Fungorum number: IF 800213 Facesoffungi number: FoF 00015

Associated with leaf spot of *Cymbidium* sp. Sexual morph: Not observed. Asexual morph: ceolomycetous. *Conidiophores* unbranched, smooth, hyaline. *Conidia*  $15\text{--}20 \times 5\text{--}10 \mu\text{m}$  ( $\bar{x} = 17 \times 5 \mu\text{m}$ ,  $n = 50$ ), aseptate, most rounded at both ends, cylindrical, some rounded at the ends, curved at the ends. *Appressoria*  $10\text{--}20 \times 5\text{--}10 \mu\text{m}$  ( $\bar{x} = 13 \times 6 \mu\text{m}$ ,  $n = 30$ ) often becoming complex with age, some rhomboid, long, some quincunx,  $10\text{--}15 \times 10\text{--}12 \mu\text{m}$  ( $\bar{x} = 12 \times 9 \mu\text{m}$ ,  $n = 30$ ) long, dark brown.

Culture characteristics – Colonies on PDA attaining 60 mm in diam in 7 days at 25°C, growth rate per day  $4.59 \pm 0.5\text{mm/d}$ , at first white, becoming greyish-brown, in reverse dark brown and margin white. Aerial mycelium greyish-brown at the centre, dense, cottony, without setae.

Material examined – China, Guangdong Province, Shenzhen Botanical Garden, *Cymbidium* sp. (*Orchidaceae*), 30 November 2020, J.W. Chen, Z.L. Mai, C. Chen (new host record) (dried cultures ZHKU 21-0078 and ZHJU 21-0079), living cultures ZHKUCC 21-0085 and ZHJUCC 21-0086.

GenBank accession numbers – *gapdh*: OL672729, OL672730; *act*: OL579738, OL672709; *chs-1* OL672719, OL672720, *tub2*: OL739539, OL739540.

Notes – The two isolates obtained in this study are phylogenetically related to *Colletotrichum syzygicola* with moderate support (73% in ML, 79% in MP) (Fig. 42). Morphological characteristics are similar to *Colletotrichum syzygicola* described by Udayanga et al. (2013). Herein we identified our strains as a new host of *C. syzygicola* on *Cymbidium* sp.

***Stachybotryaceae*** L. Lombard & Crous, Persoonia 32: 283 (2014)

*Stachybotryaceae* was introduced by Crous et al. (2014) to accommodate *Myrothecium*, *Peethamabra* and *Stachybotrys*, which are saprobes or pathogens on plants and are commonly isolated from soil. Lombard et al. (2016) revisited the family and accepted 33 genera based on morphology and LSU, ITS, *rpb2*, *cmda*, *tef1- $\alpha$*  and *tub2* sequence data. There are 39 genera accepted in *Stachybotryaceae* (Hyde et al. 2020).

***Alfaria*** Crous, Montaña-Mata & García-Jim., Persoonia 32: 239 (2014)

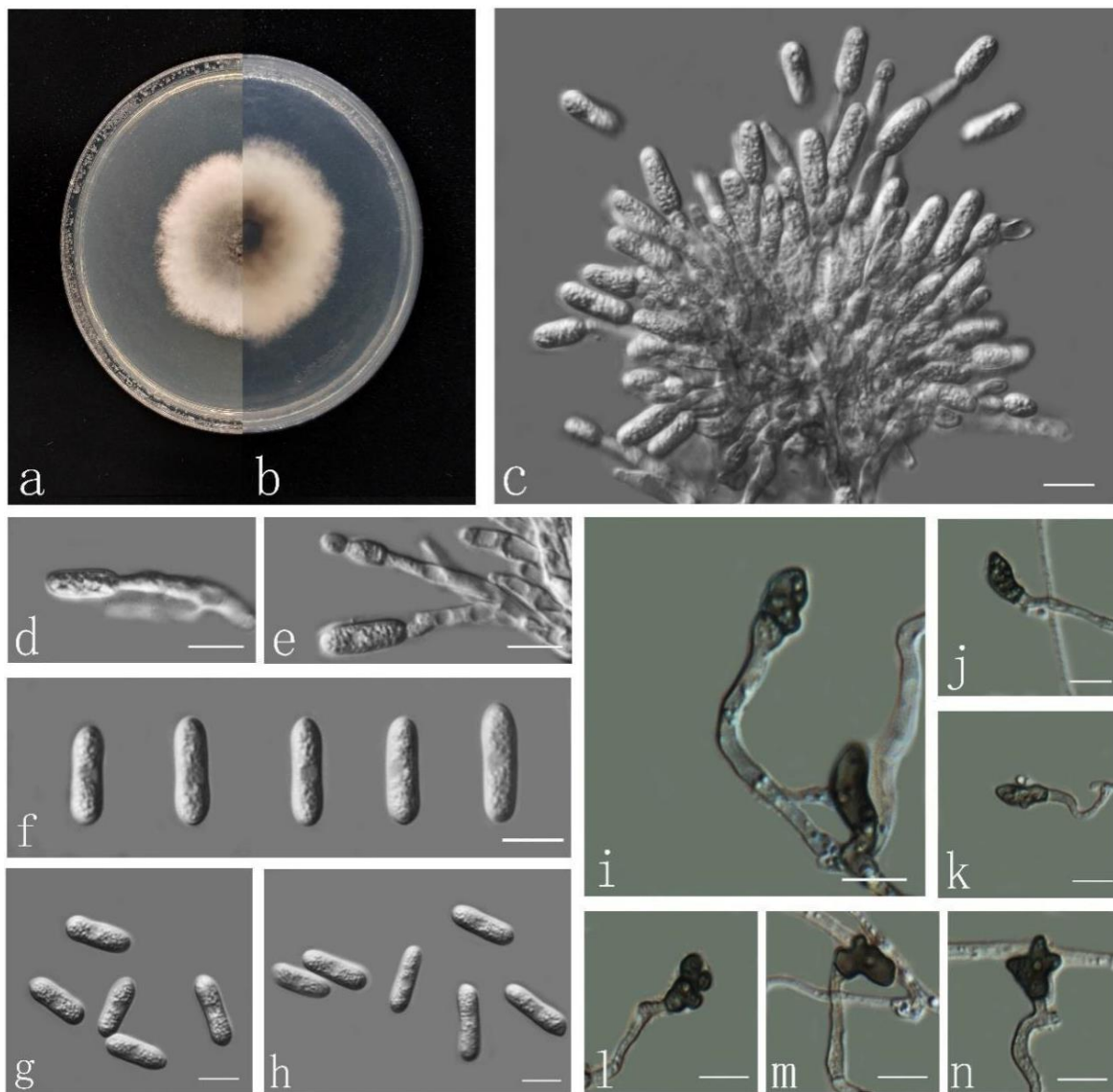
*Alfaria* was introduced by Crous et al. (2014) with the type *A. cyperi-esculentii*, which is associated with leaf apical necrosis of *Cyperus esculentus* (*Cyperaceae*). The genus is characterized by black, globose, immersed ascomata, fasciculate, subcylindrical with obtuse apices, unitunicate asci with 2–8 ascospores and hyaline, ascospores fusoid-ellipsoid and 0–3-septate. The asexual morph comprises solitary or sporodochial, verticillately or penicillately branched, hyaline

conidiophores, phialidic conidiogenous cells and cylindrical to ellipsoidal, hyaline to lightly pigmented, aseptate conidia (Crous et al. 2014, Lombard et al. 2016, Jayawardena et al. 2018).

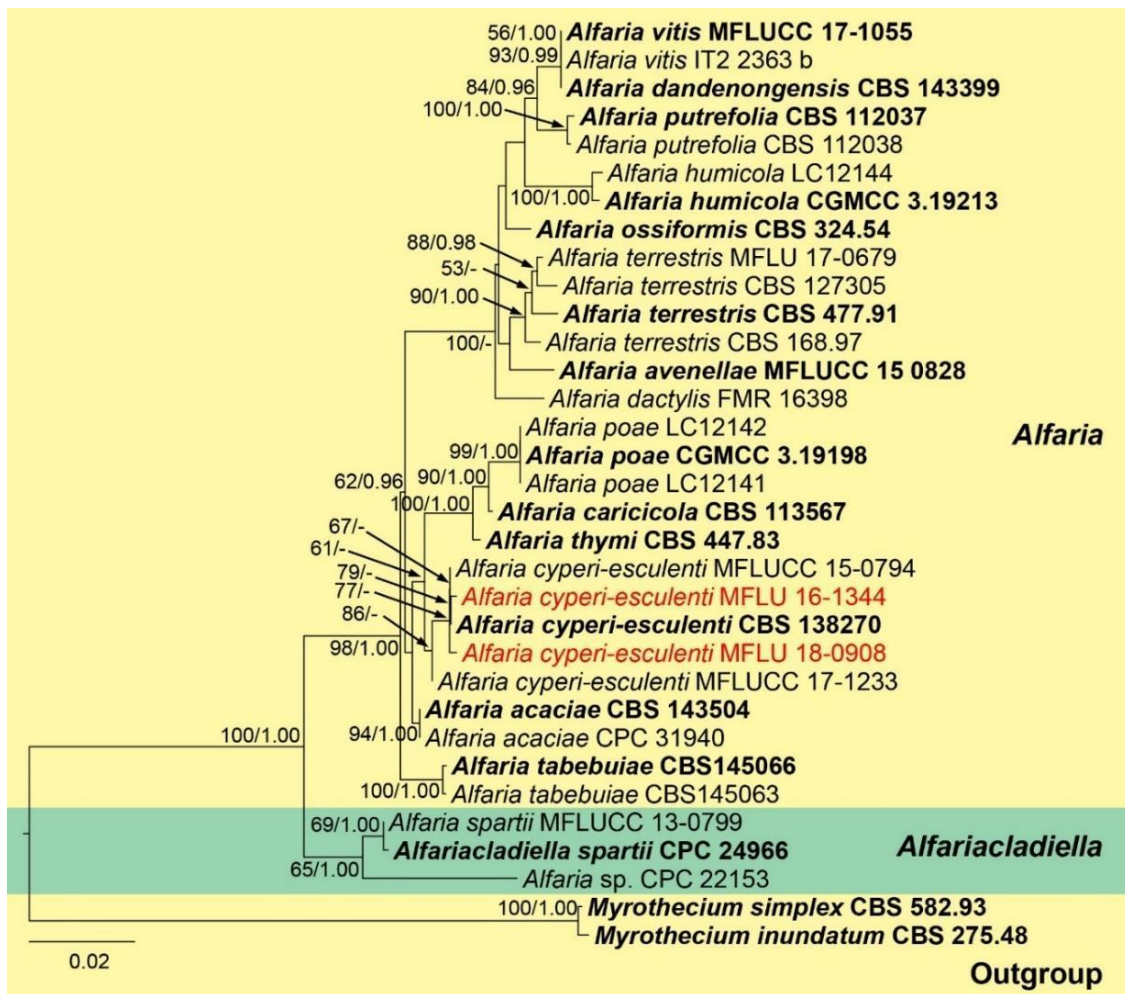
*Alfaria cyperi-esculenti* Crous, Montañó-Mata & García-Jim., in Crous et al., *Persoonia* 32: 239 (2014) Fig. 48

Index Fungorum number: IF 808924; Facesoffungi number: FoF 03602

*Saprobic* on dead aerial stems and branches of *Galium* sp. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 220–470  $\mu\text{m}$  diam., sporodochial, stromatic, superficial, cupulate to discoid, scattered to gregarious, oval to elongate or irregular in outline, composed of cells of *textura globulosa* or *textura angularis*. *Setae* arising from the base. *Conidiophores* up to 40  $\mu\text{m}$  long, arising from the basal stroma, unbranched or branched, hyaline to greenish-brown, smooth-walled. *Conidiogenous cells* 6–19  $\times$  2.5–3.8  $\mu\text{m}$  ( $\bar{x}$  = 13.7  $\times$  3.1  $\mu\text{m}$ ,  $n$  = 25), monoblastic, annellidic, cylindrical to elongate doliiform, hyaline to olivaceous green, smooth, with conspicuous collarettes and periclinal thickenings. *Conidia* 8.5–12  $\times$  3–5.3  $\mu\text{m}$  ( $\bar{x}$  = 10.4  $\times$  4.7  $\mu\text{m}$ ,  $n$  = 40), aseptate, smooth-walled, ellipsoidal, hyaline when immature, greenish-brown to dark brown when mature.



**Figure 46** – *Colletotrichum syzygicola* (ZHKUCC 21-0085, new host record). a, b Upper and reverse view on PDA after seven days. c Conidiomata and conidiogenous cells. d, e Conidiogenous cells with developing conidia. f–h Conidia. i–n Appressoria. Scale bars: c–n = 10  $\mu\text{m}$ .



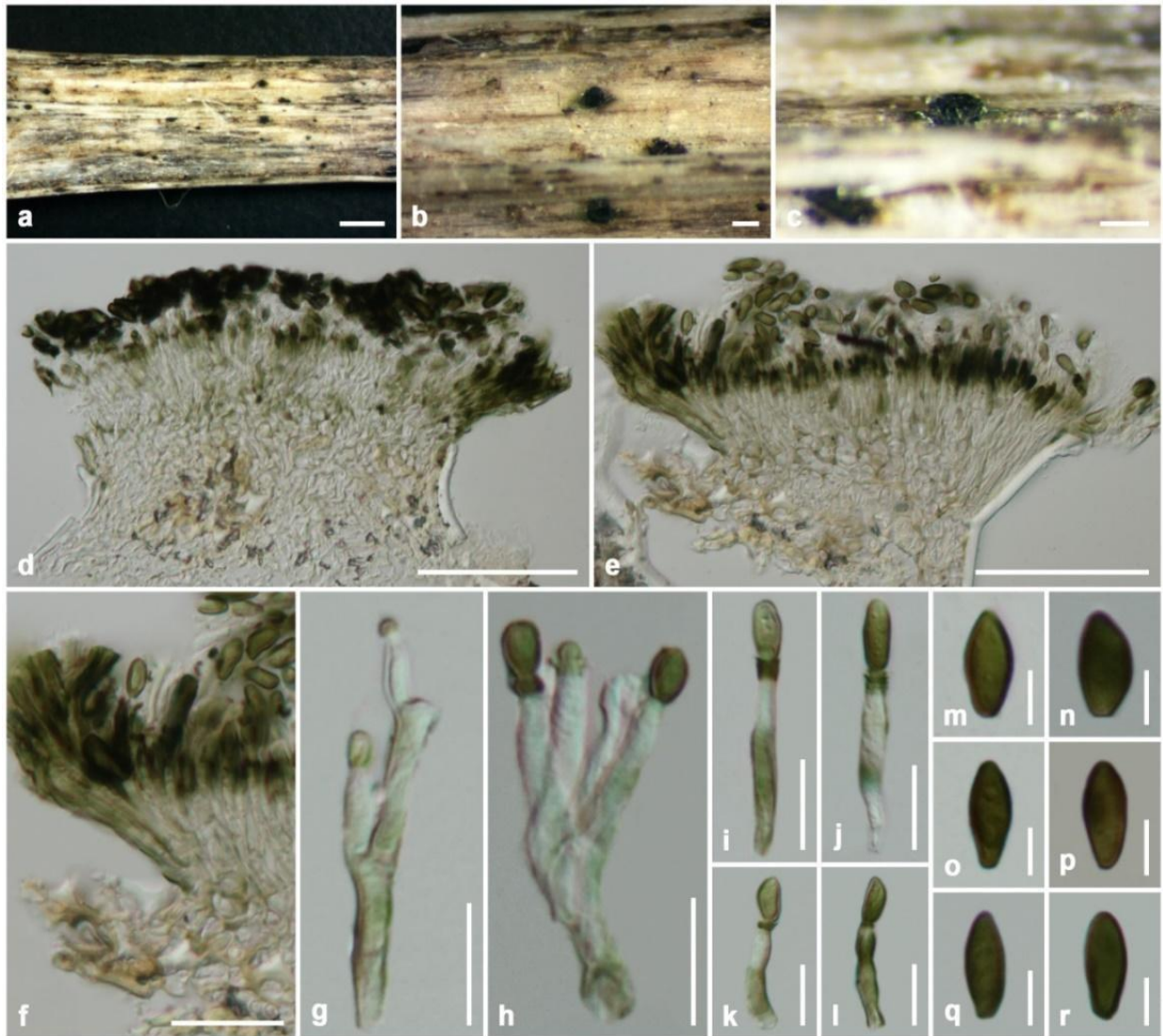
**Figure 47** – Phylogenetic tree generated by ML analysis of combined ITS, LSU, *tub2*, and *tef1- $\alpha$*  sequence data of 18 species. The analyses included 33 strains and the tree is rooted with *Myrothecium inundatum* (CBS 275.48) and *M. simplex* (CBS 582.93). The tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of -4831.516 is presented. The matrix had 323 distinct alignment patterns, with 1671 undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.2297, C = 0.2758, G = 0.2802, T = 0.2143; substitution rates AC = 1.3842, AG = 1.3396, AT = 0.8333, CG = 0.9691, CT = 6.6210, GT = 1.0000; gamma distribution shape parameter  $\alpha$  = 0.5882. RAxML bootstrap support values  $\geq 50\%$  and maximum parsimony bootstrap support  $\geq 50\%$  are shown near the nodes. Nodes with  $\geq 0.95$  (BYPP) Bayesian posterior probabilities are indicated with thickened lines. The scale bar indicates 0.02 changes per site. Ex-type/ ex-epitype strains are in bold. New isolates recovered in this are in red.

Material examined – Italy, Province of Ravenna [RA], Fognano di Brisighella, on dead aerial stem of *Galium* sp. (*Rubiaceae*), 20 March 2018, Camporesi Erio, IT3772 (MFLU 18-0908, HKAS 102380, new host record); Province of Forlì-Cesena [FC], Bagno di Romagna, near Lago Pontini, on dead aerial branch of *Cytisus* sp. (*Fabaceae*), 4 April 2016, Camporesi Erio, IT2909 (MFLU 16-1344, HKAS 102363, new host record).

GenBank accession numbers – ITS: OL587638, OL587639; LSU: OL587641, OL587642; SSU: OL587643, OL587644; *tub2*: OL606739, OL606740; *tef1- $\alpha$* : OL606737, OL606738.

Notes – Crous et al. (2014) introduced *A. cyperi-esculentii* on *Cyperus esculentus* (*Cyperaceae*) from Spain with its sexual morph. Jayawardena et al. (2018) described the asexual morph of *Alfaria cyperi-esculentii* on *Vitis vinifera* from Italy and linked sexual and asexual morphs based on phylogeny. Two isolates in this study cluster with *Alfaria cyperi-esculentii* in a multigene phylogeny. A comparison of the strains from Jayawardena et al. (2018) and this study shows similar morphology

of conidiomata (150–450  $\mu\text{m}$  vs 220–470  $\mu\text{m}$  diam.), conidiogenous cells (6–18  $\times$  1–3  $\mu\text{m}$  vs 6–19  $\times$  2.5–3.8  $\mu\text{m}$ ) and conidia (5–8  $\times$  3–4  $\mu\text{m}$  vs 8.5–12  $\times$  3–5.3  $\mu\text{m}$ ). Based on similar morphology and phylogeny, our two collections are introduced as two new host records from Italy.



**Figure 48** – *Alfaria cyperi-esculentii* (MFLU 18-0908, new host record). a-c Appearance of conidiomata on the host surface. d-f Vertical section through conidioma. g-l Conidiophores, Conidiogenous cells and conidia. m-r Conidia. Scale bars: a = 1000  $\mu\text{m}$ , b, c = 200  $\mu\text{m}$ , d, e = 50  $\mu\text{m}$ , f = 20  $\mu\text{m}$ , g-l = 10  $\mu\text{m}$ , m-r = 5  $\mu\text{m}$ .

