

Mycosphere Notes 469–520

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Abstract

Fungi are ubiquitous and essential to ecosystem functioning and biotechnology and have been estimated to have a global value of US\$ 54.57 trillion annually. This is the eleventh in a series of *Mycosphere notes* where we provide entries on new species and higher taxa, new host records,

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geographical (country) records, and habitat records of fungi. Species boundaries were defined using polyphasic approaches based on morphology and molecular phylogeny. In the set of notes, we introduce ten new species, *Conlarium multiseptatum*, *Co. yunnanense*, *Cudonia gracilistipitata*, *Cu. yunnanensis*, *Cyathicula dioscoreae*, *Cy. rusci*, *Helminthosporium guizhouense*, *Neopestalotiopsis neomaricae*, *Plectania submilleri*, and *Plenodomus shangrilaense*. In addition, we reveal ecological relationships of Ascomycota including 22 new host records (*Apiospora guizhouensis*, *A. phyllostachydis*, *Colletotrichum dematium*, *Distoseptispora suoluoensis*, *Dothiorella plurivora*, *Gloniopsis calami*, *Junewangia lamma*, *Kirschsteiniorthelia atra*, *Lasiodiplodia hormozganensis*, *Letendraea helminthicola*, *Melomastia winteri*, *Nectria asiatica*, *Neoostropa castaneae*, *Nigrograna magnolia*, *Nigrospora macarangae*, *N. oryzae*, *N. sphaerica*, *Parasporendocladia bactrospora*, *Plenodomus artemisiae*, *Pseudoacrodactys deightonii*, *Pseudofusicoccum adansoniae*, and *Torula mackenziei*); five new geographical records (*Caesiodiscus populicola*, *Codinaea aseptate*, *C. fertilis*, *Mycotribulus indonesiae*, *Tricladium terrestre*, and *Vaginatispora nypae*); seven recognitions of both new host and geographical records (*Allocryptovalsa rabenhorstii*, *Barriopsis stevensiana*, *Distoseptispora thysanolaenae*, *Massarioramusclicola chiangraiensis*, *Peroneutypa longiasca*, *Phomatospora uniseriate*, and *Thyridaria aureobrunnea*); five newly identified habitat records (*Conlarium sichuanense*, *Distoseptispora crassisporea*, *D. nonrostrata*, *Pestalotiopsis trachicarpicola*, *Talaromyces variabilis*); one new host and habitat record (*Distoseptispora dehongensis*), and one new host, geographical and habitat record (*Amphisphaeria uniseptata*). An unusual asexual Basidiomycota, *Mycotribulus indonesiae* (*Physalacriaceae*), was revealed as a new geographical record. Furthermore, we provide new molecular data for all 52 collected species belonging to two phyla, six classes, 20 orders, 30 families and 39 genera. A list of all genera discussed in Mycosphere notes 1–520 is provided. The fungal species were found as endophytes, pathogens, and saprobes on plant material and litter substrates from terrestrial, freshwater, and cave habitats in China, Italy, Iran, and Thailand. This study extends our understanding of fungal taxonomy, biodiversity, ecology, and distribution, and encourages future research in unexplored geographies, habitats and among fungal hosts that have yet to be studied.

Keywords – 10 new species – 42 new records – Ascomycota – Basidiomycota – *Allocryptovalsa* – *Amphisphaeria* – *Apiospora* – *Barriopsis* – *Caesiodiscus* – *Codinaea* – *Colletotrichum* – *Conlarium* – *Cudonia* – *Cyathicula* – *Distoseptispora* – *Dothiorella* – geographical records – habitat records – host records – *Gloniopsis* – *Helminthosporium* – *Junewangia* – *Kirschsteiniorthelia* – *Lasiodiplodia* – *Letendraea* – *Massarioramusclicola* – *Melomastia* – *Mycotribulus* – *Nectria* – *Neoostropa* – *Neopestalotiopsis* – *Nigrograna* – *Nigrospora* – *Parasporendocladia* – *Peroneutypa* – *Pestalotiopsis* – *Phomatospora* – Phylogeny – *Plectania* – *Plenodomus* – *Pseudoacrodactys* – *Pseudofusicoccum* – Sordariomycetes – *Talaromyces* – Taxonomy – *Thyridaria* – *Torula* – *Tricladium* – *Vaginatispora*

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496. *Conlarium yunnanense* H.W. Shen, Z.L. Luo & K.D. Hyde sp. nov. (entry by Shen HW)

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Xylariales Nannf.

Diatrypaceae Nitschke

516. *Alloccryptovalsa rabenhorstii* (Nitschke) C. Senwanna, Phookamsak & K.D. Hyde (entry by Du TY)

517. *Peroneutypa longiasca* Senwanna, Phookamsak & K.D. Hyde (entry by Li CJY)

Sordariomycetes family incertae sedis

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Ascomycota genus incertae sedis

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Phylum Basidiomycota

Class Agaricomycetes Doweld

Agaricales Underw.

Physalacriaceae Corner

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INTRODUCTION

Until the 21st Century, the study of fungi was a relatively neglected field of research (Hyde et al. 2024). To illustrate this, we can view the novel species described over the five decades during 1980, 1990, 2000, 2010 and 2020. There were 1,365 novel species introduced in 1990, 1,391 in 2000, 1,542 in 2010 and 3520 in 2020 (filtered data in Index Fungorum); the numbers of new taxa introduced rising each decade (Hyde et al. 2020a, Bhunjun et al. 2022, Phukhamsakda et al. 2022). While studying fungal biodiversity, researchers have discovered numerous taxa, many of which were previously known. Considerable effort was undertaken to name these taxa; however, it is

difficult to find an outlet for their publication. This research would go to waste if outlets such as Mycosphere notes (Hyde et al. 2021, 2023, Manawasinghe et al. 2022, Li et al. 2023a) and AJOM notes (Chethana et al. 2021b, 2023) would not publish this type of research. Such records are important as they 1) expand the global geographical range of a species, 2) expand the host range of the species and establish if the taxon is a generalist or host-specific, 3) provide additional molecular data on new strains of a species, often with new genes, and 4) provide voucher herbarium specimens, descriptions and photographic plates of collections of a species. This will help in documenting the phylogenetic and morphological variation in a species. Furthermore, the data may reveal a wide genotype for a species or even reveal that the collections are new species.

The present paper lists 52 entries of taxa in *Ascomycota* (51) and *Basidiomycota* (1). Ten species are new to science while the other 42 are new host, geographical, or new habitat records. Descriptions, photographic plates illustrating each species, culture characteristics where available and collection details are provided for each taxon. An update of the host and geographical distributions based on molecular data are also provided. A list of all genera published in Mycosphere notes 1–520 is also provided at the end of this paper.

MATERIALS AND METHODS

Fungal specimens were collected at random from woody, leaf, and litter substrates from terrestrial, freshwater habitats, and the cave environments in China, Thailand, Italy and Iran during 2016–2023. Morphological observation, macro and micro photography, and isolation were conducted following the methods described by Dissanayake et al. (2020a). Fungal samples and isolates including the ex-type, living, and dried cultures were deposited at the following fungaria and culture collections, respectively. Herbaria at DLU: Da Lat University, Vietnam; FUM: Ferdowsi University of Mashhad, Iran; GZAAS: Guizhou Academy of Agriculture Sciences, China; HKAS: Cryptogams Kunming Institute of Botany Academia Sinica, China; HMAS: Chinese Academy of Sciences, China; ZHKU: Zhongkai University of Agriculture and Engineering, Chian; MFLU: Mae Fah Luang University, Thailand; MHZU: Mycological Herbarium of Zhongkai University of Agriculture and Engineering, China; and the culture collections of CGMCC: China General Microbial Culture Collection Center, China; DLUCC: Dali University Culture Collection, China; GZCC: Guizhou Culture Collection, China; KUNCC: Kunming Institute of Botany Culture Collection, China; MFLUCC: Mae Fah Luang University Culture Collection, Thailand; ZHKUCC: Zhongkai University of Agriculture and Engineering Culture Collection, Thailand. Fungal pure cultures and fruiting bodies (taxa unable to obtain cultures) were used for DNA extraction. Fungal DNA extraction, PCR, gel electrophoresis, and sequencing were performed according to the methods discussed in Dissanayake et al. (2020a). The sequences generated in this study were deposited in GenBank. Phylogenetic analyses of maximum likelihood (ML) and Bayesian inference (BI) were performed on the CIPRES Science Gateway portal (Miller et al. 2012) while, maximum parsimony (MP) was implemented in PAUP v.4.0b10 (Swofford & Sullivan 2003) to understand the species boundaries. Pairwise homoplasy index (PHI) tests were carried out to determine the recombination level of species with close phylogenetic affinities, when necessary, by using Split Tree software outlined by Quaedvlieg et al. (2014). The guidelines and major criteria for defining species boundaries were followed in the identification of new fungal species as outlined by Chethana et al. (2021a) and Pem et al. (2021). Newly introduced fungal species were submitted to the Index Fungorum (2024) and Faces of Fungi database (Jayasiri et al. 2015).

RESULTS

Taxonomy

The classification follows Wijayawardene et al. (2022) and is updated where needed.

Ascomycota

Dothideomycetes O.E. Erikss. & Winka 1997

Botryosphaeriales C.L. Schoch, Crous & Shoemaker, in Schoch, Shoemaker, Seifert, Hambleton, Spatafora & Crous, *Mycologia* 98(6), 1050 (2007)

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

Barriopsis A.J.L. Phillips, A. Alves & Crous, in Phillips, Alves, Pennycook, Johnston, Ramaley, Akulov & Crous, *Persoonia* 21, 39 (2008)

Index Fungorum number: IF511712; Facesoffungi number: FoF01679

Barriopsis was introduced by Phillips et al. (2008) with *B. fusca* as the type species. *Barriopsis* is morphologically related to *Physalospora fusca*, while Phillips et al. (2008) showed morphological and phylogenetical differences from other genera in *Botryosphaeriaceae*. The genus has brown, aseptate ascospores without apiculi (Phillips et al. 2008). Currently, five species belong to this genus (Hyde et al. 2020b, Wijayawardene et al. 2022, Index Fungorum 2024). Here, we provide the updated phylogeny for *Barriopsis* taxa (Fig. 1).

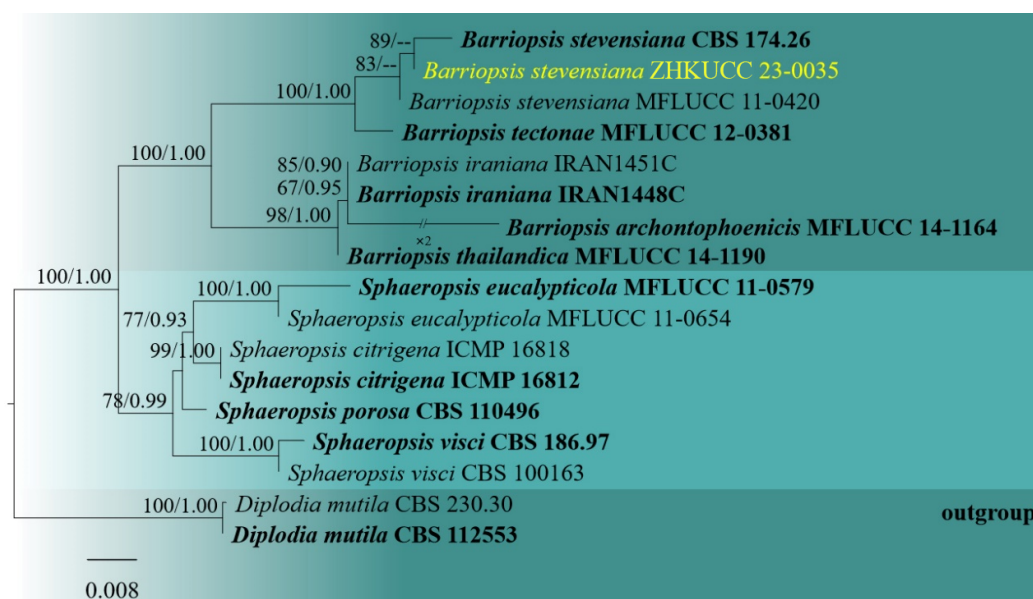


Figure 1 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU and *tef1-α* sequence data of *Barriopsis*. Seventeen strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of - 3943.229389 is presented. Evolutionary model GTR+I+G is applied for all the genes. The matrix had 236 distinct alignment patterns, with 27.56% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.233848, C = 0.253765, G = 0.287896, T = 0.224490; substitution rates AC = 1.018067, AG = 2.811741, AT = 0.803419, CG = 1.530151, CT = 4.842324, GT = 1.000000; gamma distribution shape parameter α = 1.078576. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Diplodia mutila* (CBS 230.30) and *D. mutila* (CBS 112553). Ex-type strains are in bold. The newly generated sequence is indicated in yellow.

Barriopsis stevensiana A.J.L. Phillips & Pennycook, *Fungal Diversity* 86, 56 (2017)

Fig. 2

Index Fungorum number: IF819573; Facesoffungi number: FoF07061

Saprobic on a dead twig of *Aquilaria sinensis*. Sexual morph: *Ascomata* 190–340 μm high $\times$ 280–405 μm diam. ($\bar{x}$ = 273.5 $\times$ 347 μm , n = 10), solitary, scattered, immersed, erumpent, globose to subglobose, papillate. *Ostiole* central, with periphyses. *Peridium* 30–65 μm wide, 6–12-layered, brown to dark brown cells of *textura angularis*. *Hamathecium* comprises 2.5–5 μm wide, hyaline, septate pseudoparaphyses, constricted at septa. *Asci* 110–140 (–162) $\times$ 32–50 (–55) μm ($\bar{x}$ = 129 $\times$ 42 μm , n = 10), 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, apically rounded with an ocular chamber, base with a short or long pedicel. *Ascospores* 30–38 $\times$ 12–18 μm ($\bar{x}$ = 33 $\times$

14.5 μm , $n = 30$), overlapping, 2–3-seriate at center and end, aseptate, ellipsoidal, initially hyaline, becoming pale brown to brown at maturity, smooth-walled, guttulate. Asexual morph: undetermined.



Figure 2 – Sexual morph of *Barriopsis stevensiana* (MHZU 23-0016, a new host and a geographical record). a, b Appearance of ascostromata on host surface. c Horizontal section of an ascoma. d, e Vertical sections of ascomata. f Section through the ostiole. g Pseudoparaphyses. h Peridium. i–m Asci. n–q Ascospores. r A germinating ascospore s Upper view of culture on PDA. t Reverse view of culture on PDA. Scale bars: d, e = 200 μm , f, k–m = 100 μm , g = 10 μm , h–j = 50 μm , n–r = 20 μm .

Material examined – China, Guangdong Province, Maoming City, Dianbai, on a dead twig of *Aquilaria sinensis* (*Thymeleaceae*), 3 June 2022, Tianye Du, MMA07 (MHZU 23-0016), living culture (ZHKUCC 23-0035).

GenBank numbers – ZHKUCC 23-0035: ITS: OR900225, LSU: OR898406, SSU: OR900230, *tef1-α*: OR914210.

Known distribution (based on molecular data) – Cuba (Phillips et al. 2008), Thailand (Hyde et al. 2020b), China (this study).

Known hosts (based on molecular data) – *Citrus* sp. (Phillips et al. 2008), *Cassia* sp. (Hyde et al. 2020b), *Aquilaria sinensis* (this study).

Notes – According to the phylogenetic analyses, our strain (ZHKUCC 23-0035) clustered with *B. stevensiana* strain (CBS 174.26) with 89% ML bootstrap support value (Fig. 1). The morphology of our fungal collection shares similar characteristics to *Barriopsis stevensiana* (holotype) that was isolated from dead twigs of *Citrus* sp. (Phillips et al. 2008). However, our collection (MHZU 23-0016) has shorter and wider asci (110–140 × 32–50 vs. 125–180 × 30–36 μm) than those of the holotype (Phillips et al. 2008). Based on morphology and multi-gene phylogeny we conclude our collection is *B. stevensiana*. The current study presents a new host record of *Barriopsis stevensiana* on *Aquilaria sinensis* and a new geographical record from China.

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

Index Fungorum number: IF8098; Facesoffungi number: FoF00148

Dothiorella was established by Saccardo (1880a) with *D. pyrenophora* as the type species. Members of this genus are endophytes, pathogens, and saprobes in a wide range of hosts (Liu et al. 2012a, Phillips et al. 2013, Dissanayake et al. 2016, Hyde et al. 2020b, Xiao et al. 2021, Rathnayaka et al. 2022, Li et al. 2023b, Lin et al. 2023a). *Dothiorella* is characterized by pigmented, 1-septate ascospores and conidia that become brown and 1-septate while they are attached to the conidiogenous cells (Phillips et al. 2005, Dissanayake et al. 2016). So far, 34 species are valid in *Dothiorella*, most of them reported as the asexual morph of *Dothiorella* and the sexual stage is rarely founded on nature (Dissanayake et al. 2016, Li et al. 2023b, Lin et al. 2023a). Here, we provide the updated phylogeny for the *Dothiorella* taxa (Fig. 3).

***Dothiorella plurivora* (Abdollahz., Javadi & A.J.L. Phillips) Tao Yang & Crous, in Yang, Groenewald, Jami, Cheewangkoon, Abdollahzadeh, Lombard & Crous 2016** Fig. 4

Basionym: *Spencermartinsia plurivora* Abdollahz. et al., Persoonia 32: 9 (2014).

Index Fungorum number: IF817676; Facesoffungi number: FoF05785

Saprobic on a branch of *Acer Palmatum* f. *atropurpureum*. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 320–365 μm diam × 180–220 μm high. ($\bar{x}$ = 347 × 195 μm, n = 10), solitary, immersed, becoming erumpent at maturity, dark brown to black, appear as cracks on the substrates, globose to subglobose, pycnidial, uniloculate. *Ostiole* single, circular, central, papillate. *Conidiomata* wall 11–30 μm diam. ($\bar{x}$ = 23 μm, n = 30), composed of thin-walled outer layer, with brown cells of *textura angularis*, inner layers thin, pale brown to hyaline. *Conidiogenous cells* (4–)4.4–6.5(–7) × (4.5–)5–8(–9) μm ($\bar{x}$ = 5.5 × 6.5 μm, n = 20), determinate, subglobose or cylindrical, hyaline, lining in the pycnidial cavity, holoblastic, discrete, smooth-walled. *Conidia* (17–)18.7–20.6(–21) × (8–)8.5–9.7(–11) μm ($\bar{x}$ = 19.7 × 9 μm, n = 35), ellipsoid to ovoid, straight, initially hyaline and aseptate, becoming brown and 1-septate at the maturity, while attached to conidiogenous cells, slightly constricted at the septum, rounded at both ends.

Culture characteristics – Conidia germinating on PDA within 24 h. Germ tubes produced from one side of the conidia. Colonies on PDA reaching 3 cm diam after 15 days at 25 °C, irregular circle, medium dense, flat or effuse, slightly raised, center white, edges grey.

Material examined – China, Yunnan Province, Kunming city, Kunming Botanical Garden, (25°8'19"N, 102°44'25"E, 1930m), on a decaying stem of *Acer Palmatum* f. *atropurpureum* (*Aceraceae*), 23 November 2020, Ying Gao, GY2 (HKAS 129309), living culture, KUNCC 23-16750.

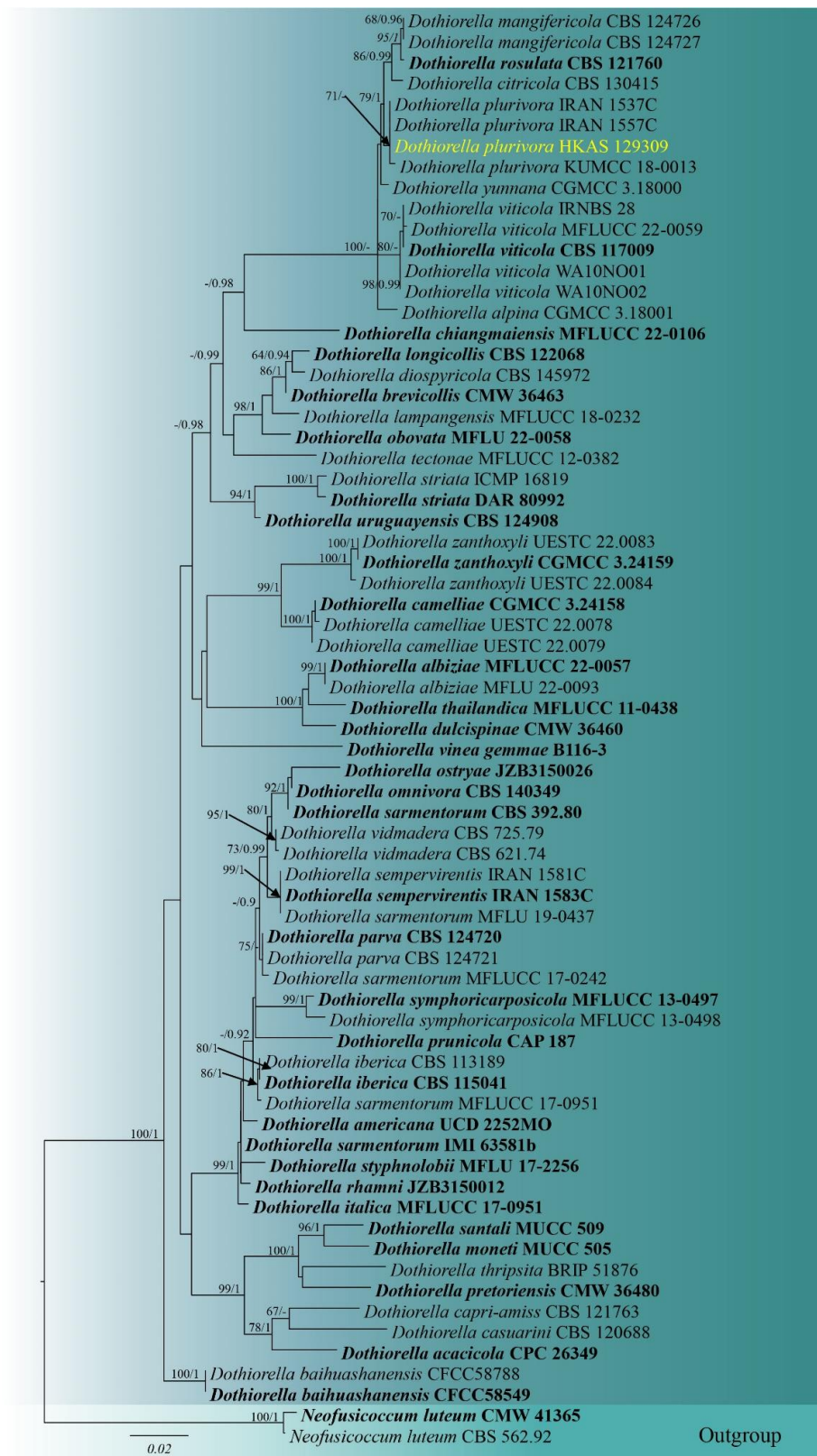


Figure 3 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, *tef1-α* and *tub2* sequence data of *Dothiorella*. Sixty-six strains are included in the combined analyses. The tree was rooted with *Neofusicoccum luteum* (CMW 41365 and CBS 562.92). The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -8361.213860 is presented. The matrix had 542 distinct alignment patterns, with 36.60% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.218627, C = 0.282109, G = 0.265810, T = 0.233455;

substitution rates AC = 1.315272, AG = 2.279085, AT = 1.104267, CG = 1.129245, CT = 5.824921, GT = 1.000000; gamma distribution shape parameter α = 0.152477. Bootstrap support values for ML greater than 65% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

GenBank numbers – HKAS 129309: ITS: OR460077, LSU: OR460080.

Known distribution (based on molecular data) – Southern Iran, Spain (Abdollahzadeh et al. 2014), China (Hyde et al. 2019, this study).

Known hosts (based on molecular data) – Soil, twigs of *Casuarina* sp., *Citrus* sp., *Cupressus sempervirens*, *Eucalyptus* sp., *Juglans regia*, *Malus domestica*, *Prunus armeniaca* and *Vitis vinifera* (Abdollahzadeh et al. 2014), dead wood (Hyde et al. 2019), *Acer Palmatum* f. *atropurpureum* (this study).

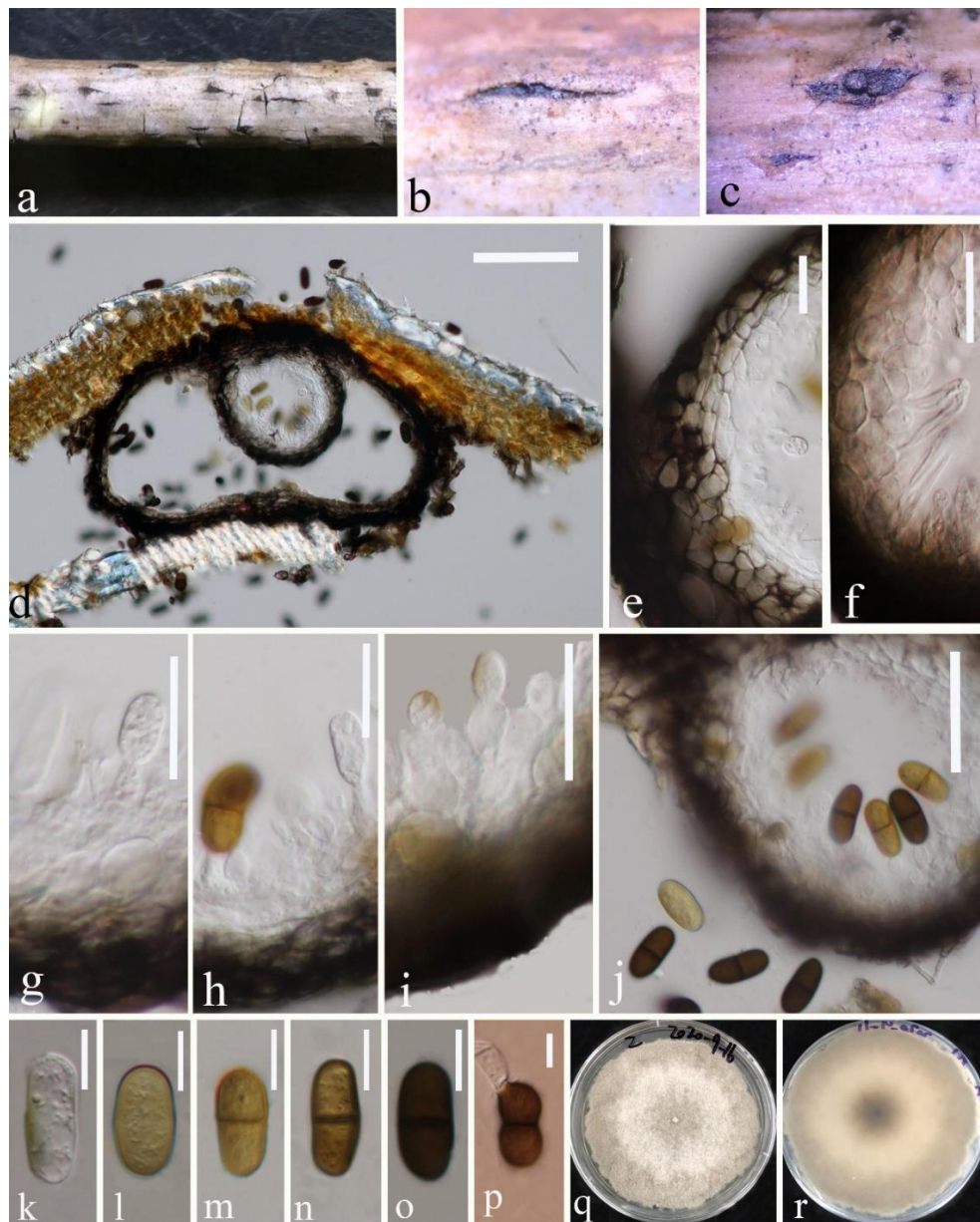


Figure 4 – *Dothiorella plurivora* (HKAS 129309, a new host record). a–c Conidiomata on host substrate. d Vertical section of a conidioma. e Conidioma wall. f–j Conidia attached to conidiogenous cells. k–o Conidia. p A germinating conidium. q Colony on PDA from above. r Cultures on PDA from reverse. Scale bars: d = 100 μ m, e–i = 20 μ m, j = 40 μ m, k–p = 10 μ m.