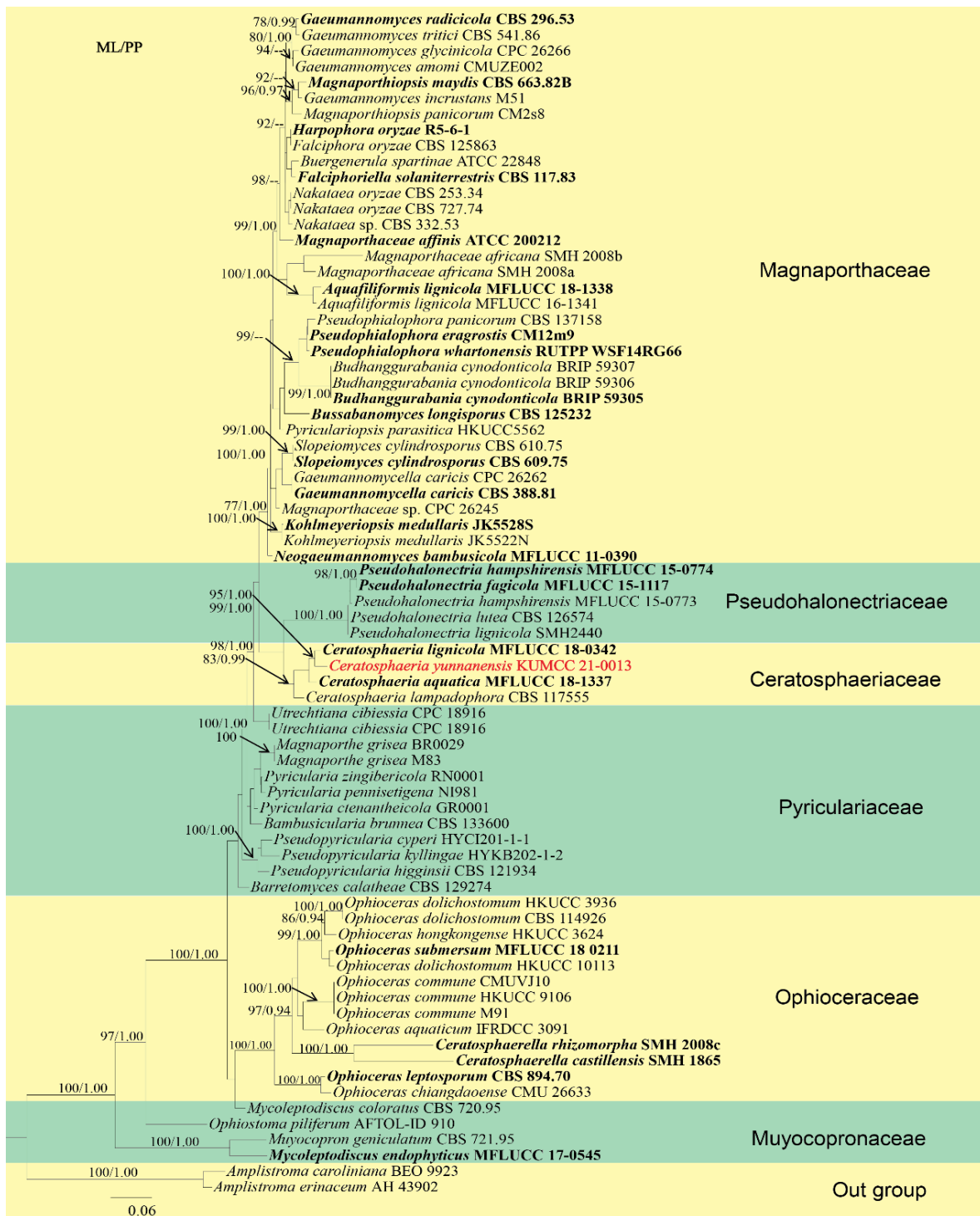
***Magnaporthaceae*** P.F. Cannon, Syst. Ascom. 13(1): 26 (1994)

*Magnaporthaceae* includes 23 genera and more than 100 species (Wijayawardene et al. 2018, Silva et al. 2019). The host has diversity in saprobes, endophytes, and plant pathogens (Luo et al. 2019, Hyde et al. 2020). Magnaporthaceous taxa are characterised by globose to subglobose perithecial ascomata with long necks, unitunicate cylindrical asci, and filiform or spindle-shaped ascospores (Silva et al. 2019).

***Ceratosphaeria*** Niessl, Verh. nat. Ver. Brünn 14: 203 (1876)

*Ceratosphaeria* was introduced by Niessl (1876) with *C. lampadophora* as the type species. This genus is characterised by globose to pyriform, immersed ascomata, cylindric-clavate asci, truncate to broadly rounded at the apex, with an apical annulus and allantoid to suballantoid, aseptate ascospores (Niessl 1876, Reľblová 2006).





**Figure 49** – Phylogenetic tree derived from maximum likelihood analysis of a combined LSU, *tef1- $\alpha$*  of 75 sequences and the aligned dataset comprised of 1665 characters including gaps (LSU: 1-824 and *tef1- $\alpha$* : 825-1665). The best scoring RAxML tree was established with a final ML optimization likelihood value of -12426.509429. The matrix had 738 distinct alignment patterns with 37.64% undetermined characters or gaps. Estimated base frequencies are as follows: A = 0.237672, C = 0.264588, G = 0.296805, T = 0.200936; substitution rates AC = 0.616617, AG = 1.708133, AT = 0.931688, CG = 1.153811, CT = 7.432532, GT = 1.000000. *Amplistroma erinaceum* (AH 43902) and *Amplistroma caroliniana* (BEO9923) were used as outgroup. Numbers above branches are the bootstrap statistics percentages (left) and Bayesian posterior probabilities (right). Branches with bootstrap values for ML and MP  $\geq 75\%$  and  $\geq 0.95$  are shown at each branch and the bar represents 0.06 substitutions per nucleotide position. Ex-type strains are in black bold and the newly generated sequences are indicated in red.

*Ceratosphaeria yunnanensis* C.F. Liao & Doilom sp. nov.

Fig. 50

Index Fungorum number: IF559274; Facesoffungi number: FoF 10583

Etymology – ‘yunnanensis’ referring to the species collected from Yunnan Province, China.

Holotype – KUN–HKAS 112878

*Saprobic* on stem of *Heteropanax fragans*. Sexual morph: *Ascomata* 110–220 × 130–250 μm ( $\bar{x}$  = 164 × 196 μm, n = 20), solitary, deeply immersed, neck erumpent through the host surface, globose to subglobose, brown to yellowish. *Neck* 60–100 μm wide ( $\bar{x}$  = 82 μm, n = 20), from the bottom to the apical part, the colour changes to brown or black to yellowish-brown, surface smooth. *Peridium* 20–50 μm wide ( $\bar{x}$  = 41 μm, n = 30), composed of 3–6 layers of brown cell to yellowish-brown cell of *textura prismatica*, thick-walled. *Paraphyses* 2–10 μm wide ( $\bar{x}$  = 6.5 μm, n = 30), hyaline, unbranched, septate, border at the base, tapering to the ends, longer than asci. *Asci* 80–120 × 5–15 μm ( $\bar{x}$  = 106 × 8 μm, n = 30), 8-spored, unitunicate, cylindrical, narrow, thin-walled with an apical ring. *Ascospores* 80–110 × 1–3 μm ( $\bar{x}$  = 88 × 2 μm, n = 30), straight or curved, S-shaped, filiform, aseptate, hyaline, tapering at both ends, with minute guttules in each cell, becoming smooth at maturity. Asexual morph: Not observed.

Culture characters – Ascospores germinating on PDA within 24 hours. Colonies on PDA reaching 1–2 cm diameter after 10 days at 25 ± 2°C, umber to pale umber at the edge, white surface forms a circular ring in the middle. Colonies rough, mycelium dense. Reverse red to yellow, no pigment produced.

Material examined – China, Yunnan Province, Kunming, on a dead stem of *Heteropanax fragans* (Roxb.) Seem., (*Araliaceae*), 12 August 2020, C.F. Liao (KUN–HKAS 112878, holotype), ex-type culture KUMCC 21-0013.

GenBank accession numbers – LSU: OL473547; ITS: OL505597; *tef1-α*: OL505597.

Notes – In the phylogenetic analysis, our taxa clustered in a sister clade to *Ceratosphaeria lignicola* (Fig. 49). *Ceratosphaeria yunnanensis* is similar to *Ceratosphaeria lignicola* concerning the deeply immersed ascomata in the substata. However, *Ceratosphaeria yunnanensis* differs from *C. lignicola* by its smaller ascomata (110–220 × 130–250 μm vs 390–470 × 500–600 μm) and thick peridium (20–50 μm vs 13.5–17.5 μm). The LSU and *tef1-α* sequence comparison of *Ceratosphaeria yunnanensis* with *Ceratosphaeria lignicola* revealed 10 and 23 nucleotides differences respectively.

**Savoryellaceae** Jaklitsch & Réblová in Jaklitsch, Index Fungorum 209: 1 (2015)

Jaklitsch (2015) introduced *Savoryellaceae* to accommodate *Savoryella*. Four genera, *Ascotaiwania*, *Canalisporium*, *Rhexoacrodictys*, and *Savoryella*, comprised the family with a total of 54 morphological species. We follow Hyde et al. (2020d) for the taxonomic treatment of *Savoryellaceae*.

**Savoryella** E.B.G. Jones & R.A. Eaton, Trans. Br. mycol. Soc. 52(1): 161 (1969)

*Savoryella*, typified by *S. lignicola*, was introduced by Jones and Eaton (1969), collected from submerged test-blocks in a water-cooling tower. *Savoryella* comprises 13 species wherein eleven are supported by molecular data (Minoura & Muroi 1978, Koch 1982, Jones and Hyde 1992, Ho et al. 1997, Abdel-Wahab & Jones 2000, Dayarathne et al. 2019, Zhang et al. 2019a). Hyde et al. (2020d) provided a historical and updated taxonomic account of *Savoryella* and we follow the treatment in this paper.

**Savoryella nypae** (K.D. Hyde & Goh) S.N. Zhang, K.D. Hyde & J.K. Liu

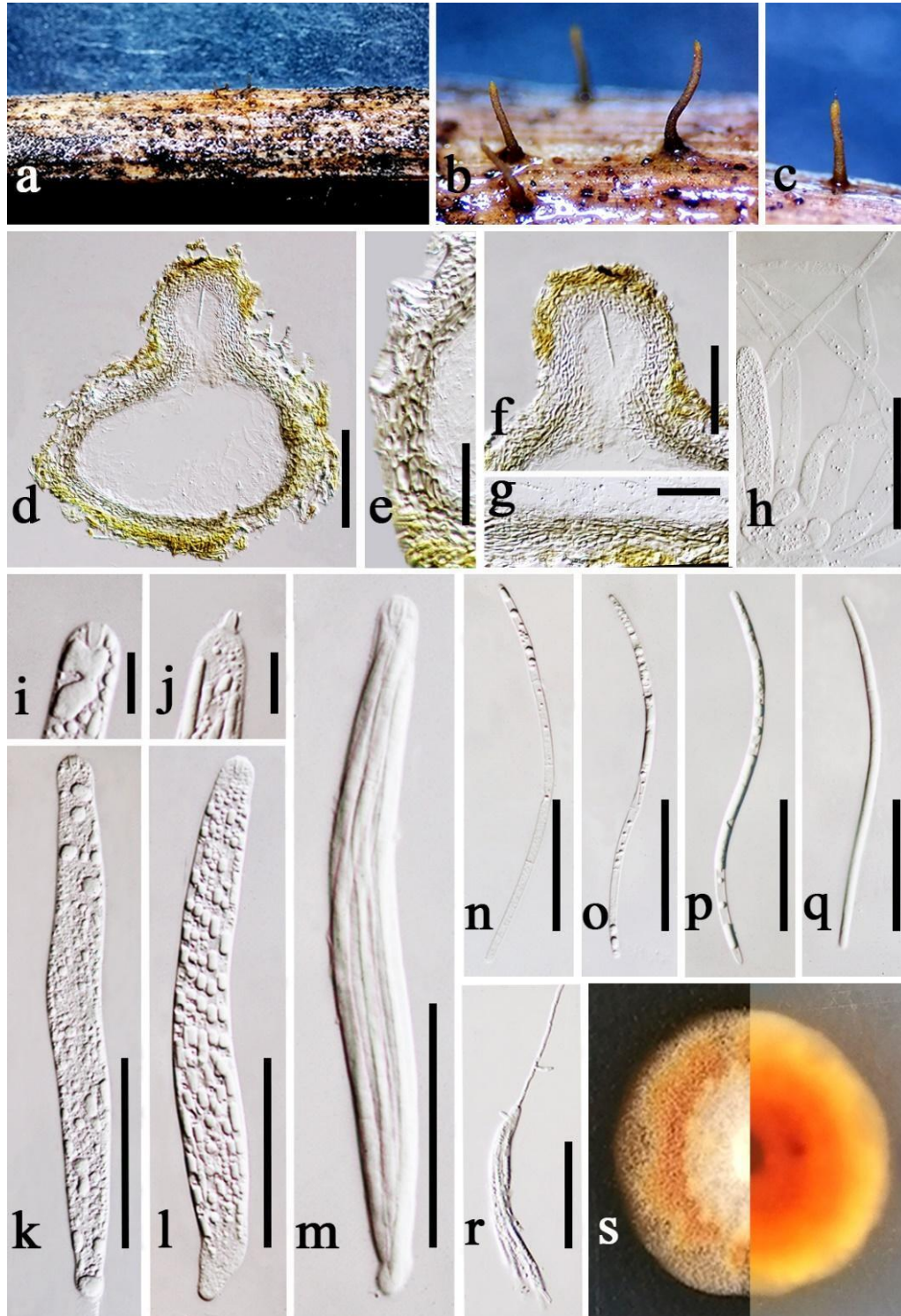
Fig. 52

Index Fungorum number: IF 556269; Facesoffungi number: FoF 05833

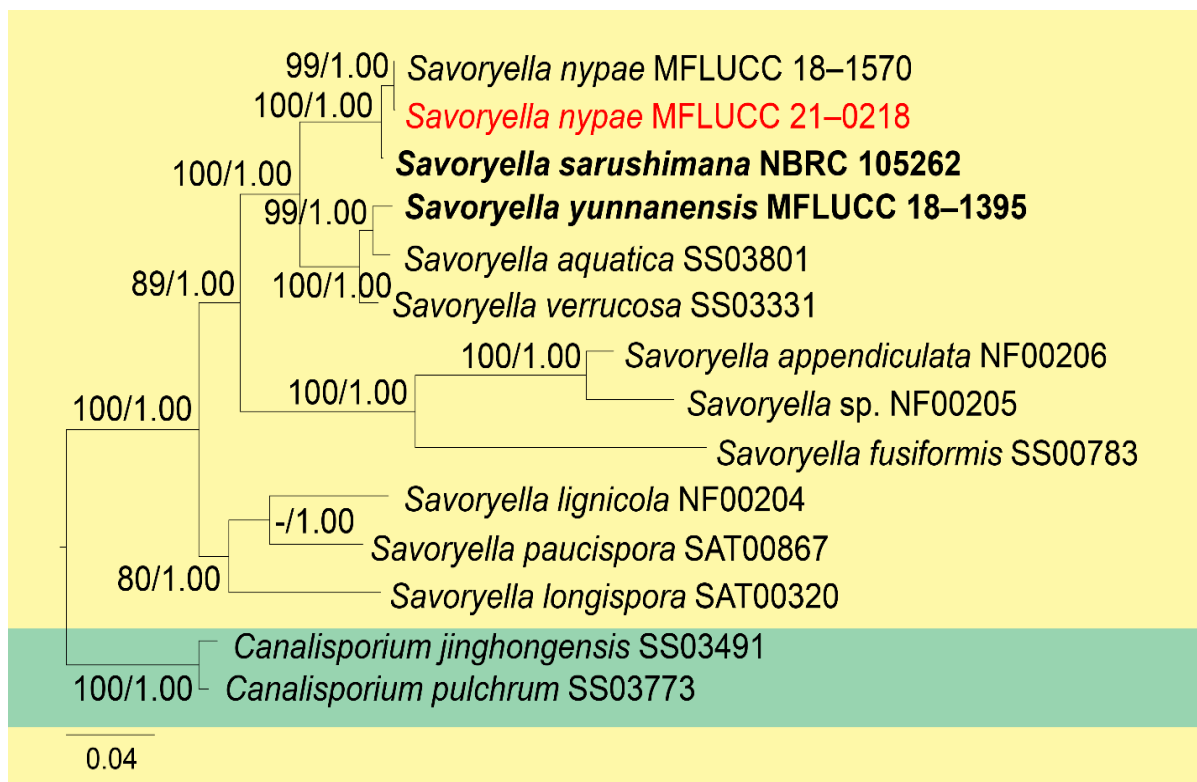
= *Trichocladium nypae* K.D. Hyde & Goh, in Hyde, Goh, Lu & Alias, Mycol. Res. 103(11): 1420 (1999)

*Saprobic* on submerged seeds of *Avicennia marina*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effuse, black, glistening, punctiform distributed on substrates. *Mycelium* 1.5–2.5 μm, hyaline to pale brown, septate, branched. *Conidiophores* inconspicuous or micronematous, mononematous, hyaline to pale brown, smooth and thin-walled. *Conidiogenous cells*

holoblastic, determinate, integrated, terminal or intercalary, cylindrical. *Conidia* 15–25 × 10–15 μm ( $\bar{x}$  = 19.8 × 13.2 μm, n = 30), rhexolytic, solitary or aggregated, pyriform to obovoid, smooth, broadly rounded at the apex, straight or slight curved, thick-walled, 2(–3)-septate, septa thick and band like, dividing the conidium into unequal cells, upper cell 10–15 μm × 9–15 μm ( $\bar{x}$  = 12.8 × 12 μm, n = 30), being largest and dark brown, middle cells brown or paler, and basal cell 2–4 × 2–4 μm ( $\bar{x}$  = 3.1 × 3.5 μm, n = 30) subhyaline or pale brown.



**Figure 50** – *Ceratosphaeria yunnanensis* (KUN–HKAS 112878, holotype). a, c Appearance of ascomata on substrate. d Section through ascoma. e, g Peridium. f Ostiole. h Paraphyses. i, j Apical ring of asci. k–m Asci. n–q Ascospores. r Germinated ascospore. s Culture characteristics on PDA. Scale bars: d = 500 μm, e, f = 200 μm, h, k–q, r = 100, g, i, j = 10 μm.



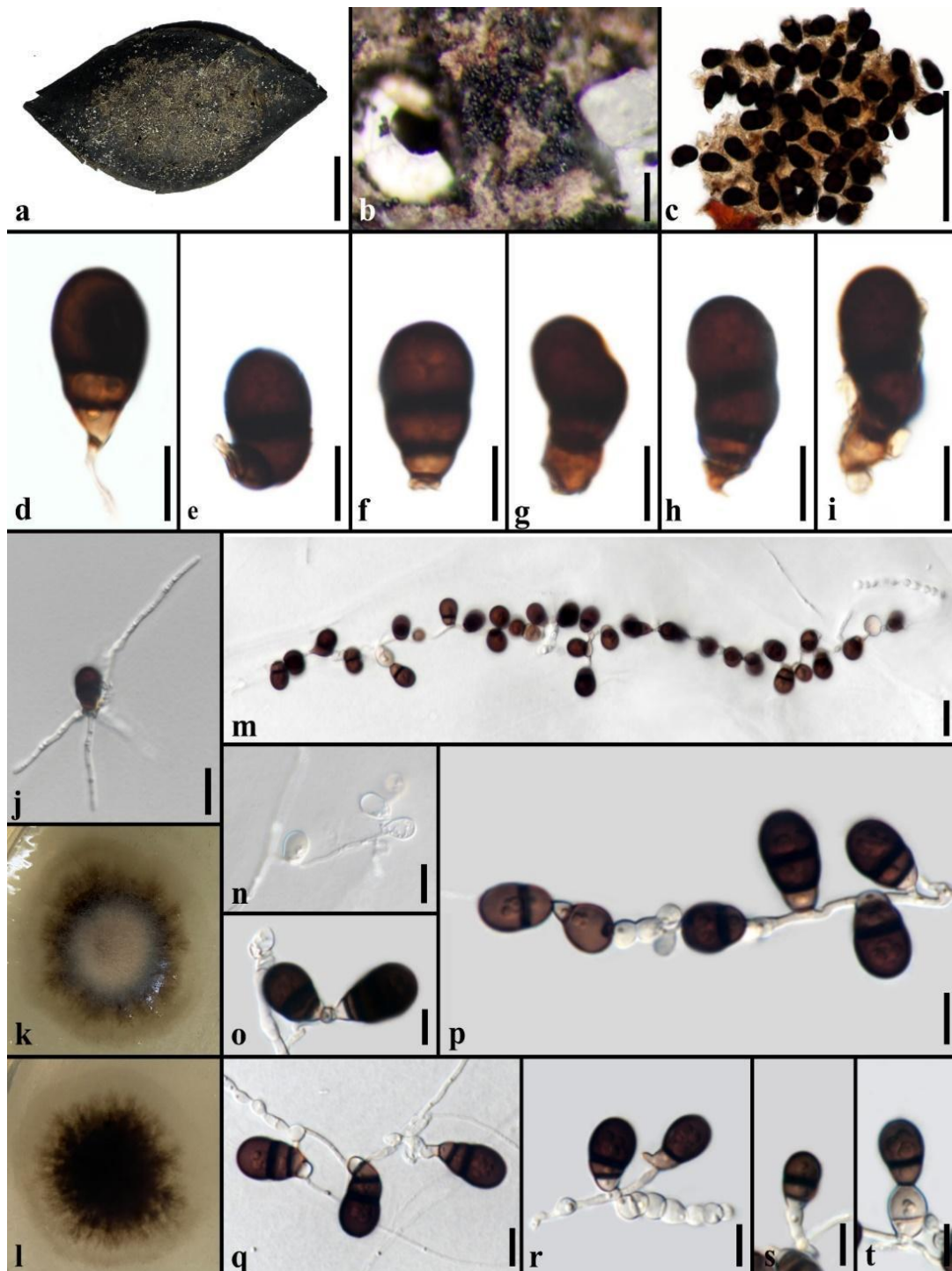
**Figure 51** – Phylogenetic tree generated by ML analysis of combined ITS, LSU, SSU, and *tef1- $\alpha$*  sequence data of *Savoryellaceae*. The analyses included 14 strains and the tree is rooted with *Canalisporium jinghongensis* (SS03491) and *Canalisporium pulchrum* (SS03773). Tree topology of the ML analysis was similar to the MP and BYPP. The best scoring RAxML tree with a final likelihood value of -62158.846229 is presented. The matrix had 3029 distinct alignment patterns, with 50.58% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.233422, C = 0.266263, G = 0.292524, T = 0.207791; substitution rates AC = 1.417135, AG = 2.562191, AT = 1.525677, CG = 1.167027, CT = 5.974681, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.297477. RAxML bootstrap support values  $\geq 75\%$  and Bayesian posterior probabilities values  $\geq 0.95$  (BYPP) are shown near the nodes. Ex-type/ex-epitype strains are in bold. New isolates recovered in this are in red.

**Culture characteristics** – Colonies on MEA attain 10 mm diam. after 15 days at 25°C, obverse light brown to brown, reverse dark brown. Mycelium in culture up to 2–3  $\mu\text{m}$  wide, hyaline to brown, septate, branched. Chlamydospore-like structures are apparent in culture and developed to conidia. Conidia in culture 11–20  $\times$  8–17 ( $\bar{x}$  = 15.1  $\times$  10.8  $\mu\text{m}$ , n = 50).

**Material examined** – Thailand, Ranong, Ko Phayam, on submerged seeds of *Avicennia marina* (Forssk.) Vierh. (*Arecaceae*), 12 September 2020, M.S. Calabon, RSB30 (MFLU 21–0255), living culture: MFLUCC 21–0218.

**GenBank accession numbers** – ITS: OL504780; LSU: OL477393; SSU: OL477394; *tef1- $\alpha$* : OL547598.

**Notes** – Zhang et al. (2019a) transferred *Trichocladium nypae* to *Savoryella* based on morphological comparison, host association, and multi-loci phylogenetic analyses. Based on the morphological comparison with the reference specimen *Savoryella nypae* (MFLUCC 18–1570) and multi-loci phylogenetic analyses confirm the present collection as *S. nypae*. This is the first report of *S. nypae* isolated from the submerged decaying seed of *Avicennia marina*. The previous isolations were from submerged petiole of *Nypa fruticans* (Hyde et al. 1999, Zhang et al. 2019a) and dead mangrove wood (Pang et al. 2011) from Brunei (Hyde et al. 1999), China (Pang et al. 2011), Malaysia (Hyde et al. 1999), and Thailand (Zhang et al. 2019a).



**Figure 52** – *Savoryella nypae* (MFLU 21–0255, new host record). a Host. b Appearance of colony on natural substrate. c–i Conidia. j Germinated conidium. Colony on MEA from (k) above and (l) below. m–t Development of conidia in culture. Scale bars: a = 1 cm, b–c = 100  $\mu$ m, d–i, n–t = 10  $\mu$ m, j, m = 20  $\mu$ m.

## Phylum Basidiomycota

### Agaricomycetes

### Agaricales

### *Agaricaceae* Chevall.1: 121 (1826)

Chevall (1826) introduced *Agaricaceae* using *Agaricus* as the type genus. He et al. (2019) accepted 60 genera in *Agaricaceae*. Sokol et al. (2021) added a new genus of *Asperosporus* to this family.

***Leucoagaricus*** Locq. ex Singer, Sydowia 2(1-6): 35 (1948)

*Leucoagaricus* have 135 estimated species, and the type species is *Leucoagaricus rubrotinctus* (He et al. 2019). Species of *Leucoagaricus* are terrestrial and saprotrophic, and species are distributed in both tropical and temperate regions (Kirk et al. 2008). Several new species have been described from Asia, such as India (Kumar & Manimohan 2009), China (Liang et al. 2010, Ge et al. 2015, Yang & Ge 2017, Yuan et al. 2014, Yu et al. 2016), Pakistan (Hussain et al. 2018, Qasim et al. 2015), and Laos (Sysouphanthong et al. 2018). In this paper, we introduce two new *Leucoagaricus* species from Laos and Thailand (Fig. 53). In the phylogenetic analysis, *Lepiota flammeotincta*, *Lep. fuliginescens* and *Lep. decorata* are placed in the *Leucoagaricus*. Vellinga (2004) indicated that *Leucoagaricus* and *Leucocoprinus* are in the *Leucoagaricus/Leucocoprinus* clade. Furthermore, Vellinga (2006, 2010) studied on type specimens of *Lep. flammeotincta*, *Lep. fuliginescens* and *Lep. decorata* and mentioned these taxa fit to *Leucoagaricus* than *Lepiota* because of their absence of clamp-connections. This is further confirmed in molecular phylogenetic analysis as them to be in *Leucoagaricus/Leucocoprinus* clade. Thus, we recommend that *Lepiota flammeotincta*, *Lepiota fuliginescens* and *Lepiota decorata* should be moved to genus *Leucoagaricus*.

***Leucoagaricus croceus*** S.M. Tang & K.D. Hyde, sp. nov.

Fig. 54

Index Fungorum number: IF 557764; Faceoffungi number: FoF 08469

Etymology – the epithet ‘croceus’ refers to the reddish-orange on the pileus.

Holotype – MFLU19-1331

*Pileus* 30–60 mm in diam., subumbonate or plano-concave with obtuse umbo, reddish-orange (7A6-8) at center, becoming white (7A1) to pastel red (7A4) towards margin; volval remnants on pileus floccose to pulverulent when basidiomata young, smooth with age; trama white, unchanging. *Stipe* 30–50 × 3–5 mm, cream (1A2) to white (1A1); context white (1A1), unchanging, clavate; basal 8–12 mm diam., subglobose, thickening toward base. *Annulus* simple, located at the middle to upper part of the stipe, white (1A1), membranous. *Basidia* 15–20 × 9–10 μm clavate, 4-spored. *Basidiospores* (3.5–)4.1–7.2(–7.9) × (2.4–)2.6–4.4(–4.6) μm,  $Q = (1.00–)1.14 \times 2.00 (–2.39) \mu\text{m}$ ,  $N = 114$ ,  $Q_m = 1.59 \pm 0.25$ , ovoid to ellipsoid, colourless, thin-walled, smooth. *Lamellar edge* appearing as a sterile strip, composed of subglobose to ellipsoid cells (15–18 × 7–9 μm) thin-walled, colourless. *Pleurocystidia* and *Cheilocystidia* are absent. *Lamellar trama* 15–25 μm wide composed of abundant elongate cells. *Pileipellis* 60–80 μm thick, composed of parallelly, thin-walled, cylindrical, light brown to reddish-brown filamentous hyphae 6–8 μm thick. *Clamp* connections absent.

Material examined – Thailand, Chiang Rai, Mae Fah Luang University, 3 June 2019, S.M. Tang (MFLU19-1331, holotype).

GenBank accession numbers – ITS: OL413492; LSU: MT515802; *rpb2*: MT518174.

Notes – In our multi-locus (ITS, LSU, *rpb2*) phylogenetic analysis (Fig. 53), *Leucoagaricus croceus* developed a clade to *L. asiaticus*. However, *L. asiaticus* has a dark brown to reddish-brown pileus and has relatively larger basidiospores 8–10 × 6–7 μm (Ge et al. 2015). *Leucoagaricus crystallifer* has basidiomata cream to pale ochre and cheilocystidia cylindrical to fusiform (Vellinga 2000). *Leucoagaricus sultanii* has yellowish-pink to dark yellowish-pink pileus and relatively wide basidia 21–27 × 7–10 μm (Hussain et al. 2018). *Leucoagaricus croceus* is also similar to *L. croceus* in their red basidiomata. However, *L. badius* has a clavate to fusiform cheilocystidia, and has narrower basidia (6–8 μm; Hussain et al. 2018). Based on both morphological and molecular phylogeny we introduce *Leucoagaricus croceus* as a novel species.

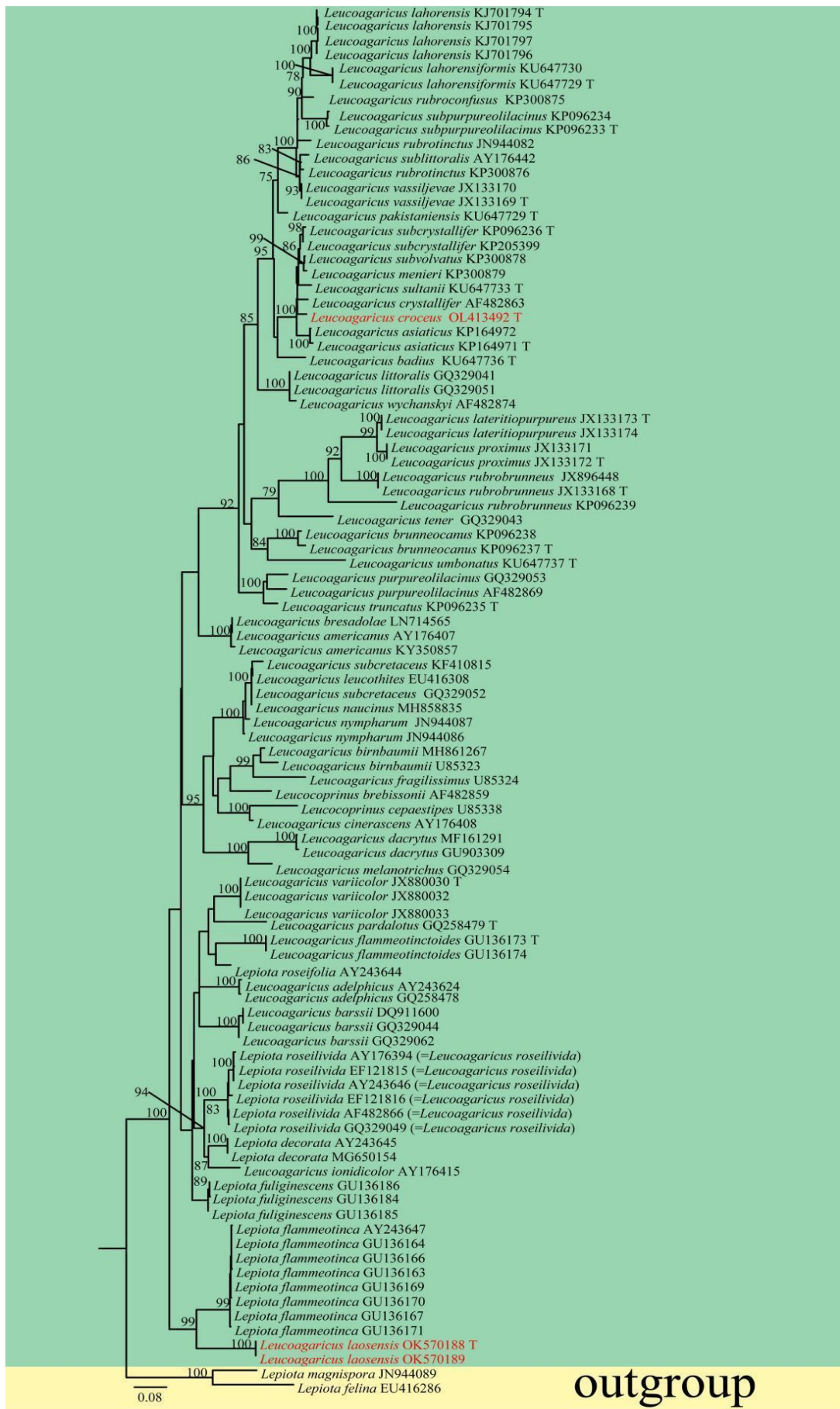
***Leucoagaricus laosensis*** Sysouph. sp. nov.

Figs 55, 56

Mycobank number: MB841760; Index Fungorum number: IF 559250; Facesoffungi number: FoF 10365

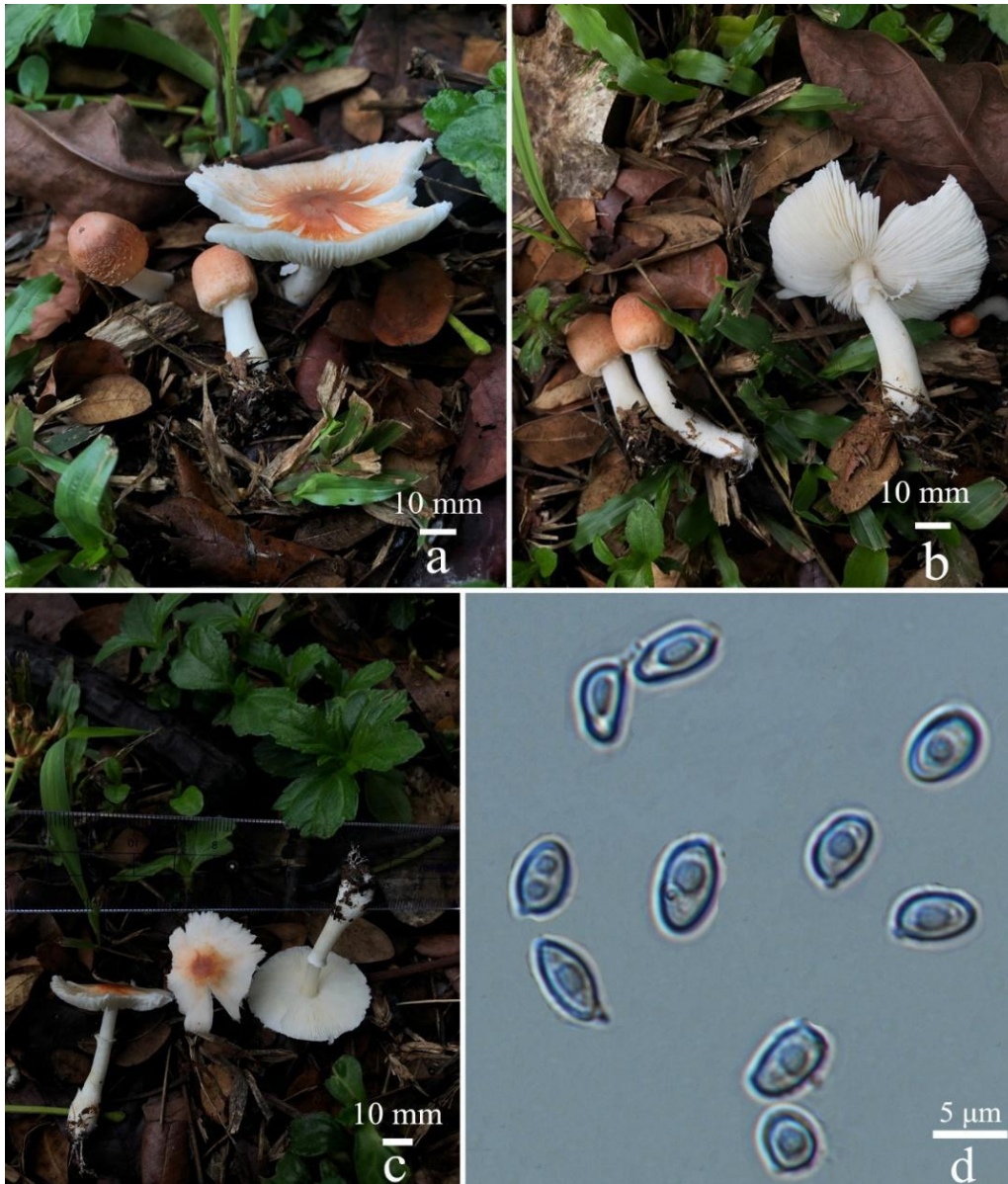
Etymology – The name “laosensis” refers to the specimens that were firstly found in Laos.

Holotype – HNL501802



**Figure 53** – Phylogram generated from maximum likelihood analysis based on combined ITS sequence data representing *Leucoagaricus*. Related sequences were taken from Hussain et al. (2018).

Ninety-six strains consisting of 823 characters after alignment with gaps. *Lepiota magnispora* (JN944089) and *L. felina* (EU416286) are used as outgroup taxa. The best scoring RAxML tree with a final likelihood value of -11514.256434 is presented. The matrix had 595 distinct alignment patterns, with 21.73% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.225629, C = 0.224430, G = 0.236067, T = 0.3413873; substitution rates AC = 1.383073, AG = 4.141789, AT = 1.520088, CG = 0.699209, CT = 4.433613, GT = 1.000000; gamma distribution shape parameter  $\alpha = 0.444032$ . ML bootstrap values equal to or greater than 70%. Newly generated sequences are indicated in red. “T” refers to sequences from type specimens.



**Figure 54** – *Leucoagaricus croceus* (MFLU19-1331, holotype). a–c Basidiomata. d Basidiospores.

*Basidiomata* small to medium size. *Pileus* 15–30 mm diam., convex to sub-umbonate with small umbo, expanding to applanate or slightly plano-concave with low center or umbo when mature, with straight margin; with very crowded fibrillose at center or umbo, light brown to dark brown (6E4–7, 6F6–8), around center with concolorous tuff, fibrillose or fibrillose squamules with uplift tip towards margin, with white to orange-white (5A2) fibrillose background; margin with concolorous fibrillose or fibrillose squamules, sulcate and fringed when mature, with or without white to light brown (6E4–5) remnants. *Lamellae* free, ventricose, 4–6 mm wide, crowded, white, with concolorous eroded edge. *Stipe* 25–35 × 5–8 mm, wider at base and tapering to apex, bulbous 12 mm wide, with

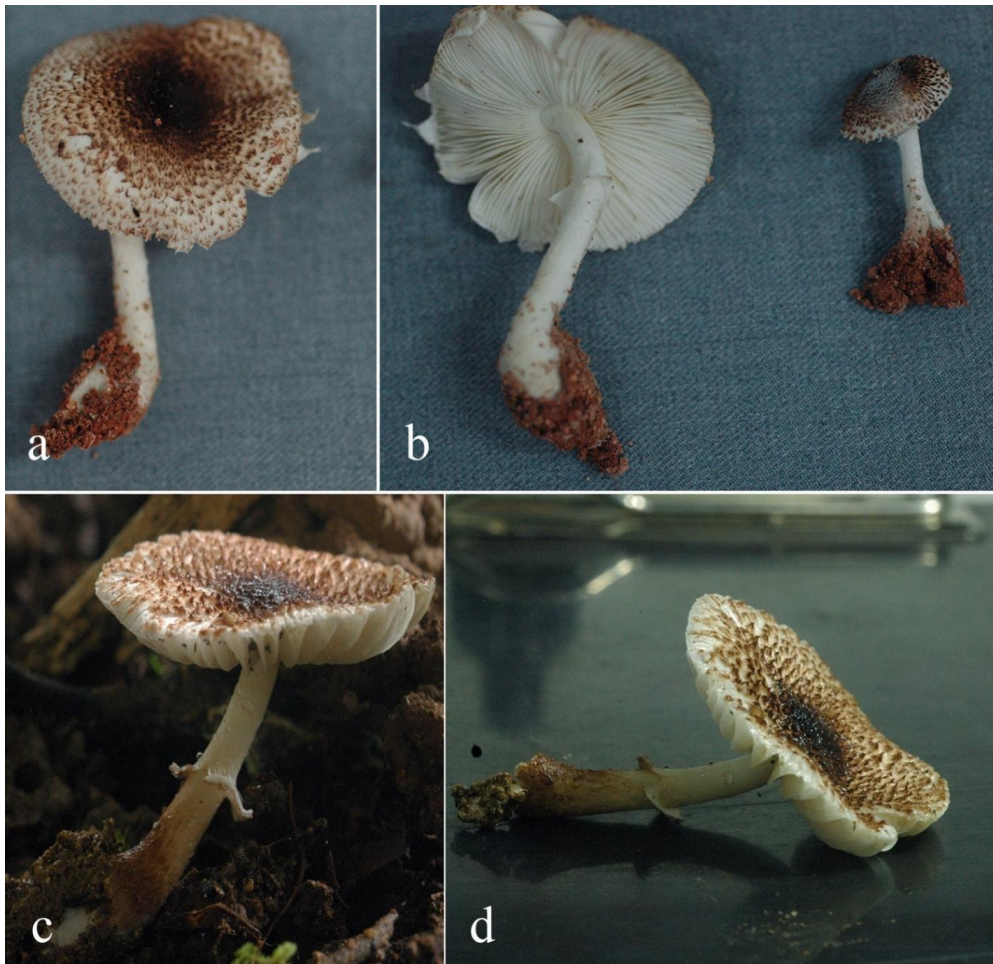


white fibrillose background, sometimes with hyaline water drops, covered with light brown to dark brown (6E4–7) fibrillose squamules from middle to base, crowded at base. *Annulus* attached at middle or slightly high on stipe, membranous, white, hanging down, with light brown to brown (6E4–7) fibrillose squamules at edge. *Context* in pileus white, up to 3 mm wide; in stipe, white, hollow. Taste not observed. Spore print white. *Basidiospores* (50.2.2)  $7.0\text{--}7.5 \times 4.3\text{--}5 \mu\text{m}$ ,  $av_l \times av_w = 7.2 \times 4.5 \mu\text{m}$ ,  $Q = 1.4\text{--}1.70$ ,  $Q_{av} = 1.60$ , in side-view ellipsoidal to oblong ovoid, slightly amygdaliform with rounded apex, in frontal view ellipsoid to oblong, hyaline, thick-walled, dextrinoid, congophilous, cyanophilous, metachromatic. *Basidia*  $17\text{--}20 \times 7\text{--}8 \mu\text{m}$ , clavate, hyaline, thin-walled, 4-spored. *Pleurocystidia* absent. *Cheilocystidia*  $20\text{--}30 \times 5\text{--}10 \mu\text{m}$ , clavate to narrowly clavate, rarely cylindrical, hyaline, thin-walled. *Pileus* covering a trichoderm made up of cylindrical elements, terminal elements  $40\text{--}90 \times 12\text{--}15 \mu\text{m}$ , slightly thick-walled, with brown parental and intracellular pigments. *Stipe* covering a trichoderm made up of cylindrical elements, terminal elements  $20\text{--}60 \times 10\text{--}15 \mu\text{m}$ , slightly thick-walled, with brown parental and intracellular pigments. *Clamp connections* absent.

Habitat and distribution – Saprotrophic, on soil with rich humus, growing solitary or in small cluster with few basidiomata. The species is only known from northern Laos.

Material examined – Laos, Oudomxay Province, Xay District, Houay Houm Village, 23 July 2014, P. Sysouphanthong (HNL501802, holotype).

GenBank accession numbers – ITS: OK570188 (holotype), OK570189.