Notes – In the phylogenetic analysis, our strain (HKAS 129309) clustered with the strains of *Dothiorella plurivora* (IRAN 1557C, ex-type; IRAN 1537C; KUMCC 18-0013) with 71% ML bootstrap support (Fig. 3). The asexual morph of *D. plurivora* (IRAN 1557C) which was isolated from twigs of *Citrus* sp. in Iran shares similar characteristics with our collection by its conidiogenous cells ($5.1\text{--}11.9 \times 3\text{--}5 \mu\text{m}$ vs. $4\text{--}7 \times 4.5\text{--}9 \mu\text{m}$) and conidia ($18\text{--}27 \times 8.9\text{--}14.4 \mu\text{m}$ vs. $17\text{--}21 \times 8\text{--}11 \mu\text{m}$) (Abdollahzadeh et al. 2014). Based on morphology and multi-gene phylogeny we conclude our collection is *D. plurivora*. The current study presents new host records of *D. plurivora* on *Acer palmatum* f. *atropurpureum* in China.

Lasiodiplodia Ellis & Everh., in Clendenin, Bot. Gaz. 21: 92 (1896)

Index Fungorum number: IF8708; Facesoffungi number: FoF00151

Lasiodiplodia was established by Ellis & Everhart (1896) with *L. theobromae* as the type species. The members of the genus are commonly found in tropical and sub-tropical climates (Jami et al. 2017, Chethana et al. 2023) and exhibit diverse lifestyles, such as endophytes (Slippers & Wingfield 2007, Chen et al. 2015, Prasher & Dhanda 2017, de Silva et al. 2019, Bhunjun et al. 2023), pathogens (Li et al. 2015, Fayette et al. 2019, El-Ganainy et al. 2022, Zhou et al. 2023) and saprobes (Abdollahzadeh et al. 2010, Liu et al. 2012a, Wu et al. 2021). *Lasiodiplodia* species are characterized by the presence of pycnidial paraphyses and longitudinal striations on mature conidia, which can distinguish *Lasiodiplodia* from other closely related genera in *Botryosphaeriaceae* (Slippers & Wingfield 2007, Phillips et al. 2013, Hyde et al. 2020b). Multi-locus phylogenetic analysis of ITS, *tef1- α* , and *tub2* sequence data showed strong phylogenetic support of *Lasiodiplodia* species within the genus (Jami et al. 2022, Slippers et al. 2013, Xia et al. 2022, Rathnayaka et al. 2023). Currently, there are 87 epithets of *Lasiodiplodia* recorded in Index Fungorum (2024) and only 76 have molecular data in GenBank (2024). Here, we provide the updated phylogeny for the *Lasiodiplodia* taxa (Fig. 5).

Lasiodiplodia hormozganensis Abdollahzadeh., Zare & A.J.L. Phillips, Persoonia 25: 6 (2010)
Fig. 6

Index Fungorum number: IF516779; Facesoffungi number: FoF16006

Saprobic on dead twig of *Camphora* sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* scattered, solitary, immersed, globose to subglobose, dark brown to black, uniloculate, ostiolate. *Ostiole* circular, centrally or laterally located. *Conidiomata* wall composed of thick-walled, brown cells of *textura angularis*. *Paraphyses* 2–4 μm wide, lay between and conidiogenous cells, hyaline, cylindrical, thin-walled, initially aseptate, becoming up to 1–7 septate when mature, rarely branched, occasionally basal, middle or apical cells swollen, rounded at the apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* $10.4\text{--}15.6 \times 3.9\text{--}5.5 \mu\text{m}$, holoblastic, discrete, hyaline, smooth, thin-walled, cylindrical. *Conidia* $(19\text{--})23\text{--}26(\text{--}28.6) \times 10.9\text{--}19 \mu\text{m}$ ($\bar{x} = 24.5 \pm 2.7 \times 15.5 \pm 2.5 \mu\text{m}$, l/w ratio = 1.6 ± 0.2 , n = 15), initially hyaline, aseptate, ellipsoid to cylindrical, with granular contents, rounded at the apex, round or truncate at the base, becoming pigmented at the maturity, 1-septate with longitudinal striations, not constricted at the septum, ellipsoid to ovoid, verruculose, with longitudinal striations.

Culture characteristics – Colonies with abundant aerial mycelium reaching to the lid of Petri plate, aerial mycelium becoming smoke-grey to olivaceous-grey at the surface and greenish grey to dark slate blue at the reverse after 2 weeks in the dark at 25 °C.

Material examined – China, Guangxi Province, Beihai city, Yintan, on a dead twig of *Camphora* sp. (*Lauraceae*), 06 October 2020, Tianye Du, BHD01 (MHZU 23-0051), living culture ZHKUCC 23-0102.

GenBank numbers – MHZU 23-0051: ITS: OR492631, *tef1- α* : OR497825 and *tub2*: OR497827.

Known distribution (based on molecular data) – Iran (Abdollahzadeh et al. 2010), Australia (Sakalidis et al. 2011), Haiti (Fayette et al. 2019), Brazil (Custódio et al. 2018, Marques et al. 2013,

Netto et al. 2014), Puerto Rico (Serrato-Diaz et al. 2020), Oman and the UAE (Al-Sadi et al. 2013), and China (Li et al. 2015, this study).

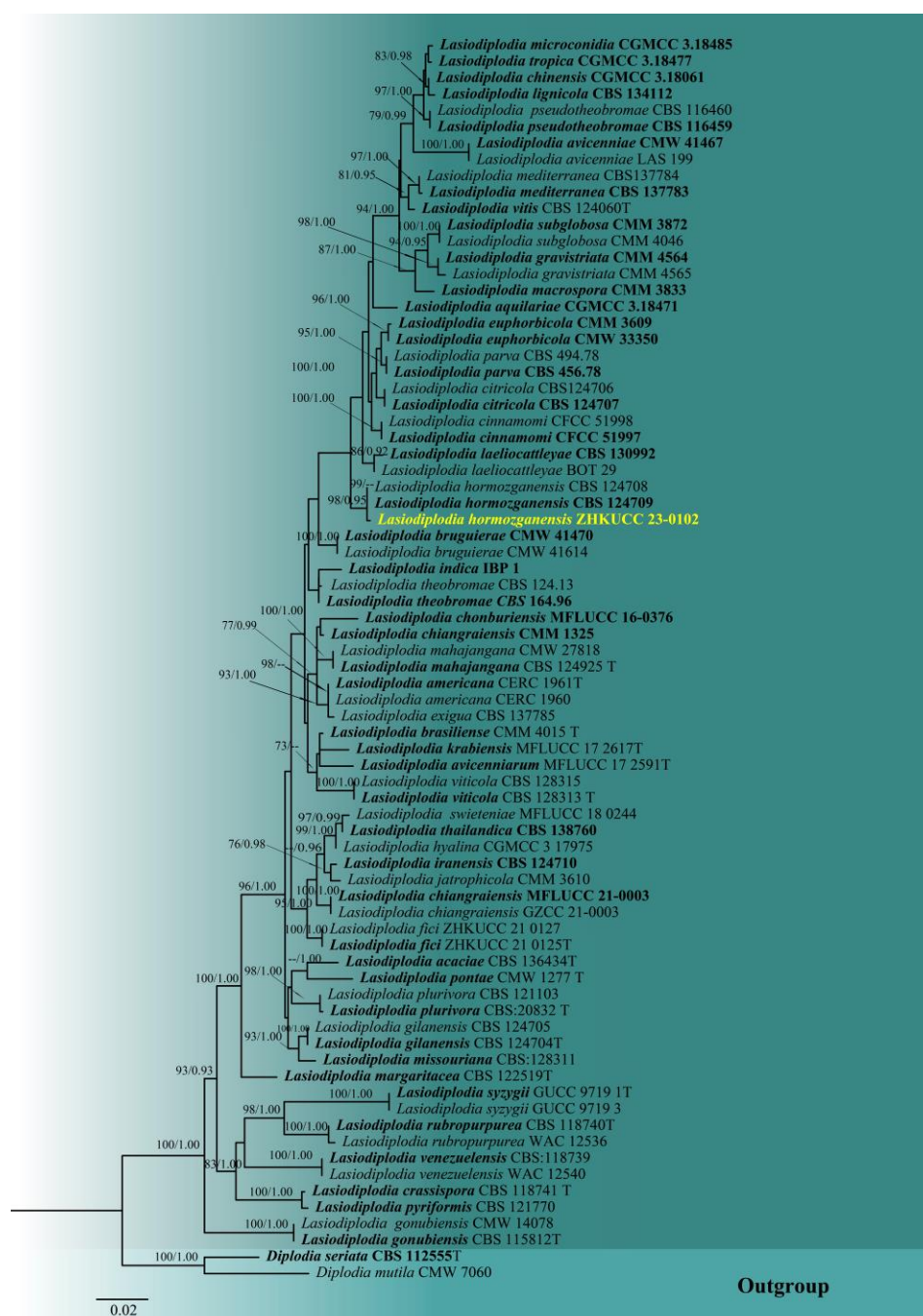


Figure 5 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, *tef1-α* and *tub2* sequence data of *Lasiodiplodia*. Seventy-five strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -5679.17 is presented. Evolutionary model GTR+I+G is applied for all the genes. The matrix had 409 distinct alignment patterns, with 18.07% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.207902, C = 0.308111, G = 0.257602, T = 0.226385; substitution rates AC = 1.164141, AG = 3.631367, AT = 1.302852, CG = 0.968296, CT = 5.435490, GT = 1.000000; gamma distribution shape parameter α = 0.190239. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Diplodia mutila* (CMW 7060) and *D. seriata* (CBS 112555). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Known hosts (based on molecular data) – *Solanum melongena* (Fayette et al. 2019), *Mangifera indica* (Abdollahzadeh et al. 2010, Al-Sadi et al. 2013), *Olea* sp. (Abdollahzadeh et al. 2010), *Adansonia digitata* (Sakalidis et al. 2011), *Ricinus communis* (Custódio et al. 2018), *Date palm* (Al-Sadi et al. 2013), *Citrus* sp. (Al-Sadi et al. 2013), *Ficus krishnae* (Prasher & Dhanda 2017), *Bougainvillea spectabilis* (Li et al. 2015), *Carica papaya* (Netto et al. 2014), and *Camphora* sp. (this study).

Notes – Phylogenetically, the strain of our new isolate (ZHKUCC 23-0102) clustered with the ex-type strain of *Lasiodiplodia hormozganensis* (CBS 124709) and *L. hormozganensis* (CBS 124708) based on combined ITS, *tef1-α* and *tub2* sequence data with 98% ML and 0.95 BYPP bootstrap support (Fig. 5). The morphological characteristics of the new isolate resembles the characters given by Abdollahzadeh et al (2010). However, our isolate has a few differences from *L. hormozganensis* (CBS 124709) in terms of maximum and minimum conidia size, (19–)23–26(–28.6) × 10.9–19 μm vs. 19.6–23.4 × 11.7–13.3 μm, respectively (Abdollahzadeh et al. 2010). *Lasiodiplodia hormozganensis* has been reported as pathogens (Custódio et al. 2018) and endophytes (Prasher & Dhanda 2017). In China, *L. hormozganensis* was reported as pathogens from *Bougainvillea spectabilis* (Li et al. 2015). Therefore, the current study presents a new host record of *L. hormozganensis* on *Camphora* sp. as a saprobe for the first time in China.

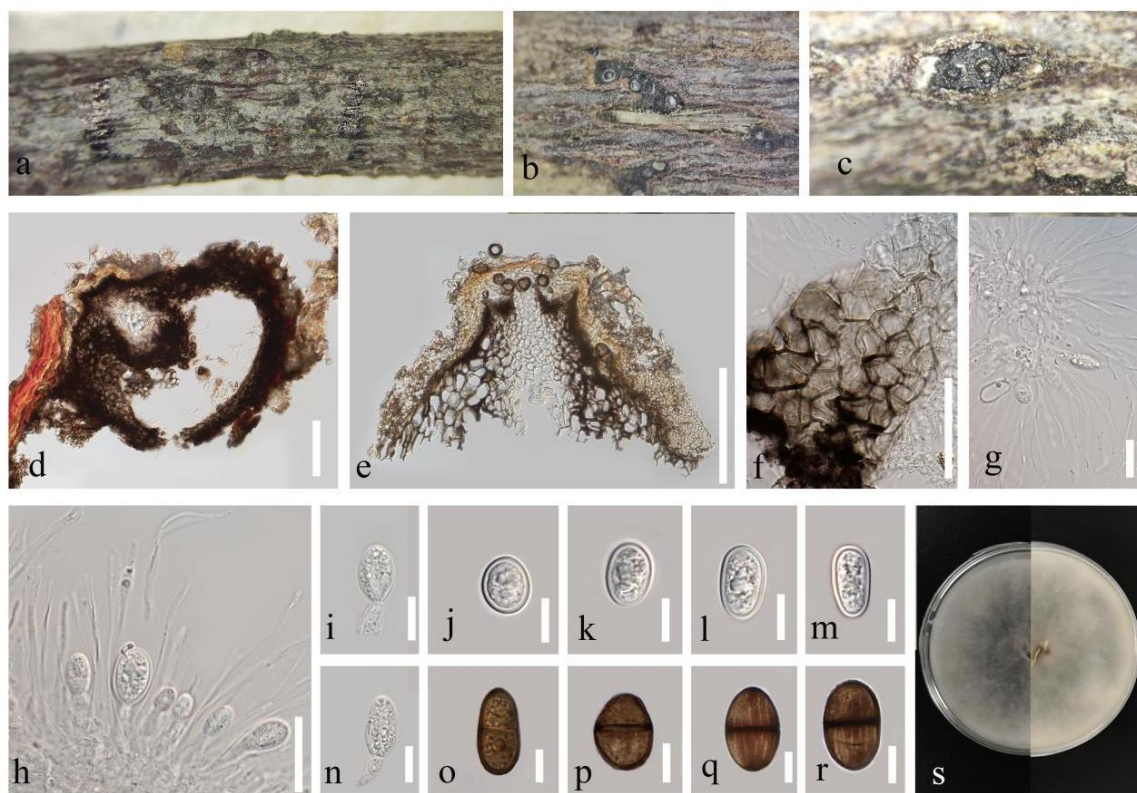


Figure 6 – *Lasiodiplodia hormozganensis* (ZHKUCC 23-0102, a new host record). a, b, c Appearance of conidiomata on *Camphora* sp. twig d Vertical section of a conidioma. e Ostiole. f Peridium. g Paraphyses. h, i, n Conidiogenous cells and developing conidia. j–m Hyaline, aseptate conidia. o–r Brown, septate conidia. s Upper and reverse view of colonies on PDA after 12 days. Scale bars: d, e = 100 μm, f = 50 μm, g, h = 20 μm, i–r = 10 μm.

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

Pseudofusicoccum Mohali, Slippers & M.J. Wingf., Stud. Mycol. 55: 249 (2006)

Index Fungorum number: IF500884; Facesoffungi number: FoF05299

Pseudofusicoccum was proposed by Crous et al. (2006) with *P. stromaticum* as the type species within *Botryosphaeriaceae*, based on asexual morph characteristics and multigene

phylogeny. The sexual morph of *Pseudofusicoccum* was described by Senwanna et al. (2020) and the majority of the species were described by their asexual morph (Chethana et al. 2023). *Pseudofusicoccum* successfully develop asexual morph in an artificial media (Senwanna et al. 2020). Based on morphology and phylogenetic evidence, *Pseudofusicoccum* was transferred from *Botryosphaeriaceae* to *Phyllostictaceae*. In the family phylogeny, *Pseudofusicoccum* clustered between *Phyllosticta* and *Neofusicoccum* (Slippers et al. 2013, Senwanna et al. 2020). The asexual morph is characterized by corticolous, coriaceous, uni- to multilocular, immersed to erumpent pycnidial conidiomata, and hyaline, aseptate, cylindrical to ellipsoid conidia covered by mucilaginous sheath (Senwanna et al. 2020). The sexual morph is characterized by scattered to clustered, uniloculate ascomata, bitunicate, cylindro-clavate asci with ocular chambers, and hyaline, uni to bi-seriate, aseptate, short clavate, smooth-walled ascospores with fine granules and surrounded by a mucilaginous sheath (Senwanna et al. 2020). *Pseudofusicoccum* has been reported as endophytes, saprobes, and phytopathogens distributed in Australia, India, South Africa, Thailand, and Venezuela. It consists of nine species (Pavlic et al. 2008, Senwanna et al. 2020, Li et al. 2023c, Sharma et al. 2022, Chethana et al. 2023). Here, we provide the updated phylogeny for *Pseudofusicoccum* (Fig. 7).

***Pseudofusicoccum adansoniae* Pavlic, T.I. Burgess & M.J. Wingf. 2008**

Fig. 8

Index Fungorum number: IF512048; Facesoffungi number: FoF00168

Saprobic on a dead twig of *Nephelium lappaceum*. Sexual morph: Ascomata 210–230 × 230–290 µm ($\bar{x}$ = 218 × 270 µm, n = 5), lignicolous, scattered, semi-immersed to erumpent, coriaceous, ostiolate. Ostioles centrally located neck, brilliant appearance of internal content. Peridium up to 30 µm thick, composed of outer dark brown and inner brown cells of *textura angularis* and *textura prismatica*. Hamathecium comprises hyaline, basal *textura globose* and subglobose cells, supporting the pseudoparaphyses which smaller than asci, sparsely present. Asci 86–120 × 13–20 µm ($\bar{x}$ = 108 × 17 µm, n = 30), bitunicate, 8-spored, clavate, fissitunicate, wide ocular chamber at the rounded apex, with thick outer wall, inner wall raised in center, narrowing downward, base horse shoe end. Ascospores 16–21 × 6–10 µm ($\bar{x}$ = 18 × 8.3 µm, n = 30), hyaline, clavate, overlapping, biserial, with asymmetrical ends, apically wide, rounded end, narrowing towards the base, smooth walled. Asexual morph: see Doilom et al. (2015).

Material examined – Thailand, Chiang Mai, Mae Taeng, Pa Pae, 50150. 19°07'25.6"N 98°44'18.9"E, on decaying twigs of *Nephelium lappaceum*. 04 May 2023, Mekala Niranjan, 2343 (MFLU 24-0024), living culture (MFLUCC 23-0651).

Culture characteristics – Ascospores germinated on PDA within 24 h at 28 °C. One-week old culture grown 90 mm diam after 2 weeks at 28 °C. Colony circular, gray apical appearance, with umbonate elevation with filamentous margin, hyaline mycelial extension from base, shiny appearance, non-pigmented, opaque property and brown background.

GenBank Numbers – MFLUCC 23-0651: ITS: OR906152, LSU: OR906201.

Known distribution (based on molecular data) – Australia (Pavlic et al. 2008), India (Sharma et al. 2022), Thailand (Doilom et al. 2015, Senwanna et al. 2020, Chethana et al. 2023, this study).

Known hosts (based on molecular data) – *Adansonia gibbose*, *Acacia synchronica*, *Eucalyptus* sp. and *Ficus opposita* (Pavlic et al. 2008), *Tectona grandis*, *Hevea brasiliensis* (Doilom et al. 2015, Senwanna et al. 2020), *Artemisia annua* (Sharma et al. 2022), *Epipremnum pinnatum*, *Mangifera indica* (Chethana et al. 2023) and *Nephelium lappaceum* (this study).

Notes – In the phylogenetic analysis, our strain (MFLUCC 23-0651) grouped with *Pseudofusicoccum adansoniae* (ArSRK01) strain with 96% ML, 94% MP and 1.00 BYPP bootstrap support (Fig. 7). Our collection is similar to the sexual morph (MFLUCC 19-0239) described by Senwanna et al. (2020) by having a multiloculate corticolous, raised ascostromata and peridium composed of *textura angularis* whereas our isolate consists of basal *textura angularis* layers and a lateral side composed of *textura prismatica* cells. The holotype of *P. adansoniae* was reported as an endophyte with asexual morph, from dying branches of *Adansonia gibbose* (Pavlic et al. 2008). The MFLU 19-0239 collection has cylindro-clavate asci and a funnel-shaped inner wall with large

granulated ascospores whereas our collection has a large clavate asci with a raised inner wall,

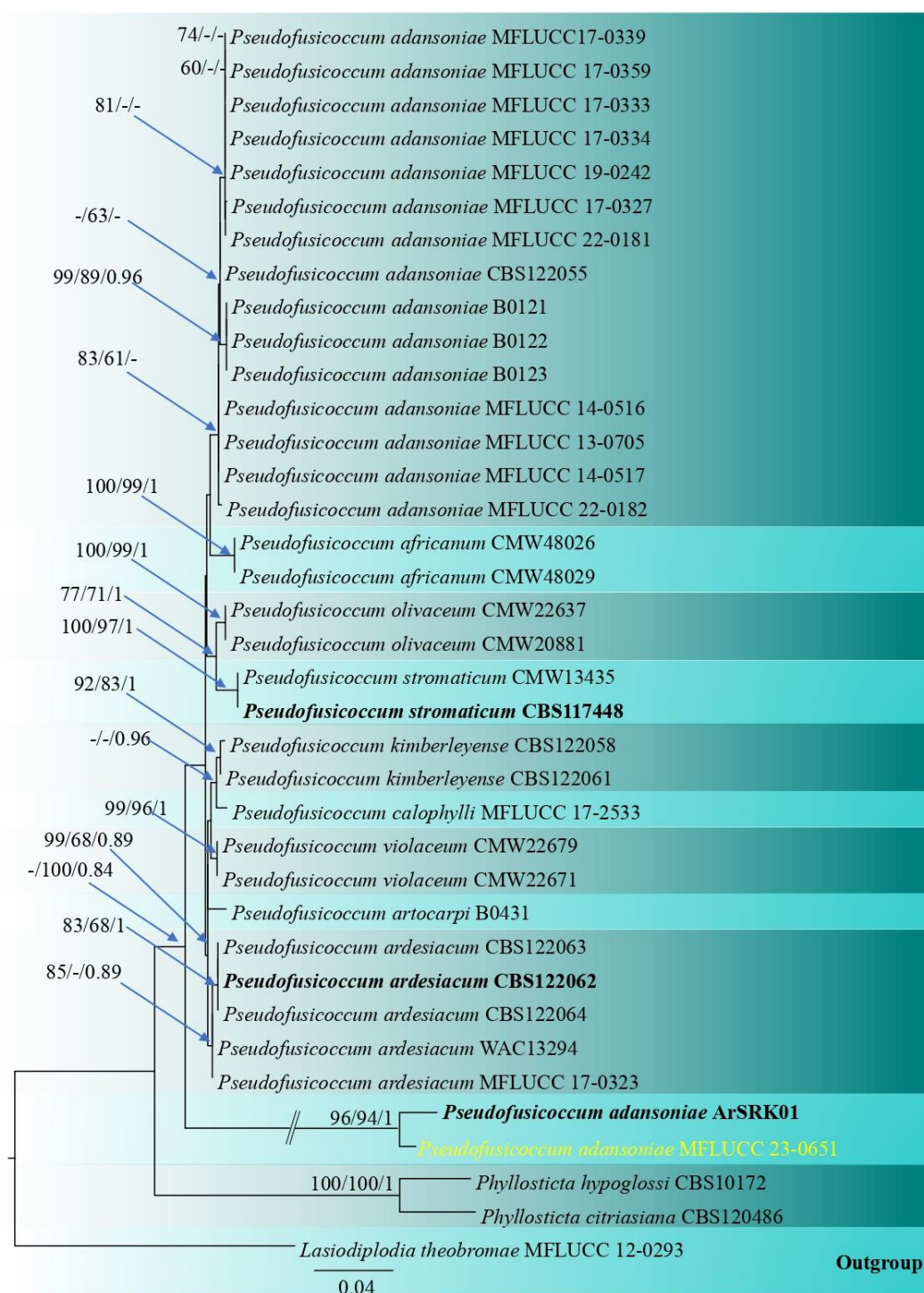


Figure 7 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, *tef1*- α and *tub2* sequence data of *Pseudofusicoccum* and *Phyllosticta*. Thirty-seven strains are included in the combined analyses. The best RAxML tree with a final likelihood value of -7471.647982 is presented. Evolutionary model GTR+I+G is applied for all the genes. The matrix had 563 distinct alignment patterns, with 44.75% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.211779, C = 0.284052, G = 0.273656, T = 0.230513; substitution rates AC = 0.691520, AG = 1.541233, AT = 0.965788, CG = 1.008488, CT = 3.200239, GT = 1.000000; gamma distribution shape parameter α = 1.265492. Bootstrap support

values for ML and MP greater than 60% and Bayesian posterior probabilities greater than 0.95 are given near nodes. The tree was rooted with *Lasiodiplodia theobromae* (MFLUCC 12-0293). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

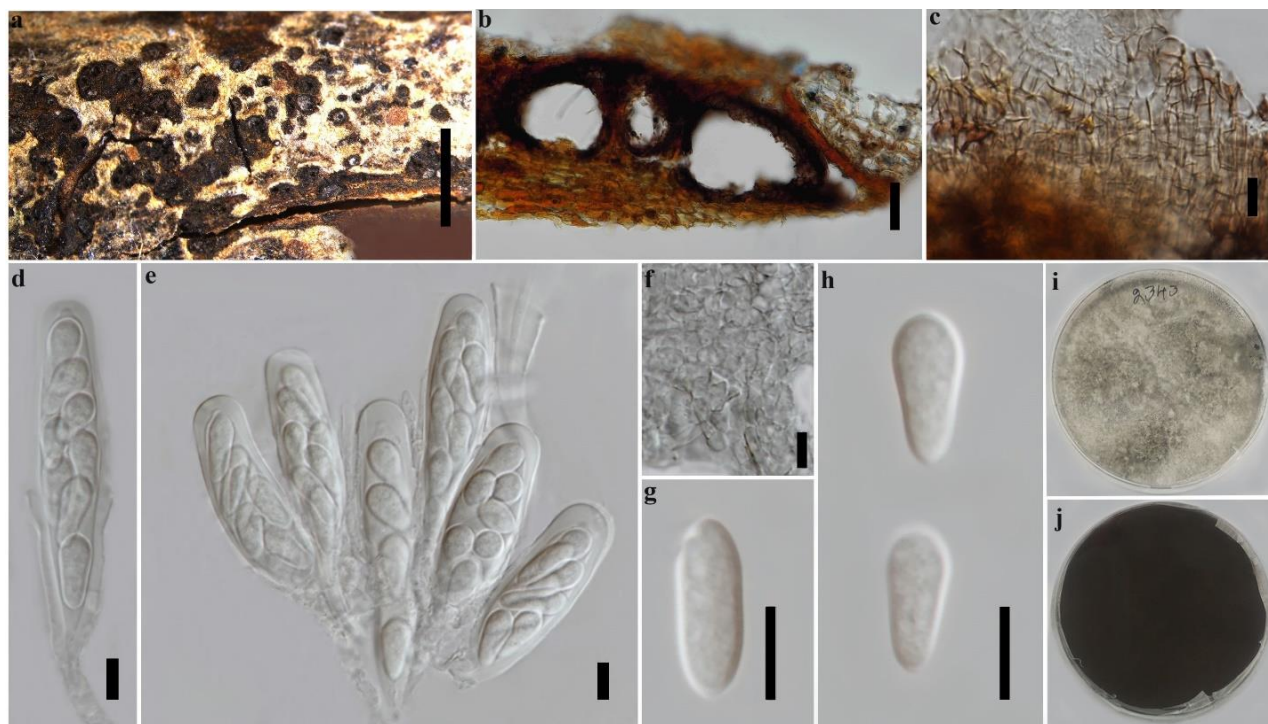


Figure 8 – *Pseudofusicoccum adansoniae* (MFLU 24-0024, a new host record). a Ascomata on host surface. b Vertical sections of ascomata. c Peridium. d–e Asci. f Hamathecium. g, h Ascospores. i, j Colonies on PDA medium (i: upper and j: reverse). Scale bars: a = 250 µm, b = 100 µm, c–h = 10 µm.

lack of granules in the ascospores which are surrounded by a mucilaginous sheath. In the colony morphology, *P. adansoniae* (MFLUCC 19-0239) has a light brown to whitish grey center, whereas in our culture, it turns into dark gray-brown. In our phylogenetic analysis, ArSRK01 and MFLUCC 23-0651 (*P. adansoniae*) form a sister clade but distance from existing *P. adansoniae* species. Therefore, additional taxon sampling of both asexual and sexual morph is required to confirm the accurate placement of *P. adansoniae*. The present study expands the host occurrence of *P. adansoniae* on *Nephelium lappaceum* from Thailand.

Dyfrlomycetales K.L. Pang, K.D. Hyde & E.B.G. Jones, in Hyde et al., Fungal Diversity 63, 7 (2013).

Pleurotremataceae Walt. Watson, New Phytol. 28, 113 (1929).

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

Index Fungorum number: IF3118; Facesoffungi number: FoF07673

Melomastia was introduced by Saccardo (1875) to accommodate *M. friesii* as the type species. Schröter (1894) synonymized *M. friesii* under *M. mastoidea*. Norphanphoun et al. (2017) demonstrated *M. italica* and *Dyfrlomycetes maolanensis* which form separate lineages within *Pleurotremataceae*, and synonymized *Dyfrlomycetes maolanensis* under *Melomastia maolanensis*. They also transferred *Melomastia* into *Pleurotremataceae* based on morphology and multi-gene phylogeny. Li et al. (2022) synonymized 11 species *Dyfrlomycetes* under *Melomastia* based on morpho-molecular studies. Phylogenetic analysis conducted by Kularathnage et al. (2023) revealed that two of the aforementioned 11 species viz. *M. chromolaenae* and *M. tiomanensis* form a distinct basal clade with other *Melomastia* species. Consequently, they were reinstated into *Dyfrlomycetes*. This genus is characterized by immersed, globose, black ascomata with an erumpent apex;

cylindrical, uniseriate asci with a J-, subapical ring; and ovoid, 2-septate ascospores constricted at the septum, with or without a gelatinous sheath (Barr 1994, Kang et al. 1999, Norphanphoun et al. 2017, Li et al. 2022). Most *Melomastia* species are isolated as saprobes from woody branches, twigs, and culms from terrestrial, freshwater, marine and mangrove habitats in both temperate and tropical countries (Norphanphoun et al. 2017, Phukhamsakda et al. 2020, Li et al. 2022, Kularathnage et al. 2023, Naziazeno & Aptroot 2023). Currently, 61 species are listed under *Melomastia* in the Index Fungorum (2024). Dong et al. (2023), recently expanded the taxonomy of the genus by introducing a novel species. Here, we provide the multi-gene phylogeny for *Melomastia* taxa (Fig. 9) and report a new host record of *Melomastia winteri*.

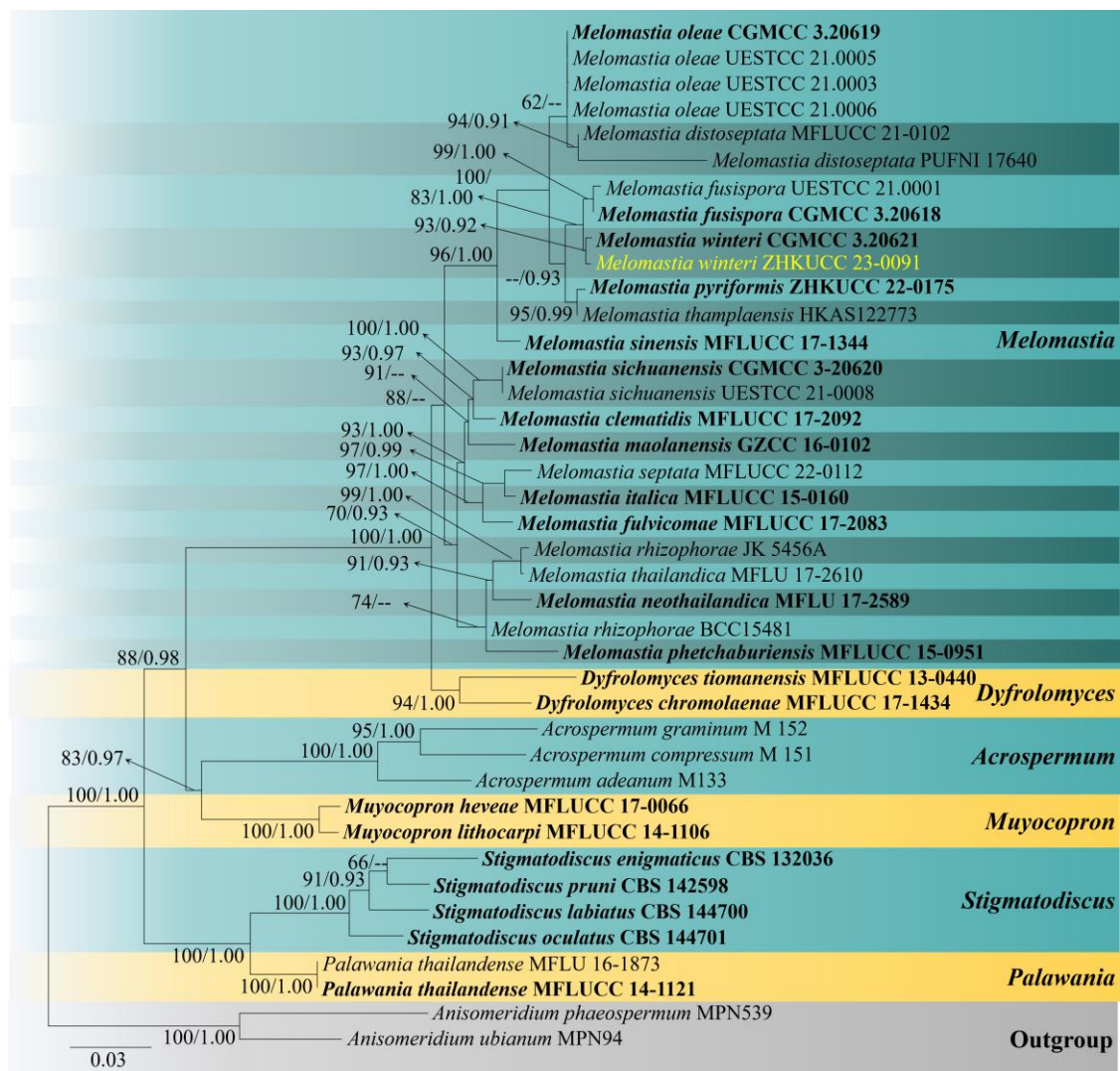


Figure 9 – Phylogram generated from the maximum likelihood analysis based on the combined LSU, SSU and *tef1*- α sequence data of *Melomastia*. Forty strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -13760.045564 is presented. The evolutionary model GTR+I+G is applied to all the genes. The matrix had 956 distinct alignment patterns, with 37.67% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.238388, C = 0.257603, G = 0.292239, T = 0.211770; substitution rates AC = 0.802988, AG = 2.204655, AT = 1.231135, CG = 0.855696, CT = 7.108307, GT = 1.000000; gamma distribution shape parameter α = 0.745973. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Anisomeridium phaeospermum* (MPN539) and *A. ubianum* (MPN94). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Melomastia winteri W.L. Li, Maharachch. & Jian K. Liu, in Li, Maharachchikumbura, Cheewangkoon & Liu, Journal of Fungi 8(1, no. 76): 14 (2022). Fig. 10

Index Fungorum number: IF841502; Facesoffungi number: FoF10536

Saprobic on dead branches of *Aquilaria* sp. Sexual morph: *Ascomata* 300–400 × 350–450 µm ($\bar{x}$ = 366 × 380 µm, n = 10), semi-immersed to immersed, solitary, gregarious, coriaceous to carbonaceous, globose, dark brown to black, ostiolate. *Ostioles* central, coriaceous to carbonaceous, dark brown to black, periphyses filling the ostiolar canal. *Peridium* 36–68 µm ($\bar{x}$ = 52.17 µm, n = 10) wide, two-layered, outer layer thick, carbonaceous and inner layer composed of 3–4 layers of hyaline to lightly brown cells of *textura angularis* to *textura prismatica*. *Hamathecium* comprises 1–3 µm wide, filiform, unbranched, septate, dense, cellular pseudoparaphyses. *Asci* 120–192 × 5–9 µm ($\bar{x}$ = 165.06 × 7.17 µm, n = 30), 8-spored, bitunicate, cylindrical, slightly flexuous, apically round, with a distinct ocular chamber, cylindrical pedicellate 5–15 × 2–5 µm ($\bar{x}$ = 10.48 × 3.47 µm, n = 30). *Ascospores* 19–28 × 5–8 µm ($\bar{x}$ = 22.40 × 6.27 µm, n = 30), partially overlapping, uniseriate, fusiform with pointed ends, hyaline, 3-septate, strongly constricted at the median septum, with guttules in each cell, lacking a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 2.5 cm after 5 days at room temperature (20–25 °C), white, dense, margin erose, somewhat fluffy, sparse aerial mycelium on the surface; reverse pale yellow.

Material examined – China, Yunnan Province, China, Yunnan Province, Xishuangbanna, Menghai city, Agarwood plantation, on dead leaves of *Aquilaria* sp. (*Thymelaeaceae*), 15 September 2021, Tianye Du, YNA64 (ZHKU 23-0040), living culture, ZHKUCC 23-0091.

GenBank numbers – ZHKU 23-0040: LSU: PP000846, SSU: PP000845, *tef1-α*: PP025857.

Known distribution – China (Li et al. 2022, this study).

Known hosts or substrata – *Olea europaea* (Li et al. 2022), *Aquilaria* sp. (this study).

Notes – Based on multi-locus phylogenetic analyses of LSU, SSU and *tef1-α*, our new strain (ZHKUCC 23-0091) clustered with the type strain of *M. winteri* (CGMCC 3.20621) with 93% ML 0.92 BYPP bootstrap support (Fig. 9). *Melomastia winteri* was introduced by Li et al. (2022) with the sexual morph isolated from leaf spots of *Olea europaea*. Our new isolate shares similar morphology to *M. winteri* (CGMCC 3.20621) in having cylindrical asci with a distinct ocular chamber and a cylindrical pedicel, and partially overlapping, uniseriate, fusiform, 3-septate ascospores deeply constricted at the median septum, with pointed ends, guttules in each cell, and lacking a mucilaginous sheath (Liu et al. 2022). Based on morphology and phylogeny, our new isolate is identified as *Melomastia winteri*. This is the first report of *M. winteri* isolated from *Aquilaria* sp.

Hysteriales Lindau, in Engler & Prantl, Nat. Pflanzenfam., Teil. I (Leipzig) 1(1): 265 (1897)

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

Glioniopsis De Not., Giornale Botanico Italiano 2 (7–8): 12, 23 (1847)

Index Fungorum number: IF2090; Facesoffungi number: FoF08055

Glioniopsis was introduced by De Notaris (1847) as a polyphyletic genus without designating a type species (Boehm et al. 2009a, b). Subsequently, Zogg (1962) defined the type species of the genus as *G. praelonga* (= *G. decipiens*) and synonymized several names under the type. Additionally, *G. curvata* with smaller ascospores was added to the genus (Zogg 1962). Currently, 70 epithets are listed in Index Fungorum (2024) and only ten species have sequence data to represent the generic placement. Several *Glioniopsis* species are polyphyletic (Hyde et al. 2020b). The sexual morph of the genus is characterized by hyaline or pigmented dictyospores that are frequently inequilateral, obovoid, obtuse to sub- to acuminate at the ends, one or more longitudinal septa, constricted at the first-formed septum, occasionally constricted at the other septa, and enclosed by a gelatinous sheath, which can be dissipate at the maturity. An aposphaeria-like asexual morph is produced (Boehm et al. 2009a). Molecular data for members of this genus comprise ITS, LSU, *tef1-α*, and *rpb2*. Based on morphology and multigene phylogeny (Fig. 11), we report a new host record of *Glioniopsis calami* from *Dipterocarpus alatus* woody litter.

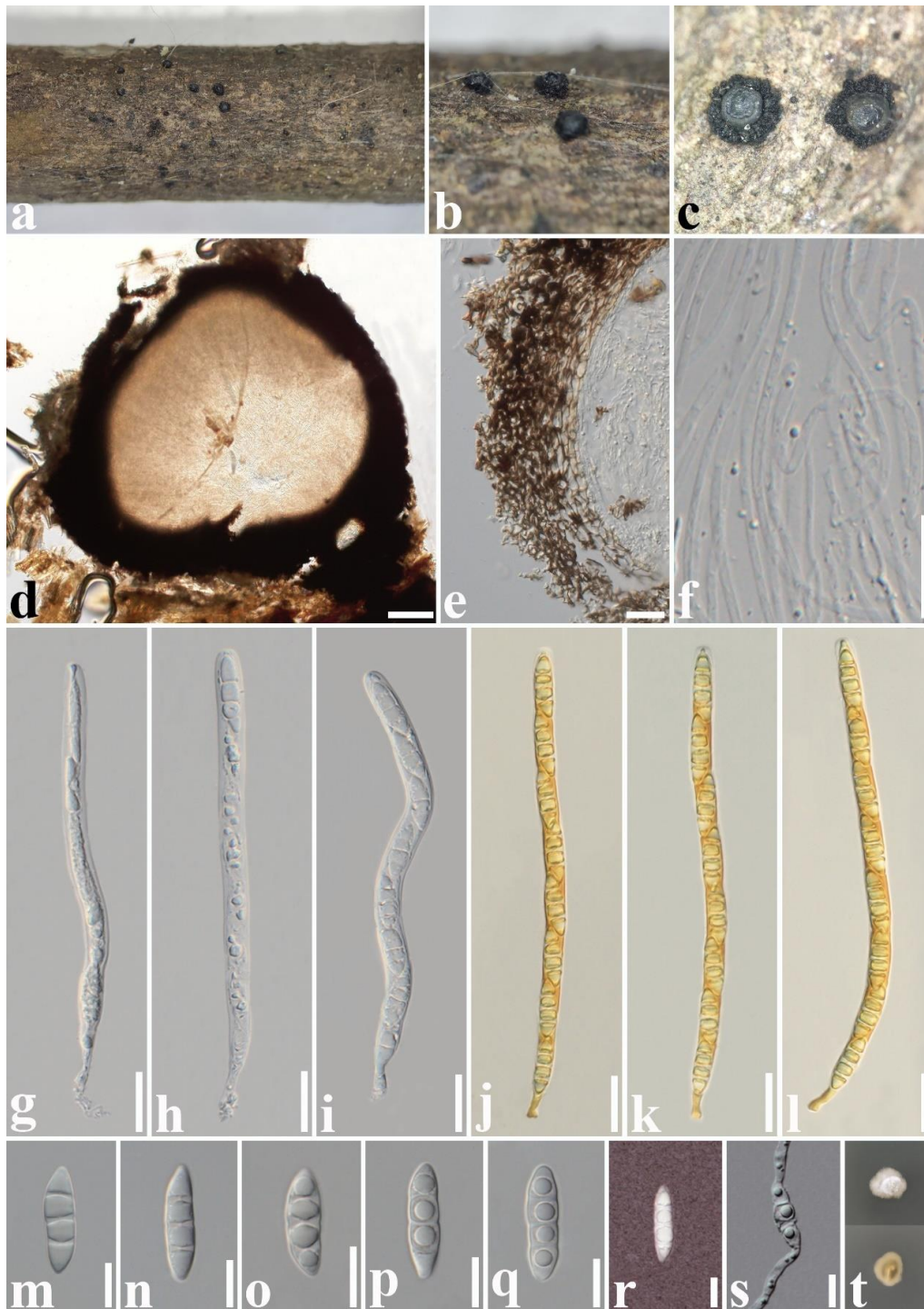


Figure 10 – *Melomastia winteri* (ZHKU 23-0040, a new host record). a–c Ascomata on the substrate. d Vertical section of an ascoma. e Peridium. f Pseudoparaphyses. g–i Asci. j–l Asci in Lugol's iodine. m–q Ascospores. r Ascospores stained in India ink. s A germinating ascospore. t Colony on PDA (above and below). Scale bars: d = 100 μ m, e–l = 20 μ m, m–s = 10 μ m.

Glioniopsis calami S. Konta & K.D. Hyde, in Hyde et al., Fungal Diversity 80: 34 (2016)
Fig. 12

Index Fungorum number: IF552234; Facesoffungi number: FoF 02366

Saprobic on *Dipterocarpus alatus* woody litter. Sexual morph: *Ascomata* 150–294 $\times$ 126.7–269 μ m ($\bar{x}$ = 242 $\times$ 182.5 μ m, n = 5), hysetrothecial, erumpent, solitary or aggregated, ellipsoid to significantly elongate, straight to curved, fragile, carbonaceous, black, with a longitudinal slit-like opening. *Peridium* 23–40.8 μ m wide ($\bar{x}$ = 31, n = 25), comprising two layers, outer layers

composed of thick, black to dark brown carbonaceous cells, inner layer composed of thin, hyaline to brown cells arranged in *textura angularis*. *Hamathecium* comprises 1.2–2.4 µm wide ($\bar{x}$ = 1.8, n = 15), cylindrical, branched, hyaline, septate, anastomosing pseudoparaphyses. Asci 48–77 × 12.5–19.5 µm ($\bar{x}$ = 62 × 16 µm, n = 20), 8-spored, bitunicate, saccate, mostly clavate to cylindric-clavate, moderately curved, with a short knob-like pedicel, apically rounded, with a well-developed ocular chamber. *Ascospores* 14.5–20.5 × 6–9.5 µm ($\bar{x}$ = 17.8 × 7.6 µm, n = 30), overlapping bi-seriate, initially hyaline, becoming pale brown to brown at maturity, dictyosporous, fusiform, ellipsoidal to cylindrical, mostly with 3–6 transverse and 2–4 vertical septa, constricted at the septa, asymmetric. Asexual morph: Not observed.

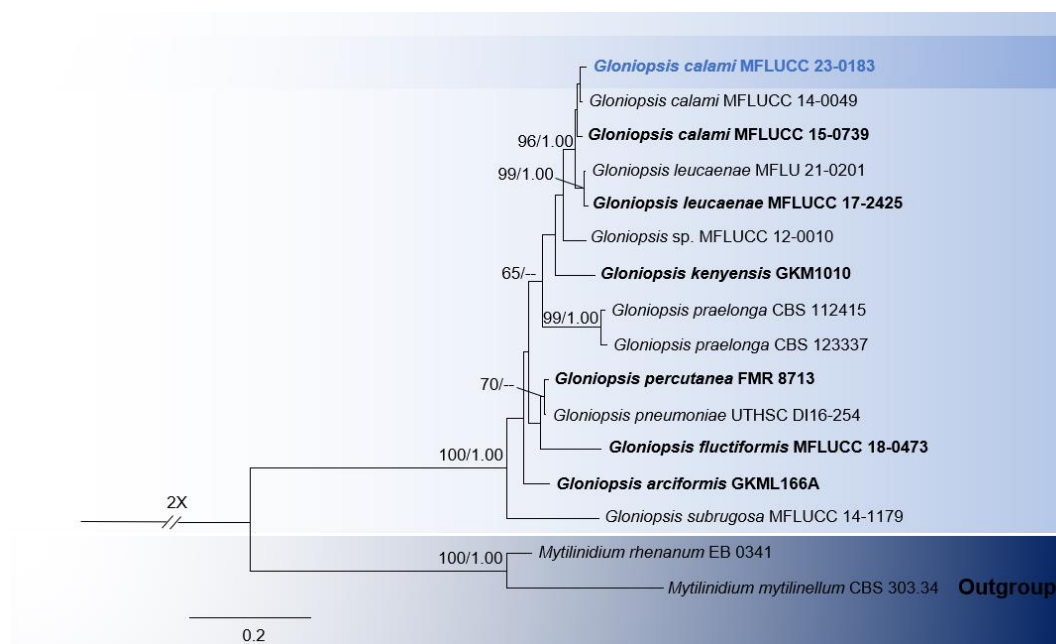


Figure 11 – Phylogram generated from Bayesian Inference (BI) analysis based on combined ITS, LSU, *rpb2* and *tef1-α* sequence data. Sixteen strains are encompassed in the combined analyses, which comprised 3,476 characters (666 characters for ITS, 894 characters for LSU, 955 characters for *rpb2*, and 961 characters for *tef1-α*) in the combined dataset. The best RAxML tree with a final likelihood value -11532.417308 is presented. Estimated base frequencies were as follows: A = 0.237170, C = 0.255073, G = 0.279680, T = 0.228076; substitution rates AC = 1.147620, AG = 3.250204, AT = 1.128420, CG = 0.549903, CT = 7.069937, GT = 1.000000; gamma distribution shape parameter α = 0.305952. The evolutionary models SYM+G, TIM1+I+G, TrNef+G, and TrN+G were applied to ITS, LSU, *rpb2* and *tef1-α* sequence data respectively. Bootstrap support values for ML equal to or greater than 65% and Bayesian posterior probabilities equal to or greater than 1.00 are indicated near nodes, in turn. The strain codes are noted after the species names. The tree is rooted with *Mytilinidium rhenanum* (EB 0341) and *M. mytilinellum* (CBS 303.34). Ex-type strains are in bold. The newly generated sequence is indicated in bold and blue.

Material examined – Thailand, Doi Tung National Park, Chiang Rai, on decaying wood of *Dipterocarpus alatus* (*Dipterocarpaceae*), 26 March 2022, N. Afshari, 2C1T1R6a (MFLU 23-0361), living culture MFLUCC 23-0183.

GenBank numbers – LSU: OR467493, *tef1-α*: OR481003, *rpb2*: OR492616.

Known distribution (based on molecular data) – Thailand, Chiang Mai and Chiang Rai provinces (Hyde et al. 2020b), Phang-Nga Province (Hyde et al. 2016), Chiang Rai Province (this study).

Known hosts (based on molecular data) – On dead *Calamus* sp. (*Arecaceae*) (Hyde et al. 2016), on decaying submerged wood in freshwater pond of an unidentified host, and on dead wood

of an unidentified host (Hyde et al. 2020b), decaying wood of *Dipterocarpus alatus* (*Dipterocarpaceae*) (this study).

Notes – In the multi-gene phylogenetic analysis, our strain (MLFUCC 23-0183) clustered together with *Glioniopsis calami* (MFLUCC 14-0049, MFLUCC 15-0739) strains, sister to *G. leucaenae* (MFLU 21-0201, MFLUCC 17-2425) based on ITS, LSU, *rpb2*, and *tef1-α* sequence dataset (Fig. 11). Our collection shares similar morphology with *G. calami* in the shape and size of ascomata, peridium, asci and ascospore characters (Hyde et al. 2016, 2020b). *Glioniopsis calami* has been collected from southern Thailand on *Calamus* sp. (Hyde et al. 2016) and from northern Thailand on unidentified wood (Hyde et al. 2020b) while, we report our collection as a new host record from *Dipterocarpus alatus* in northern Thailand.



Figure 12 – *Glioniopsis calami* (MFLU 23-0361, a new host record). a, b Appearance of ascomata on woody substrate. c Section of an ascoma. d Pseudoparaphyses and asci. e–h Asci. i–q Ascospores. r A germinated ascospore. s, t Colony on PDA (s-above, t- reverse). Scale bars: a = 1 mm, b = 200 μm, c, r = 50 μm, d–h = 20 μm, i–q = 10 μm.

Kirschsteiniotheliales Hern. -Restr., R.F. Castañeda, Gené & Crous, Studies in Mycology 86: 72 (2017)

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

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

Index Fungorum number: IF25723; Facesoffungi number: FoF08040

Kirschsteiniothelia was introduced with *Kirschsteiniothelia atra* as the type species (Hawksworth 1985). *Kirschsteiniothelia* is commonly found on dead wood in tropical and subtropical areas in both freshwater and terrestrial habitats (Boonmee et al. 2012, Mehrabi et al. 2017, Bao et al. 2018, Rodríguez-Andrade et al. 2019, Sun et al. 2021, Verma et al. 2021, Xu et al. 2023). The sexual morph of this genus is characterized by superficial, semi-immersed, globose ascomata, bitunicate, cylindrical to clavate asci with eight, ellipsoidal, septate (1–2), brown ascospores (Hawksworth 1985, Boonmee et al. 2012, Bao et al. 2018, Sun et al. 2021, Xu et al. 2023). Dendryphiopsis-like and sporidesmium-like are two different types of asexual morphs of *Kirschsteiniothelia* (Boonmee et al. 2012, Sun et al. 2021). Forty-eight *Kirschsteiniothelia* species are listed in Species Fungorum (2024). The support for a single species for *K. aethiops* is quite weak and the hosts are diverse (mangrove vs terrestrial), therefore this is likely to be a species complex. Further collections from various hosts and habitats (see known hosts and habitats below) are required to address these discrepancies. Here, we provide a tentative new host record of *Kirschsteiniothelia atra* from Iran (Fig. 13).

Kirschsteiniothelia atra (Corda) D. Hawksw., Fungal Diversity 69: 37 (2014)

Fig. 14

Index Fungorum number: IF804962; Facesoffungi number: FoF14763

Saprobic on dead wood of *Fagus orientalis*. Asexual morph: *Mycelium* mostly immersed, septate, branched, brown. *Conidiophores* 150–250 $\mu\text{m} \times 5\text{--}10\text{ }\mu\text{m}$ ($\bar{x} = 180\text{ }\mu\text{m} \times 6.7\text{ }\mu\text{m}$, $n = 20$), macronematous, mononematous, cylindrical, branched at the top, forming a stipe and head, light brown to brown. *Conidiogenous cells* 22–30 $\times 6\text{--}10\text{ }\mu\text{m}$ ($\bar{x} = 25\text{ }\mu\text{m} \times 7\text{ }\mu\text{m}$, $n = 20$), tretic, integrated, originate from the terminal cell of conidiophore, brown. *Conidia* 35–60 $\times 12\text{--}20\text{ }\mu\text{m}$ ($\bar{x} = 48 \times 13\text{ }\mu\text{m}$, $n = 30$), acrogenous, cylindrical with rounded ends, pale to mid-dark brown, 3–4 transverse septate, strongly darken at the septa. Sexual morph: Undetermined.

Culture characteristics – Colonies growing on PDA, reaching 50 mm in diameter after 15 days at 25 °C under dark conditions, flat, entire margin, initially olivaceous to pale brown and eventually black after 15 days, mycelium immersed to superficial and sporulating after 30 days on PDA.

Material examined – Iran, Mazandaran, Sari, Pol sefid, Sangdeh forest, on dead *Fagus orientalis* (Fagaceae), 6 October 2017, Omid Karimi, (FUM 20-016).

GenBank number – ITS: MG602687.

Known distribution – Australia (Hyde 1993), China (Su et al. 2016), Cuba (Mercado 1984), Czech Republic (Reblova & Svrcek 1997), France (Aptroot 1995), Germany (Schmid-Heckel 1988), India (Subramanian & Sekar 1987, Prasher & Kumar-Verma 2016), Iran (Gharizadeh et al. 2004, this study), Japan (Otani & Tubaki 1976, Tanaka & Hosoya 2006), Mexico (Aptroot 1995), New Zealand (Ellis 1971), Poland (Chlebicki 2006), Russia (Aptroot 1995), Sweden (Eriksson 1992, Nordén et al. 1997), USA (Goos & Uecker 1992).

Known hosts – *Alnus glutinosa* (Mulenko et al. 2008), *Carpinus betulus* (Reblova & Svrcek 1997, Chlebicki 2006), *Carpinus* sp. (Chen & Hsieh 2004), *Cedrus deodara* (Prasher & Kumar-Verma 2016), *Corylus avellane* (Schmid-Heckel 1988, Nordén et al. 1997), *Fagus orientalis* (this study), *Hedera helix* (Aptroot 1995), *Lonicera coerulea* (Aptroot 1995), *Phoenix dactylifera* (Hyde 1993), *Quercus robur* (Eriksson 1992).

Note – The phylogenetic analysis based on the combined ITS and LSU data revealed that our strain (FUM 20-016) clustered with *Kirschsteiniothelia atra* strains (MFLUCC 16-1104 and S-783) with 99% ML and 0.90 BYPP bootstrap support (Fig. 13). Our collection (FUM 20-016) morphologically resembles *K. atra* in having macronematous, mononematous, cylindrical, branched, brown conidiophores, tretic, integrated conidiogenous cells, and acrogenous, cylindrical,

rounded end, brown, 3–4-transversely septate conidia (Su et al. 2016). Based on morphology and phylogenetic analysis we conclude our isolate is *K. atra* and this is a new host record of this fungus from *Fagus orientalis* in Iran.