**Figure 55** – Fresh basidiomata of *Leucoagaricus laosensis* *in situ*. a–b HNL501802. c–d HNL501782.

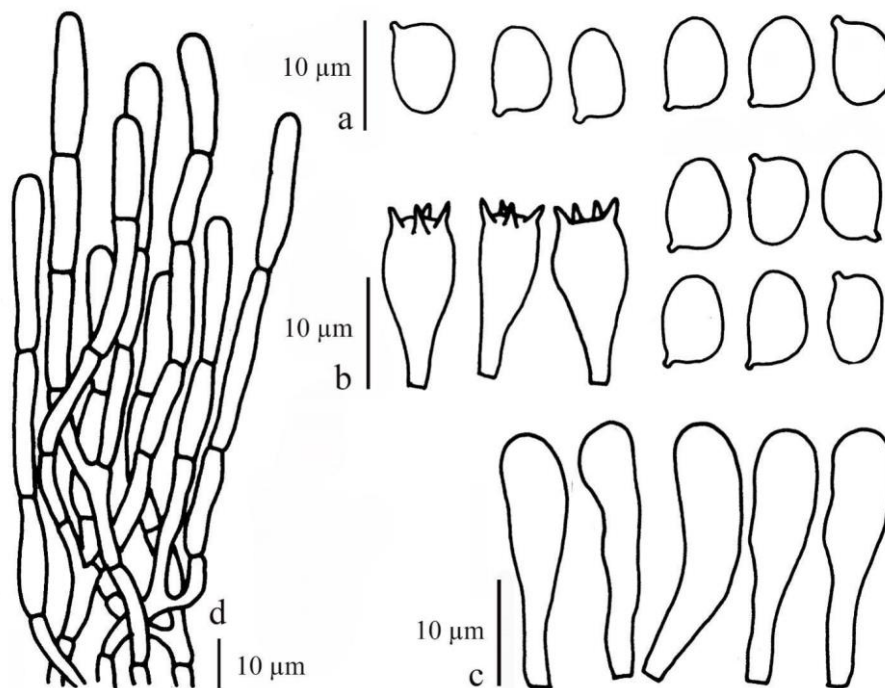
Notes – *Leucoagaricus laosensis* can be recognized by small to medium size, convex to sub-umbonate pileus and covered by light brown to dark brown fibrillose to fibrillose squamules, oblong

to ellipsoidal ovoid basidiospores, clavate basidia, clavate to narrowly clavate cheilocystidia, and trichodermal structure of pileus and stipe covering. According to the colour of pileus covering, it is rare species related to *Leucoagaricus laosensis*. *Leucoagaricus infuscatus* from the USA, is similar to *Leucoagaricus laosensis* by the size of basidiomata (18–24 mm) and applanate to shallowly plano-convex pileus covered with brown fibrillose. However, *Leucoagaricus infuscatus* has distant lamellae, smooth stipe and whitish on watery pinkish-cream background, narrower basidiospores ( $5.6\text{--}7.6 \times 3.4\text{--}4.4 \mu\text{m}$ ), longer cheilocystidia ( $26\text{--}57 \times 4.0\text{--}12 \mu\text{m}$ ), a cutis structure of pileus covering (Vellinga 2007).

***Physalacriaceae*** Corner, Beih. Nova Hedwigia 33: 10 (1970)

***Mucidula*** Pat., Hyménomyc. Eur. (Paris): 95 (1887)

*Mucidula* is belonging to *Physalacriaceae* (Yang et al. 2019, He et al. 2019) and *M. mucida* is the types species. They are characterised by white to pale brown armillarioid basidiomata with a greasy to viscid pileus surface, annulus on the stalk, and globose basidiospores. There are two species *M. brunneomarginata* and *M. mucida* of this genus and *M. mucida* is separated into three varieties: *M. mucida* var. *asiatica*, *M. mucida* var. *mucida*, and *M. mucida* var. *venosolamellata*. Species identification is based on the distribution differences and pileipellis and lamella features (Petersen & Hughes 2010).



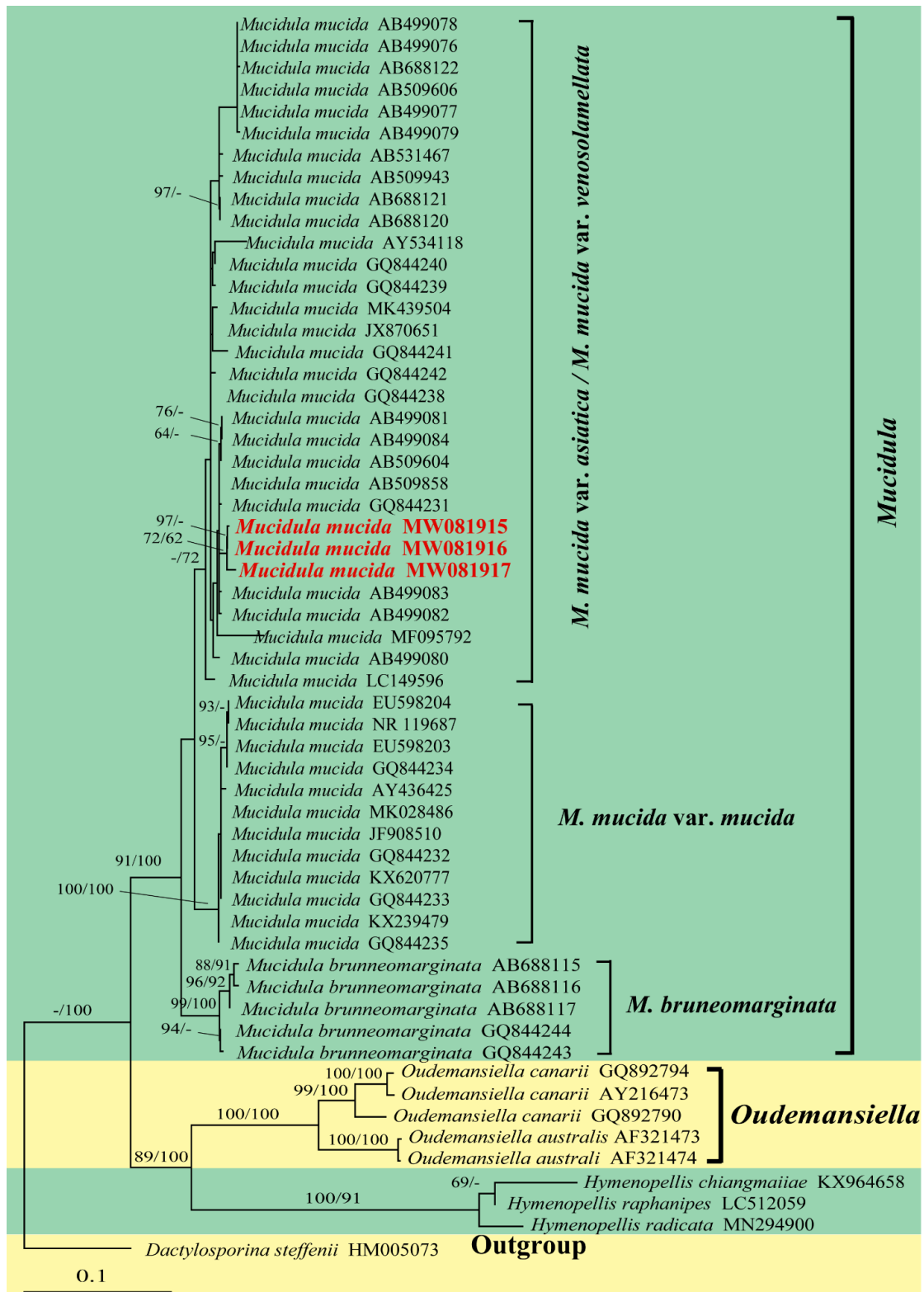
**Figure 56** – *Leucoagaricus laosensis* (HNL501782, holotype). Micro morphological characters. a Basidiospores. b Basidia. c Cheilocystidia. d Elements on pileus covering.

***Mucidula mucida* var. *venosolamellata*** (Imazeki & Toki) R.H. Petersen, in Petersen & Hughes, Nova Hedwigia, Beih. 137: 265 (2010) Fig. 60

Index Fungorum number: IF 456952; Facesoffungi number: FoF 10364

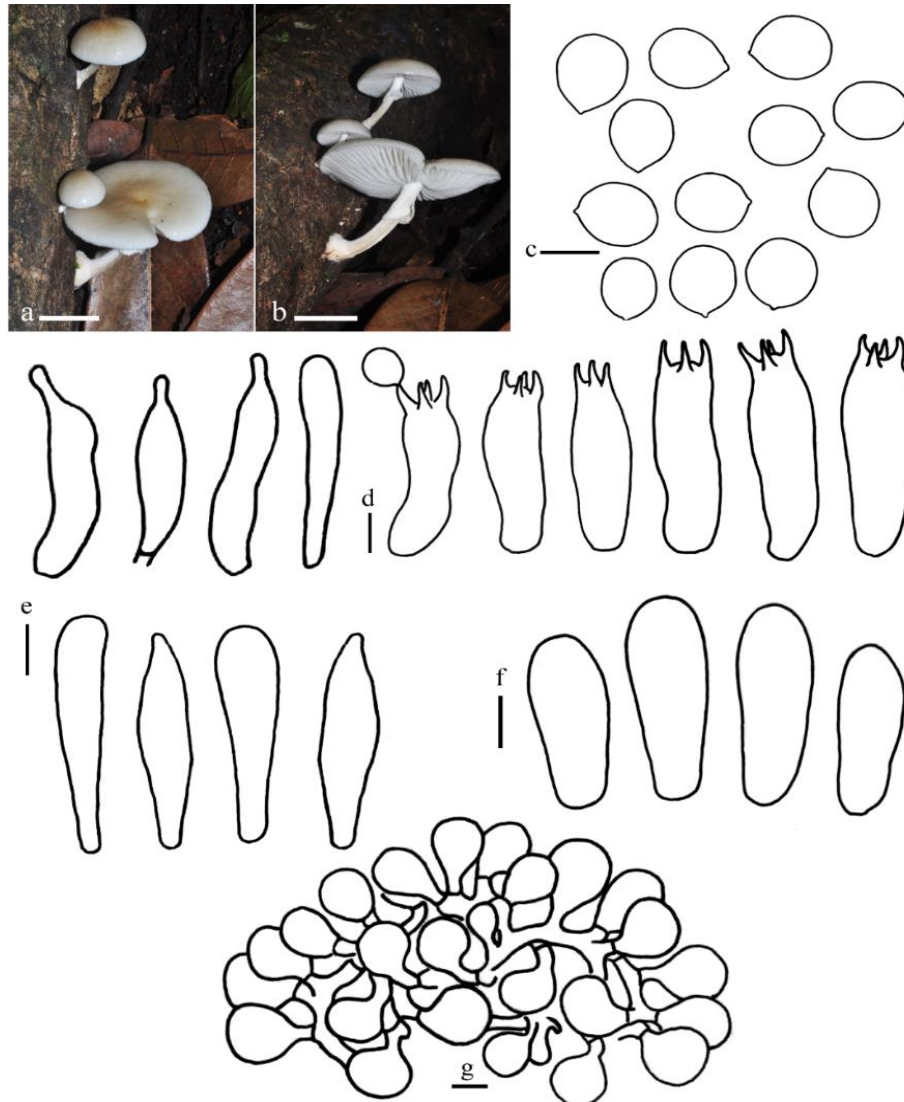
*Pileus* 30–50 mm diam., firstly convex to broadly convex, expanding to plano-convex, becoming hemispheric when mature, with straight to slightly inflexed margin; soft and viscid when wet, smooth or glabrous when dry, white to dirty white (1A1), yellowish-white to greyish-yellow (4A2–4B3) at the center; margin white, striate. *Lamellae* adnate, white, broad to broadly ventricose, 5–8 mm thick, with concolorous eroded edge. *Stipe* 20–60 × 0.5–1 mm, cylindrical with wide bulbous 10–15 mm, covered with white fibrillose, with white fibrillose squamules to squamules at base zone

or bulbous, on white to yellowish-white (3A2, 4A2) background. *Annulus* present at above of stipe, white, membranous. *Context* white in pileus, 2–4 mm thick; solid and white in stipe. Spores print white.



**Figure 57** – Phylogenetic tree generated by ML analysis of ITS sequence data of *Mucidula* species. The analyses included 57 species and the tree was rooted with *Dactylosporina steffenii* (HM005073). Tree topology of the ML analysis was similar to the MP and BYPP. The best scoring RAxML tree with a final likelihood value of -3823.834840 is presented. The matrix had 348 distinct alignment patterns, with 6.85% of undetermined characters or gaps. Estimated base frequencies were as follows:

A = 0.209642, C = 0.228142, G = 0.235041, T = 0.327175; substitution rates AC = 0.890824, AG = 1.893300, AT = 0.595315, CG = 1.040815, CT = 2.222406, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.597222. Maximum parsimony analysis of 402 constant characters and 239 informative characters resulted in 100 equally most parsimonious tree of 10 steps (CI = 0.792, RI = 0.896, RC = 0.710, HI = 0.208). RAxML bootstrap support values  $\geq 50\%$  and maximum parsimony bootstrap support values  $\geq 50\%$  are shown near the nodes. The scale bar indicates 0.1 change per site. New isolates recovered are in red.



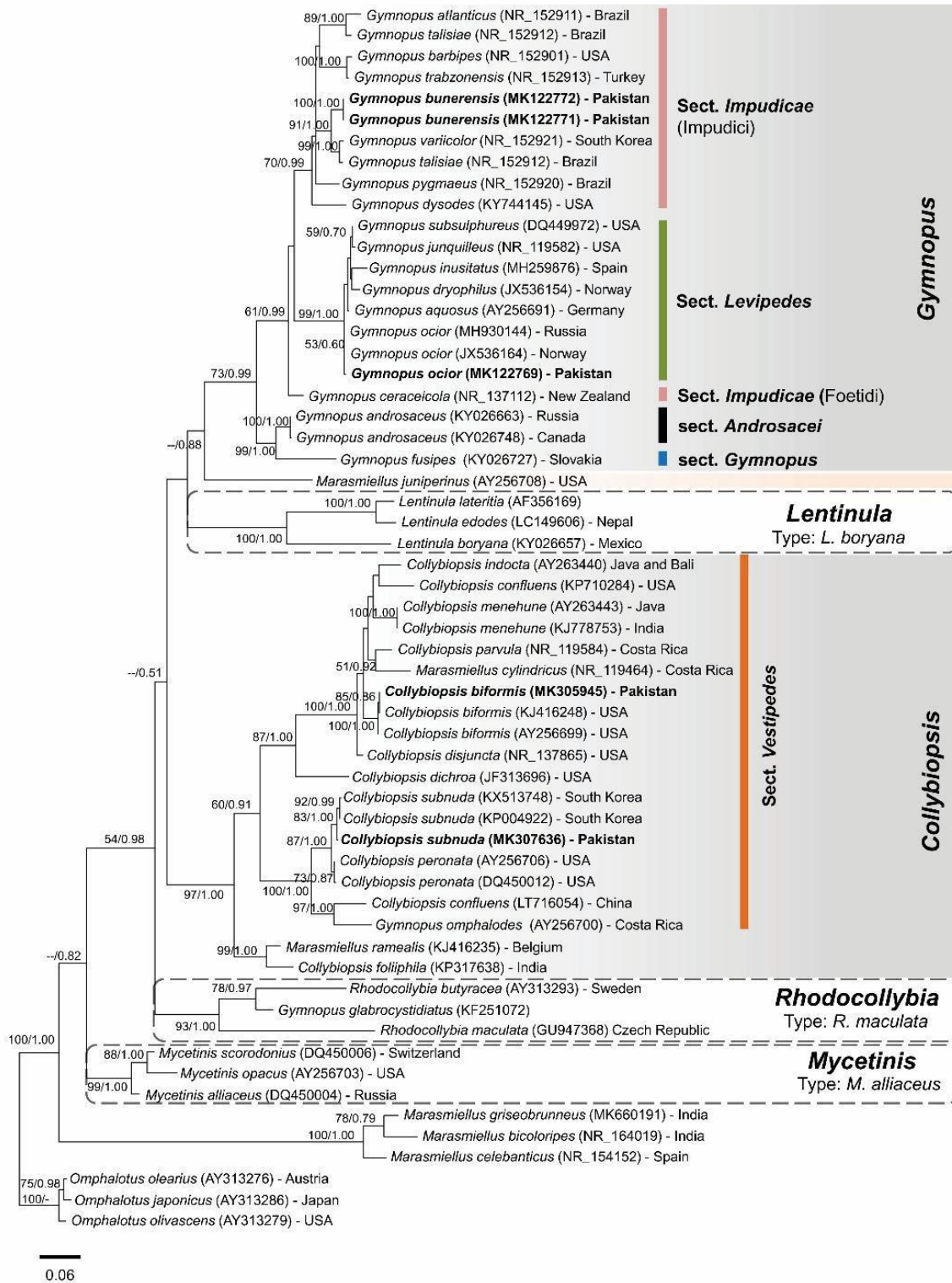
**Figure 58** – *Mucidula mucida* (HNL503504, new geographical record). a–b Fresh basidiomata of *Mucidula mucida* on-field captured by Phongoun Sysouphanthong. c Basidiospores. d Basidia. e Cheilocystidia. f Pleurocystidia. g Pileipellis ixotricchoderm. Scale bars: a–b = 20 mm. c–g = 10  $\mu$ m.

*Basidiospores* 20–25  $\times$  15–20  $\mu$ m, Q = 1.09–1.45, subglobose to broadly ellipsoid, smooth, hyaline, thick-walled. *Basidia* 50–70  $\times$  15–20  $\mu$ m, clavate to broadly clavate, thick-walled, 4-spores, sometimes 2-spored. *Cheilocystidia* 15–20  $\times$  5–10  $\mu$ m, variable in shape, clavate, narrowly clavate, fusiform, occasionally capitate, thin-walled. *Pleurocystidia* 40–60  $\times$  15–20  $\mu$ m, cylindrical to subcylindrical, thin-walled. *Pileipellis* an ixotricchoderm to subhymeniderm made up of clavate to broadly terminal cells, 15–20  $\times$  5–7  $\mu$ m. *Clamp-connections* present.

Habitat and distribution – saprotrophic on dead wood, the species was found in China, Japan, Russia (Ushijima et al. 2012, Vizzini et al. 2012). This is the first record from Laos.

Material examined – Laos, Xiang Khouang Province, Phoukout District, Gnophe, Na Phouang, hamlet, 27 May 2018, P. Sysouphanthong (HNL503504); Vientiane Capital, Xaythany District, Houay Yang Forest Reserve, 30 March 2018, P. Sysouphanthong (HNL503530); *ibidem* 16 January 2016, P. Sysouphanthong (HNL503214).

GenBank accession numbers – ITS: MW081915, MW081916, MW081917.



**Figure 59** – Phylogenetic tree generated by ML analysis based on combined ITS and LSU sequence data of *Gymnopus*, *Collybiopsis* and its closely related taxa. The analyses included 60 strains and the

tree is rooted with *Omphalotus olearius* (AY313276), *Omphalotus japonicus* (AY313286) and *Omphalotus ovilascens* (AY313279). Tree topology of the ML analysis was similar to the MP and BYPP. The best scoring RAxML tree with a final likelihood value of -6984.942184 is presented. The matrix had 1349 distinct alignment patterns, with 2.68% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.249358, C = 0.249262, G = 0.232205, T = 0.0269175; substitution rates AC = 1.530869, AG = 1.342665, AT = 3.376816, CG = 1.078744, CT = 6.284633, GT = 1.000000; gamma distribution shape parameter  $\alpha = 0.214635$ . RAxML bootstrap support  $\geq 50\%$  and Bayesian posterior probabilities  $\geq 0.60$  (BYPP) are indicated above the nodes. The scale bar indicates 0.06 changes per site. New sequences recovered in this study are in bold black.



**Figure 60** – a Basidiocarps of *A. Gymnopus ocior*. b *G. bunerensis*. c *Collybiopsis biformis*. d *Collybiopsis subnuda* in the field. Scale bars: a–d = 50 mm.

Notes – In the phylogenetic tree the *Mucidula* varieties are closely related (Fig. 60). *Mucidula mucidu* var. *asiatica* have lamellae venose-reticulate anastomoses and pileipellis have narrowly clavate cells, while *M. mucidu* var. *venosolamellata* lack anastomoses on the lamellae, with ixotricchoderm pileipellis with slender hyphae and different from *M. mucida* var. *mucida* by pileipellis composed of coralloid terminal cells and smaller basidiospores size ( $13\text{--}22 \times 12\text{--}19.7 \mu\text{m}$ ) (Petersen & Hughes 2010, Ushijima et al. 2012, Vizzini et al. 2012). *Mucidula mucida* specimen from Laos is characteristic with plano-convex pileus, gelatinous surface, and lamellae adnate. Furthermore, distinguished ixotricchoderm to subhymeniderm on the pileipellis. Therefore, those morphologies are fit well with *M. mucidu* var. *venosolamellata* from China and Japan with similar macro-shapes, and micro characteristics. The terminal cells of pileipellis ( $15\text{--}20 \times 5\text{--}7 \mu\text{m}$ ), cheilocystidia ( $15\text{--}20 \times 5\text{--}10 \mu\text{m}$ ) and pleurocystidia ( $40\text{--}60 \times 15\text{--}20 \mu\text{m}$ ) of Laos specimens are smaller than Japanese specimen (terminal cells of pileipellis  $21\text{--}68.5 \times 4\text{--}11 \mu\text{m}$ , cheilocystidia  $106\text{--}$

115 × 17–62, pleurocystidia 103–227 × 20–60 µm) and Chinese specimen (terminal cells of pileipellis 22–40 × 10–15 µm, cheilocystidia 78–140 × 9–20 µm, pleurocystidia 157–200 × 20–40 µm) (Ushijima et al. 2012, Vizzini et al. 2012). These variations in morphology might be a result of different geographical habitat and environmental conditions that can change the phenotype of mushrooms (Hewitt et al. 2016).

**Omphalotaceae** Bresinsky, in Kämmerer, Besl & Bresinsky, Pl. Syst. Evol. 150(1-2): 113 (1985)

For taxonomic treatments of this family, we follow Antonín & Noordeloos (1997), Matheny et al. (2006) and Antonín & Noordeloos (2010).

**Collybiopsis** (J. Schröt.) Earle, Bull. New York Bot. Gard. 5: 415 (1909)

For the taxonomic treatments of this genus, we follow Petersen & Hughes (2021).

**Collybiopsis biformis** (Peck) Halling, in Antonín, Halling & Noordeloos, Mycotaxon 63: 363 (1997)  
Figs 60, 61

Index Fungorum number: IF 437617; Facesoffungi number: FoF 10622

*Basidiocarps* medium-sized. *Pileus* 20–40 mm in diam., convex, umbilicate to slightly depressed disc, dry, with smooth margin, reddish-brown (10R4/4) to dull reddish (10R6/3). *Lamellae* adnate, thin, subdistant to close, whitish-pink (7.5Y9/2); edges even; lamellulae unevenly distributed. *Stipe* 23–33 × 6–9 mm, reddish-brown (5YR4/6), equal, somewhat broad at the base, laterally compressed and longitudinally grooved, straight, covered with white (2.5R9/2) pubescence. *Odour and taste* not observed. *Basidiospores* (3.5–) 3.8–6.8 (–7) × (1.7) 1.8–2.7 (–3) µm, L × W= 5.8 × 2.4 µm, Q = (1.9–) 2–2.8 (–2.9), Qe = 2.4, lacrymoid, inamyloid, smooth. *Basidia* 10–15 × 3–4 µm, clavate, 4-spored. *Pleurocystidia* absent. *Cheilocystidia* 15–30 × 5–8 µm, sub-cylindric contorted to strangulated or variously lobed. *Pileipellis* composed of hyphae, 3–5 µm diam., thick-walled (0.5–0.8 µm), branched, radially oriented outgrowths of 13–16 µm long, cylindrical. *Stipitipellis* hyphae 2–3 µm in diam, thick-walled (0.75–0.9 µm wide), arranged in parallel. *Caulocystidia* contorted to irregularly lobed, 10–20 µm long. *Clamp connections* observed in all tissues.

Habitat – Grows on gravely soil in an Oak forest dominated by *Quercus incana* Royl.

Material examined – Pakistan, Khyber Pakhtunkhwa Province, Swat District, 34°47' N, 72°17' E. 2100 m a.s.l, 14 July 2015, A. Naseer and A. N. Khalid, ASSW28 (LAH35820).

GenBank accession numbers – ITS MK305945.

Notes – *Collybiopsis biformis* is characterized by a reddish-brown, convex, dry, striate pileus with smooth margin; white, thin, subdistant lamellae with adnate attachment; equal, slightly pubescent stipe; lacrymoid and inamyloid spores; sub-cylindric contorted to strangulated or variously lobed cheilocystidia; radially oriented outgrowths on pileus hyphae and contorted to irregularly lobed caulocystidia. Our description agrees quite well with the original description, except in spore size (6.4–8.6 × 3.2–4.4 µm), basidia 19.6–28 × 4.2–5.6 µm, and cheilocystidia 21.6–50.8 µm, which are significantly larger in the original description (Halling 2004). However, the reasons for the micromorphological variations can be well explained after the holotype is re-examined. This collection represents the first report of *C. biformis* for Pakistan.

**Collybiopsis subnuda** (Ellis ex Peck) R.H. Petersen, in Petersen & Hughes, Mycotaxon 136(2): 344 (2021)  
Figs 60, 62

Index Fungorum number: IF 437643; Facesoffungi number: FoF 10624

*Basidiocarps* medium sized. *Pileus* 21–30 mm wide, convex to broadly convex with incurved margin at young stage becoming decurved to uplifted at maturity, dull reddish-brown (5YR5/3,5/4) to dull brown (7.5YR6/3) or reddish-brown (5YR5/6,5/8); surface dry, glabrous. *Lamellae* distant to subdistant, adnexed, entire, whitish (7.5Y9/2) to dull orange (5YR7/3,7/4); lamellulae evenly distributed, small and short. *Stipe* 50–70 × 2–5 mm, central, tapered toward the apex, fibrous, light brown (7.5YR7/4,7/6), to light reddish-brown (7.5YR8/3), whitish pubescence at the base. *Basidiospores* [n/b/p] 30/2/1], (5.0–) 5.8–7.9 (–8.3) × (1.9–) 2–2.76 (–2.8) µm, L × W= 6.7 × 2.3 µm,

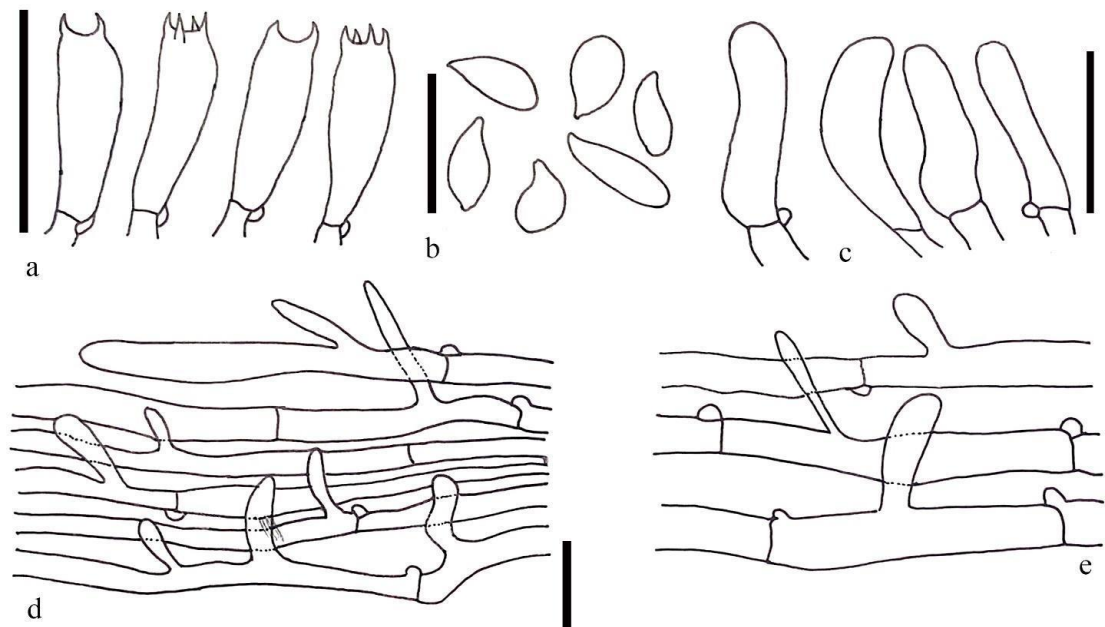
$Q = (2.1-)$  2.5–3.4 (–4),  $Q_e = 2.9$ , lacrymoid to ellipsoid, thin walled, smooth. *Basidia* 21–26 × 4–5  $\mu\text{m}$ , clavate to subclavate, 2–4-spored. *Cheilocystidia* 14–30 × 4.6–8  $\mu\text{m}$ , flexuose, ventricose-fusoid to mucronate, thick-walled. *Pleurocystidia* absent. *Pileipellis hyphae* 4–5  $\mu\text{m}$  wide, cylindrical, septate, branched, thick-walled (0.8–1  $\mu\text{m}$ ) with rare projections. *Stipitipellis hyphae* 5.2–6.5  $\mu\text{m}$  wide, thick-walled (0.7–0.9  $\mu\text{m}$ ). *Clamp-connections* present in all tissues. Odour and taste not observed. KOH on tissues not observed.

Habitat – On litter of both fallen needles and branches of *Pinus roxbergii*.

Material examined – Pakistan, Khyber Pakhtunkhwa Province, District Battagram, 34°33' and 34°47' latitude and 72°55' and 73°14' longitude, at 2040 m a.s.l, 21 July 2017, M. B Khan LAH35879.

GenBank accession numbers – ITS MK307636.

Notes – In the phylogenetic analysis (Fig 59), our isolate from Pakistan clustered together with *Collybiopsis subnuda* strains from South Korea with 83% ML bootstrap and 1.0 BYPP support. Our description agrees well with the original description by Halling (2004) for *Collybiopsis subnuda*. The present collection differs *C. subnuda* type description by basidia size (22.8–35 × 5.6–10.8  $\mu\text{m}$ ), spores (8.6–10.8 (–12) × 3.2–4.4  $\mu\text{m}$ ) and cheilocystidia (29–37.8 (–52.5) × 7.6–8.6  $\mu\text{m}$ ) all of which are significantly larger than our taxon. However, the reasons for the micromorphological variations can be explained after the holotype is re-examined. This collection represents the first record of *C. subnuda* for Pakistan.



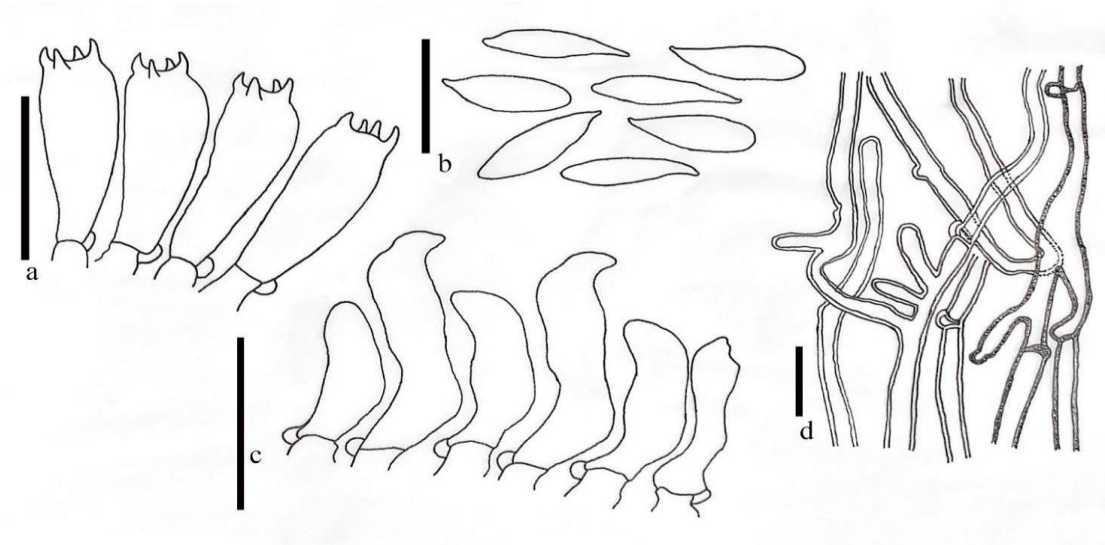
**Figure 61** – *Collybiopsis biformis* (LAH35820, new geographical record). a Basidia. b Basidiospores. c Cheilocystidia. d Pileipellis. e Stipitipellis. Drawings by Muhammad Ishaq. Scale bars: a, c = 20  $\mu\text{m}$ , b, d, e = 10  $\mu\text{m}$ .

### *Gymnopus* (Pers. 1801: 302) Roussel (1806: 62)

*Gymnopus* is a large agaricoid genus with a worldwide distribution. There are 373 published names in the (Index Fungorum 2020). The genus includes delicate to semi-fleshy mushrooms commonly found on leaves and woody litter in tropical and temperate ecosystems (Mata & Ovrebo 2009). Ecologically, *Gymnopus* species are saprotrophic and considered important for the recycling of nutrients (Singer 1986, Mata & Ovrebo 2009). According to Antonín & Noordeloos (1997), the genus originally consisted of four sections viz. *Gymnopus*, *Levipedes*, *Vestipedes*, and *Striipedes*, among which the sect. *Vestipedes* included two subsections: *Impudicae* and *Vestipedes*. Antonín & Noordeloos (2010) raised the subsection. *Impudicae* to the sectional rank and the position of sect.



*Impudicae* within the genus *Gymnopus* was further confirmed (Wilson & Desjardin 2005, Mata et al. 2007, Ryoo et al. 2016).



**Figure 62** – *Collybiopsis subnudus* (LAH35879, new geographical record). a Basidia. b Basidiospores. c Cheilocystidia. d Pileipellis. Drawings by Muhammad Ishaq. Scale bars: a, c = 20  $\mu$ m, b, d = 10  $\mu$ m.

*Gymnopus bunerensis* Ishaq, M, Fiaz, M & Khalid sp. nov.

Figs 60, 63

MycoBank number: MB829211; Facesoffungi number: FoF 10621

Etymology – “*bunerensis*” refers to the holotype locality i.e. Buner District.

Holotype – LAH35878

*Basidiocarps* medium-sized, *Pileus* 20–40 mm in diam., initially campanulate, becoming saucer-shaped at maturity, somewhat depressed at the disk, margin incurved when young, uplifted with maturity, eroded; surface fibrillose, reddish-brown (7.5R4/8) at center, violet-brown (5YR5/4) towards margin, plicate-striate. *Lamellae* 0.5–1 mm broad, adnate, unequal, with entire margin, creamy to pale yellow (10YR8/4); distant to subdistant with unevenly distributed lamellulae. *Stipe* 20–40  $\times$  2–4 mm, central, terete to somewhat equal, minutely pubescent, dark reddish-brown, basal mycelium absent. *Smell* unpleasant.

*Basidiospores* [n/b/p] [60/3/2] (3.6–) 4.3–5.9 (–6.3)  $\times$  (2.4–) 2.7–3.7 (–3.9)  $\mu$ m, L  $\times$  W = 4.9  $\times$  3.1  $\mu$ m, Q = (1.2–) 1.4–1.8 (–2), Q<sub>e</sub> = 1.6, oblong, subcylindrical to ellipsoid, smooth, thin-walled, hyaline in KOH, inamyloid; apiculus small. *Basidia* 11–23  $\times$  5–6  $\mu$ m, narrowly clavate to clavate, thin-walled, hyaline in 5% KOH, inamyloid, 2–4-spored; sterigmata 7–10  $\mu$ m long. *Cheilocystidia* 14–23  $\times$  4–5  $\mu$ m, narrowly fusiform to fusiform, thin-walled, brown in 5% KOH, oil granules present with KOH. *Pileipellis* composed of hyphae, 6–8  $\mu$ m wide, thick-walled (0.5–0.8  $\mu$ m) sometimes with diverticulate outgrowths, radially oriented, branched. *Stipitipellis* hyphae 3–6  $\mu$ m wide, parallelly arranged, thick-walled (0.6–1  $\mu$ m), cylindrical to subcylindrical, branched, sometimes with diverticulate outgrowths. *Caulocystidia* 29–71  $\times$  3–5  $\mu$ m, narrowly clavate to narrowly conical, obtuse, seldom lobed, strangulated or irregular shape, thick-walled (0.7–0.9). *Clamp-connections* present in all the tissues.

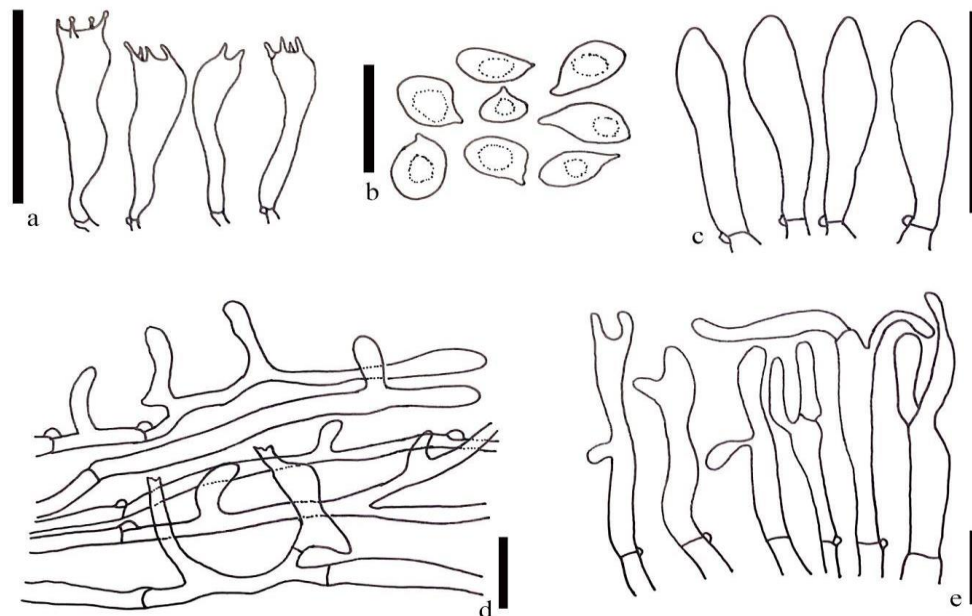
*Habitat* – Frequently grows on decayed materials of leaves and branches of *Pinus roxburghii* Sargent, in coniferous forests.

*Material examined* – Pakistan, Khyber Pakhtunkhwa Province, Malakand Division, Buner District, 34°09'N, 34°–43'N and 72°10'E, 72°47' E, 3183 m a.s.l, on soil under *Pinus roxburghii*, 17 July 2017, Muhammad Ishaq (LAH35878, holotype). Additional specimen (paratype) examined Pakistan, Khyber Pakhtunkhwa Province, Hazara Division, Battagram District, 34°33' and 34°47'

latitude and 72°55' and 73°14' longitude, at 2085 a.s.l., 07 August 2016, Muhammad Binyamin Khan (LAH35877).

GenBank accession numbers – ITS: MK122772; LSU: MK122770.

Notes – *Gymnopus bunerensis* is similar to *G. similis* Antonín, Ryoo, Ka and Tomšovský (2016: 268), but *G. similis* differs by its larger basidiospores ( $6\text{--}9 \times 2.7\text{--}4 \mu\text{m}$ ), and the presence of irregular to rostrate or coralloid cheilocystidia (Ryoo et al. 2016). A phylogenetically close taxon (Fig. 59) *G. variicolor* Antonín, Ryoo, Ka and Tomšovský (2016: 268) is distinct by the striate to striate-sulcate, purplish-brown, dark to reddish-brown pileus and larger stipe ( $30\text{--}80 \times 2.5\text{--}5 \text{ mm}$ ) of violaceous brown to reddish-brown color and basidiospores ( $6\text{--}8.5 \times 3.2\text{--}4.5 \mu\text{m}$ ) compared to *G. bunerensis* (Ryoo et al. 2016). *Gymnopus iocephalus* (Berk. and Curtis) Halling (1997: 364) is distinct from the new species and differs by its purplish-lilac, vinaceous lilac, light pinkish-lilac to pale vinaceous lilac pileus, larger basidiospores ( $6.5\text{--}8.6 \times 3.2\text{--}4.4 \mu\text{m}$ ) and absence of cheilocystidia (Halling 2004). *Gymnopus impudicus* differs from *G. bunerensis* by a combination of characters viz., smaller pileus (10–25 mm diam.), larger basidiospores ( $6.4\text{--}10.9 \times 3.5\text{--}4.8 \mu\text{m}$ ) and larger basidia ( $30.7\text{--}34.5 \times 5.7\text{--}6.2 \mu\text{m}$ ) (Antonín & Noordeloos 1997). Another phylogenetically close taxon *G. talisiae* is morphologically distinct as it has a larger pileus (20–60 mm) with a smooth pale greyish-orange, brownish-orange, light brown to brown surface. Furthermore, it has yellowish-white, orange-white, orange grey to reddish-blond lamellae, as well as a larger stipe ( $30\text{--}70 \times 2\text{--}5 \text{ mm}$ ), basidiospores ( $4\text{--}5\text{--}8 \times 2\text{--}4 \mu\text{m}$ , and basidia  $23\text{--}29 \times 5\text{--}7 \mu\text{m}$  (Coimbra et al. 2015).



**Figure 63** – *Gymnopus bunerensis* (LAH35878, holotype). a Basidia. b Basidiospores. c Cheilocystidia. d Pileipellis. e Caulocystidia. Drawings by Muhammad Ishaq. Scale bars: a, c, d, e = 20  $\mu\text{m}$ , b = 10  $\mu\text{m}$ .

*Gymnopus ocior* (Pers.) Antonín and Noordel. Mycotaxon 63: 365, 1997

Figs 60, 64

Index Fungorum number: IF 437636; Facesoffunginumber: FoF 10623

*Basidiocarps* small to medium. *Pileus* 21–32 mm in diam., parabolic to pulvinate, smooth, dark reddish (10R2/3) at disc, becoming orange-brown (10R3/3) towards the margin, margins smooth, decurved. *Lamellae* adnexed, distant to subdistant, broad, unequal, entire, smooth, orange-brown (10YR7/6). *Lamellulae* present, regular, margins entire. Stipe  $43 \times 3 \text{ mm}$ , equal to clavate at the base, hollow, smooth, yellowish-brown (7/6 10YR) at apex become reddish-brown (10R4/8) towards base. Odour and taste not observed. *Basidiospores* [20/2/1], ( $5.0\text{--}6.2\text{--}7.1\text{--}7.5$ )  $\times$  ( $2.5\text{--}3.5\text{--}3.9\text{--}4.2$ )  $\mu\text{m}$ ,  $L \times W = 6.6 \times 3.6 \mu\text{m}$ ,  $Q = (1.2\text{--}1.7\text{--}2\text{--}2.8)$ ,  $Q_e = 1.9$ , ellipsoid to obovoid, thin-walled,

hyaline with 5% KOH, inamyloid, non-guttulate. *Basidia* 19.9–31.5 × 6.2–9.3 μm, narrowly clavate, thin-walled, 2–4-spored. *Cheilocystidia* 19.8–32 × 4.3–8.9 μm, narrowly clavate, clavate to diverticulate, thin-walled. *Pleurocystidia* absent. *Pileipellis* hyphae 4.3–5.8 μm in diam., thin-walled, septate *Dryophila*-type, branched, hyaline in 5% KOH. *Stipitipellis* hyphae 5.2–6.4 μm in diameter, thin-walled, cylindrical, septate, branched. *Clamp connections* present in all tissues.