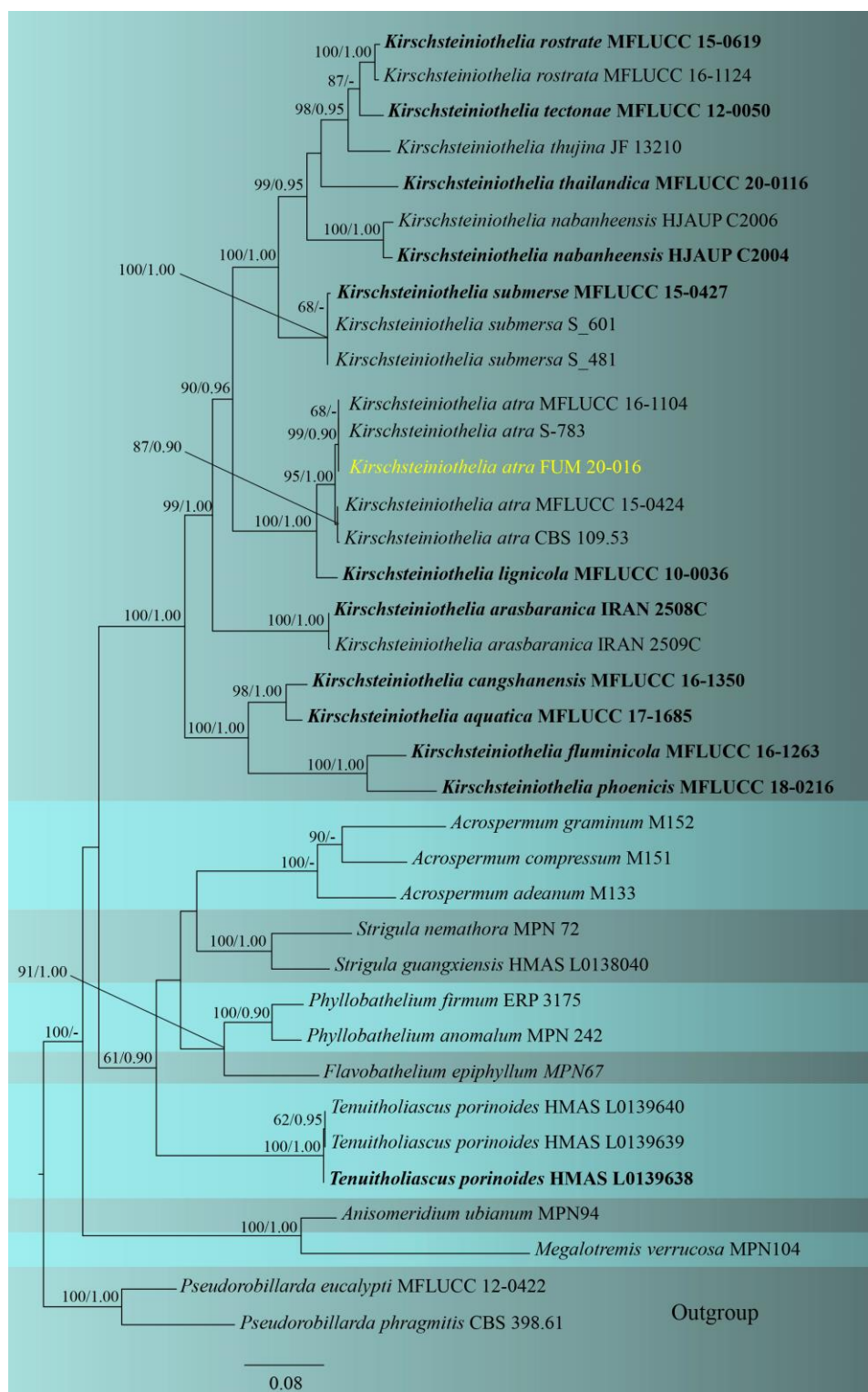


Figure 13 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Thirty-seven strains are included in the combined analyses. Maximum likelihood bootstrap support values greater than or equal to 60% and Bayesian posterior probabilities greater than or equal to 0.90 are given near nodes, respectively. The newly generated sequences are indicated in yellow. All the type specimens are in bold. The best-scoring RAxML tree with a final likelihood value of -14019.668883 is presented. Estimated base frequencies were

as follows: A = 0.225868, C = 0.25568, G = 0.310821, T = 0.207631; substitution rates AC = 1.287961, AG = 2.917321, AT = 1.278427, CG = 1.371353, CT = 6.772959, GT = 1.000000; gamma distribution shape parameter α = 0.282300. The tree was rooted with *Pseudorobillarda eucalypti* (MFLUCC 12-0422) *Pseudorobillarda phragmitis* (CBS 398.61).

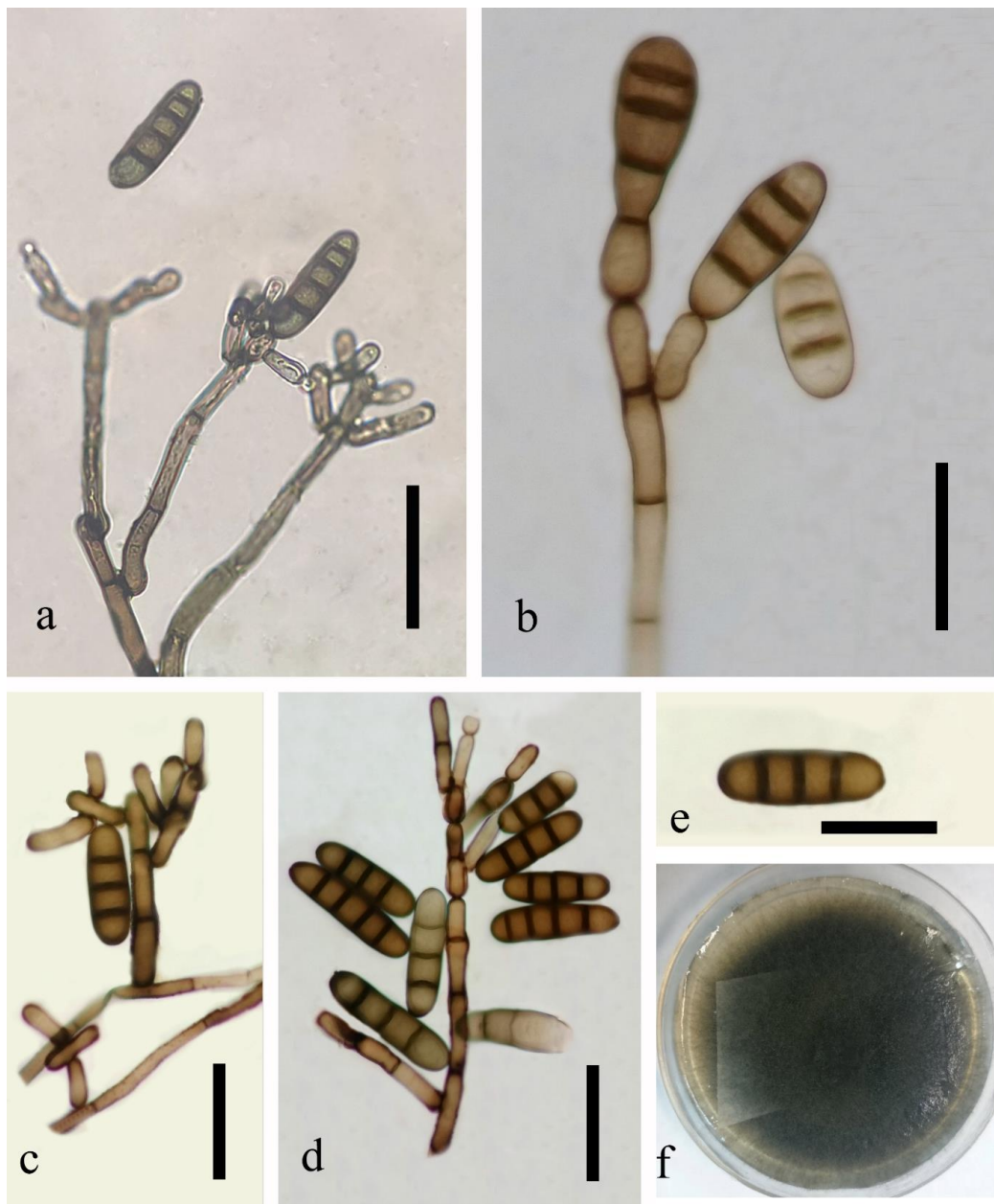


Figure 14 – Asexual morph of *Kirschsteiniothelia atra* (FUM 20-016, a new host record). a, b Conidiophores with conidia c–e Conidiogenous cells and conidia f Colony on PDA after 15 days. Scale bars: a, b = 20 μ m, c–e = 10 μ m.

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

Didymosphaeriaceae Munk

Letendraea Sacc.

Index Fungorum number: IF2812; Facesoffungi number: FoF00044

Saccardo (1880b) introduced *Letendraea* with *L. eurotioides* as the type species. *Letendraea eurotioides* is characterized by superficial, globose to conical ascomata, filiform pseudoparaphyses, obclavate to cylindrical, 8-spored asci, and fusoid to oblong, 1-septate ascospores (Ariyawansa et al. 2014). Species of *Letendraea* are saprobic in terrestrial habitats, pathogenic associated with leaf

spot disease in *Cordyline* sp. (Ariyawansa et al. 2014) and are also recorded from marine environments (Huang et al. 2019). Taxonomists have placed *Letendraea* in different families by considering morphological characteristics. Kodsueb et al. (2006) placed *Letendraea* in *Melanommataceae* due to similar morphology with *Karstenula rhodostoma* and Zhang et al. (2012b) referred *Letendraea* to *Montagnulaceae*. However, based on multi-gene phylogenies, Ariyawansa et al. (2014) revealed that *Letendraea* belongs to *Didymosphaeriaceae*. Fifteen *Letendraea* species are listed in Species Fungorum (2024), but sequence data is available for only a few species.

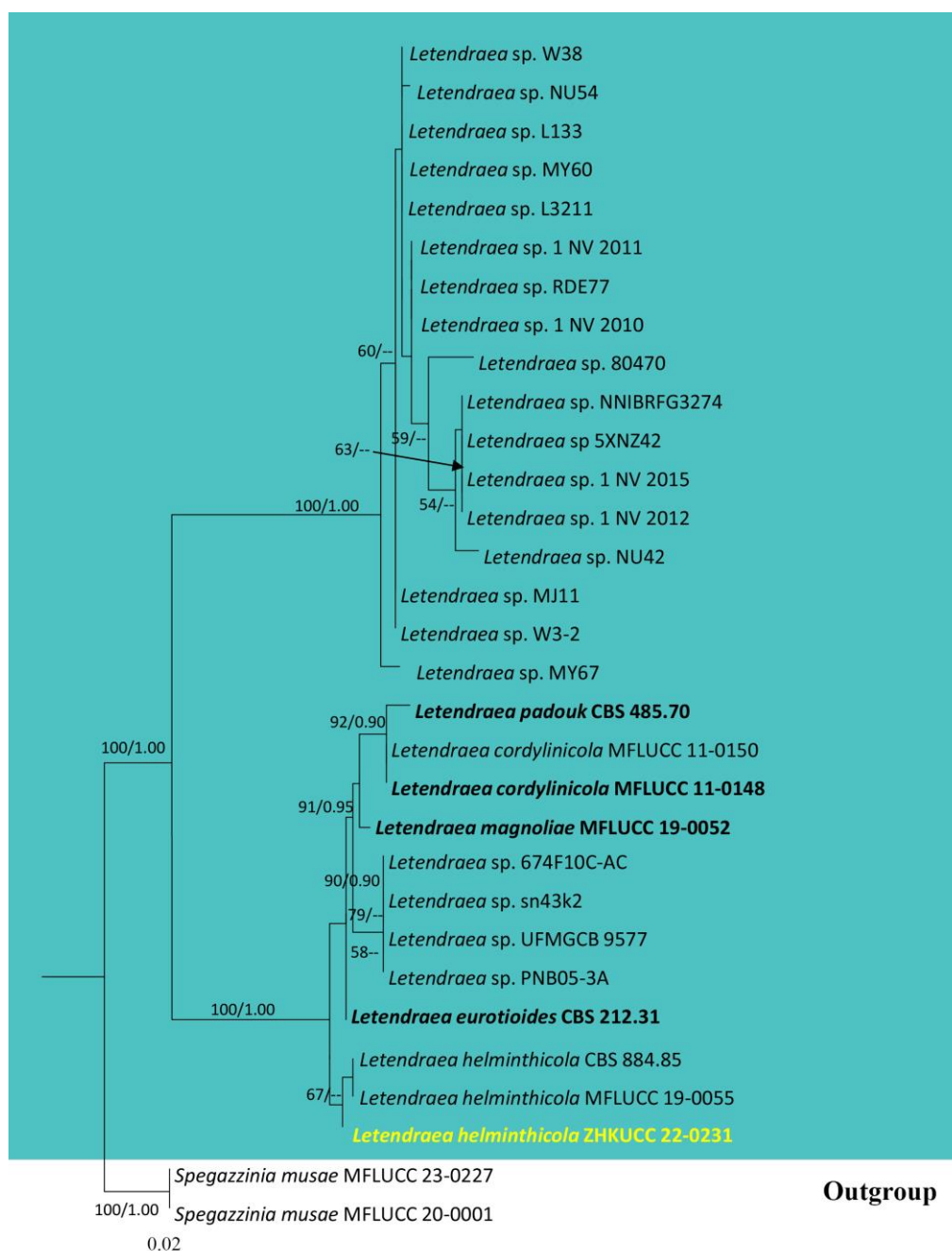


Figure 15 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of 31 strains, which comprised 1,492 characters (ITS = 607, LSU = 885). The best scoring RAxML tree with a final likelihood value of -3376.742825 is presented. The matrix had 283 distinct alignment patterns, with 41.66% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.230861, C = 0.254110, G = 0.290892, T = 0.224136; substitution rates: AC = 1.442773, AG = 1.468182, AT = 2.173572, CG = 1.202084, CT =

6.283883, GT = 1.0; gamma distribution shape parameter α = 0.123415. Bootstrap support values for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (the rounding of values to 2 decimal proportions) from Bayesian inference analysis are labeled at each node. Ex-type strains are in bold, while the new isolate is indicated in yellow bold. The tree is rooted to *Spiegazzinia musae* (MFLUCC 23-0227, MFLUCC 20-0001).

Letendraea helminthicola (Berk. & Broome) Weese, Trans. Br. mycol. Soc. 21(3-4): 277 (1938) [1937] Fig. 16

Index Fungorum number: IF252540; Facesoffungi number: FoF09440

Saprobic on bamboo stems, visible as black dots on the host surface. Sexual morph: *Ascomata* 190–330 μm wide, 210–350 μm high, densely gregarious, erumpent through epidermis, sometimes superficial, subglobose to turbinate, flattened at the base, black, tuberculate, ostiolate, rounded to truncate at apex. *Ostiolar canal* lined with short periphyses growing downwards. *Peridium* 20–25 μm wide, 2–5-layers, composed of dark brown to brown cells of *textura angularis*. *Pseudoparaphyses* 1.5–3 μm wide, rarely branched, septate. *Asci* 80–90 $\times$ 8–10 μm , bitunicate, 8-spored, elliptical, short pedicellate. *Ascospores* 12–18 $\times$ 4–7 μm , overlapping, uniseriate, oblong-fusoid, pointed at ends, straight or sometimes curved, 1-septate at middle, constricted at the septum, dark brown. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 2 cm diameter after 7 days at 25 °C, colonies circular, margin filiform to slightly undulate, flat to slightly raised, dense, velvety appearance, off-white mycelia and colony from above: cream and light brown; reverse: brown.

Material examined – China, Yunnan Province, on decaying stems of *Bambusa* sp. (*Poaceae*), 18 January 2019, ND Kularathnage, MHZU 23-0244 (living culture ZHKUCC 23-0231).

GenBank numbers – ITS: OR997674; LSU: OR997717.

Known distribution – China, India, Mauritius, Mexico, Thailand (Andaman Sea and Gulf of Thailand), Spain

Known hosts – *Cinnamomum* sp., rice, *Eucalyptus deglupta*, *Eucalyptus urophylla*, *Nervilia fordii*, *Magnolia liliifera* (de Silva et al. 2021), *Suaeda salsa*, *Annella* sp., *Taxus globosa*, coral, marine sponge, polyester coating, textile wastewater.

Notes – The combined ITS and LSU phylogenetic analyses showed that our collection clustered with *Letendraea helminthicola* with 100% ML and 1.00 BYPP bootstrap support (Fig. 15). Our isolate shares similar morphological characteristics with *Letendraea helminthicola*. The sexual morph of *L. helminthicola* was introduced as hyper-pathogenic on *Helminthosporium appendiculatum* by Petch (1938) from the UK. The asexual morph of this species was described by de Silva et al. (2021). This species has been reported from China (Yunnan, Taiwan) on healthy leaves of *Magnolia candolli* and on dead branches of *Cinnamomum* sp. This is the first report of *Letendraea helminthicola* on *Bambusa* sp. in China.

Massariaceae Nitschke, Verh. Naturhist. Vereines Preuss. Rheinl.: 73 (1869)

Massarioramusculicola Huanral., Thambug. & K.D. Hyde, Phytotaxa 371 (1): 20 (2018)

Index Fungorum number: IF554425; Facesoffungi number: FoF04478

Massarioramusculicola is a monotypic genus introduced to accommodate *M. chiangraiensis* as the type species (Huanraluek et al. 2018). *Massarioramusculicola* is similar to *Neomassaria*, however, can be differentiated by having a peridium with two strata comprising dark brown to hyaline cells and 3-septate, fusiform ascospores (Huanraluek et al. 2018). *Massarioramusculicola chiangraiensis* was recorded as a saprobe with sexual morphs from dead twigs in terrestrial environments in Thailand (Huanraluek et al. 2018). Herein, we provide a new host and a country record of *M. chiangraiensis* (Fig. 17).

Massarioramusculicola chiangraiensis Huanral., Thambug. & K.D. Hyde, Phytotaxa 371 (1): 20 (2018) Fig. 18

Index Fungorum number: IF554426; Facesoffungi number: FoF04479

Saprobic on dead twig of *Coffea* sp. Sexual morph: *Ascomata* 150–250 μm high $\times$ 170–240 μm diam. ($\bar{x}$ = 191 $\times$ 193 μm , n = 15), immersed to semi-immersed, solitary or scattered, coriaceous, globose to subglobose, black, uniloculate, ostiolate. *Ostiole* central, with periphyses in the canal. *Peridium* 15–25 μm wide ($\bar{x}$ = 20 μm , n = 20), composed of two strata; outer stratum comprising 4–6 layers of dark brown to black, thick-walled cells of *textura angularis* fusing at the outside with the host tissues, inner stratum comprising several layers of lightly pigmented to hyaline, thin-walled cells of *textura angularis*. *Hamathecium* comprises 1–2 μm wide ($\bar{x}$ = 1.7 μm , n = 20), cylindrical to filiform, trabeculae, branched, septate pseudoparaphyses embedded in a gelatinous matrix. *Asci* 60–80 $\times$ 8–12 μm ($\bar{x}$ = 71 $\times$ 10.2 μm , n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, with short, rounded pedicel, apically rounded with a distinct ocular chamber. *Ascospores* 20–24 $\times$ 4–6 μm ($\bar{x}$ = 21 $\times$ 4.6 μm , n = 25), overlapping 1–2-seriate, fusiform, 1–3-septate, slightly constricted at the septa, smooth-walled, hyaline, straight or slightly curved, guttulate at the maturity, surrounded by a thin mucilaginous sheath. Asexual morph: Not observed.

Material examined – China, Yunnan Province, Lincang City, on a dead twig of *Coffea* sp. (*Rubiaceae*), 28 July 2022, Li Lu, LC3-C8 (MHZU 23-0084), living culture ZHKUCC 23-0678 = ZHKUCC 23-0679.

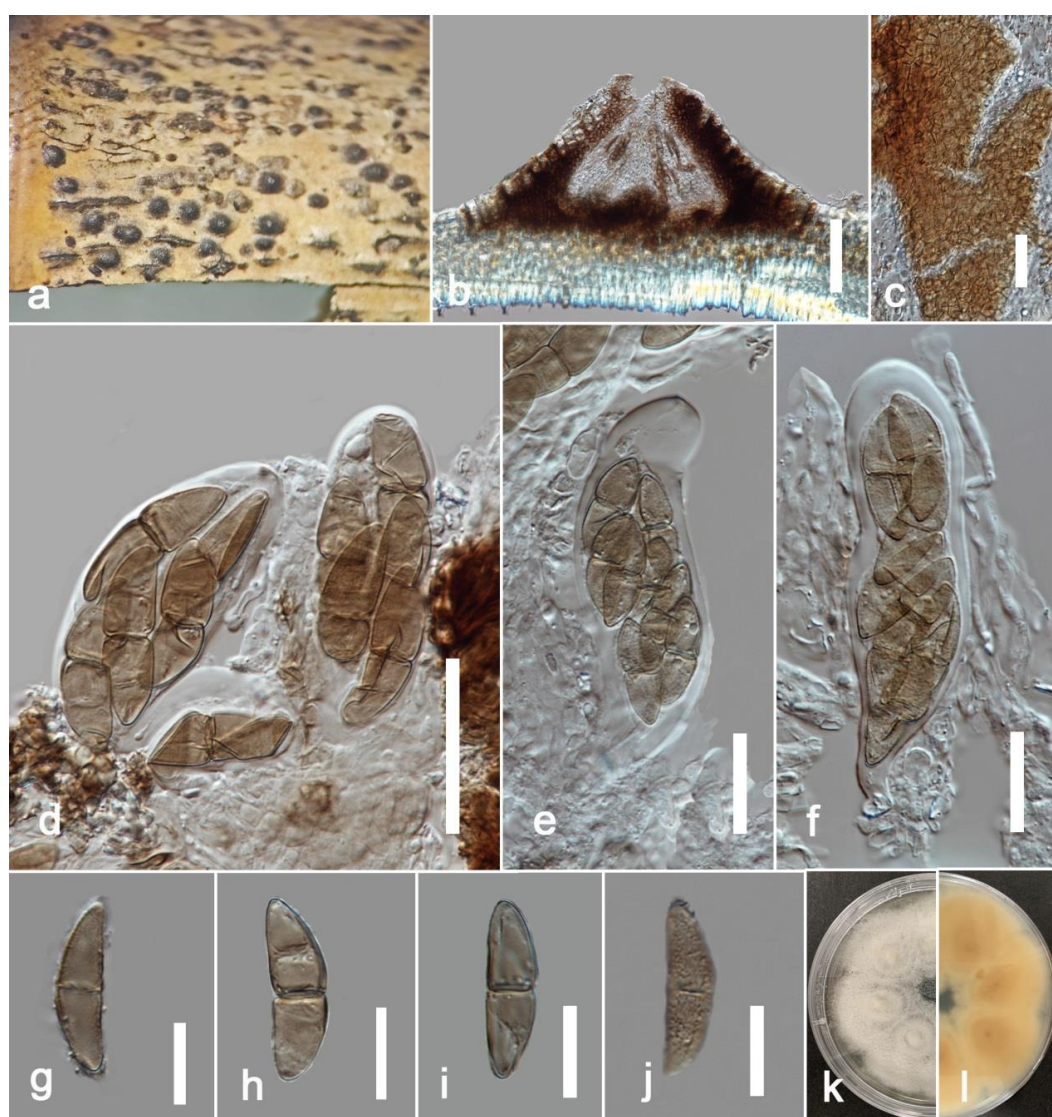


Figure 16 – *Letendraea helminthicola* (MHZU 23-0244, a new host record). a Ascomata on host substrate. b Cross section of an ascoma. c Peridium. d–f Asci. g–j Ascospores. k Surface view of

colonies on PDA. l Reverse view of colonies on PDA. Scale bars: b = 100 μ m, d–f = 20 μ m, c, g–j = 10 μ m.

Culture characters – Ascospores germinating on PDA within 12 hours. Colonies on PDA reaching 30–40 mm within 4 weeks at 25 °C. Culture from above circular to slightly irregular, flat to slightly raised, dense, surface light red, fluffy, reverse saffron to brown, yellowish at the margin.

GenBank numbers – ZHKUCC 23-0678: LSU: OR836013, SSU: OR836019, *rpb2*: OR832763; ZHKUCC 23-0679: LSU: OR836014, SSU: OR836020, *rpb2*: OR832764.

Known distribution (based on molecular data) – China (this study), Thailand (Huanraluek et al. 2018).

Known hosts (based on molecular data) – dead twig of an undetermined host (Huanraluek et al. 2018), dead twig of *Coffea* sp. (this study).

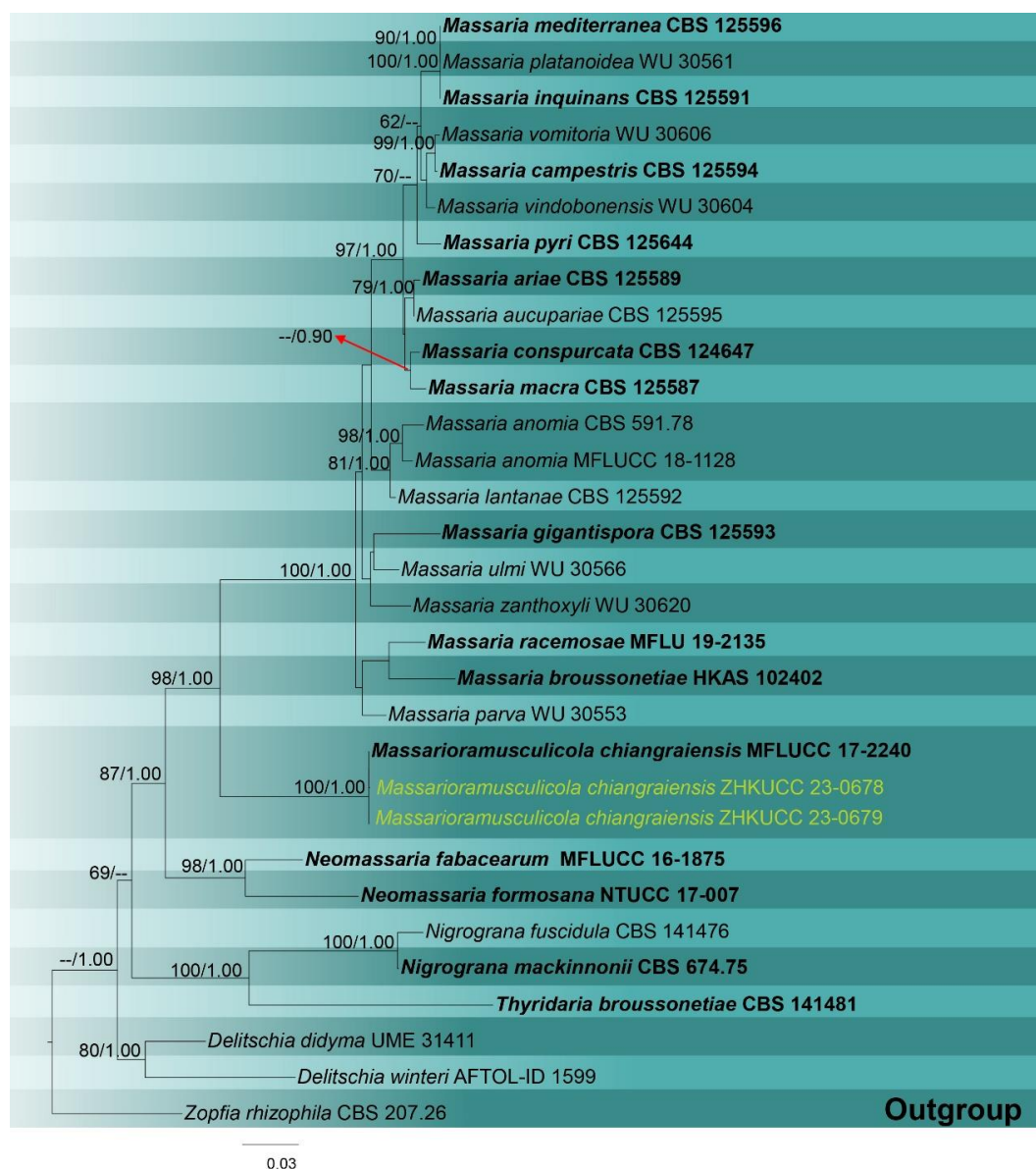


Figure 17 – Phylogram generated from the maximum likelihood analysis based on the combined LSU, SSU and *rpb2* sequence data. Thirty-one strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAXML tree with a final likelihood value of -12352.346556 is presented. The evolutionary model GTR+I+G is applied to all the genes. The matrix had 876 distinct alignment patterns, with 27.97% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.265291, C =

0.210605, G = 0.277032, T = 0.247072; substitution rates AC = 1.629000, AG = 4.051773, AT = 1.273955, CG = 1.030927, CT = 9.095774, GT = 1.000000; gamma distribution shape parameter α = 0.158830. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Zopfia rhizophila* (CBS 207.26). All type strains are in bold. The newly generated sequences are indicated in yellow.