Habitat – Grows on fallen dead leaves and branches of *Pinus wallichiana* A. B. Jacks.

Material examined – Pakistan, Province Gilgit-Baltistan, Fairy Meadows, District Diamer, 35° 26' 5.78" N, 73° 56' 31.59" E, at 3300 m a.s.l. near Nanga Parbat, 18 July 2016, Abeera Ali and Abdul Nazir Khalid, LAH24250.

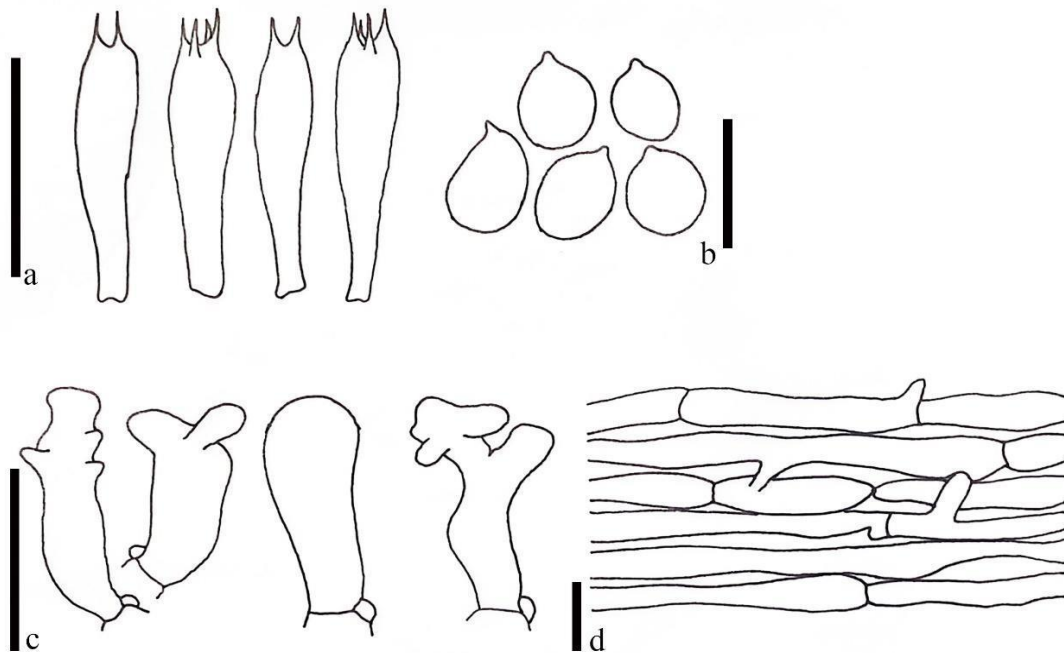
GenBank accession numbers – ITS MK122769.

Notes – The present collection matches well with the original description of *Gymnopus ocior* (Antonín et al. 2013). *Gymnopus ocior* is characterized by its dark red to orange-brown pileus with parabolic to pulvinate centre and distant to subdistant, broad, adnexed orange-brown lamellae. This species has equal to clavate stipe which is yellowish-brown toward the apex and reddish-brown towards the base. Basidiospores are ellipsoid to obovoid, inamyloid. Cheilocystidia are narrowly clavate, clavate to diverticulate. *Dryophila*-like structures are available in the pileipellis. Our collection differs from the original description by smaller size spores (5.0–7.0 × 2.5–4.0) μm, larger cheilocystidia (16–60 × 6–12 μm), and yellowish-white lamellae (Antonín et al. 2013). This is the first record of *G. ocior* from Pakistan.

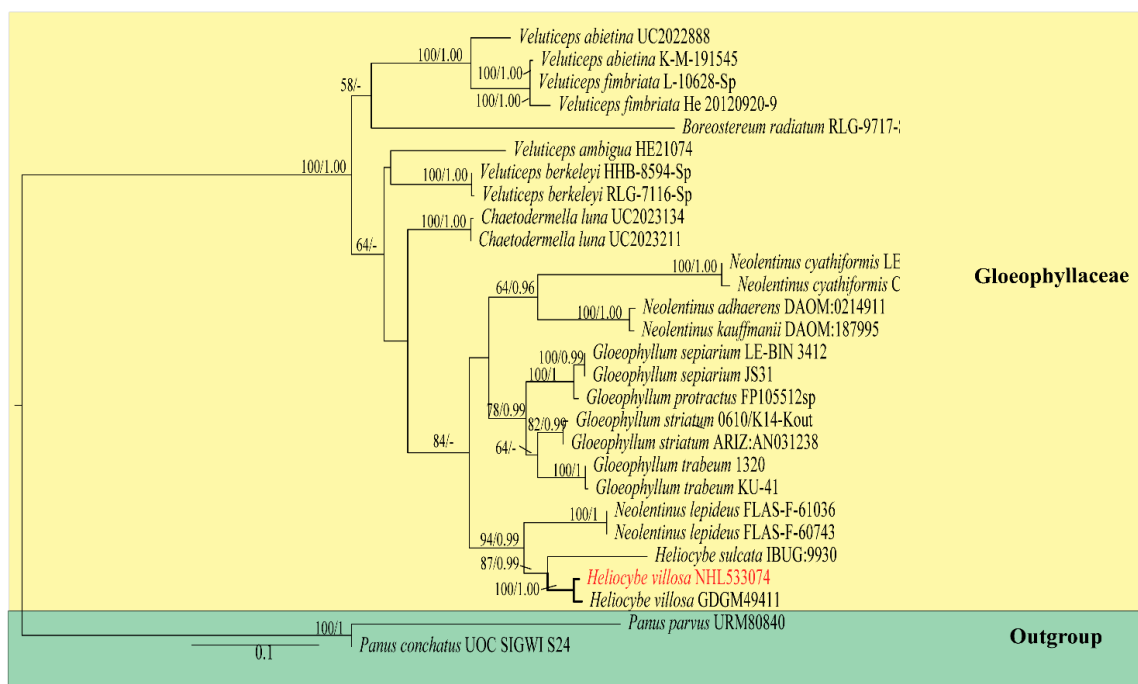
***Gloeophyllaceae*** Jülich, *Bibliotheca Mycol.* 85: 368 (1982) [1981]

***Heliocybe*** Redhead & Ginns, *Trans. Mycol. Soc. Japan* 26(3): 359 (1985)

*Heliocybe* belongs to the *Gloeophyllaceae* Jülich, the genus was established by Redhead & Ginns (1985), and *H. sulcata* is the type species (He et al. 2019). The *Heliocybe* species are brown rot fungi (Saitta et al. 2011, Rune 1994). There are two species in the genus which are *H. sulcata* and *H. villosa*. *Heliocybe sulcata* differs from *H. villosa* by having more robust basidiomata and yellowish-brown scales instead of brownish-orange (Gilbertson et al. 1976, Garcia-Sandoval et al. 2011 and Zhang et al. 2018). In this present study, we introduce a new geographical record from Laos (Fig. 65)



**Figure 64** – *Gymnopus ocior* (LAH 24250, new geographical record). a Basidia. b Basidiospores. c Cheilocystidia. d Pileipellis. Drawings by Muhammad Ishaq. Scale bars: a, c = 20 μm, b, d = 10 μm.



**Figure 65** – Phylogenetic tree generated by ML analysis base on ITS sequence data of *Gloeophyllaceae*. The analyses included 30 strains and the tree is rooted with *Panus parvus* (URM80840) and *Panus conchatus* (UOC SIGWI S24). Tree topology of the ML analysis was similar to the MP and BYPP. The best scoring RAxML tree with a final likelihood value of -3798.997404 is presented. The matrix had 272 distinct alignment patterns, with 2.88% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.228661, C = 0.235234, G = 0.239303, T = 0.296802; substitution rates AC = 0.535465, AG = 1.759859, AT = 0.931225, CG = 0.225490, CT = 3.124545, GT = 1.000000; gamma distribution shape parameter  $\alpha$  = 0.322384. RAxML bootstrap support values  $\geq 50\%$  and nodes with  $\geq 0.95$  (BYPP) Bayesian posterior probabilities are indicated with thickened lines. The scale bar indicates 0.1 change per site. New sequences recovered in this study are red.

*Heliocybe villosa* Ming Zhang & T.H. in Zhang, Li & Song, Phytotaxa 349(2): 174 (2018)

Fig. 66

Index Fungorum number: IF 570533; Facesoffunginumber: FoF 10365

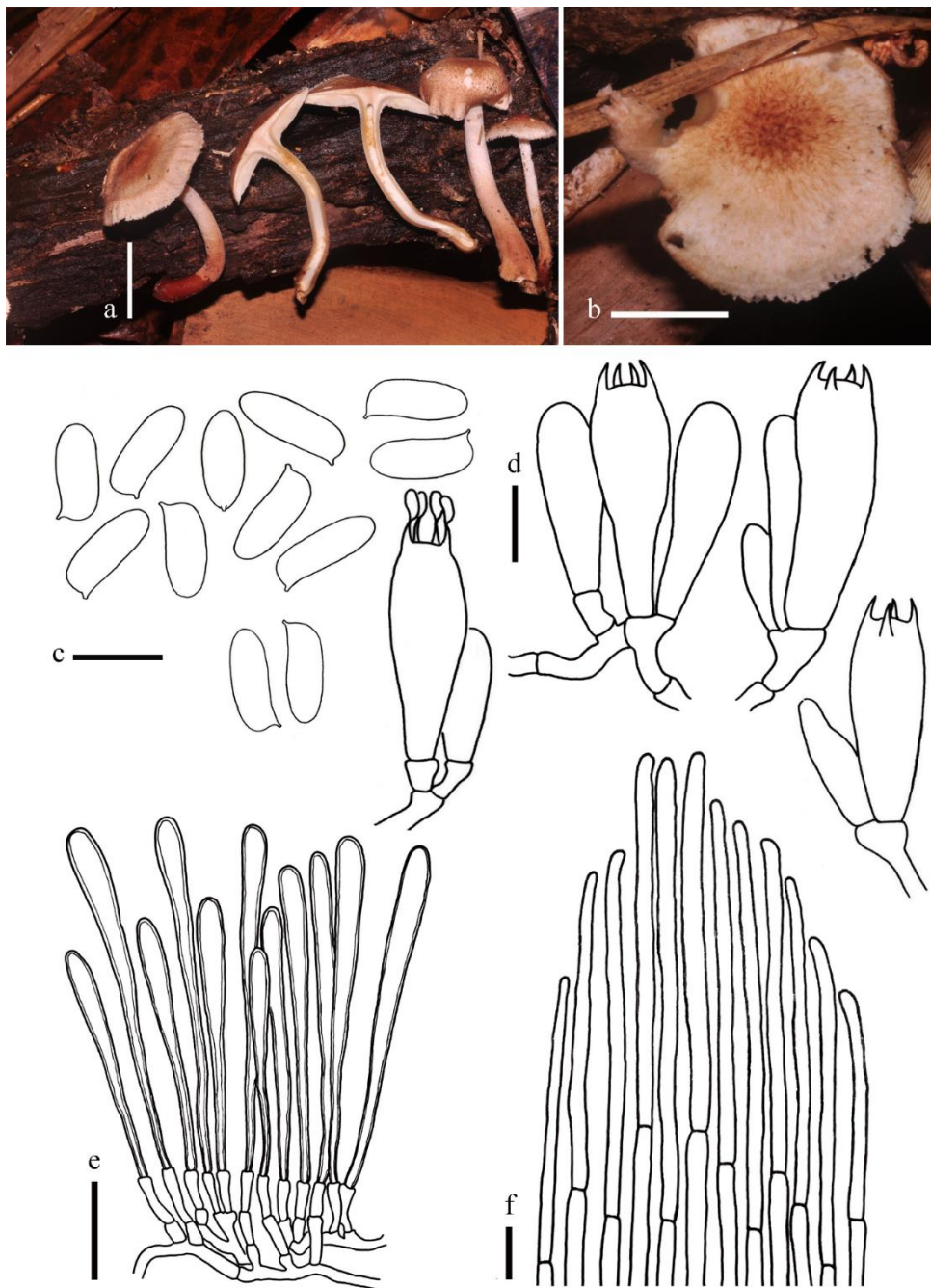
*Pileus* 30–50 mm diam., hemispherical to campanulate when young, expanding to sub-umbonate to umbonate, with slightly appanate when mature, with straight margin; covered by fibrillose to fibrillose squamules, crowded at center, when young, brownish-orange to light brown (7C6, 7D7), with brown to light brown (7D7, 7E7) when mature, darker at center or umbo, on white to reddish-white (7A2) background; margin with concolorous fibrillose. *Lamellae* adnate to subdecurrent, crowded, broad, 2–3 mm wide, with more than 5 lamellulae series, white to cream (3A1) when young, becoming brownish-yellow (5C8) to light brown (6D8) when mature. *Stipe* 30–80 × 2–4 mm, equal or less sub-bulbous to more swollen base, covered with crowded soft hairs, brown to light brown (7D7, 7E7) from base towards center, paler from center to apex, on white to light brown (7D7) background. *Annulus* absent. *Context* 5–7 mm thick in pileus white to cream; white and hollow in stipe, concolorous with surface. Taste and odor not observed. Spores print white. *Basidiospores* (5.7–)5.7–7.3(–9.1) × (2.2–)2.4–3.3–4.4)  $\mu\text{m}$ , Q = 1.5–2.87, ellipsoid to oblong ovoid in sideview oblong in frontal view, smooth, hyaline and thin-walled. *Basidia* 9.2–15.3 × 3.4–4.6  $\mu\text{m}$ , clavate to narrowly clavate, hyaline, thin-walled, sterigmata 2–3  $\mu\text{m}$  long, 4-spored, sometimes 2-spored. *Pleurocystidia* absent. *Cheilocystidia* 47.8–108.3 × 2.7–8.3  $\mu\text{m}$ , cylindrical to narrowly clavate, brown, thick-walled, septate and branched at base. *Pileipellis* a trichoderm made up of cylindrical elements, pale brown to dark brown pigment, 5  $\mu\text{m}$  wide, up to 250  $\mu\text{m}$  long. *Stipitipellis*

a cutis composed of hyaline to yellow-brown hyphae and cylindrical elements, 3–5  $\mu\text{m}$  wide. *Clamp-connections* absent.

Material examined – Laos, Vientiane Capital, Xaythany District, Houay Yang Forest Reserve, 15 September 2015, Phongsouphanthong (HNL503374); *ibidem*, 21 October 2015, Phongsouphanthong (HNL503410).

GenBank accession numbers – ITS: OK067323.

Notes – *Heliocybe villosa* was described from China, and it is recognized to have brownish-orange, fibrillose, pileus covering (Zhang & Song 2018). Two specimens of *H. villosa* from Laos are similar to the type species from China. However, the Laos specimens have distinct long narrowly clavate cheilocystidia, but cheilocystidia were not observed in the type specimens. Furthermore, the molecular analysis based on available data of ITS sequences supported the Laos specimens as being similar to the type specimens. This is the first record from Central Laos.



**Figure 66** – a, b Fresh basidiomata of *Heliocybe villosa* in the field (a = HNL503374. b = HNL503410, new geographical record). Micromorphology features c Basidiospores. d Basidia.

e Cheilocystidia. f Trichodermal pileipellis. Scale bar: a–b = 50  $\mu$ m, c–d = 10  $\mu$ m, e = 10  $\mu$ m, f = 20  $\mu$ m.

## Acknowledgements

Kevin D. Hyde would like to thank Thailand Science Research and Innovation (TSRI) grant “Macrofungi diversity research from the Lancang-Mekong Watershed and Surrounding areas” (Grant no. DBG6280009) and Chiang Mai University for the award of Visiting Professor. The project was also funded by the High-level Talents in Zhongkai University of Agriculture and Engineering (Grant no. J2201080102) for sequencing. Napalai Chaiwan would like to thank the Thailand Research Fund (No. PHD60K0147) and T.S Bulgakov for collecting the specimen. Saowaluck Tibpromma would like to thank the International Postdoctoral Exchange Fellowship Program (No. Y9180822S1), CAS President’s International Fellowship Initiative (PIFI) (No. 2020PC0009), China Postdoctoral Science Foundation and the Yunnan Human Resources, and Social Security Department Foundation for funding her postdoctoral research. Samantha C. Kaunaratna thanks the CAS President’s International Fellowship Initiative (PIFI) for funding his postdoctoral research (No. 2018PC0006) and the National Science Foundation of China (NSFC) for funding this work under the project code 31851110759. Yusufjon Gafforov thanks Ministry of Innovative Development of the Republic of Uzbekistan (Projects nos. P3-20170921183 and A-FA-2021-144) and State scientific and technical program of Uzbekistan. Mark S. Calabon is grateful to Department of Science and Technology - Science Education Institute (DOST-SEI) Philippines and Mushroom Research Foundation. Muhammad Ishaq thanks Muhammad Binyamin Khan, ARooj Naseer and Abeera Ali for providing specimens for the study. Ishara S. Manawasinghe would like to thank Dr Shaun Pennycook, Nomenclature Editor, Mycotaxon, for his guidance on the species names.

## References

- Abdel-Wahab MA, Jones EBG. 2000 – Three new marine ascomycetes from driftwood in Australian sand dunes. *Mycoscience* 41, 379–388.
- Antonín V, Noordeloos ME. 1997 – A monograph of *Marasmius*, *Collybia* and related genera in Europe. Part 2: *Collybia*, *Gymnopus*, *Rhodocollybia*, *Crinipellis*, *Chaetocalathus*, and additions to *Marasmiellus*. *Libri Botanici* 17,1–256.
- Antonín V, Noordeloos ME. 2010 – A monograph of marasmioid and collybioid fungi in Europe. IHW Verlag, Eching, 478 pp.
- Antonín V, Sedláč P, Tomšovský M. 2013 – Taxonomy and phylogeny of European *Gymnopus* subsection *Levipedes* (Basidiomycota, *Omphalotaceae*). *Persoonia* 31, 179–187.
- Ariyawansa HA, Hyde KD, Jayasiri SC, Buyck B et al. 2015 – Fungal diversity notes 111–252 taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 75, 27–274.
- Ariyawansa HA, Phookamsak R, Tibpromma S, Kang JC et al. 2014 – A molecular and morphological reassessment of *Diademaceae*. *The Scientific World Journal*. 675348, 1–11.
- Ariyawansa HA, Tanaka K, Thambugala KM, Phookamsak R et al. 2014 – A molecular phylogenetic reappraisal of the *Didymosphaeriaceae* (= *Montagnulaceae*). *Fungal Diversity* 68, 69–104.
- Ariyawansa HA, Thambugala KM, Manamgoda DS, Jayawardena R et al. 2015 – Towards a natural classification and backbone tree for *Pleosporaceae*. *Fungal Diversity* 71, 85–139.
- Asgari B, Zare R, Gams W. 2007 – *Coniochaeta ershadii*, a new species from Iran, and a key to well-documented *Coniochaeta* species. *Nova Hedwigia* 84, 175–187.
- Bakhshi M, Arzanlou M, Groenewald JZ, Quaedvlieg W et al. 2019 – *Parastagonosporella fallopiae* gen. et sp. nov. (*Phaeosphaeriaceae*) on *Fallopia convolvulus* from Iran. *Mycological Progress*. 18, 203–214.
- Bao DF, Su HY, Maharachchikumbura SSN, Liu JK et al. 2019 – Lignicolous freshwater fungi from China and Thailand: Multi-gene phylogeny reveals new species and new records in *Lophiostomataceae*. *Mycosphere* 10, 1080–1099.

- Barbosa FR, Da 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, Raja HA, Shearer CA, Gusmão LFP. 2013 – Some freshwater fungi from the Brazilian semi-arid region, including two new species of hyphomycetes. Cryptogam Mycol 34, 243–258.
- Bhunjun CS, Niskanen T, Suwannarach N, Wannathes N et al. 2022 – The numbers of fungi: are the most speciose genera truly diverse? Fungal Diversity. Doi 10.1007/s13225-022-00501-4
- Bhunjun CS, Jayawardena RS, Wei DP, Huanraluek N et al. 2019 – Multigene phylogenetic characterisation of *Colletotrichum artocarpicola* sp. nov. from *Artocarpus heterophyllus* in northern Thailand. Phytotaxa 418, 273–286.
- Brahmanage RS, Dayarathne MC, Wanasinghe DN, Thambugala KM et al. 2020 – Taxonomic novelties of saprobic Pleosporales from selected dicotyledons and grasses. Mycosphere 11, 2481–541.
- Brockmann I. 1976 – Untersuchungen über die Gattung *Discostroma clements* (Ascomycetes) Sydowia 28, 275–338.
- Barr ME. 1979 – A classification of Loculoascomycetes. Mycologia, 71, 935–957.
- Boehm EW, Mugambi GK, Miller AN, Huhndorf SM et al. 2009 – A molecular phylogenetic reappraisal of the *Hysteriaceae*, *Mytilinidiaceae* and *Gloniaceae* (Pleosporomycetidae, Dothideomycetes) with keys to world species. Studies in Mycology 64, 49–83.
- Boonmee S, Phookamsak R, Hongsanan S, Doilom M et al. 2017 – Mycosphere notes 51–101. Revision of genera in *Perisporiopsidaceae* and *Pseudoperisporiaceae* and other Ascomycota genera incertae sedis. Mycosphere 8, 1695–1801.
- Boonmee S, Wanasinghe DN, Calabon MS, Huanraluek N et al. 2021 – Fungal diversity notes 1387–1511: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 111, 1–335.
- Calabon MS, Hyde KD, Jones EBG, Luo ZL et al. 2022 – Freshwater fungal numbers. Fungal Diversity (In press).
- Cao B, Haelewaters D, Schoutteten N, Begerow D et al. 2021 – Delimiting species in Basidiomycota: a review. Fungal Diversity 109, 181–237.
- Cesati V, De Notaris G. 1863 – Schema di classificazione degli sferiacei italici aschigeri: più o meno appartenenti al genere *Sphaerianell* l'antico significato attribuitogli da Persoo. Commentario della Società Crittogamologica Italiana 1: 205.
- Chaiwan N, Gomdola D, Wang S, Monkai J et al. 2021 – <https://gmsmicrofungi.org>: an online database providing updated information of microfungi in the Greater Mekong Subregion. Mycosphere 12, 1513–1526.
- Cheek M, Nic Lughadha E, Kirk P, Lindon H et al. 2020 – New scientific discoveries: Plants and fungi. Plants, People, Planet, 2, 371–388.
- Chethana KWT, Li XH, Zhang W, Hyde KD et al. 2016 – Trail of decryption of molecular research on *Botryosphaeriaceae* in woody plants. Phytopathologia Mediterranea 55, 147–171.
- Chethana KWT, Manawasinghe IS, Hurdeal VG, Bhunjun CS et al. 2021 – What are fungal species and how to delineate them?. Fungal Diversity 109, 1–25.
- Chevallier FF. 1826 – Flore Générale des Environs de Paris [General Flora of the Area Around Paris]. Ferra Jeune, France, 1–674.
- Chunyu J, Yong W, Shiping W, Yulan J. 2013 – Morphological characteristics and molecular phylogeny analysis of newly recorded fungal species *Phialocephala humicola* in China. Guizhou Agricultural Science 41, 86–89.
- Clements FE, Shear CL. 1931 – The Genera of Fungi. HW Wilson Co. Publ., Minneapolis, MN, U.S.A.
- Clements FE. 1909 – The Genera of Fungi. H. W. Wilson Co., Minneapolis, MN.
- Corda A. 1842 – Icones fungorum hucusque cognitorum. 5, 1–92.
- Corda ACJ. 1839 – Corda Icones fungorum hucusque cognitorum 3, 1–55.
- Crane JL, Miller AN. 2016 – Studies in genera similar to *Torula*: *Bahusaganda*, *Bahusandhika*, *Pseudotorula*, and *Simmonsella* gen. nov. IMA Fungus 7, 29–45.

- Crous PW, Carris LM, Giraldo A, Groenewald JZ et al. 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, 163–198.
- Crous PW, Cowan DA, Maggs-Kölling G, Yilmaz N et al. 2021 – Fungal planet description sheets: 1182–1283. Persoonia: Molecular Phylogeny and Evolution of Fungi 46, 313–528.
- Crous PW, Shivas RG, Quaedvlieg W, van der Bank M et al. 2014a – Fungal Planet Description Sheets: 214–280. Persoonia 32, 184–306.
- Crous PW, Slippers B, Wingfield MJ, Rheeder J et al. 2006 Phylogenetic lineages in the *Botryosphaeriaceae*. Studies in Mycology 55, 235–253.
- Crous PW, Wingfield MJ, Le Roux JJ, Richardson DM et al. 2015b – Fungal planet description sheets: 371–399. Persoonia. 35, 264–327.
- 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.
- Day MJ, Hall JC, Currah RS. 2012 – Phialide arrangement and character evolution in the helotiale anamorph genera *Cadophora* and *Phialocephala*. Mycologia 104, 371–381.
- Dayarathne MC, Jones EBG, Maharachchikumbura SSN, Devadatha B et al. 2020 – Morpho-molecular characterization of microfungi associated with marine based habitats. Mycosphere, 11, 1–188.
- Dayarathne MC, Maharachchikumbura SSN, Jones EBG, Dong W et al. 2019 – Phylogenetic revision of *Savoryellaceae* and evidence for its ranking as a subclass. Frontiers in Microbiology 10. Doi 10.3389/fmicb.2019.00840
- Dayarathne MC, Phookamsak R, Hyde KD, Manawasinghe IS et al. 2016a – *Halodiatrype*, a novel diatrypaceous genus from mangroves with *H. salinicola* and *H. avicenniae* spp. nov. Mycosphere 7, 612–627.
- Dayarathne MC, Wanasinghe DN, Devadatha B, Abeywickrama et al. 2020b – Modern taxonomic approaches to identifying diatrypaceous fungi from marine habitats, with a novel genus *Halocryptovalsa* Dayarathne & K.D. Hyde, gen. nov. Cryptogamy. Mycology 41, 21–67.
- Devadatha B, Sarma V, Wanasinghe D, Hyde KD et al. 2017– Introducing the new Indian mangrove species, *Vaginatispora microarmatispora* (*Lophiostomataceae*) based on morphology and multigene phylogenetic analysis. Phytotaxa 329, 139–149.
- Dissanayake AJ, Bhunjun CS, Maharachchikumbura SSN, Liu JK. 2020 – Applied aspects of methods to infer phylogenetic relationships amongst fungi. Mycosphere 11, 2652–2676.
- Doilom M, Hyde KD, Phookamsak R, Dai DQ et al. 2018 – Mycosphere Notes 225–274: types and other specimens of some genera of Ascomycota. Mycosphere 9, 647–754.
- Ellis MB. 1976 – More Dematiaceous Hyphomycetes. Commonwealth Mycological Institute, Kew.
- Farr DF, Rossman AY. 2021 – Fungal Databases, U.S. National Fungus Collections, ARS, USDA., from <https://nt.ars-grin.gov/fungaldatabases/> (Retrieved on October 30, 2021).
- Fiuza PO, Silva CR, Santos TAB, Raja H et al. 2018 – *Roselymyces*, a new asexual genus of the Xylariales (Ascomycota) from Brazil. Sydowia 70, 59–65.
- García D, Stchigel AM, Cano J, Caldusch M et al. 2006 – Molecular phylogeny of *Coniochaetales*. Mycological Research 110, 1271–1289.
- Garcia-Sandoval R, Wang Z, Binder M, Hibbett DS. 2011 – Molecular phylogenetics of the *Gloeophyllales* and relative ages of clades of Agaricomycotina producing a brown rot. Mycologia 103, 510–524.
- Ge ZW, Yang ZL, Qasim T, Nawaz R et al. 2015b – Four new species in *Leucoagaricus* (*Agaricaceae*, Basidiomycota) from Asia. Mycologia 107, 1033–1044.
- Ge ZW, Yang ZL, Qasim T, Nawaz R et al. 2015 – Four new species in *Leucoagaricus* (*Agaricaceae*, Basidiomycota) from Asia. Mycologia 107, 1033–1044.
- Gilbertson RL, Burdsall Jr HH, Canfield ER. 1976 – Fungi that decay mesquite in southern Arizona. Mycotaxon 3, 487–551.



- Glawe A, Jacobs KA. 1987 – Taxonomic notes on *Eutypella vitis*, *Cryptosphaeria populina*, and *Diatrype stigma*. *Mycologia* 79, 135–139.
- Goh J, Mun HY, Jeon YJ, Chung N et al. 2020 – First report of six Sordariomycetes fungi isolated from plant litter in freshwater ecosystems of Korea. *Korean Journal of Mycology* 48, 103–116.
- Grünig CR, Sieber TN, Rogers SO, Holdenrieder O. 2002 – Genetic variability among strains of *Phialocephala fortinii* and phylogenetic analysis of the genus *Phialocephala* based on rDNA its sequence comparisons. *Canadian Journal of Botany* 80, 1239–1249.
- Hashimoto A, Hirayama K, Takahashi H, Matsumura M et al. 2018 – Resolving the *Lophiostoma bipolare* complex: Generic delimitations within *Lophiostomataceae*. *Studies in Mycology* 90, 161–189.
- He MQ, Zhao RL, Hyde KD, Begerow D et al. 2019 – Notes, outline and divergence times of Basidiomycota. *Fungal Diversity* 99, 105–367.
- Hewitt SK, Foster DS, Dyer PS, Avery SV. 2016 – Phenotypic heterogeneity in fungi: importance and methodology. *Fungal Biology Reviews* 30, 176–184.
- Hinkle AE. 2007 – Population structure of Pacific *Cordyline fruticosa* (Laxmanniaceae) with implications for human settlement of *Polynesia*. *American Journal of Botany* 94, 828–839.
- Ho WH, Hyde KD, Hodgkiss IJ. 1997 – Ascomycetes from tropical freshwater habitats: The genus *Savoryella*, with two new species. *Mycological Research* 101, 803–809.
- Holm L, Holm K. 1988 – Studies in the *Lophiostmataceae* with emphasis on the Swedish species. *Symbolae Botanicae Upsalienses* 28, 1–50.
- Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN et al. 2020a – Refined families of Dothideomycetes: Orders and families incertae sedis in Dothideomycetes. *Fungal Diversity* 24, 1–302.
- Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN et al. 2020b – Refined families of Dothideomycetes: Dothideomycetidae and Pleosporomycetidae. *Mycosphere* 11, 1553–2107.
- Huang R, Xu Y, Ye B, Ding W et al. 2019 – Letenketals A and B, two novel spirocyclic polyketides from a marine crab-derived *Letendraea* sp. fungus. *Phytochemistry Letters* 30, 165–168.
- Hughes SJ. 1958 – Revisiones hyphomycetum aliquot cum appendice de nominibus rejiciendis. *Canadian Journal of Botany* 36, 727–836.
- Huhndorf SM, Miller AN, Fernández FA. 2004 – Molecular systematics of the Sordariales: the order and the family *Lasiosphaeriaceae* redefined. *Mycologia* 96, 368–387.
- Hussain S, Jabeen S, Khalid AN, Ahmad H et al. 2018 – Underexplored regions of Pakistan yield five new species of *Leucoagaricus*. *Mycologia* 110, 387–400.
- Hyde KD. 1992 – Intertidal mangrove fungi from the west coast of Mexico, including one new genus and two new species. *Mycological Research* 96, 25–30.
- Hyde KD. 1995 – Tropical Australasian fungi. IX. *Vaginatispora aquatica* gen. et sp. nov. *Nova Hedwia* 61, 233–241.
- Hyde KD, Chaiwan N, Norphanphoun C, Boonmee S et al. 2018 – *Mycosphere* notes 169–224. *Mycosphere* 9, 271–430.
- Hyde KD, de Silva NI, Jeewon R, Bhat JD et al. 2020a – AJOM new records and collections of fungi: 1–100. *Asian Journal of Mycology* 3: 22–294.
- Hyde KD, Dong Y, Phookamsak R, Jeewon R et al. 2020b – Fungal diversity notes 1151–1276: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 100, 5–277.
- Hyde KD, Goh TK, Lu BS, Alias SA. 1999 – Eleven new intertidal fungi from *Nypa fruticans*. *Mycological Research* 103, 1409–1422.
- Hyde KD, Jeewon R, Chen YJ, Bhunjun CS et al. 2020c – The numbers of fungi: is the descriptive curve flattening? *Fungal Diversity* 103, 219–271.
- Hyde KD, Hongsanan S, Jeewon R, Bhat DJ et al. 2016 – Fungal diversity notes 367–490: taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 80, 1–270.
- Hyde KD, Jones EBG, Liu JK, Ariyawansa H et al. 2013 – Families of Dothideomycetes. *Fungal Diversity* 63, 1–313.

- Hyde KD, Nilsson RH, Alias SA, Ariyawansa HA et al. 2014 – One stop shop: backbone trees for important phytopathogenic genera: I Fungal Diversity 67, 21–125.
- Hyde KD, Norphanphoun C, Abreu VP, Bazzicalupo A et al. 2017 – Fungal diversity notes 603–708: taxonomic and phylogenetic notes on genera and species. Fungal Diversity 87, 1–235.
- Hyde KD, Norphanphoun C, Maharachchikumbura SSN, Bhat DJ et al. 2020d – Refined families of Sordariomycetes. Mycosphere 11, 305–1059.
- Hyde KD, Tennakoon DS, Jeewon R, Bhat DJ et al. 2019 – Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 96, 1–242.
- Index Fungorum. 2021 – <http://www.indexfungorum.org/Names/Names.asp> (Accessed on October 30, 2021).
- Jacobs A, Coetzee MPA, Wingfield BD, Jacobs K et al. 2003 – Phylogenetic relationships among *Phialocephala* species and other ascomycetes. Mycologia 95, 637–645.
- Jacobs K, Wingfield MJ, Jacobs A, Wingfield BD. 2001 – A taxonomic re-evaluation of *Phialocephala phycomyces*. Canadian Journal of Botany 79, 110–117.
- Jaklitsch W. 2015 – Nomenclatural novelties. Index Fungorum 209, 1–1.
- Jaklitsch WM, Gardiennet A, Voglmayr H. 2016 – Resolution of morphology-based taxonomic delusions: *Acrocordiella*, *Basiseptospora*, *Blogiascospora*, *Clypeosphaeria*, *Hymenopleella*, *Lepteutypa*, *Pseudapiospora*, *Requienella*, *Seiridium* and *Strickeria*. Persoonia 37, 82–105.
- Jang S, Jang Y, Lim YW, Kim et al. 2016 – Phylogenetic identification of Korean *Gymnopus* spp. and the first report of 3 Species: *G. iocephalus*, *G. polygrammus*, and *G. subnudus*. Mycobiology 44, 131–136.
- Jayasiri SC, Hyde KD, Jones EBG, McKenzie EHC et al. 2019 – Diversity, morphology and molecular phylogeny of Dothideomycetes on decaying wild seed pods and fruits. Mycosphere 10, 1–186.
- Jayasiri SC, Hyde KD, Jones EBG, Peršoh D et al. 2018 – Taxonomic novelties of hysteriform Dothideomycetes. Mycosphere 9, 803–837.
- Jayawardena RS, Bhunjun CS, Hyde KD, Gentekaki E et al. 2021 – *Colletotrichum*: lifestyles, biology, morpho-species, species complexes and accepted species. Mycosphere 12, 519–669.
- Jayawardena RS, Hyde KD, Chethana KWT, Daranagama DA et al. 2018 – Mycosphere Notes 102–168: Saprotrophic fungi on *Vitis* in China, Italy, Russia and Thailand. Mycosphere 9, 1–114.
- Jayawardena RS, Hyde KD, de Farias ARG, Bhunjun CS et al. 2021 – What is a species in fungal plant pathogens?. Fungal Diversity 109, 239–266.
- Jeewon R, Hyde KD. 2016 – Establishing species boundaries and new taxa among fungi: recommendations to resolve taxonomic ambiguities. Mycosphere 7, 1669–1677.
- Jones EBG, Eaton RA. 1969 – *Savoryella lignicola* gen. et sp.nov. from water-cooling towers. Transactions of the British Mycological Society 52, 161–IN14.
- Jones EBG, Hyde KD. 1992 – Taxonomic studies on *Savoryella* Jones et Eaton (Ascomycotina). Bot Mar 35, 83–92.
- Jones EBG, Pang KL, Abdel-Wahab MA, Scholz B et al. 2019 – An online resource for marine fungi. Fungal Diversity 96, 347–433.
- Jong SC, Davis EE. 1972 – *Phialocephala humicola*, a new hyphomycete. Mycologia 64, 1351–1356.
- Karlsen-Ayala E, Gazis R, Smith ME. 2021 – *Asperosporus subterraneus*, a new genus and species of sequestrate *Agaricaceae* found in Florida nursery production. Fungal Systematics and Evolution 8, 91–100.
- Kiyuna T, An KD, Kigawa R, Sano C et al. 2012 – Bristle-like fungal colonizers on the stone walls of the Kitora and Takamatsuzuka Tumuli are identified as *Kendrickiella phycomyces*. Mycoscience 53, 446–459.
- Kirk PM, Cannon P, Minter D, Stalpers J. 2008 – Ainsworth & Bisby's dictionary of the fungi, 10th edn. CAB International, Wallingford, UK.

- Kirk PM, Cannon PF, Minter DW, Stalpers JA. 2008 – Ainsworth & Bisby's dictionary of the fungi, 10th edn. CABI, Wallingford.
- Koch J. 1982 – Some lignicolous marine fungi from Sri Lanka. *Nordic Journal of Botany* 2, 163–169.
- Kumar TKA, Manimohan P. 2009 – The genera *Leucoagaricus* and *Leucocoprinus* (Agaricales, Basidiomycota) in Kerala State, India. *Mycotaxon* 108, 385–428.
- Kuntze O. 1891 – *Revisio generum plantarum* 3, 375–1011.
- Li JF, Phookamsak R, Jeewon R, Bhat DJ et al. 2017 – Molecular taxonomy and morphological characterization reveal new species and new host records of *Torula* species (*Torulaceae*, Pleosporales). *Mycological Progress* 16, 447–461.
- Liang JF, Yang ZL, Xu JP, Ge ZW. 2010 – Two new unusual *Leucoagaricus* species (*Agaricaceae*) from tropical China with blue-green staining reactions. *Mycologia* 102, 1141–1152.
- Liew ECY, Aptroot A, Hyde KD. 2002 – An evaluation of the monophyly of *Massarina* based on ribosomal DNA sequences. *Mycologia* 94, 803–813.
- Liu F, Groenewald BJZ, Cai L, Crous PW. 2019 – *Sporocadaceae*, a family of coelomycetous fungi with appendage-bearing conidia. *Studies in Mycology* 92, 287–415.
- Liu JK, Hyde KD, Jones EBG, Ariyawansa HA et al. 2015 – Fungal diversity notes 1–110: taxonomic and phylogenetic contributions to fungal species. *Fungal Diversity* 72, 1–197.
- Lombard L, Houbraken J, Decock C, Samson RA et al. 2016 – Generic hyper-diversity in *Stachybotriaceae*. *Persoonia* 36, 156–246.
- 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 and Earth Sciences* 1, 1–64.
- Luo ZL, Hyde KD, Liu JK, Maharachchikumbura SSN et al. 2019 – Freshwater Sordariomycetes. *Fungal Diversity* 99, 451–660.
- Maggi O, Persiani AM. 1984 – *Codinaea coffeae* and *Phialocephala xalapensis*, two new hyphomycetes from Mexico. *Mycotaxon* 20, 251–258.
- Maharachchikumbura SN, Hyde KD, Jones EBG, McKenzie EHC et al. 2016 – Families of Sordariomycetes. *Fungal Diversity* 79, 1–317.
- Maharachchikumbura SS, Ariyawansa HA, Wanasinghe DN, Dayarathne MC et al. 2019 – Phylogenetic classification and generic delineation of *Hydeomyces desertipleosporoides* gen. et sp. nov. (*Phaeosphaeriaceae*) from Jebel Akhdar Mountain in Oman. *Phytotaxa* 391, 28–38.
- Maharachchikumbura SSN, Chen Y, Ariyawansa HA, Hyde KD et al. 2021 – Integrative approaches for species delimitation in Ascomycota. *Fungal Diversity* 109, 155–179.
- Maharachchikumbura SSN, Hyde KD, Jones EBG, McKenzie EHC. 2015 – Towards a natural classification and backbone tree for Sordariomycetes. *Fungal Diversity* 72, 199–301.
- Malloch D, Cain RF. 1971 – New cleistothecial *Sordariaceae* and a new family *Coniochaetaceae*. *Canadian Journal of Botany* 49, 869–880.
- Manamgoda DS, Udayanga D, Cai L, Chukeatirote E et al. 2013 – Endophytic *Colletotrichum* from tropical grasses with a new species *C. endophytica*. *Fungal Diversity* 61, 107–115.
- Manawasinghe IS, Phillips AJL, Hyde KD, Chethana KWT et al. 2016 – Mycosphere Essays 14: Assessing the aggressiveness of plant pathogenic *Botryosphaeriaceae*. *Mycosphere* 7, 883–892.
- Manawasinghe IS, Phillips AJL, Xu J, Balasuriya A et al. 2021 – Defining a species in fungal plant pathology: beyond the species level. *Fungal Diversity* 109, 267–282.
- Mapook A, Hyde KD, McKenzie EH, Jones EBG et al. 2020 – Taxonomic and phylogenetic contributions to fungi associated with the invasive weed *Chromolaena odorata* (Siam weed). *Fungal Diversity* 101, 1–175.
- Mata JL, Halling RE, Petersen RH. 2004 – New species and mating system reports in *Gymnopus* (Agaricales) from Costa Rica. *Fungal Diversity* 16, 113–129.
- Mata JL, Hughes KW, Petersen RH. 2007 – An investigation of *Omphalotaceae* (Fungi: *Euagarics*) with emphasis of the genus *Gymnopus*. *Sydowia* 58, 191–289.