Figure 18 – Sexual morph of *Massarioramusclicola chiangraiensis* (MFLU 23-0084, a new host and new geographical record). a, b Appearance of ascostroma on host surface. c Section through ascoma. d Section through peridium. e Hamathecium. f–i Asci. j Geminated ascospore. k, l culture on PDA from above and reverse. m–r Ascospores (q ascospore stained with Lugol's iodine; r ascospore stained with Indian ink). Scale bars: c = 100 μ m, d–j = 20 μ m, m–r = 10 μ m.

Notes – This species is typical of *Massarioramusclicola* as it has trabeculate pseudoparaphyses (*sensu* Liew et al. 2000), cylindrical to cylindric-clavate asci and fusiform to subclavate hyaline ascospores (Huanraluek et al. 2018). According to the phylogenetic analyses, our strains (ZHKUCC 23-0678 and ZHKUCC 23-0679) clustered with *Massarioramusclicola*

chiangraiensis (MFLUCC 17–2240, ex-type) with 100% ML and 1.00 BYPP bootstrap support (Fig. 17). The sexual morph of our fungal collection resembles *M. chiangraiensis* (the holotype) which was isolated from a dead twig of an undetermined host (Huanraluek et al. 2018). Huanraluek et al. (2018), used only LSU sequence data to introduce *Massarioramusclicola*. We updated the combined phylogeny of LSU, SSU, and *rpb2* and revealed *Massarioramusclicola* is a distinct genus in *Massariaceae*. This study provides *rpb2* sequences for the type species (*M. chiangraiensis*) for the first time. This study presents a new host record and a country record of *M. chiangraiensis* from *Coffea* sp. in China.

Massariaceae Munk

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

Index Fungorum number: IF8495; Facesoffungi number: FoF06499

Link (1809) established *Helminthosporium* to accommodate *H. velutinum* as the type species.

The genus is characterized by macronematous, cylindrical, erect, septate conidiophores with tretic conidiogenous cells and clavate or obclavate, distoseptate conidia with bud scars at the base (Luttrell 1964, Voglmayr & Jaklitsch 2017). *Helminthosporium* includes well-known species as saprobes and pathogens exhibiting a worldwide distribution and a wide range of hosts. The genus currently includes 781 species (Index Fungorum 2024), and most of them are not congeneric with the generic type in the development of conidia and conidiophores. In addition, only 25 species have sequence data, and most species are based on morphological studies. In this study, we introduced a new species *Helminthosporium guizhouense* based on morphological evidence and phylogenetic analysis (Fig. 19).

Helminthosporium guizhouense Y.Y. Yang, A.R. Gomes de Farias & K.D. Hyde, sp. nov. Fig. 20

Index Fungorum number: IF902274; Facesoffungi number: FoF15237

Etymology – Referring to the collecting site “Guizhou Province, China”, where the holotype was collected

Holotype – HKAS 130313

Saprobic on a dead branch of *Quercus fabrei*. Sexual morph: Undetermined. Asexual morph: *Colony* on the natural substrate punctiform, effuse, black, hairy. *Mycelium* mostly immersed towards the surface, septate, forming stroma-like aggregations of light to dark-brown pseudoparenchymatous cells. *Conidiophores* 387–953 × 12–25 µm ($\bar{x}$ = 590 × 16, n = 10), macronematous, mononematous, unbranched, arising solitarily or in small groups from the stroma cells, erect, straight or flexuous, simple, thick-walled, subcylindrical, smooth, dark to blackish brown, paler near the apex, multiple-septate. *Conidiogenous cells* monotretic, terminal, with well-defined small pores at the apex, rarely laterally beneath the upper 1–2 septa. *Conidia* 72–121 × 18–26 µm ($\bar{x}$ = 91 × 21, n = 25), tapering to 5–10 µm at the distal end, with a fuscous truncate 7–9 µm wide scar at the base, obclavate, angular lunate, straight or flexuous, smooth, (2–) 6–11 (–16)-distoseptate, pale olive when immature, thin-walled, pale brown.

Culture characteristics – Slow growing on PDA media, reaching 6.3 cm after incubation at 25 °C for 21 days, white, circular, velvety, reverse creamy white, with black at the center.

Material examined – China, Guizhou Province, Zunyi City, Zhengan County, on a dead branch of *Quercus fabrei* (*Fagaceae*), 6 October 2021, Y.Y. Yang, YYY142 (HKAS 130313, holotype), ex-type living culture KUNCC 24-18300.

GenBank numbers – LSU: PP981904, ITS: PP981907, SSU: PP977159, and *tef1-α*: PQ041228.

Notes – In the phylogenetic analysis of combined LSU, ITS, *rpb2* and *tef1-α* sequence data, our strain (HKAS 130313) formed a separate lineage with *Helminthosporium hispanicum* (WU 38843), *H. syzygii* (CBS 145570), *H. chengduense* (UESTC 22.0025) and *H. chengduense* (CGMCC3.23575) with 100 ML and 1.00 BYPP statistical support (Fig. 19). Sequence comparison for the ITS region between *H. guizhouense* (HKAS 130313) and *H. hispanicum* (WU 38843)

showed a 2.71% (15/553 bp, excluding gap) base pair difference. In addition, *H. guizhouense* shares similar morphological characteristics with *H. hispanicum* by having terminal, intercalary conidiogenous cells and solitary conidia with distosepta. However, the conidiophores (387–953 × 12–25 µm) of *H. guizhouense* are longer than *H. hispanicum* (130–540 × 13–22.5 µm) (Voglmayr & Jaklitsch 2017). The conidia of *H. guizhouense* are also initially pale olive, while in *H. hispanicum* they are hyaline. Hence, based on morphology and multi-gene phylogeny, we introduce *H. guizhouense* as a new species.

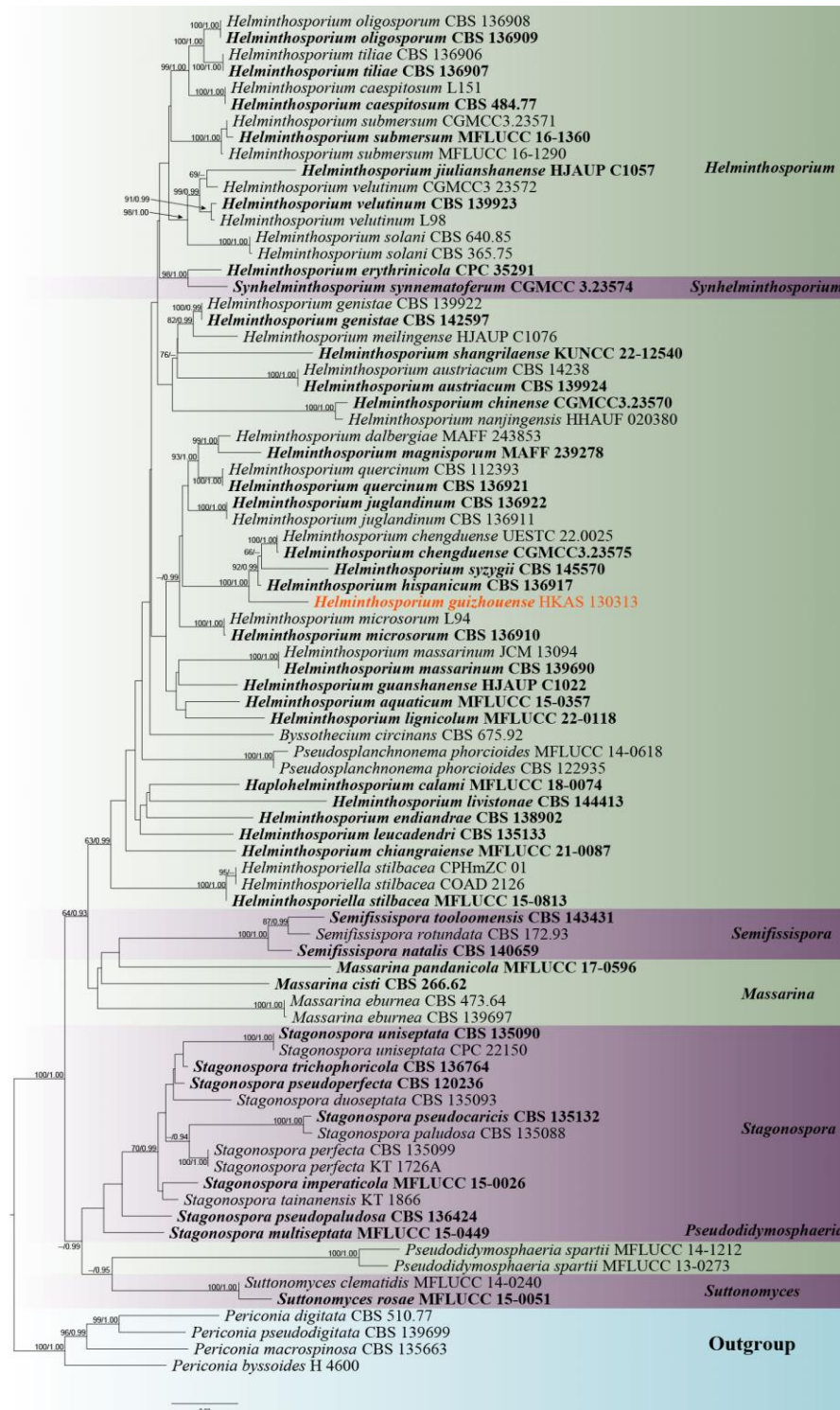


Figure 19 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, SSU and *tef1-α* sequence data of the genus *Helminthosporium*. Eighty-two strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar

to the Bayesian analysis. The best RAxML tree with a final likelihood value of -25294.82 is presented. The evolutionary model GTR+I+G is applied to all the genes. The matrix had 1389 distinct alignment patterns, with 32.75% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.234938, C = 0.250654, G = 0.268824, T = 0.245584; substitution rates AC = 1.740057, AG = 3.253679, AT = 1.865780, CG = 1.115589, CT = 7.637143, GT = 1.000000; gamma distribution shape parameter α = 0.478784. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree is rooted in *Periconia digitata* (CBS 510.77), *P. pseudodigitata* (CBS 139699), *P. macrospinoa* (CBS 135663), and *P. byssoidea* (H 4600). Estimated base frequencies were as follows: A = 0.234938, C = 0.250654, G = 0.268824, T = 0.245584; substitution rates AC = 1.740057, AG = 3.253679, AT = 1.865780, CG = 1.115589, CT = 7.637143, GT = 1.000000; gamma distribution shape parameter α = 0.478784. Ex-type strains are in bold. The newly generated sequences are indicated in red.

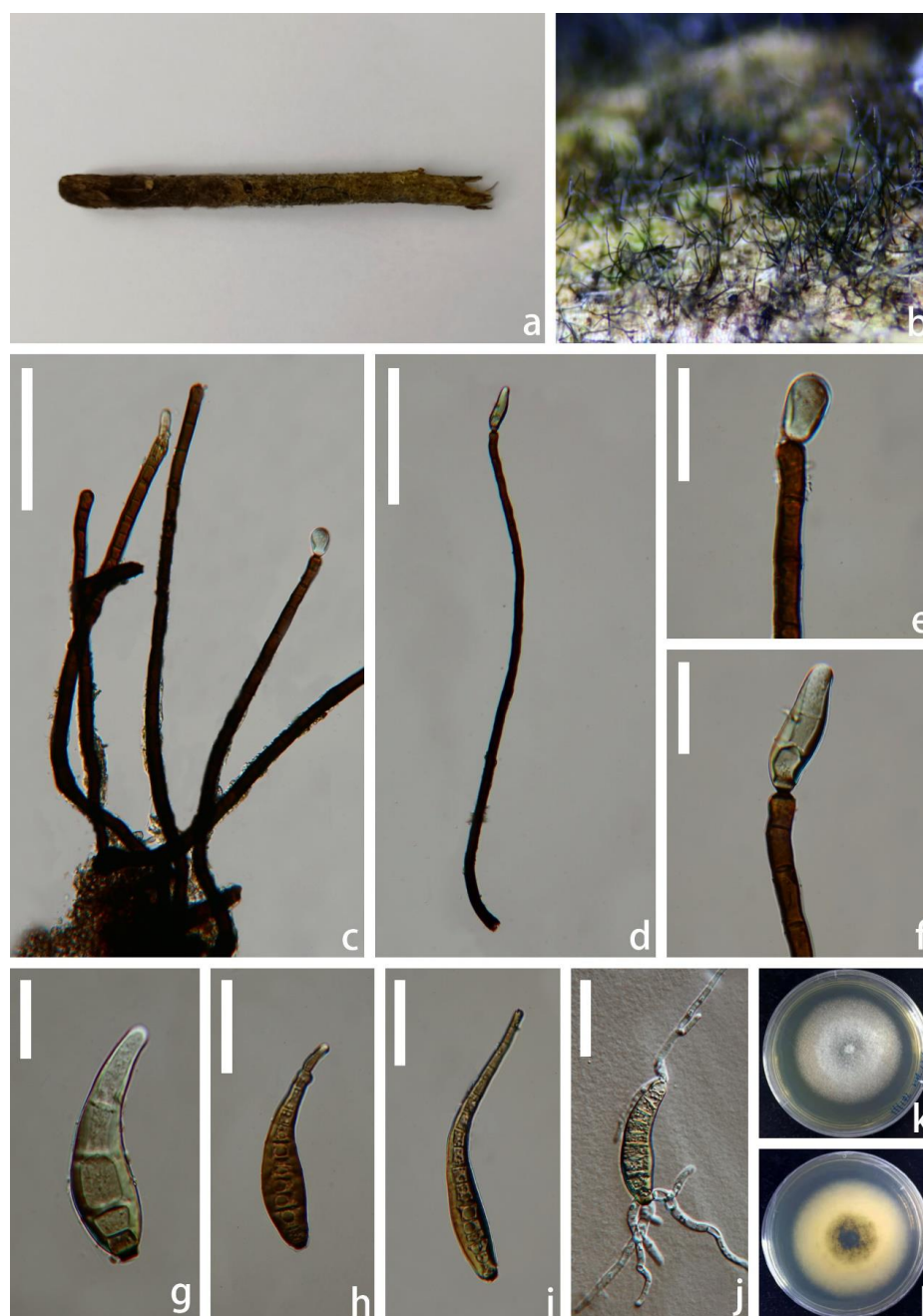


Figure 20 – *Helminthosporium guizhouense* (HKAS 130313, holotype). a Natural substrate. b Colonies on the substrate. c, d Conidiophores with conidiogenous cells and conidia. e, f Apical

conidiophores and conidiogenesis. g–i Conidia. j Germinated conidium. k, l Culture on PDA after 23 days. Scale bars: c = 150 µm, d = 200 µm, e–f, h–j = 50 µm, g = 30 µm.

Vaginatispora K.D. Hyde, Nova Hedwigia 61(1-2): 234 (1995)

Index Fungorum number: IF27644; Facesoffungi number: FoF00828

Vaginatispora was introduced by Hyde (1995) and typified with *V. aquatica*. The genus currently comprises eleven species (Index Fungorum 2024) and they can be commonly found on dead wood in mangrove and terrestrial habitats (Hyde et al. 2019, 2020b; Jayasiri et al. 2019). This genus is characterized by immersed, globose to subglobose, dark ascomata, cylindric-clavate, bitunicate asci and fusiform, septate, guttulate, hyaline ascospores, with a distinctively and thickened mucilaginous sheath (Hyde et al. 2020b, Chethana et al. 2023). Here, we provide the updated phylogenetic tree for *Vaginatispora* (Fig. 21). The support for a single species for *V. nypae* is quite weak and the habitats are diverse (mangrove vs terrestrial), therefore this is likely to be a species complex. Further collections from various habitats are required to address these discrepancies.

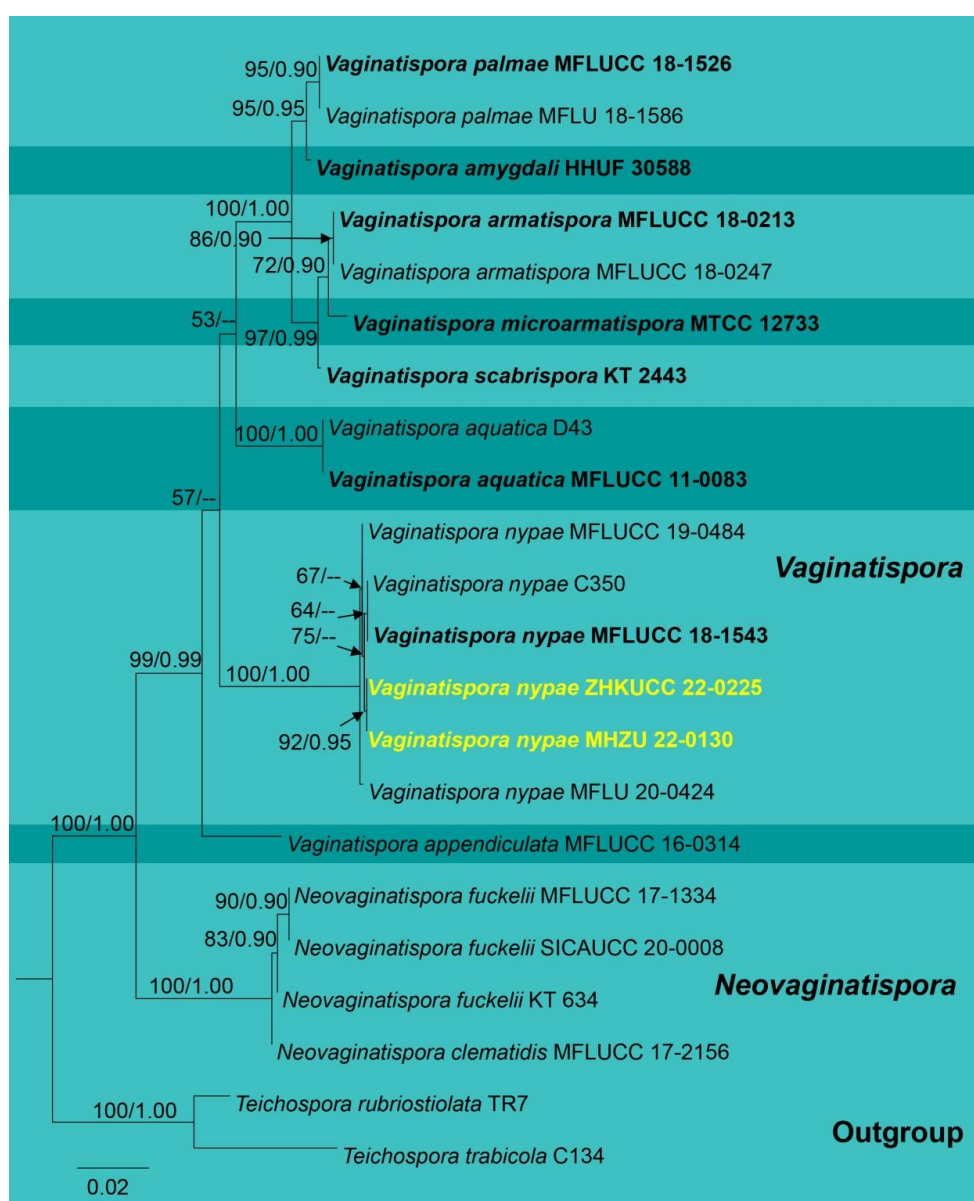


Figure 21 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of 22 taxa, which comprised 1422 characters (ITS = 574, LSU = 848). The best scoring RAxML tree with a final likelihood value of -4273.259975 is presented. The matrix had

330 distinct alignment patterns, with 16% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.238777, C = 0.245021, G = 0.287585, T = 0.228618; substitution rates: AC = 1.943766, AG = 1.158736, AT = 1.167107, CG = 1.119023, CT = 7.849639, GT = 1.0; gamma distribution shape parameter α = 0.140526. Bootstrap support values for maximum likelihood (ML) equal to or greater than 50% and clade credibility values greater than 0.90 (the rounding of values to 2 decimal proportions) from Bayesian inference analysis are labeled at each node. Ex-type strains are in bold, while the new isolate is indicated in yellow bold. The tree is rooted to *Teichospora rubriostiolata* (TR7) and *T. trabicola* (C134).

Vaginatispora nypae Jayasiri, E.B.G. Jones & K.D. Hyde, *Mycosphere* 10(1): 84 (2019) Fig. 22

Index Fungorum number: IF555558; Facesoffungi number: FoF05264

Saprobic on dried twigs of an unidentified host. Sexual morph: *Perithecia* 300–340 × 250–360 μ m ($\bar{x}$ = 327 × 323 μ m, n = 10), immersed to semi-immersed, solitary, scattered, globose to subglobose, wide papillate, dark brown, coriaceous, ostiolate. *Ostiole* central, slit-like. *Peridium* 40–90 μ m wide, composed of 5–7 layered, blackish dark brown cells of *textura angularis*. *Hamathecium* comprises 2.5–3 μ m wide, anastomosing, septate, branched, hyaline, pseudoparaphyses. *Asci* 60–110 × 10–15 μ m ($\bar{x}$ = 90 × 12 μ m, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, with short pedicel, sometimes sessile, apically rounded, with minutely an ocular chamber. *Ascospores* 23–33 × 4–7 μ m ($\bar{x}$ = 28 × 6 μ m, n = 20), overlapping 1–2-seriate, hyaline, fusiform with narrow, acute ends, 1-septate, constricted at the septum, guttulate, with a distinctively and thickened mucilaginous sheath, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 3 cm diameter after 4 weeks at 25 °C, circular, slightly raised, wavy margin, initially white, turn in to pinkish green inner zone and white outer zone when old, plenty of whitish aerial mycelia around center, Reverse olive-green center with white outer zone.

Material examined – China, Guangdong Province, Guangzhou City, Baiyun Mountain, on submerged decaying twigs, 16 August 2021, JZ Fu, WBHS 9 (ZHKU 22-0130); living culture ZHKUCC 22-0225.

GenBank numbers – ZHKUCC 22-0225: ITS: OR997672, LSU: OR997715; ZHKUCC 22-0225: ITS: OR997673; LSU: OR997716.

Known distribution – Thailand (Jayasiri et al. 2019; Hyde et al. 2020b), China (this study)

Known hosts – on fallen fruit pericarp of *Nypa fruticans* (Jayasiri et al. 2019), on submerged decaying twigs (Hyde et al. 2020b, this study).

Notes – In the phylogenetic analysis, our strain clustered with the type strain of *Vaginatispora nypae* (MFLUCC 18–1543) forming a distinct clade with 100% ML and 1.00 BYPP bootstrap support (Fig. 21). Morphologically, our collection is very similar to the type collection of *V. nypae* by the characteristics of ascomata, asci and ascospores (Jayasiri et al. 2019). *Vaginatispora nypae* has been reported from fallen fruit pericarp of *Nypa fruticans* (*Arecaceae*) and decaying plant twigs (Jayasiri et al. 2019; Hyde et al. 2020b). Therefore, based on morphology and phylogenetic evidences, we identify our collection (ZHKU 22-0130) as *Vaginatispora nypae*. This is the first report of this species in China and here we describe it as a new geographical record.

Leptosphaeriaceae M.E. Barr

Plenodomus Preuss, *Linnaea* 24: 145 (1851)

Index Fungorum number: IF9445; Facesoffungi number: FoF06403

Preuss (1851) established *Plenodomus* to accommodate the type *P. rabenhorstii*, however, due to the material of *P. rabenhorstii* being lost, *P. lingam* was replaced as the type species of *Plenodomus* (Torres et al. 2005, Hyde et al. 2020b). The genus currently includes 102 species (Index Fungorum 2024), and these species have often been reported as saprobic or pathogenic on different plants. The taxa are widely distributed and have been recorded in both temperate and

tropical countries (Zhao et al. 2021, Xu et al. 2022). In this study, we introduced a new species *Plenodomus shangrilaense* and a new host record *Plenodomus artemisiae* based on morphological evidence and phylogenetic analyses (Fig. 23). The support for a single species for *Plenodomus artemisiae* is quite weak and the hosts are diverse (*Artemisia* vs *Erigeron annuus* (both *Asteraceae*), therefore this is likely to be a species complex. Further collections from various hosts are required to address these discrepancies.

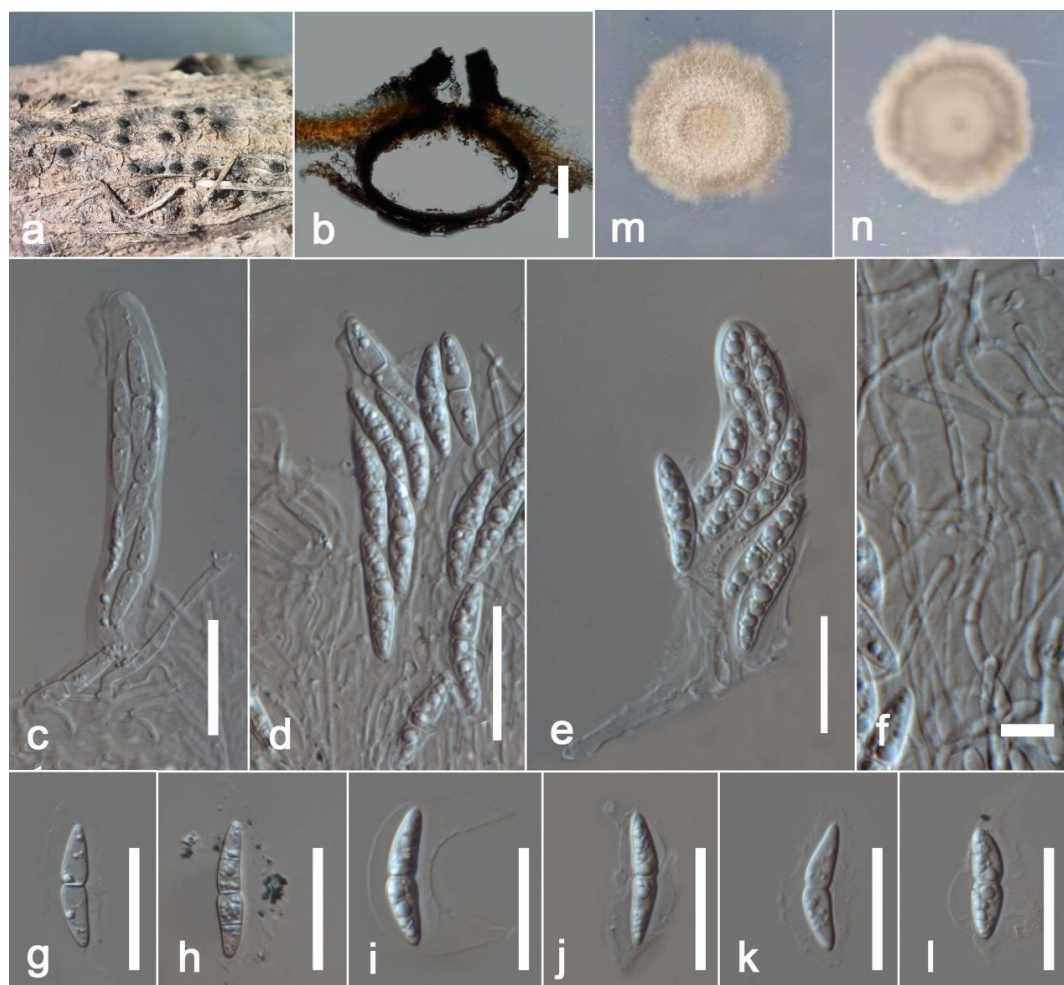


Figure 22 – *Vaginatispora nypae* (ZHKU 22-0130, a new geographical record). a Appearance of ascomata on woody substrate. b Vertical cross-section of an ascoma. c-e Asci. f Pseudoparaphyses. g-l Ascospores. m Surface view of colony on PDA. n Reverse view of colony on PDA. Scale bars: b = 150 μ m, f = 10 μ m, c-e, g-l = 30 μ m.

Plenodomus artemisiae A. Karunarathna, Phookamsak and K.D. Hyde, in Phookamsak et al., Fungal Diversity 95: 23. Fig. 24

Index Fungorum number: IF556118; Facesoffungi number: FoF05696

Saprobic on the dead stems of *Erigeron annuus*. Sexual morph: *Ascomata* 147–233 μ m $\times$ 119–212 μ m ($\bar{x}$ = 193 $\times$ 150 μ m, n = 10), solitary to gregarious, black, superficial, scattered, base seated in the substrate, globose or subglobose and flat-globose, uni-loculate, glabrous, papillate, ostiolate. *Ostioles* central, with paraphyses in the canal. *Peridium* 20–29 μ m wide ($\bar{x}$ = 26 μ m, n = 20), thick-walled of unequal thickness, composed of several layers with the cells of *textura angularis* and *textura globulosa*, inner layer hyaline to pale brown, outer layer black. *Hamathecium* comprises 18–2.6 μ m wide, filiform, hyaline, septate, cellular pseudoparaphyses embedded in a gelatinous matrix. *Asci* 56–82 $\times$ 8.6–12.6 μ m ($\bar{x}$ = 69 $\times$ 10 μ m, n = 30), 8-spored, bitunicate, fissitunicate, arising from base, short pedicellate, rounded at the apex with a distinct ocular chamber, cylindrical to cylindric-clavate. *Ascospores* 31–42 $\times$ 3.8–5 μ m ($\bar{x}$ = 35 $\times$ 4.5 μ m, n = 30),

overlapping, 2–3-seriate, initially hyaline, becoming pale yellowish at maturity, lunate to narrowly fusiform, 5-septate, often constricted at medium septum, with tapering and rounded ends, guttulate, without sheath or appendages. Asexual morph: Undetermined.

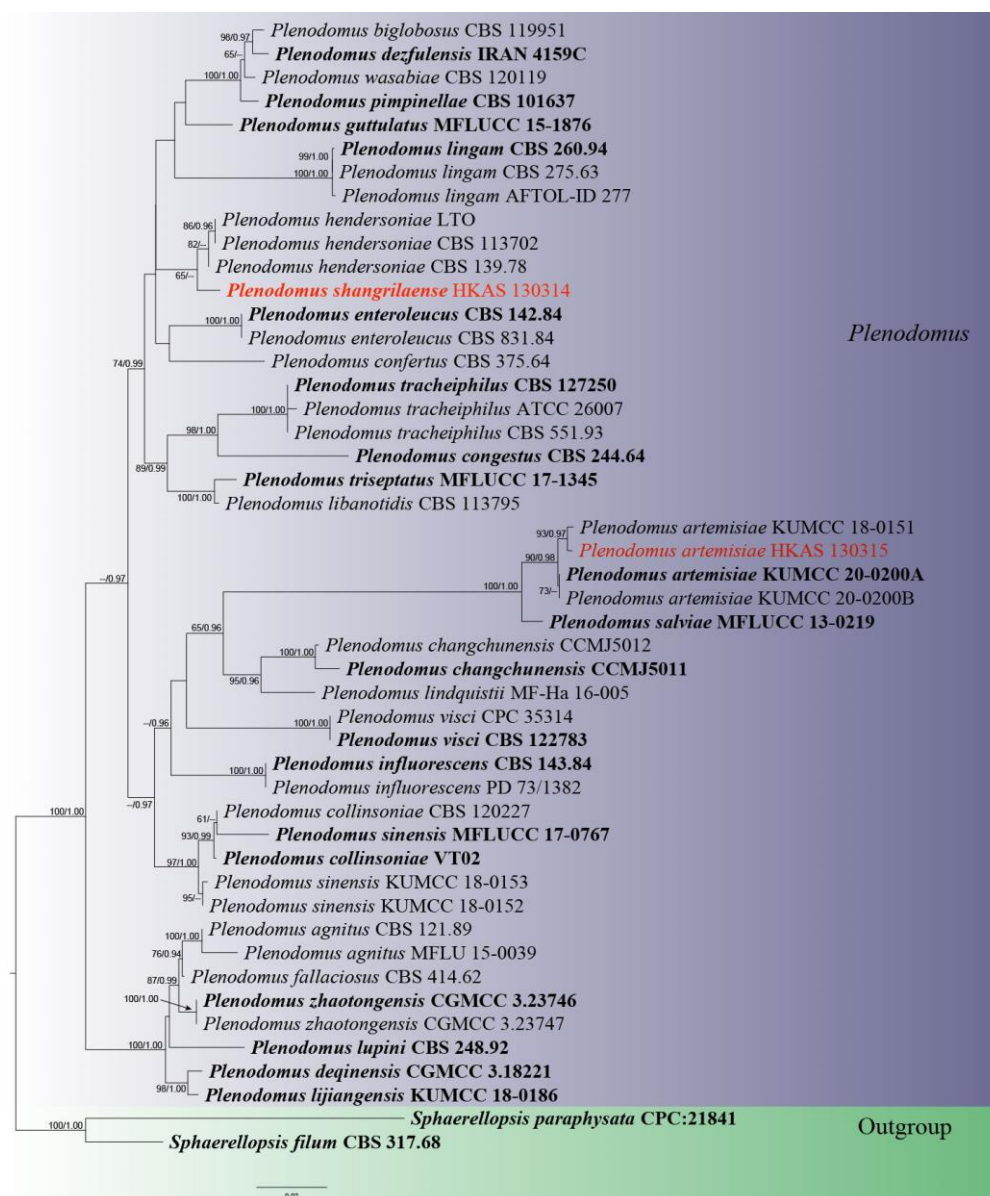


Figure 23 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, SSU and *tub2* sequence data of *Plenodomus*. Forty-eight strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -10731.13 is presented. The evolutionary model GTR+I+G is applied to all the genes. The matrix had 577 distinct alignment patterns, with 29.39% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.237924, C = 0.233228, G = 0.271434, T = 0.257414; substitution rates AC = 1.273144, AG = 2.746549, AT = 1.264770, CG = 1.052806, CT = 6.016241, GT = 1.000000; gamma distribution shape parameter α = 0.445940. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree is rooted in *Sphaerellopsis paraphysata* (CPC:21841), *S. filum* (CBS 317.68). Estimated base frequencies were as follows: A = 0.237924, C = 0.233228, G = 0.271434, T = 0.257414; substitution rates AC = 1.273144, AG = 2.746549, AT = 1.264770, CG = 1.052806, CT = 6.016241, GT = 1.000000; gamma distribution shape parameter α = 0.445940. Ex-type strains are in bold. The newly generated sequences are indicated in red.

Material examined – China, Guizhou Province, Zunyi City, Zhengan County, on a dead branch of *Erigeron annuus* (Asteraceae), 5 May 2022, Y.Y. Yang, YYY407 (HKAS 130315).

GenBank numbers – ITS: PP981909, LSU: PP981906, SSU: PP977160, *tub2*: PQ041230.

Known distribution – Yunnan Province, Guizhou Province, China (Phookamsak et al. 2019, Doilom et al. 2021, this study)

Known hosts – *Artemisia* sp., *A. argyi* (Phookamsak et al. 2019, Doilom et al. 2021), *Erigeron annuus* (this study)

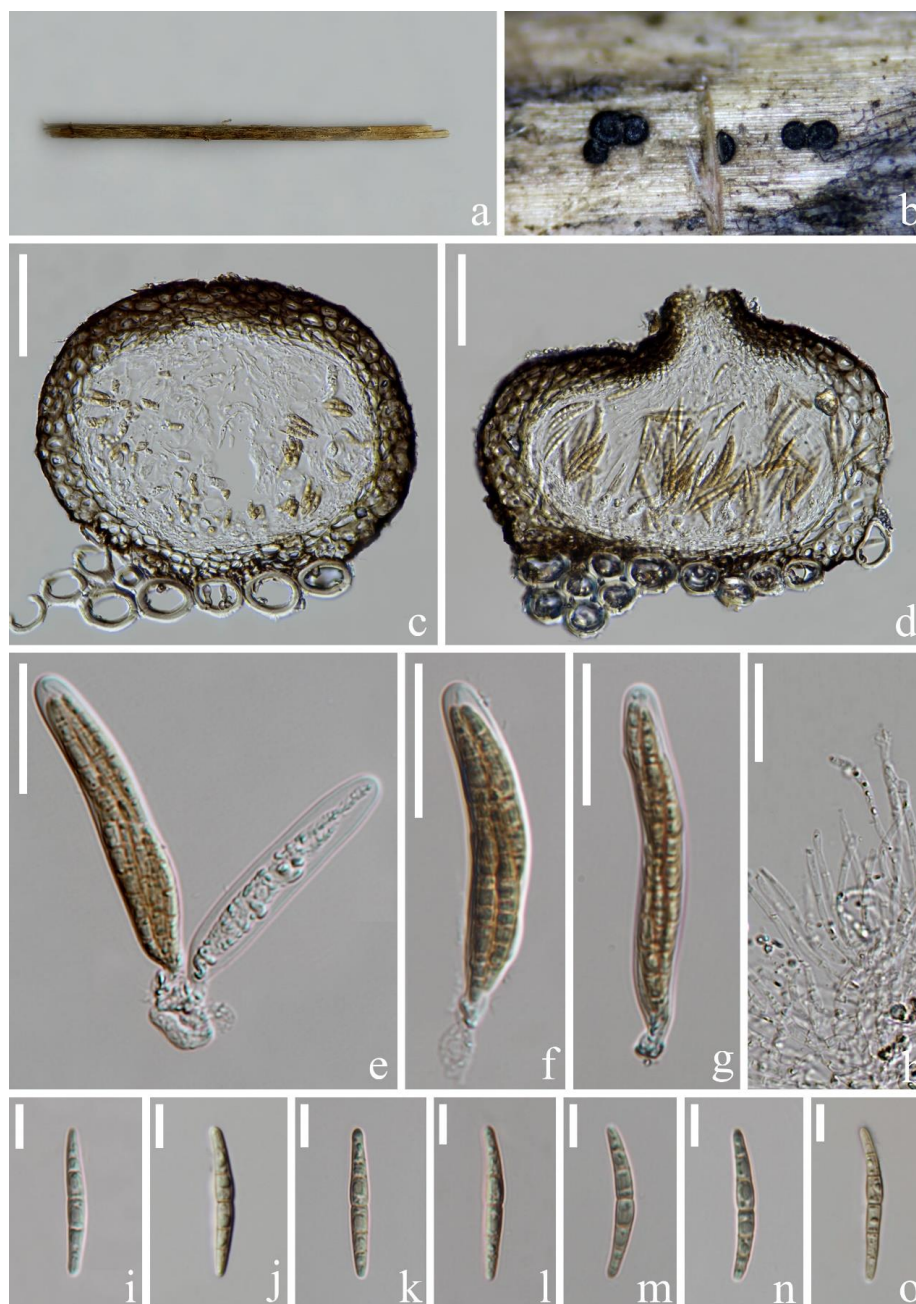


Figure 24 – *Plenodomus artemisiae* (HKAS 130315, a new host record). a Natural substrate. b Ascomata on host substrate. c, d Vertical sections of ascomata. e–g Asci. h Pseudoparaphyses. i–o Ascospores. Scale bars: c, d = 50 μ m, e–h = 30 μ m, i–o = 10 μ m.

Notes – Phylogenetic analyses supported the close affinity of our strain (HKAS 130315) to *Plenodomus artemisiae* (KUMCC 18-0151), and the two were grouped with 93% ML and 0.97 BYPP bootstrap support (Fig. 23). They share similar characteristics by having black, compressed globose, uniloculate, and obscurely papillate ascomata, numerous, septate, hyaline

pseudoparaphyses, and narrowly fusiform, constricted at the median septum with guttulate ascospores. Here, we conclude our collection is *P. artemisiae* based on morphological and molecular evidence. *Plenodomus artemisiae* was reported from dead branches and stems of *Artemisia* species in Yunnan Province, China (Phookamsak et al. 2019, Doilom et al. 2021). Our new collection is the first report of *P. artemisiae* on *Erigeron annuus* and identify as a new host record.

Plenodomus shangrilaense Y.Y. Yang, A.R. Gomes de Farias & K.D. Hyde, sp. nov. Fig. 25
Index Fungorum number: IF902273; Facesoffungi number: FoF15236

Etymology – Referring to the collecting site “Shangri-La Province, China”, where the holotype was collected.

Holotype – HKAS 130314

Saprobic on dead branch of *Rhododendron telmateium*. Sexual morph: *Ascomata* 270–404 × 247–437 µm ($\bar{x}$ = 313 × 313 µm, n = 6), gregarious, raised, superficial, visible as black spots on the host surface, globose, black, uni-loculate, glabrous, ostiolate, papillate. *Ostiole* central, well-developed dark brown papilla, ostiolar canal filled with paraphyses. *Peridium* 32–57 µm wide ($\bar{x}$ = 45 µm, n = 10), composed of thick-walled cells of *textura angularis* to *textura globulosa*, unequal thickness, brown. *Hamathecium* comprises 1–2 µm diam., filiform, hyaline, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 88–139 × 9–15 µm ($\bar{x}$ = 111 × 13 µm, n = 15), 8-spored, bitunicate, fissitunicate, arising from base, cylindric-clavate, short pedicellate with foot-like pedicel, thin- and smooth-walled, rounded at the apex with a distinct ocular chamber. *Ascospores* 51–71 × 4.5–5.5 µm ($\bar{x}$ = 59 × 5.1 µm, n = 20), pale yellowish at maturity, overlapping, 2–3-seriate, 7–9-septate, lunate to long fusiform, straight or slightly curved, with tapering and rounded ends, without sheath or appendages. Asexual morph: Not observed.

Material examined – China, Yunnan Province, Shangri-La City, Gezan Village, on a dead branch of *Rhododendron* sp. (*Ericaceae*), 19 June 2022, Y.Y. Yang, YYY406 (HKAS 130314, holotype).

GenBank numbers – ITS: PP981908, LSU: PP981905, *tub2*: PQ041229.

Notes – In the multigene phylogenetic analysis, our strain (HKAS 130314) formed a separate lineage sister to *Plenodomus hendersoniae* strains (LTO, CBS 113702, CBS 139.78) with 65% ML bootstrap support (Fig 23). Sequence comparison for the ITS region between *P. shangrilaense* (HKAS 130314) and *P. hendersoniae* (LTO) showed a 2.87% (17/591 bp, excluding gaps) base pair difference. *Plenodomus shangrilaense* shares similar morphological characters with *P. salviae* in having cellular pseudoparaphyses, cylindrical asci with 8 spores and long fusiform ascospores without sheaths or appendages. However, *P. shangrilaense* has larger ascomata (270–404 × 247–437 µm vs. 130–250 × 150–280 µm), asci (88–139 × 9–15 µm vs. 57–88 × 8.6–11.4 µm), ascospores (51–71 × 4.5–5.5 µm vs. 30–48 × 3.1–4.3 µm) and more ascospore septation (7–9 vs. 5) than *P. salvia* (Ariyawansa et al. 2015). Therefore, we introduce *P. shangrilaense* as a new species based on morphology and phylogenetic evidence.

Nigrogranaceae Jaklitsch & Voglmayr, Stud. Mycol. 85: 54 (2016)

Nigrograna Gruyter, Verkley & Crous, Stud. Mycol. 75: 31 (2012)

Index Fungorum number: IF564794; Facesoffungi number: FoF08318

Nigrograna was introduced by de Gruyter (2012) with *Nigrograna mackinnonii* ($\equiv$ *Pyrenochaeta mackinnonii*) as the type species. Ahmed et al. (2014) reclassified *N. mackinnonii* as a synonym of *Biatrispora marina* due to its morphological resemblance to the type species of *Biatrispora*. Jaklitsch & Voglmayr (2016) revealed morphological and ecological differences between *Nigrograna mackinnonii* and *Pyrenochaeta mackinnonii*, while Hongsanan et al. (2020) treated *Biatrispora* and *Nigrograna* as two separate genera. *Nigrograna* species have been reported as pathogens, saprobes, and endophytes worldwide (Kolařík 2018, Zhao et al. 2018, Chethana et al. 2023). The genus is characterized by black, globose to subglobose ascomata, clavate, fissitunicate, short pedicellate asci, brown, septate, fusoid to narrowly ellipsoid, and

smooth or verruculose ascospores (Jaklitsch & Voglmayr 2016, Dong et al. 2020). Currently, 36 species are listed in this genus (Index Fungorum 2024). Here, we provide the updated phylogeny for the *Nigrograna* taxa (Fig. 26).

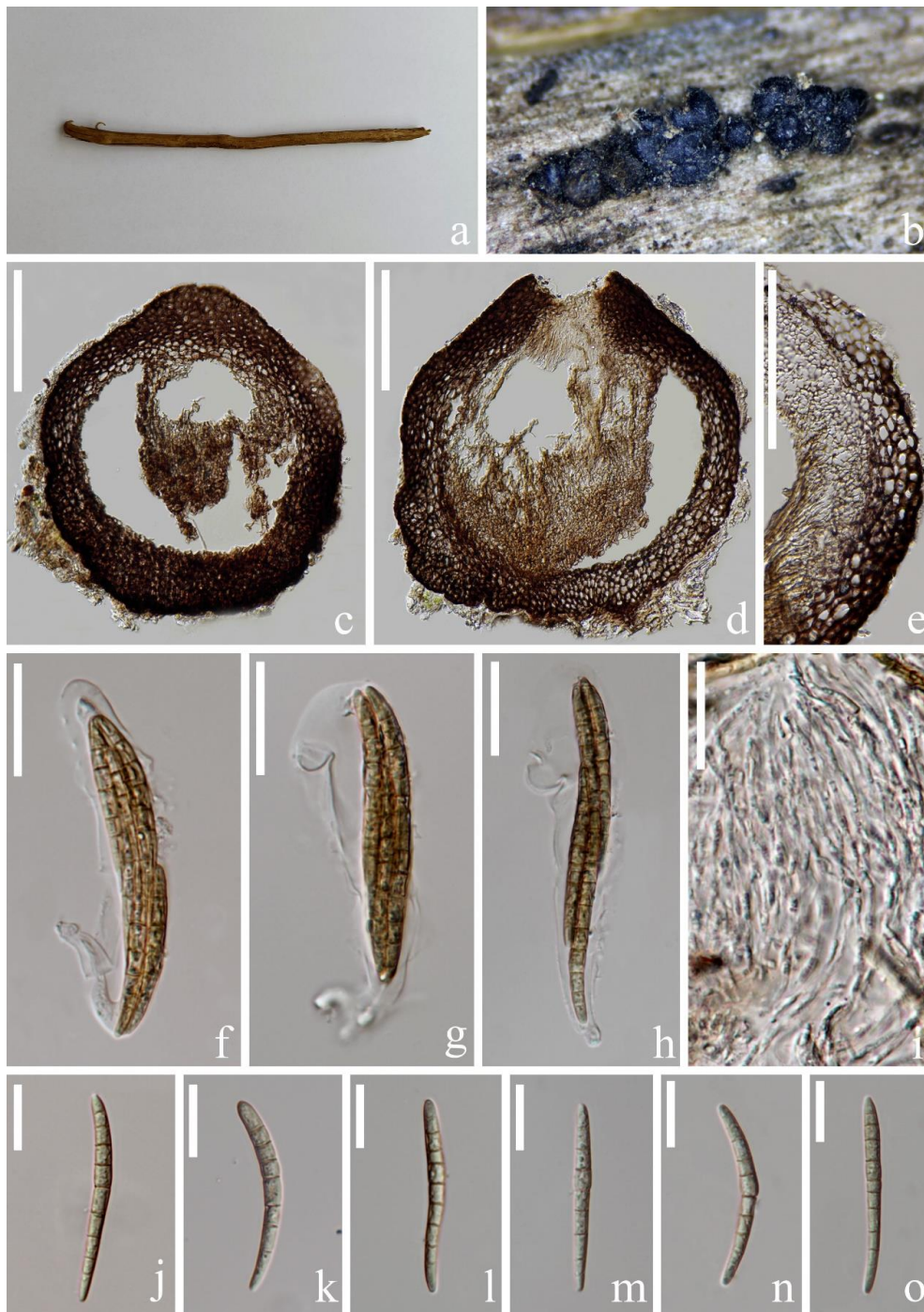


Figure 25 – *Plenodomus shangrilaense* (HKAS 130314, holotype). a Natural substrate. b Ascomata on host substrate. c, d Vertical sections of ascomata. e Peridium. f–h Asci. i Pseudoparaphyses. j–o Ascospores. Scale bars: c–e = 100 μ m, f–i = 30 μ m, j–o = 20 μ m.

Nigrograna magnoliae Wanas, in D.N. Wanasinghe, N.N. Wijayawardene, J.C. Xu, R. Cheewangkoon & P.E. Mortimer, PLoS ONE 15(7), e0235855 (2020) Fig. 27

Index Fungorum number: IF557331; Facesoffungi number: FoF06278

Saprobic on dead twig of *Aquilaria* sp. Sexual morph: Ascomata 90–260 μ m high $\times$ 170–340 μ m diam. ($\bar{x}$ = 192 $\times$ 260 μ m, n = 10), solitary, immersed, scattered to gregarious, ellipsoidal to

subglobose, pale brown to dark brown, ostiolate. *Ostiole* central, cylindrical, with periphyses. *Peridium* 20–40 μm wide, 2–4-layered, composed of *textura angularis* cells, inner layer with hyaline, thin-wall cells, outer layer with brown to dark brown, thick-walled cells. *Hamathecium* comprises 2–4 μm wide, hyaline, aseptate pseudoparaphyses. *Asci* 63–73 (–78) $\times$ 10–13 (–14) μm ($\bar{x}$ = 69.5 $\times$ 11.5 μm , n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 12–16 $\times$ 5–8 μm ($\bar{x}$ = 14.5 $\times$ 6.5 μm , n = 30), overlapping, 1–2-seriate, initially hyaline to pale yellow, becoming yellow to brown at maturity, mostly 3-septate, guttulate, phragmosporous, fusoid. Asexual morph: See Wanasinghe et al. (2020).

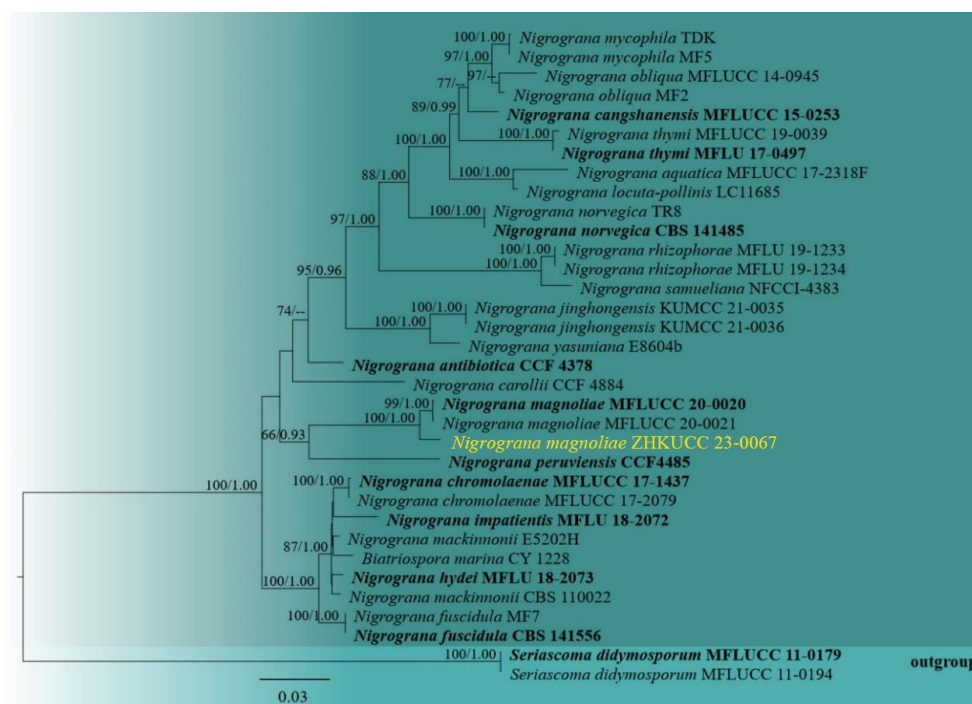


Figure 26 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, SSU, and *tef1- α* sequence data of *Nigrograna*. Thirty-four strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -17314.713275 is presented. The evolutionary model GTR+I+G is applied for all the genes. The matrix had 1038 distinct alignment patterns, with 46% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.249454, C = 0.245681, G = 0.268395, T = 0.236470; substitution rates AC = 1.488030, AG = 4.372465, AT = 1.512313, CG = 1.224882, CT = 11.395425, GT = 1.000000; gamma distribution shape parameter α = 0.608959. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Seriascoma didymosporum* (MFLUCC 11-0179) and *S. didymosporum* (MFLUCC 11-0194). Ex-type strains are in bold. The newly generated sequence is indicated in yellow.

Material examined – China, Yunnan Province, Xishuangbanna, Menghai city, on a dead twig of *Aquilaria* sp. (*Thymeleaceae*), 15 September 2021, Tianye Du, YNA24 (MHZU 23-0031), living culture ZHKUCC 23-0067.

GenBank numbers – ZHKUCC 23-0067: ITS: OR900223, LSU: OR900223, SSU: OR900228, *tef1- α* : OR914208.

Known distribution (based on molecular data) – China (Wanasinghe et al. 2020, this study).

Known hosts (based on molecular data) – *Magnolia denudata* (Wanasinghe et al. 2020), *Aquilaria* sp. (this study).

Notes – According to the phylogenetic analyses, our collection (ZHKUCC 23-0067) clustered with *P. adansoniae* strains (MFLUCC 20-0020 and MFLUCC 20-0021) with 100% ML and 1.00 BYPP bootstrap support (Fig. 26). Our collection shares similar characteristics to *Nigrograna magnoliae* (the holotype) isolated from dead aerial twigs of *Magnolia denudata* (Wanasinghe et al. 2020). However, our collection (MHZU 23-0031) has smaller ascomata ($\bar{x} = 192 \times 260 \mu\text{m}$ vs. $\bar{x} = 243.7 \times 186.2 \mu\text{m}$) and asci ($\bar{x} = 69.5 \times 11.5 \mu\text{m}$ vs. $\bar{x} = 74.2 \times 9.5 \mu\text{m}$) than those of the holotype (Wanasinghe et al. 2020). Therefore, based on morphology and phylogenetic analyses, we conclude that our collection is *N. magnoliae*. This is a new host record on *Aquilaria* sp. in China.