- Mata JL, Ovrebo CL. 2009 – New reports and illustrations of *Gymnopus* for Costa Rica and Panama. *Fungal Diversity* 38, 125–131.
- Matsushima T. 1975 – *Icones Microfungorum A Matsushima Lectorum*. Published by the author, Kobe.
- Matsushima T. 1980 – *Matsushima Mycological Memoirs No. 1: Saprophytic Microfungi from Taiwan*. Published by the author, Kobe.
- Matsushima T. 1989 – *Matsushima Mycological Memoirs No. 6*. Published by the author, Kobe.
- Matheny PB, Curtis JM, Hofstetter V, Aime MC et al. 2006 – Major clades of Agaricales: a multilocus phylogenetic overview. *Mycologia* 98, 982–95.
- Mehrabi M, Asgari B, Hemmati R. 2019 – Two new species of *Eutypella* and a new combination in the genus *Peroneutypa* (*Diatrypaceae*). *Mycological Progress* 18, 1057–1069.
- Minoura K, Muroi T. 1978 – Some freshwater ascomycetes from Japan. *Transactions of the Mycological Society of Japan* 19, 129–134.
- Monteiro JS, Castañeda-Ruiz RF, Gusmão LFP. 2016 – *Thozetella coronata* and *T. ypsiloidea* spp. nov. from the Brazilian Amazon forest. *Mycotaxon* 131, 605–611.
- Moyo P, Damm U, Mostert L, Halleen F. 2018a – *Eutypa*, *Eutypella*, and *Cryptovalsa* species (*Diatrypaceae*) associated with *Prunus* species in South Africa. *Plant Disease* 102, 1402–1409.
- Moyo P, Mostert L, Spies CFJ, Damm U, Halleen F. 2018b – Diversity of *Diatrypaceae* species associated with dieback of grapevines in South Africa, with the description of *Eutypa cremea* sp. nov. *Plant Disease* 102, 220–230.
- Munk A. 1953 – The system of the pyrenomycetes. A contribution to a natural classification of the group Sphaeriales sensu Lindau. *Dansk Botanisk Arkiv* 15, 1–163.
- Nag Raj TR. 1993 – *Coelomycetous anamorphs with appendage-bearing conidia* Mycologue publications, Canada.
- Nitschke TRJ. 1869 – Grundlage eines systems der Pyrenomyceten. *Verhandlungen des Naturhistorischen Vereins der Preussischen Rheinlande, Westfalens und des Regierungsbezirks Osnabrück* 26, 70–77.
- Niessl G. 1876 – *Notizen u'ber neue und kritische Pyrenomyceten*. Verlag des Vereines.
- Norphanhoun C, Doilom M, Daranagama DA, Phookamsak R et al. 2017 – Revisiting the genus *Cytospora* and allied species. *Mycosphere* 8, 51–9.
- Pang KL, Jheng JS, Jones EBG. 2011 – *Marine Mangrove Fungi of Taiwan*. National Taiwan Ocean University, Taiwan.
- Paulus B, Gadek P, Hyde K. 2004 – Phylogenetic and morphological assessment of five new species of *Thozetella* from an Australian rainforest. *Mycologia* 96, 1074–1087.
- Pem D, Jeewon R, Bhat DJ, Doilom M et al. 2019 – *Mycosphere Notes 275–324: A morphotaxonomic revision and typification of obscure Dothideomycetes genera (incertae sedis)*. *Mycosphere* 10, 1115–1246.
- Pem D, Jeewon R, Chethana KWT, Hongsanan S et al. 2021 – Species concepts of Dothideomycetes: classification, phylogenetic inconsistencies and taxonomic standardization. *Fungal Diversity* 109, 283–319.
- Persoon CH. 1794 – *Neuer Versuch einer systematischen Eintheilung der Schwammme*. *N Mag Die Bot Ihrem Ganzen Umfange* 1, 63–128.
- Persoon CH. 1797 – *Tentamen dispositionis methodicae fungorum in classes, ordines genera et familias*. Lipsiae.
- Petersen RH, Hughes KW. 2010 – *The Xerula/Oudemansiella Complex (Agaricales) Introduction*. *Nova Hedwigia*, 9–615.
- Phillips AJL, Alves A, Abdollahzadeh J, Slippers B et al. 2013 – *The Botryosphaeriaceae: genera and species known from culture*. *Studies in Mycology* 76, 51–167.
- Phillips AJ, Hyde KD, Alves A, Liu JKJ. 2019 – Families in Botryosphaeriales: a phylogenetic, morphological and evolutionary perspective. *Fungal Diversity* 94, 1–22.

- Phookamsak R, Hyde KD, Jeewon R, Bhat DJ et al. 2019 – Fungal diversity notes 929–1035: taxonomic and phylogenetic contributions on genera and species of fungi. *Fungal Diversity* 95, 1–273.
- Phookamsak R, Liu JK, McKenzie EH, Manamgoda DS et al. 2014 – Revision of *Phaeosphaeriaceae*. *Fungal Diversity* 68, 159–238.
- Phukhamsakda C, McKenzie EH, Phillips AJ, Jones EBG et al. 2020 – Microfungi associated with *Clematis* (*Ranunculaceae*) with an integrated approach to delimiting species boundaries. *Fungal diversity* 102, 1–203.
- Pinruan U, Hyde KD, Lumyong S, McKenzie EHC, Jones EBG. 2007 – Occurrence of fungi on tissues of the peat swamp palm *Licuala longicalycata*. *Fungal Diversity* 25, 157–173.
- Pinruan U, Pinnoi A, Hyde KD, Jones EBG. 2014 – Tropical peat swamp fungi with special reference to palms. In: Jones EBG, Hyde KD, Pang KL (eds) *Freshwater Fungi*. De Gruyter, Berlin, Boston, pp. 371–388.
- Prihastuti H, Cai L, Chen H, McKenzie EHC et al. 2009 – Characterization of *Colletotrichum* species associated with coffee berries in northern Thailand. *Fungal Diversity* 39, 89–109.
- Qasim T, Amir T, Nawaz R, Niazi A et al. 2015 – *Leucoagaricus lahorensis*, a new species of *L. sect. Rubrotincti*. *Mycotaxon* 130, 533–541.
- Rabenhorst L. 1857 – Ein Notizblatt für kryptogamische Studien. *Hedwigia* 1, 116.
- Ramaley AW. 1997 – *Barrina*, a new genus with polysporous asci. *Mycologia* 89, 962–966.
- Reblová M. 2006 – Molecular systematics of *Ceratostomella* sensu lato and morphologically similar fungi. *Mycologia* 98, 68–93.
- Redhead SA, Ginns JH. 1985 – A reappraisal of agaric genera associated with brown rots of wood. *Transactions of the Mycological Society of Japan* 26, 349–381. [in Japanese].
- Ronquist F, Huelsenbeck JP. 2003 – MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19, 1572–1574.
- Rune F. 1994 – *Neolentinus* – a well-founded genus in *Pleurotaceae* that includes *Heliocybe*. *Mycological Research* 98, 542–544.
- Ryoo R, Antonín V, KA KH, Tomšovský M. 2016 – Marasmioid and gymnopoid fungi of the Republic of Korea. 8. *Gymnopus* section *Impudicae*. *Phytotaxa* 286, 75–88.
- Saccardo PA. 1880a – Conspectus generum fungorum italiae inferiorum nempe ad Sphaeropsideas, Melanconieas et Hyphomyceteas pertinentium, systemate sporologico dispositu. *Michelia* 2, 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, 39–135.
- Saitta A, Bernicchia A, Gorjón SP, Altobelli E et al. 2011 – Biodiversity of wood-decay fungi in Italy. *Plant Biosystems-An International Journal Dealing with all Aspects of Plant Biology* 145, 958–968.
- Samarakoon BC, Phookamsak R, Karunarathna SC, Jeewon R et al. 2021 – New host and geographic records of five pleosporalean hyphomycetes associated with *Musa* spp. (Banana). *Studies in Fungi* 6, 92–115.
- Samarakoon MC, Gafforov Y, Liu N, Maharachchikumbura SS et al. 2018 – Combined multi-gene backbone tree for the genus *Coniochaeta* with two new species from Uzbekistan. *Phytotaxa* 336, 43–58.
- Samuels GJ, Muller E. 1979 – Life- History Studies of Brazilian ascomycetes. 7. *Rhytidhysterium rufulum* and the genus *Eutrybliella*. *Sydowia* 32, 277–292.
- Shoemaker RA, Babcock CE. 1992 – Applanodictyosporous Pleosporales: *Clathrospora*, *Comoclathris*, *Graphyllum*, *Macrospora*, and *Platysporoides*. *Canadian Journal of Botany* 70, 1617–1658.
- Silva RM, Oliveira RJ, Bezerra JD, Bezerra JL et al. 2019 – *Bifusisporella sorghi* gen. et sp. nov. (*Magnaporthaceae*) to accommodate an endophytic fungus from Brazil. *Mycological Progress* 18, 847–854.

- Silvestro D, Michalak I. 2016 – RaxmlGUI: A graphical front end for RAxML. *Organisms Diversity & Evolution* 12, 335–337.
- Sivichai S, Jones EBG, Hywel-Jones N. 2002 – Fungal colonisation of wood in a freshwater stream at Tad Ta Phu, Khao Yai National Park, Thailand. *Fungal Diversity* 10, 113–129.
- Singer R. 1948 – Diagnoses fungorum novorum agaricalium. *Sydowia* 2, 35–36.
- Species Fungorum. 2021 – <http://www.speciesfungorum.org/Names/Names.asp> (Accessed on October 30, 2021).
- Song J, Liang JF, Mehrabi-Koushki M, Krisai-Greilhuber I et al. 2020 – Fungal Systematics and Evolution: FUSE 5. *Sydowia* 71, 141–245.
- Spegazzini CL. 1881 – Fungi argentini additis nonnullis brasiliensibus montevidensibusque.
- Stamatakis A, Hoover P, Rougemont J. 2008 – A rapid bootstrap algorithm for the RAxML webservers. *Systematic Biology* 75, 758–771.
- Sutton BC. 1975 – Coelomycetes V. *Coryneum Mycological Papers* 138, 1–224.
- Sturm J. Deutschlands Flora. 1829 – Abt. III. Die Pilze Deutschlands 2, 1–136.
- Swofford DL, Sullivan J. 2003 – Phylogeny inference based on parsimony and other methods using PAUP\*. *The phylogenetic handbook: A practical approach to DNA and protein phylogeny*, Cambridge University Press, New York.
- Sysouphanthong P, Bouamanivong S, Salichanh T, Xaybouangeun N et al. 2018 – *Leucoagaricus houaynhangensis* (Agaricaceae), A new yellowish-green species from Lao People's Democratic Republic. *Chiang Mai Journal of Science* 45, 1287–1295.
- Tanaka K, Endo M, Hirayama K, Okane I et al. 2011 – Phylogeny of *Discosia* and *Seimatosporium*, and introduction of *Adisciso* and *Immersidiscosia* genera nova. *Persoonia* 26, 85–98.
- Tanney J, Miller AN. 2017 – Asexual-sexual morph connection in the type species of *Berkleasium*. *IMA Fungus* 8, 99–105.
- Tanney JB, Seifert KA. 2020 – *Mollisiaceae*: An overlooked lineage of diverse endophytes. *Studies in Mycology* 95, 293–380.
- Tennakoon DS, Hyde KD, Wanasinghe DN, Bahkali AH et al. 2016 – Taxonomy and phylogenetic appraisal of *Montagnula jonesii* sp. nov. (*Didymosphaeriaceae*, Pleosporales) from Italy. *Mycosphere* 7, 1346–1356.
- Tennakoon DS, Kuo CH, Maharachchikumbura SS, Thambugala KM et al. 2021 – Taxonomic and phylogenetic contributions to *Celtis formosana*, *Ficus ampelas*, *F. septica*, *Macaranga tanarius* and *Morus australis* leaf litter inhabiting microfungi. *Fungal Diversity* 108, 1–215.
- Thambugala KM, Ariyawansa HA, Li YM, Boonmee S et al. 2014 – Dothideales. *Fungal Diversity* 68, 105–158.
- Thambugala KM, Hyde KD, Eungwanichayapant PD, Romero AI et al. 2016 – Additions to the genus *Rhytidhysterion* in *Hysteriaceae*. *Cryptogamie Mycologie* 37, 99–116.
- Thambugala KM, Hyde KD, Tanaka K, Tian Q et al. 2015 – Towards a natural classification and backbone tree for *Lophiostomataceae*, *Floricolaceae*, and *Amorosiaceae* fam. nov. *Fungal Diversity* 74, 199–266.
- Thambugala KM, Wanasinghe DN, Phillips AJL, Camporesi E et al. 2017 – Mycosphere notes 1-50: Grass (*Poaceae*) inhabiting Dothideomycetes. *Mycosphere* 8, 697–796.
- Thongkantha S, Jeewon R, Vijaykrishna D, Lumyong S et al. 2009 – Molecular phylogeny of *Magnaporthaceae* (Sordariomycetes) with a new species *Ophioceras chiangdaoense* from *Dracaena loureioides* in Thailand. *Fungal Diversity* 34, 157–173.
- Tibpromma S, Hyde KD, Bhat JD, Mortimer PE et al. 2018 – Identification of endophytic fungi from leaves of *Pandanaceae* based on their morphotypes and DNA sequence data from southern Thailand. *MycKeys* 33, 25–67.
- Tokumasu S, Tubaki K, Manoch L. 1990 – A preliminary list of hyphomycetes isolated from pine leaf litter of Thailand. *Reports of the Tottori Mycological Institute* 28, 185–190.
- Udayanga D, Manamgoda DS, Liu XZ, Chukeatirote E. 2013 – What are the common anthracnose pathogens of tropical fruits? *Fungal Diversity* 61, 165–179.

- Ushijima S, Shimomura N, Nagasawa E, Maekawa N. 2012 – Taxonomic reevaluation of a fungus described as “*Mucidula mucida*” in Japan. *Mushroom Science and Biotechnology* 20, 22–30.
- Valenzuela-Lopez N, Cano-Lira JF, Guarro J, Sutton DA et al. 2018 – Coelomycetous Dothideomycetes with emphasis on the families *Cucurbitariaceae* and *Didymellaceae*. *Studies in Mycology* 90, 1–69.
- Vellinga EC. 2000 – Notulae ad floram agaricinam neerlandicam – XXXVIII – *Leucoagaricus* subgenus *Sericeomyces* Persoonia 17, 473–480.
- Vellinga EC. 2004 – Genera in the family *Agaricaceae* – Evidence from nrITS and nrLSU sequences. *Mycological Research* 108, 354–377.
- Vellinga EC. 2006 – Lepiotaceous fungi in California, U.S.A. – 3. Pink and lilac species in *Leucoagaricus* sect. *Piloselli*. *Mycotaxon* 98, 213–224.
- Vellinga EC. 2007 – Lepiotaceous fungi in California, U.S.A. – 5. *Lepiota oculata* and its look-alikes. *Mycotaxon* 102, 267–280.
- Vellinga EC. 2010 – Lepiotaceous fungi in California, U.S.A. *Leucoagaricus* sect. *Piloselli*. *Mycotaxon* 112, 393–444.
- Vellinga EC, Noordeloos ME. 2001 – Glossary in Noordeloos ME, Kuyper ThW, Vellinga EC (eds). *Flora agaricina neerlandica* 5, 6–11. A.A. Balkema Publishers, Lisse/Abingdon/Exton (PA)/Tokyo. 169.
- Vellinga EC. 2000 – Notes on *Lepiota* and *Leucoagaricus*. Type studies on *Lepiota magnispora*, *Lepiota barssii* and *Agaricus americanus*. *Mycotaxon* 76, 429–438.
- Vizzini A, Gelardi M, Ercole E, Perrone L et al. 2012 – On the status of *Mucidula venosolamellata* and *M. mucida* var. *asiatica* Physalacriaceae, Agaricales. *Bollettino dell'Associazione Micologica ed Ecologica Roman* 87, 3–18.
- Walker J. 1980 – *Gaeumannomyces*, *Linocarpon*, *Ophiobolus* and several other genera of scolecospored ascomycetes and *Phialophora* conidial states, with a note on hyphopodia. *Mycotaxon* 11, 1–129.
- Wanasinghe DN, Jones EBG, Camporesi E, Dissanayake AJ et al. 2016 – Taxonomy and phylogeny of *Laburnicola* gen. nov. and *Paramassariosphaeria* gen. nov. (*Didymosphaeriaceae*, *Massarineae*, Pleosporales). *Fungal Biology* 120, 1354–1373.
- Wanasinghe DN, Jones EBG, Dissanayake AJ, Hyde KD. 2016 – Saprobic Dothideomycetes in Thailand: *Vaginatisspora appendiculata* sp. nov. (*Lophiostomataceae*) introduced based on morphological and molecular data. *Studies in Fungi* 1, 56–68.
- Wanasinghe DN, Phukhamsakda C, Hyde KD, Jeewon R et al. 2018 – Fungal diversity notes 709–839: taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on *Rosaceae*. *Fungal Diversity* 89, 1–236.
- Wang Y, Jie CY, Hyde KD, Jiang YL et al. 2017 – *Chloridium terricola* sp. nov. from China. *Mycotaxon* 132, 79–86.
- Weber E, Görke C, Begerow D. 2002 – The *Lecythophora-Coniochaeta* complex: II. Molecular studies based on sequences of the large subunit of ribosomal DNA. *Nova Hedwigia* 74, 187–200.
- Weber E. 2002 – The *Lecythophora-Coniochaeta* complex, I. Morphological studies on *Lecythophora* species isolated from *Picea abies*. *Nova Hedwigia* 74, 159–185.
- Wei MJ, Zhang H, Dong W, Boonmee S, Zhang D. 2018 – Introducing *Dictyochoeta aquatica* sp. nov. and two new species of *Chloridium* (*Chaetosphaeriaceae*, Sordariomycetes) from aquatic habitats. *Phytotaxa* 362, 187–199.
- Wijayawardene NN, Hyde KD, Al-Ani LKT, Tedersoo L et al. 2020 – Outline of Fungi and fungus-like taxa. *Mycosphere* 11, 1060–1456.
- Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M et al. 2022 – Outline of Fungi and fungus-like taxa – 2021. *Mycosphere* 13, 53–453.
- Wijayawardene NN, Hyde KD, Lumbsch HT, Liu JK et al. 2018 – Outline of Ascomycota. *Fungal Diversity* 88, 167–263.

- Wijayawardene NN, Hyde KD, Rajeshkumar KC, Hawksworth DL et al. 2017 – Notes for genera: *Ascomycota*. *Fungal Diversity* 86, 1–594.
- Wikee S, Lombard L, Crous PW, Nakashima C. 2013 – *Phyllosticta capitalensis*, a widespread endophyte of plants. *Fungal Diversity* 60, 91–105.
- Wijayawardene NN, Hyde KD, Wanasinghe DN, Papizadeh M et al. 2016 – Taxonomy and phylogeny of dematiaceous coelomycetes. *Fungal Diversity* 77, 1–316.
- Wikee S, Lombard L, Nakashima C, Motohashi K et al. 2013 – A phylogenetic re-evaluation of *Phyllosticta* (Botryosphaeriales). *Studies in Mycology* 76, 1–29.
- Wilson AW, Desjardin DE. 2005 – Phylogenetic relationships in the gymnopoid and marasmiod fungi (Basidiomycetes, euagarics clade). *Mycologia* 97, 667–679.
- Whitton SR, McKenzie EHC, Hyde KD. 2012 – Fungi associated with *Pandanaceae*. Springer Netherlands, London.
- Wu N, Dissanayake AJ, Manawasinghe IS, Rathnayaka AR et al. 2021 – <https://botryosphaeriales.org/>, an online platform for up-to-date classification and account of taxa of Botryosphaeriales. *Database* 2021, 1–9.
- Yang CL, Xu XL, Wanasinghe DN, Jeewon R et al. 2019 – *Neostagonosporella sichuanensis* gen. et sp. nov. (*Phaeosphaeriaceae*, Pleosporales) on *Phyllostachys heteroclada* (*Poaceae*) from Sichuan Province, China. *MycoKeys* 46, 119–150.
- Yang ZL, Ge ZW. 2017 – Six new combinations of lepiotaceous fungi from China. *Mycosystema* 36, 542–551.
- Yang ZL, Zhang LF, Mueller GM, Kost GW et al. 2009 – A new systematic arrangement of the genus *Oudemansiella* s. str. (*Physalacriaceae*, Agaricales). *Mycosystema* 28, 1–13.
- Yu F, Liang JF, Ge ZW, Li YK. 2016 – Morphological and molecular evidence for a new species of *Leucoagaricus* from China. *Sydowia* 68, 41–47.
- Yuan HS, Lu X, Dai YC, Hyde KD et al. 2020 – Fungal diversity notes 1277–1386: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 104, 1–266.
- Zhang SN, Abdel-Wahab MA, Jones EBG, Hyde KD, Liu JK. 2019a – Additions to the genus *Savoryella* (*Savoryellaceae*), with the asexual morphs *Savoryella nypae* comb. nov. and *S. sarushimana* sp. nov. *Phytotaxa* 408, 195–208.
- Zhang Y, Crous PW, Schoch CL, Hyde KD. 2012 – Pleosporales. *Fungal Diversity* 53, 1–221.
- Zhang H, Hyde KD, Zhao YC, Mackenzie EHC et al. 2014 – Freshwater ascomycetes: *Lophiostoma vaginatisspora* comb. nov. (Dothideomycetes, Pleosporales, *Lophiostomataceae*) based on morphological and molecular data. *Phytotaxa* 176, 184–191.
- Zhang JF, Liu JK, Jeewon R, Wanasinghe DN, Liu ZY. 2019b – Fungi from Asian Karst formations III. Molecular and morphological characterization reveal new taxa in *Phaeosphaeriaceae*. *Mycosphere* 10, 202–220.
- Zhang M, Li T, Song B. 2018 – *Heliocybe villosa* sp. nov., a new member to the genus *Heliocybe* (*Gloeophyllales*). *Phytotaxa* 349, 173–178.
- Zhang N, Castlebury LA, Miller AN, Huhndorf SM et al. 2006 – An overview of the systematics of the Sordariomycetes based on a four-gene phylogeny. *Mycologia* 98, 1076–1087.
- Zhang W, Groenewald JZ, Lombard L, Schumacher RK et al. 2020 – Evaluating species in Botryosphaeriales. *Persoonia* 46, 63–115.
- Zhang Y, Zhang J, Wang Z, Fournier J et al. 2014 – Neotypification and phylogeny of *Kalmusia*. *Phytotaxa* 176, 164–173.