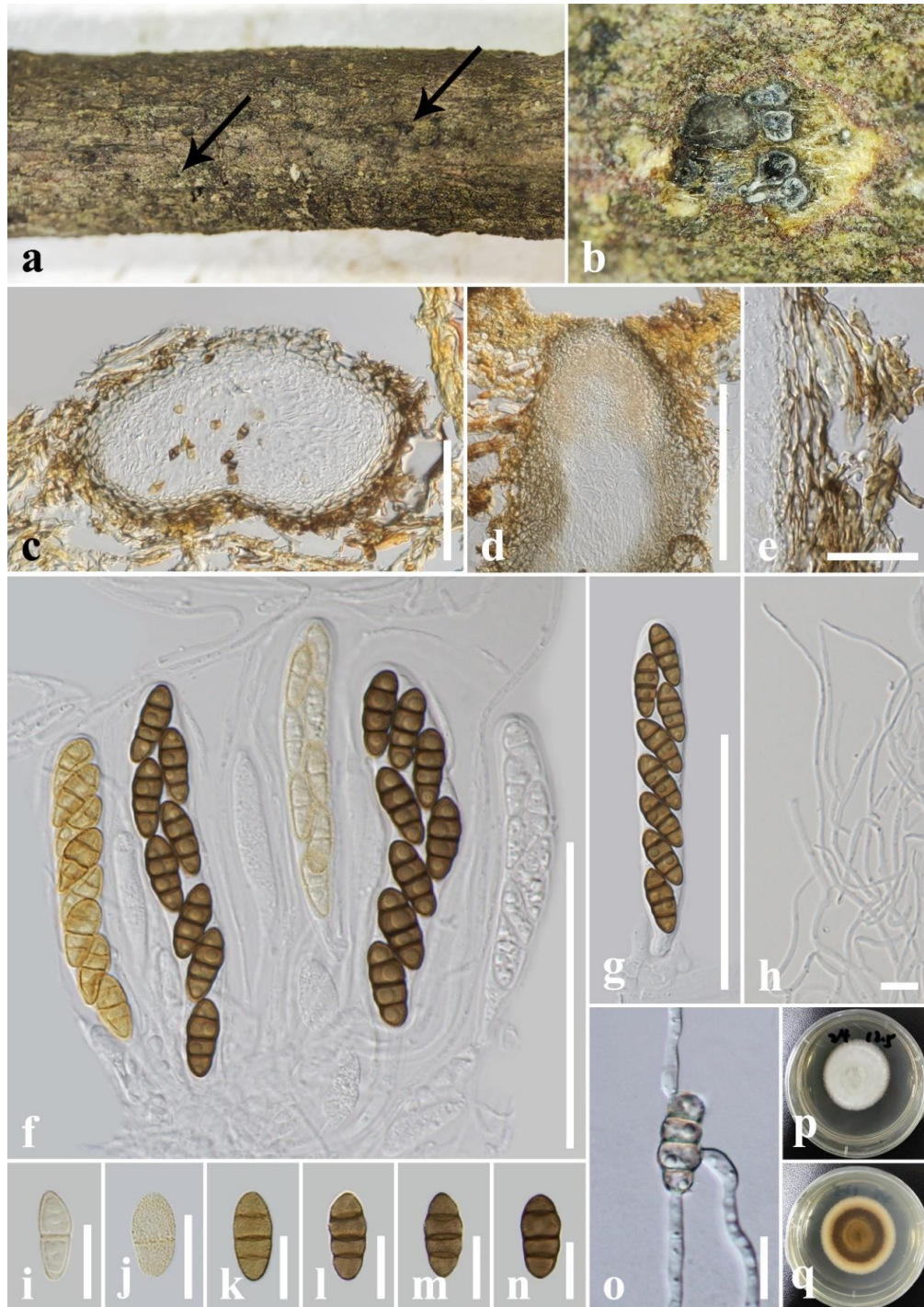


Figure 27 – Sexual morph of *Nigrograna magnoliae* (MHZU 23-0031, a new host record). a, b Appearance of ascostroma on host surface. c Section of an ascoma. d Section of an ostiole. e Peridium. f, g Asci. h Pseudoparaphyses. i–n Ascospores. o A germinating ascospore. p Upper

view of culture on PDA. q Reverse view of culture on PDA. Scale bars: c = 100 μ m, d = 200 μ m, e = 20 μ m, f, g = 50 μ m, h–o = 10 μ m.

Thyridariaceae Q. Tian & K.D. Hyde, Fungal Diversity 63 (1), 254 (2013)

Thyridaria Sacc., Grevillea 4 (29), 21 (1875)

Index Fungorum number: IF5463; Facesoffungi number: FoF08375

Thyridaria was introduced by Saccardo (1875) with *T. brousseauetiae* as the type species (Barr 1990). The taxonomic placement of *Thyridaria* has been highly debated and it was placed in *Didymosphaeriaceae*, *Lophiostomataceae*, *Melanommataceae*, *Platystomaceae*, *Pleosporaceae*, and *Sphaeriaceae* by various authors (Wehmeyer 1941, 1957, Munk 1957, Luttrell 1973, Müller & von Arx 1973, Dennis 1978, Barr 1979a, b, 2003, Mugambi & Huhndorf 2009a, b). Hyde et al. (2013) introduced *Thyridariaceae* to accommodate *Thyridaria* in *Pleosporales*. Barr (2003) summarized and suggested that the genus could be characterized by ample subiculum surrounding ascomata, which formed under the periderm or in woody plant substrates, with ascospores having both thickened and darkened septa and walls. Currently, 52 species belong to this genus (Wijayawardene et al. 2022). However, only four species have sequence data in GenBank. Here, we provide the updated phylogeny for *Thyridaria* taxa (Fig. 28).

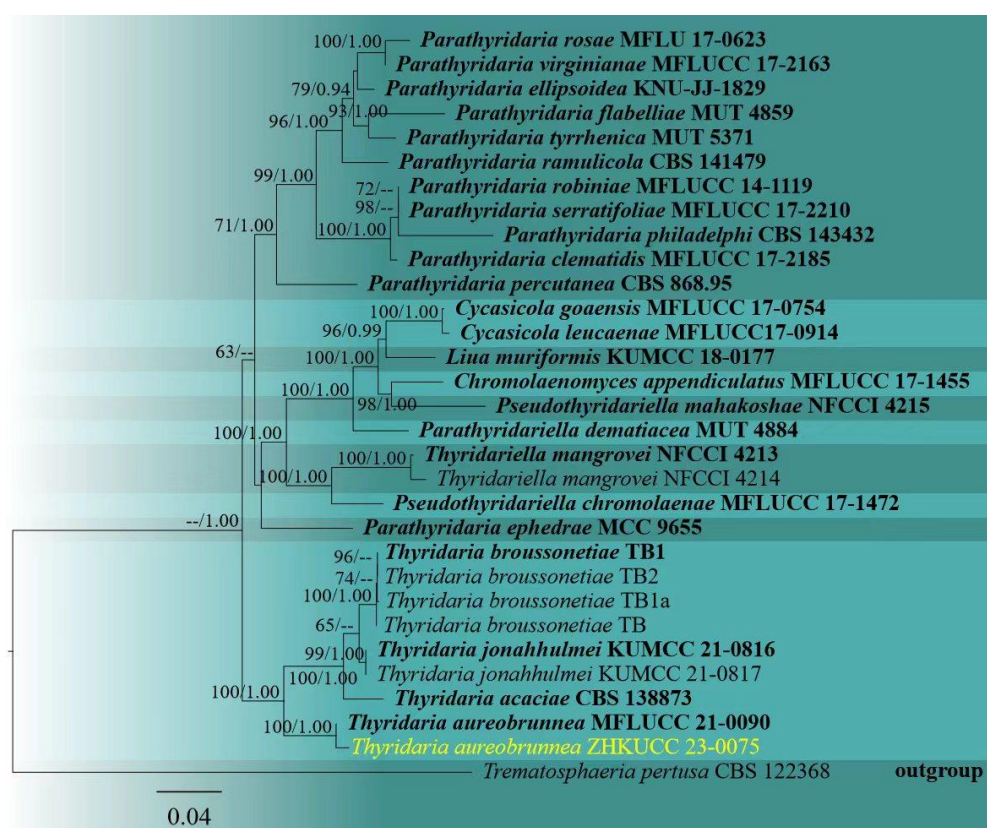


Figure 28 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, SSU, *tef1- α* and *rpb2* sequence data of *Pseudofusicoccum*. Thirty-one strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -26478.441465 is presented. Evolutionary model GTR+I+G is applied for all the genes. Estimated base frequencies were as follows: A = 0.247395, C = 0.258396, G = 0.271901, T = 0.222308; substitution rates AC = 1.380857, AG = 3.307741, AT = 1.588080, CG = 0.989910, CT = 7.988678, GT = 1.000000; gamma distribution shape parameter α = 0.457139. The matrix had 1670 distinct alignment patterns, with 52.58% of undetermined characters or gaps. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively.

The tree was rooted with *Trematosphaeria pertusa* (CBS 122368). Ex-type strains are in bold. The newly generated sequence is indicated in yellow.

Thyridaria aureobrunnea S. Boonmee, N. Huanraluek & K.D. Hyde

Fig. 29

Index Fungorum number: IF558540; Facesoffungi number: FoF09193

Saprobic on dead twig of *Aquilaria* sp. Sexual morph: *Ascomata* 150–280 µm high × 160–280 µm diam. ($\bar{x}$ = 220 × 230 µm, n = 10), solitary, scattered, immersed, erumpent, globose to subglobose, ostiolate. *Ostiole* central, papillate, brittle. *Peridium* 15–30 µm wide, 2–4-layered, composed of *textura angularis* cells, inner layer hyaline, with thin-wall cells, outer layer brown to dark brown, thick-walled cells. *Hamathecium* comprises 2 µm wide, hyaline, branched, aseptate, anastomosing pseudoparaphyses. *Asci* 60–85 × 7–11 µm ($\bar{x}$ = 72 × 8.5 µm, n = 20), 8-spored, bitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 11–15 × 3–5 µm ($\bar{x}$ = 13 × 4.5 µm, n = 30), overlapping, 1–2-seriate, initially hyaline, becoming pale brown to brown at maturity, straight or curved, 2–3-septate, mostly 3-septate, darkened and constricted at the septa, guttulate. Asexual morph: Undetermined.

Material examined – China, Yunnan Province, Xishuangbanna, Menghai City, on a dead twig of *Aquilaria* sp. (*Thymeleaceae*), 15 September 2021, Tianye Du, YNA61 (MHZU 23-0039, living culture (ZHKUCC 23-0075).

GenBank numbers – ZHKUCC 23-0075: ITS: OR900224, LSU: OR898405, *tef1*-α: OR914209, *rpb2*: OR914207.

Known distribution (based on molecular data) – Thailand (Boonmee et al. 2021), China (this study).

Known hosts (based on molecular data) – decaying wood (Boonmee et al. 2021), *Aquilaria* sp. (this study).

Notes – According to the phylogenetic analyses, our collection (ZHKUCC 23-0075) clustered with *P. adansoniae* strain (MFLUCC 21-0090) with 100% ML and 1.00 BYPP bootstrap support (Fig. 28). The morphology of our collection shares similar characteristics to *Thyridaria aureobrunnea* (the holotype) isolated from a decaying wood in Thailand (Boonmee et al. 2021). However, our sexual morph (MHZU 23-0039) has larger asci ($\bar{x}$ = 72 × 8.5 µm vs. $\bar{x}$ = 52 × 7.5 µm) than those of the holotype (Boonmee et al. 2021). Therefore, based on morphology and phylogenetic analyses, we conclude that our collection is *T. aureobrunnea*. This is a new host record on *Aquilaria* sp. and a new geographical record from China.

Torulaceae Corda, Deutschlands Flora, Abt. III. Die Pilze Deutschlands 2: 71 (1829)

Torula Pers., Ann. Bot. (Usteri) 15: 25 (1794)

Index Fungorum number: IF701482; Facesoffungi number: FoF01740

Torula was proposed by Persoon (1794) to accommodate *T. herbarum* as the type. Later, Crous et al. (2015) accepted *Torula* in *Torulaceae* (*Pleosporales*) based on phylogenetic analysis. *Torula* is an asexual and hyphomycetous genus that commonly inhabits terrestrial and aquatic habitats in temperate to tropical regions and reported as saprobes (Su et al. 2018, de Silva et al. 2022, Tian et al. 2023). The genus is characterized by terminal or lateral, monoblastic or polyblastic conidiogenous cells and dark brown, cylindrical to subcylindrical, solitary to catenate, acrogenous, simple, phragmosporous, septate conidia (Crane & Miller 2016, Li et al. 2017a, Hyde et al. 2020b, de Silva et al. 2022). *Torula* has an ancient origin and consists of 542 species epithets in Index Fungorum (2024), but only a few species have molecular data. *Torula* species can be distinguished by their conidial size, number of septa, and chains (Crous et al. 2015, Dong et al. 2023, Tian et al. 2023).

Torula mackenziei J.F. Li, Phookamsak & K.D. Hyde, Mycological Progress 16 (4): 455 (2017)

Fig. 31

Index Fungorum number: IF819537; Facesoffungi number: FoF02714

Saprobic on dead twig of *Coffea arabica*. Sexual morph: Undetermined. Asexual morph: Colonies on the host substrate, sporadic, black, powdery. Mycelium immersed through the substrate, composed of septate, branched, smooth, hyaline to light brown hyphae. Conidiophores 5–7 μm long $\times$ 3–5 μm wide ($\bar{x}$ = 6.4 $\times$ 4 μm , n = 10), macronematous, mononematous, solitary, erect, branched, light brown, thick-walled, without apical branches, ellipsoid to subglobose, arising from hypha, sometimes reduced to conidiogenous cells. Conidiogenous cells 4–5.5 μm long $\times$ 3.5–6 μm wide ($\bar{x}$ = 4.8 $\times$ 4.8 μm , n = 10), polyblastic, terminal, dark brown to black, paler at apex, smooth to minutely verruculose, thick-walled, globose to ellipsoid. Conidia 10–19 μm long $\times$ 5–8 μm wide ($\bar{x}$ = 15 $\times$ 6.5 μm , n = 20) acrogenous, catenated, phragmosporous, light brown to dark brown, smooth to minutely verruculose, 1–3-septate, slightly constricted at some septa, rounded at both ends, often paler at apex, composed of moniliform cells, mainly subcylindrical.

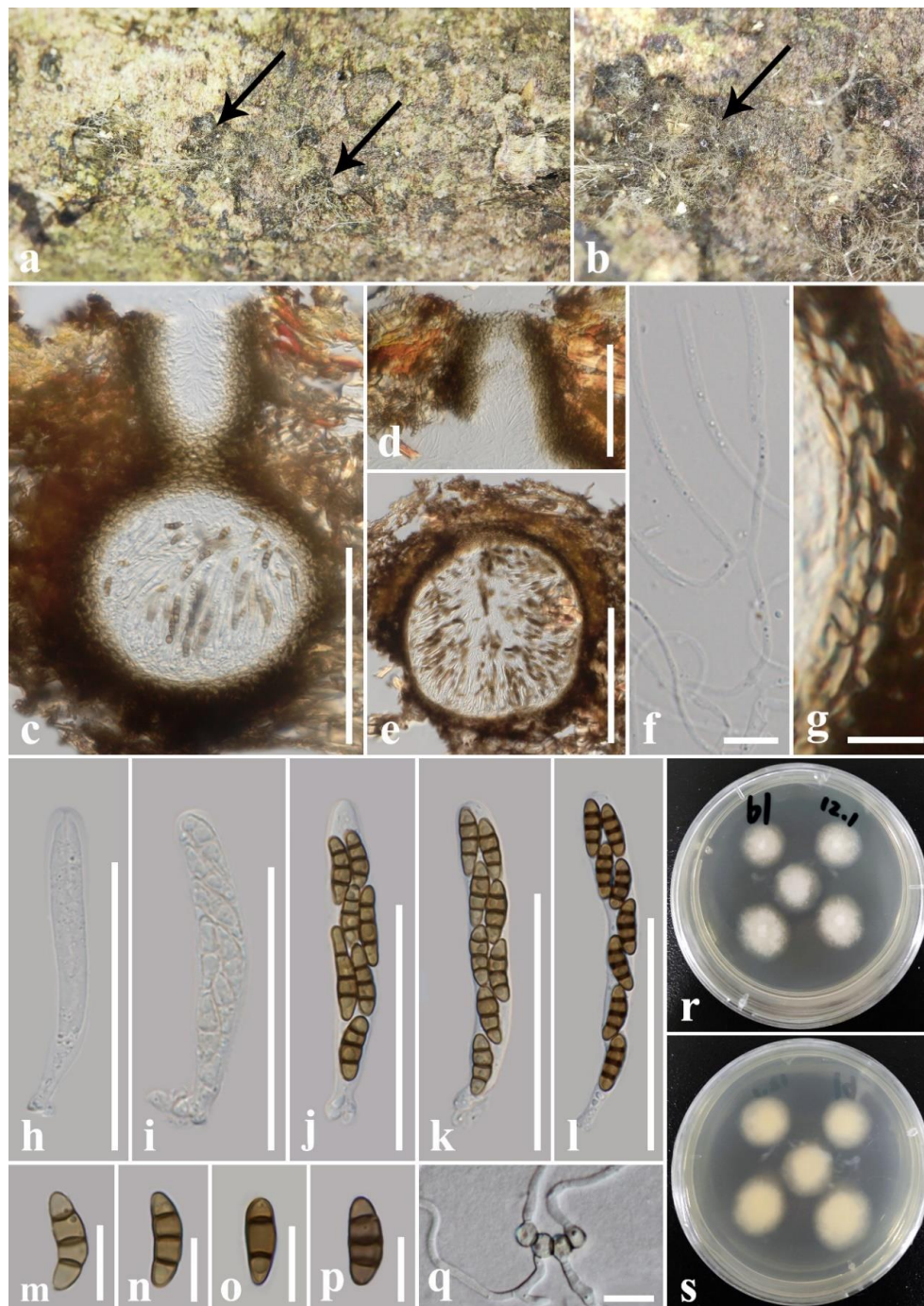


Figure 29 – Sexual morph of *Thyridaria aureobrunnea* (MHZU 23-0039, a new host and a geographical record). a, b Appearance of ascostromata on host surface. c, e Sections of ascomata.

d Section of an ostiole. f Pseudoparaphyses. g Peridium. h–l Asci. m–p Ascospores. q A germinating ascospore. r Upper view of culture on PDA. s Reverse view of culture on PDA. Scale bars: c, e = 200 μ m, d = 100 μ m, h–l = 50 μ m, f, g, m–p = 10 μ m.

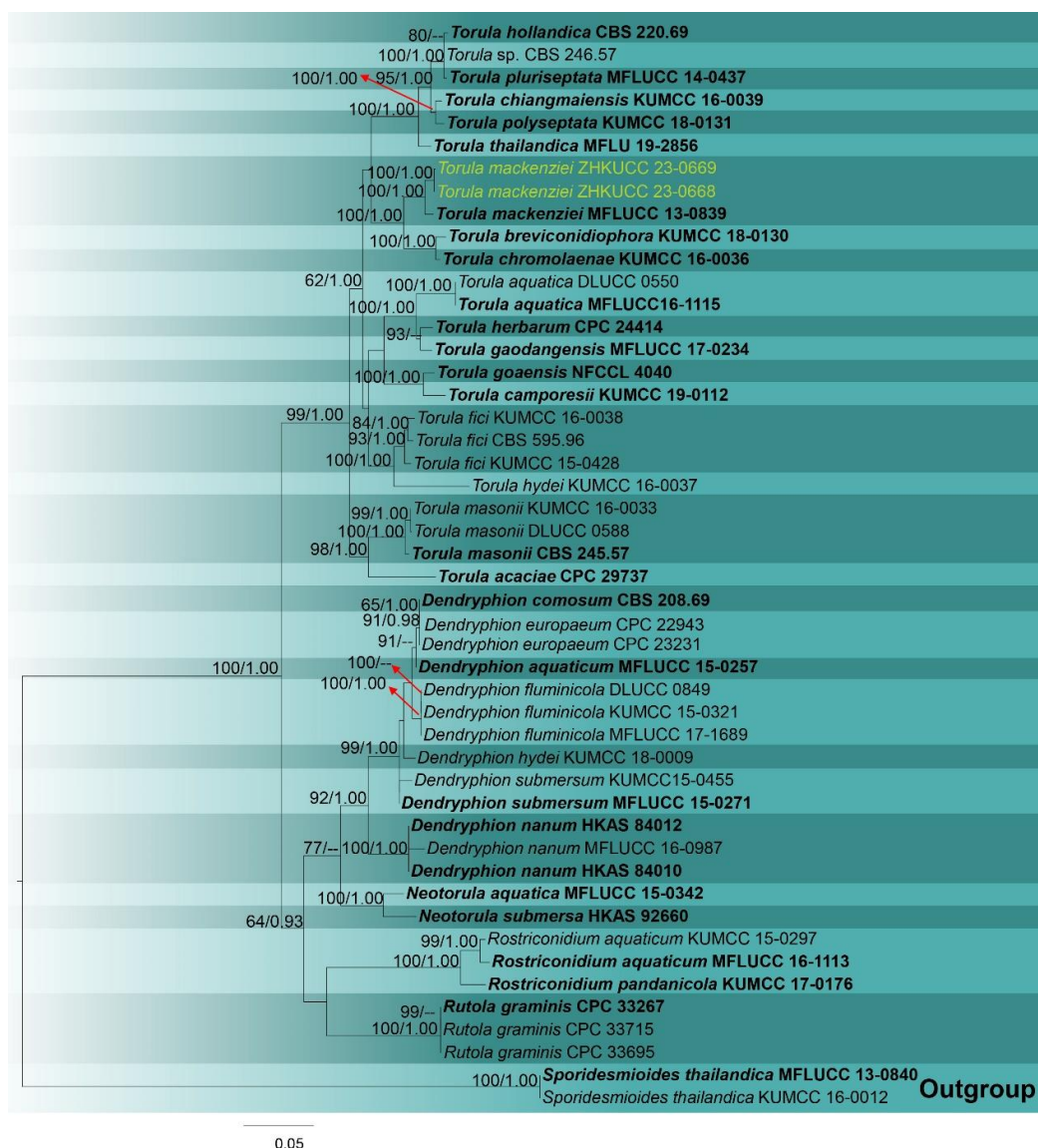


Figure 30 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, SSU, *rpb2* and *tef1- α* sequence data. Forty-eight strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -20011.228479 is presented. The evolutionary model GTR+I+G is applied for all the genes. The matrix had 1429 distinct alignment patterns, with 39.82% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.245893, C = 0.259812, G = 0.271391, T = 0.222905; substitution rates AC = 1.659997, AG = 3.281475, AT = 1.493369, CG = 0.981860, CT = 7.973947, GT = 1.000000; gamma distribution shape parameter α = 0.176316. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Sporidesmioides thailandica* (MFLUCC 13-0840 and KUMCC 16-0012). All type strains are in bold. The newly generated sequences are indicated in yellow.

Material examined – China, Yunnan Province, Dali City, on a dead twig of *Coffea arabica* (Rubiaceae), 25 July 2022, Li Lu, DL-C3 (MHZU 23-0079), living cultures ZHKUCC 23-0668 = ZHKUCC 23-0669.

Culture characters – Conidia germinating on PDA within 12 hours. Colonies on PDA reaching 20 mm within 4 weeks at 25 °C. Culture from above, cream, circular, margin entire, flat, slightly effuse in middle, cottony; reverse yellowish.

GenBank numbers – ZHKUCC 23-0668: ITS: OR826583, LSU: OR836015, SSU: OR836021, *rpb2*: OR832765, *tef1-α*: OR832757; ZHKUCC 23-0669: ITS: OR826584, LSU: OR836016, SSU: OR836022, *rpb2*: OR832766, *tef1-α*: OR832758.

Known distribution (based on molecular data) – China (Yunnan, Sichuan) (this study, Tian et al. 2023), Thailand (Li et al. 2017a).

Known hosts (based on molecular data) – *Coffea arabica* (Rubiaceae) (this study), dead branches of unknown hosts (Tian et al. 2023), dead branch of *Bidens pilosa* (Li et al. 2017a).



Figure 31 – *Torula mackenziei* (MHZU 23-0079, a new host record). a, b Colonies on a dead branch of *Coffea arabica*. c, d Hyphae, conidiophores, and conidiogenous cells. e Conidia in catenated chain. f A germinated conidium. g Culture on PDA from above and reverse. h Budding on conidia. i–m Immature and mature stages of conidia. Scale bars: c = 30 μm, d–m = 10 μm.

Notes – Phylogenetic analyses of the combined ITS, LSU, SSU, *rpb2* and *tef1-α* sequence dataset revealed that our strains (ZHKUCC 23-0668 and ZHKUCC 23-0669) grouped with *T. mackenziei* (MFLUCC 13-0839) with 100% ML and 1.00 BYPP bootstrap support (Fig. 30). The nucleotide base comparison of ITS, LSU, SSU, *rpb2* and *tef1-α* regions shows that our strain (ZHKUCC 23-0668) differs from the type strain of *T. mackenziei* (MFLUCC 13-0839) by 7/497 bp

(1.4%), 0/880 bp (0%), 1/849 bp (0.1%), 24/895 bp (2.6%) and 2/904 bp (0.2%) respectively. *Torula mackenziei* was introduced by Li et al. (2017a) based on morphology and phylogeny. The fungus has been reported on dead branches of *Bidens pilosa* in Thailand and dead branches of unidentified hosts in China. Our collection (MHZU 23-0079) was found on the twigs of *Coffea arabica* in China. The morphology of our isolates is similar to *T. mackenziei* (holotype). However, our collection has longer conidiophores and wider conidia than in the original description (conidiophores: 5–7 μm $\times$ 3–5 μm vs. s 3–4.3 μm $\times$ 3.4–3.7 μm ; conidia: 10–19 μm long $\times$ 5–8 μm vs. a 9.4–18.5 μm long $\times$ (3.8–)4.4–4.7 μm) (Li et al. 2017a). Thus, following Chethana et al. (2021a) and conclusions based on morphology and phylogeny, we identify our new collection is *T. mackenziei* and it is a new host record from *Coffee*.

Eurotiomycetes O.E. Erikss. & Winka, Myconet 1(1): 6 (1997).

Eurotiales G.W. Martin ex Benny & Kimbr.

Trichocomaceae E. Fisch., in Engler & Prantl, Nat. Pflanzenfam., Teil. I (Leipzig) 1(1): 310 (1898) [1900].

Talaromyces C.R. Benj., Mycologia 47(5): 681 (1955).

Index Fungorum number: IF5347; Facesoffungi number: FoF00458

Talaromyces was introduced by Benjamin (1955) to accommodate sexual morphs of *Penicillium* that produce smooth-walled ascomata covered with interwoven hyphae. The genus is typified by *Talaromyces flavus*. Members of *Talaromyces* colonize many substrates, including living or decaying plant material, soil, air, compost, dung, dust, foodstuffs, arthropods, and animals worldwide in both terrestrial and marine environments (Wijayawardene et al. 2017, Sun et al. 2020, Zhang et al. 2022a). Some *Talaromyces* species are important endophytes with antagonistic properties against plant pathogens, colonizing the rhizosphere and have been employed in crop protection through artificial inoculations, which has great potential in sustainable agriculture (Naraghi et al. 2010, Kazerooni et al. 2019, Nicoletti et al. 2023). Currently, there are more than 150 species belonging to eight sections (*Bacillispori*, *Helici*, *Islandici*, *Purpurei*, *Tenues*, *Subinflati*, *Talaromyces* and *Trachyspermi*) of *Talaromyces* (Yilmaz et al. 2014, Sun et al. 2020, Index Fungorum 2024, Zhang et al. 2022a). Here, we provide the updated phylogeny for *Talaromyces*, section *Islandici* (Fig. 32).

Talaromyces variabilis (Sopp) Samson, N. Yilmaz, Frisvad & Seifert, in Samson, Yilmaz, Houben, Spierenburg, Seifert, Peterson, Varga & Frisvad, Stud. Mycol. 70: 177 (2011). Fig. 33

Index Fungorum number: IF560676; Facesoffungi number: FoF15297

Isolated from soil in a cave habitat. Asexual morph: *Colony* growing on PDA. *Hyphae* 1–3 μm wide, hyaline, septate, smooth, branched. *Conidiophores* smooth, bi-verticillate. *Stipes* smooth, branched, 2–3 per stipe. *Metulae* 3–5, divergent, 6–22 $\times$ 2–3 μm ($\bar{x}$ = 11.01 $\times$ 2.65 μm , n = 60). *Phialides* 6–14 $\times$ 1.5–3 μm ($\bar{x}$ = 9.26 $\times$ 2.36 μm , n = 80), acerose to ampulliform, 3–5 per metulae. *Conidia* 2.5–5.5 $\times$ 2–3.5 μm ($\bar{x}$ = 3.62 $\times$ 2.67 μm , n = 150), smooth, fusiform, obround, ovoid, subglobose, arranged in chains. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA attaining 2 cm after 7 days at room temperature (20–25 °C), circular to irregular, plain, margins wide, irregular. Mycelia white, texture velutinous; sporulation dense; conidial mass yellowish green to vivid green; soluble pigments absent; exudates absent; reverse green to buff at the periphery, and white at margins.

Material examined – China, Yunnan Province, Kunming, Fuming County, Gem Cave (N 25°17'31.49", E 102° 40' 08.59"), 21 May 2020, Samantha C. Karunarathna, A17-C1 (ZHKU 23-0279), living culture ZHKUCC 23-1031; *ibid.*, A17-A, living culture ZHKUCC 23-1028; *ibid.*, A17-B, living culture ZHKUCC 23-1029; *ibid.*, A17-C, living culture ZHKUCC 23-1030; *ibid.*, A9, living culture ZHKUCC 23-1032; *ibid.*, A9-A, living culture ZHKUCC 23-1033.

GenBank numbers – ZHKUCC 23-1028: ITS: PP029405: *BenA*: PP077040, *CaM*: PP077052, *rpb2*: PP077046; ZHKUCC 23-1029: ITS: PP029406: *BenA*: PP077041, *CaM*: PP077053, *rpb2*:

PP077047; ZHKUCC 23-1030: ITS: PP029407: *BenA*: PP077042, *CaM*: PP077054, *rpb2*:
 PP077048; ZHKUCC 23-1031: ITS: PP029408: *BenA*: PP077043, *CaM*: PP077055, *rpb2*:
 PP077049; ZHKUCC 23-1032: ITS: PP029409: *BenA*: PP077044, *CaM*: PP077056, *rpb2*:
 PP077050; ZHKUCC 23-1033: ITS: PP029410: *BenA*: PP077045, *CaM*: PP077057, *rpb2*:
 PP077051.

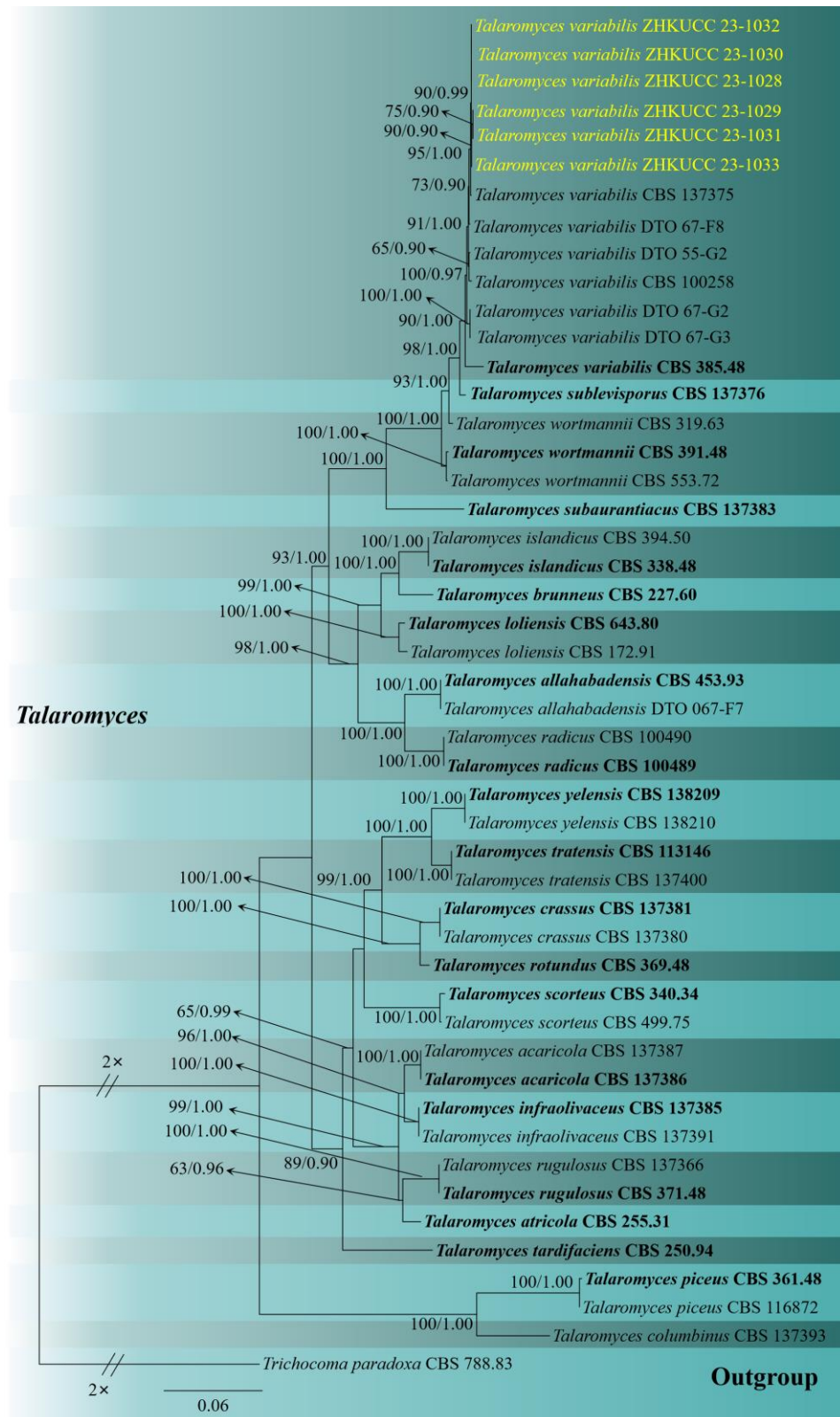


Figure 32 – The phylogram generated from the maximum likelihood analysis is based on the combined ITS, *BenA*, *CaM* and *rpb2* sequence data for *Talaromyces* section *Islandici*. Forty-eight

strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -13648.805389 is presented. The evolutionary model GTR+I+G is applied to all the genes. The matrix had 867 distinct alignment patterns, with 3.28% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.229079, C = 0.267924, G = 0.272640, T = 0.230357; substitution rates AC = 1.033618, AG = 3.478624, AT = 1.068762, CG = 0.809810, CT = 4.827112, GT = 1.000000; gamma distribution shape parameter α = 1.035181. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Trichocoma paradoxa* (CBS 788.83). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Known distribution – China (this study), South Korea (Adhikar et al. 2021).

Known hosts or substrata – Cave substrata (this study), soil (Adhikar et al. 2021).

Notes – In the multi-locus phylogenetic analysis of ITS, *BenA*, *CaM* and *rpb2*, our new strains (ZHKUCC 23-1028–ZHKUCC 23-1033) clustered with the strains of *T. variabilis* (CBS 137375, CBS 100258, CBS 385.48, DTO 67-F8, DTO 55-G2, DTO 67-G3, and DTO 67-G2) with 95% ML and 1.00 BYPP bootstrap support (Fig. 32). Also, our strains share similar morphological characteristics to *T. variabilis* in having bi-verticillate conidiophores, acerose to ampulliform phialides, and smooth, obround, ovoid, subglobose conidia arranged in chains. *Talaromyces variabilis* was first described as *Penicillium variable* by Sopp (1912). Samson et al. (2011) transferred *P. variable* to *Talaromyces* and synonymized it as *T. variabilis* based on the combined phylogeny of ITS and *rpb1*. Thus, based on morphology and phylogenetic analysis, the new isolates are identified as *T. variabilis*. This is the first report of *T. variabilis* isolated from a cave habitat.

Lecanoromycetes O.E. Erikss. & Winka

Ostropomycetidae V. Reeb, Lutzoni & Cl. Roux

Ostropales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 68 (1932)

Stictidaceae Fr. [as 'Stictci'], Summa veg. Scand., Sectio Post. (Stockholm): 345 (1849)

Neoostropa Y.Y. Yang, A.R. Gomes de Farias & K.D. Hyde 2023

Index Fungorum number: IF900059 Facesoffungi number: FoF13373

Neoostropa was introduced to accommodate *N. castaneae* as the type species by Yang et al. (2023a). *Neoostropa* is characterized by immersed, solitary, multilocular, perithecial ascomata, cylindrical, long asci with thickened caps, and hyaline, aseptate, guttulate ascospores. This genus has only one species, collected from a forest in Yunnan Province, China. Here, we provide an updated phylogeny for the *Stictidaceae* taxa (Fig. 34).

Neoostropa castaneae Yang et al. Current Research in Environmental & Applied Mycology (Journal of Fungal Biology) 13(1):123–135 (2023) Fig. 35

Index Fungorum number: IF900060, Facesoffungi number: FoF13349

Saprobic on dead stem of *Photinia* × *fraseri*. Sexual morph: *Ascomata* 450–534 µm high, 280–357 µm wide ($\bar{x}$ = 502 × 317 µm, n = 10), appear as white cracks on the host surface, apothecial, immersed to erumpent, solitary, subglobose, white, apex partly protruding beyond the surface layers of the stem, exposing the discs. *Discs* white, convex, and covered by thick pruinose substance. *Exciple* 6–14 µm width ($\bar{x}$ = 9.5, n = 20), comprising interwoven and hyaline hyphae, with numerous crystalline inclusions to the wall in the upper part of the ascomata. *Hamathecium* comprises asci and paraphyses. *Paraphyses* 1.3–2.8 µm (x = 2, n = 40), thick, hyaline, long filiform, unbranched, aseptate. *Asci* (167–)213–283(–324) × (6.6–)7–9(–10) µm ($\bar{x}$ = 248 × 8, n = 30), 8-spored, hyaline, cylindrical, slightly cylindric-clavate, thick-walled, apically rounded, with a minute ocular chamber. *Ascospores* (1.7–)1.9–2.5(–3) µm wide ($\bar{x}$ = 2.2, n = 45), the same length as asci, filiform, hyaline, multi-guttulate, multi-septate, spiral arrangement, but intertwining irregularly in the upper part of the asci. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and the colony slowly growing on PDA media, reaching 3 cm after incubation for 2 months at 27 °C, circular, dense, umbonate, undulate. Front light grey and reverse yellow-orange.

Material examined – China, Yunnan Province, Kunming city, Kunming Botanical Garden, (25°8'19"N, 102°44'25"E, 1930m), on decaying stem of *Photinia* × *fraseri* (*Rosaceae*), 10 April 2022, Ying Gao, KG1A (HKAS 124665), (CGMCC 3.24556, living culture), *ibid.*, KG1B (HMAS 352289), (CGMCC 3.24557, living culture).

GenBank numbers – CGMCC 3.24556: ITS: OR464185, LSU: OR464187, mtSSU: OR464189; CGMCC 3.24557: ITS: OR464186, LSU: OR464188, mtSSU: OR464190.

Known distribution (based on molecular data) – China (Yang et al. 2023a, this study).

Known hosts (based on molecular data) – *Castanea henryi* (Yang et al. 2023a), *Photinia* × *fraseri* (this study).

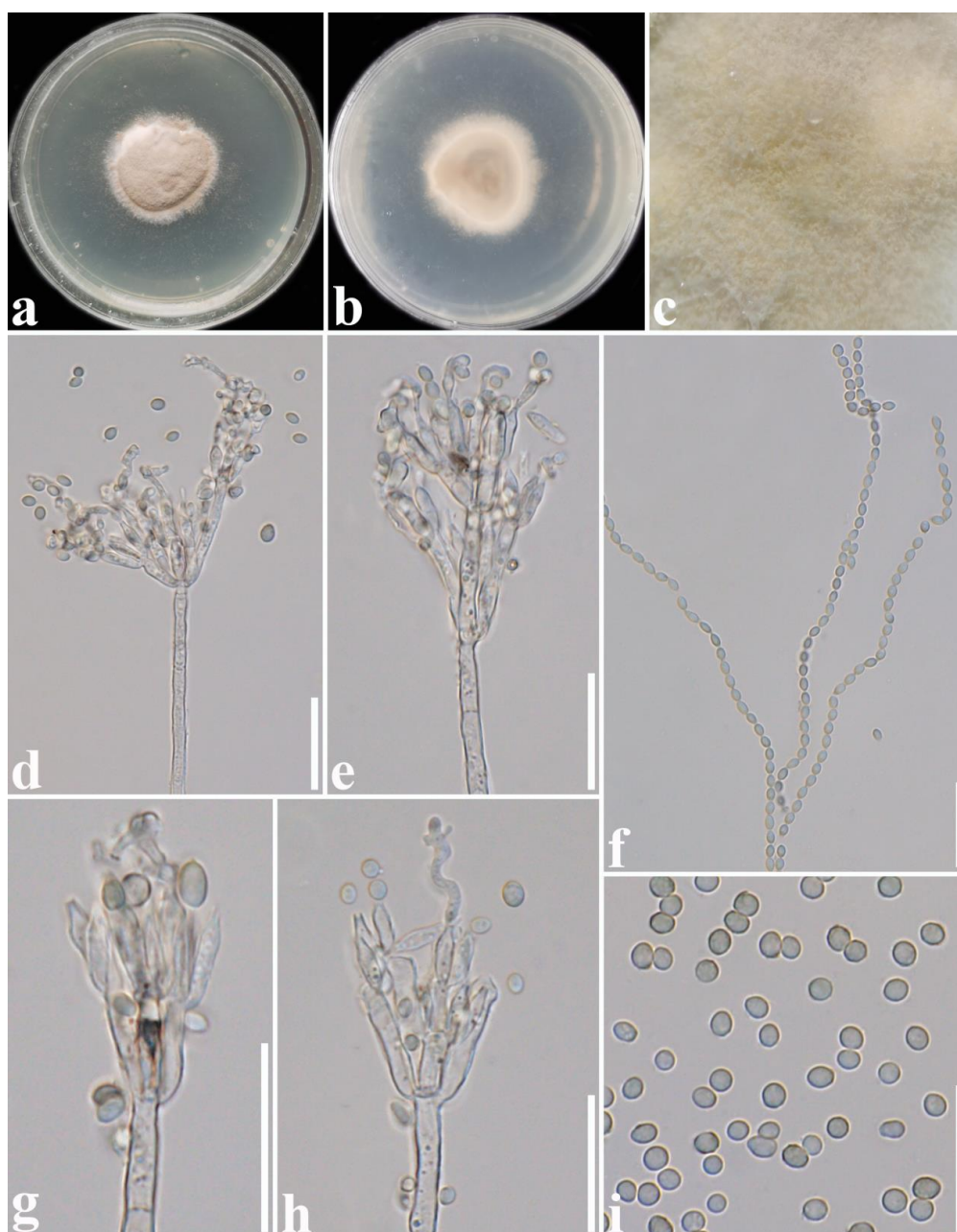


Figure 33 – *Talaromyces variabilis* (ZHKU 23-0279, a new record in cave habitat). a, b Colony on PDA (a) above and (b) below. c Sporulating conidiomata on PDA (20 days old culture). d, e, g, h Conidiophores, Conidiogenous cells with conidia. f Conidia arranged in chains. i Conidia. Scale bars: d–i = 20 µm.

Note – The BLAST search results for LSU, ITS, and mtSSU sequences data showed close hits to *Neoostropa castaneae* (99.75%/99.15%/99.73%), and the newly generated sequences clustered together with the strains of *N. castaneae* with 100% ML and 1.00 BYPP bootstrap support (Fig. 34). Also, the new isolate shares similar morphological characteristics to *N. castaneae*. However, the morphology of our collection (HKAS 124665, HMAS 352289) differs from *N. castaneae* (KUNCC 22-12390, holotype; KUNCC 22-12391) in ascospore width and septation (1.7–3 μm , multi-septate vs. 1–1.6 μm , aseptate). Based on the morphology and multi-gene phylogeny, we conclude our strains are *N. castaneae*. Here, we provide the first record of *N. castaneae* on *Photinia x fraseri* in China.

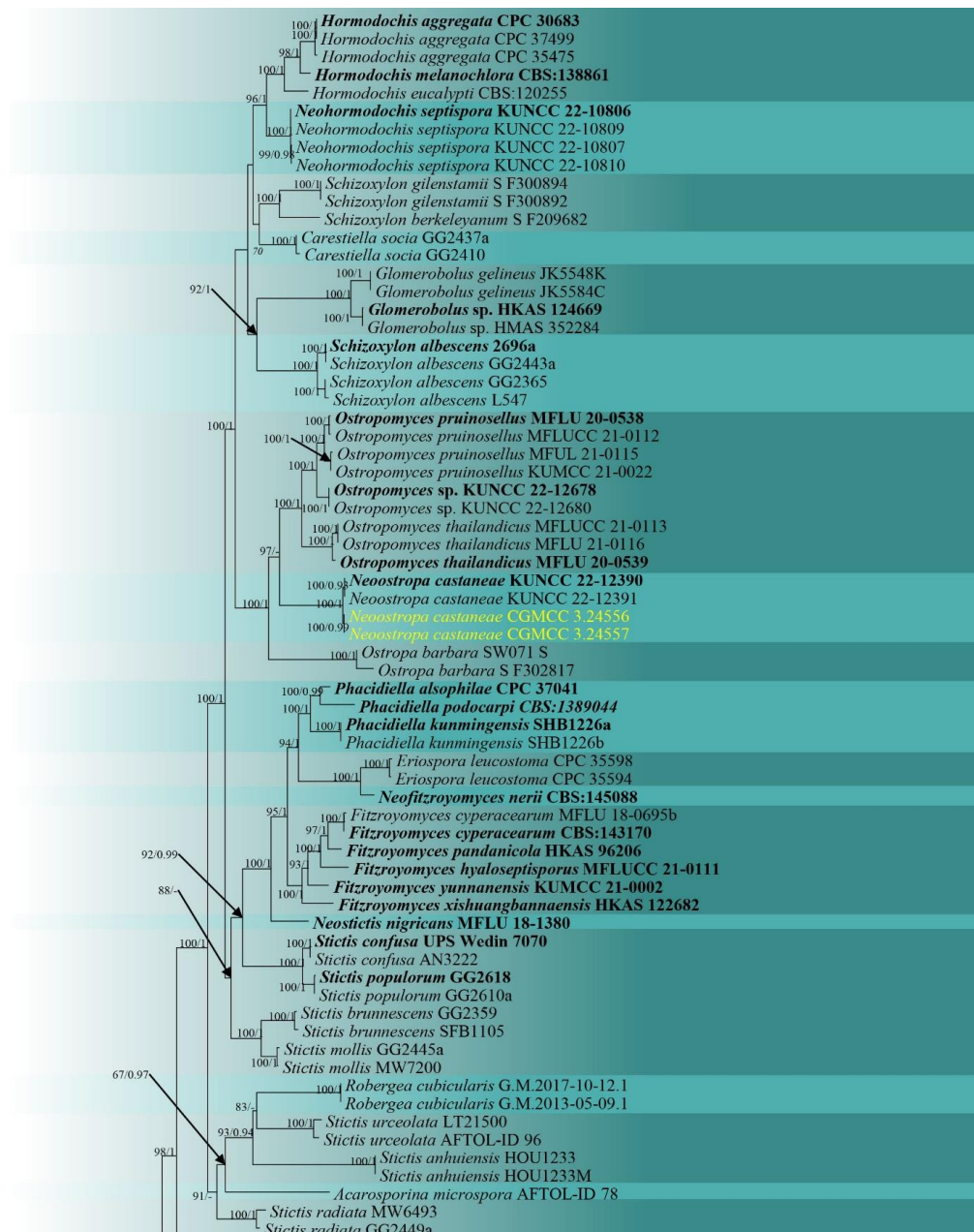


Figure 34 – Phylogenetic tree of *Stictidaceae* species based on maximum likelihood analysis of a combined multigene alignment (LSU, ITS, mtSSU, and *rpb2*). Hundred and two strains are included in the combined analyses. The best RAXML tree with a final likelihood value of -52712.148227 is presented. The evolutionary model GTR+I+G is applied to all the genes. The matrix had 2710 distinct alignment patterns, with 54.18% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.275144, C = 0.218376, G = 0.263393, T = 0.243088; substitution rates AC = 1.340123, AG = 2.893395, AT = 1.754171, CG = 0.923331, CT

= 6.233358, GT = 1.000000; gamma distribution shape parameter α = 0.330441. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. Tree was rooted with *Trapelia glebulosa* (KS22) and *Placopsis perrugosa* (KS132). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

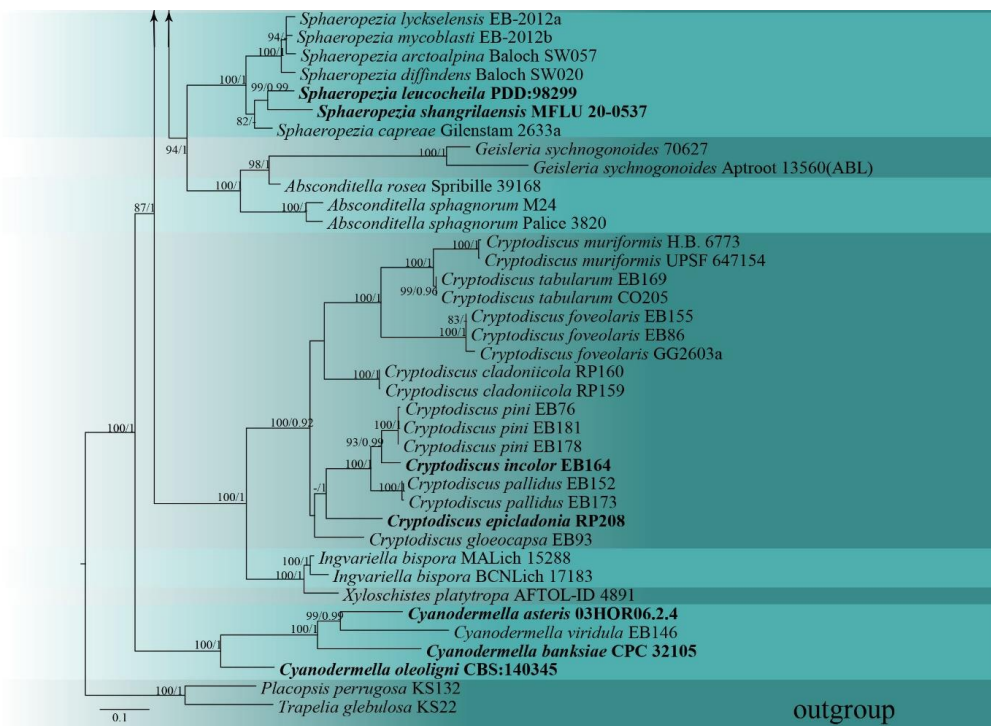


Figure 34 – Continued.

Leotiomyces O.E. Erikss. & Winka, Myconet 1(1): 7 (1997)

Helotiales Nannf., Nova Acta R. Soc. Scient. upsala., Ser. 4 8(no. 2): 68 (1932)

Helotiaceae Rehm [as ‘*Helotieae*’], Rabenh. Krypt.-Fl., Edn 2 (Leipzig) 1.3(lief. 37): 647 (1892) [1896]

Cyathicula De Not., Comm. Soc. crittog. Ital. 1(fasc. 5): 381 (1863) [1864]

Index Fungorum number: IF1367; Facesoffungi number: FoF15221

Cyathicula was introduced with the type species *C. coronata* (Clement & Shearer 1931). Initially, some *Cyathicula* specimens were identified as *Conchatium* or *Crocicreas* (Svrček 1985), yet phylogenetic analyses and morphological observation showed that they differ (Baral 2005, Chlebická & Chlebicki 2007, Baral et al. 2015). *Cyathicula* species are characterized by cylindric to clavate paraphyses, which differ from lanceolate or cylindrical paraphyses in *Crocicreas* (Carpenter 1981). Most *Cyathicula* species have been reported in Asia, Europe and the USA (Rehm 1893, Carpenter 1981, Chlebická & Chlebicki 2007). Currently, 30 species are listed in this genus (Wijayawardene et al. 2022). Herein, we provide an updated phylogeny for the *Cyathicula* taxa (Fig. 36).

Cyathicula dioscoreae Lestari, Camporesi & K.D. Hyde, sp. nov.

Fig. 37

Index Fungorum number: IF901542; Facesoffungi number: FoF15280

Etymology – Referring to the host genus name ‘*Dioscorea*’

Holotype – MFLU 23- 0461

Saprobic on a dead aerial stem of *Dioscorea communis*. Sexual morph: *Apothecia* 262–802 μm high $\times$ 222–420 μm diam. ($\bar{x}$ = 489 $\times$ 347 μm , n = 10) in dried form, solitary or in small clusters, stipitate. *Receptacle* cupulate, greyish white. *Disc* concave. *Ectal excipulum* 40–51 μm ($\bar{x}$ = 41.6 μm , n = 10) in the lower part, composed of thick-walled, dark to pale brown, gelatinous cells of *textura porrecta*. *Medullary excipulum* 29–40 μm ($\bar{x}$ = 34 μm , n = 10) in lower part, composed

of thin-walled, hyaline cells of *textura porrecta*. *Paraphyses* 2–3.1 μm ($\bar{x}$ = 2.8 μm , n = 10) wide, filiform, numerous, smooth, aseptate, sometime branched at 1/3 length, rounded at the apex, similar to the length with the asci. *Asci* 45–52 $\times$ 4.9–6.3 μm ($\bar{x}$ = 48 $\times$ 5.7 μm , n = 10), unitunicate, 8-spored, cylindrical, short pedicellate, mostly conical at the apex, arising from croziers. *Ascospores* 8.7–11 $\times$ 2.3–2.8 μm ($\bar{x}$ = 10 $\times$ 2.5 μm , n = 10), 1–2-seriate, fusoid, hyaline, aseptate, smooth-walled, with guttules at the both ends. Asexual morph: Undetermined.

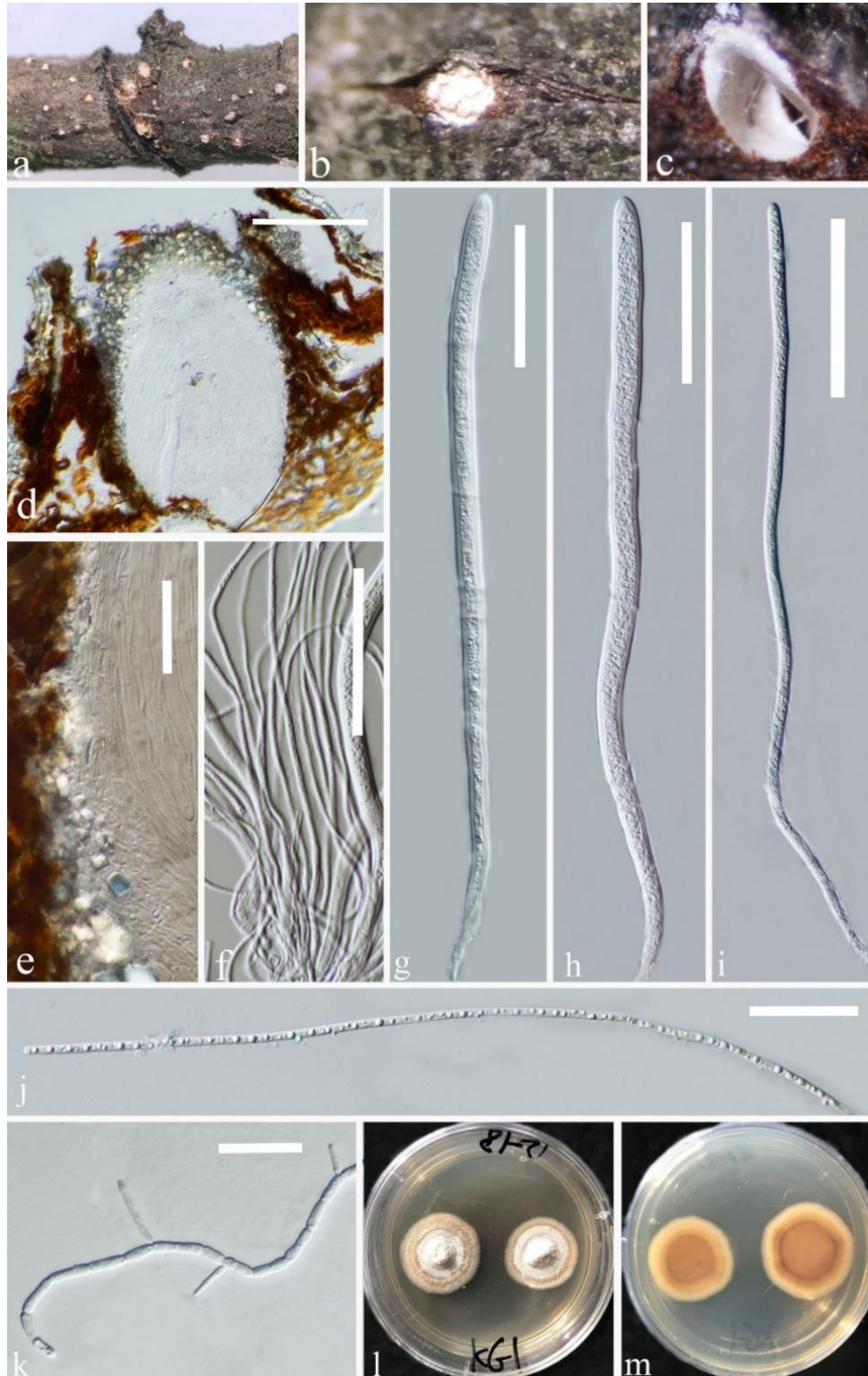


Figure 35 – *Neoostropa castaneae* (HKAS 124665, a new host record). a, b Ascomata on the host. c, d Vertical sections of ascomata. e Exciple. f Paraphyses. g–i Asci. j Ascospore. k A germinating

ascospore. l, m Front and reverse views of colony on PDA. Scale bars: d = 200 μ m, e–h = 50 μ m, i = 100 μ m, j, k = 30 μ m.

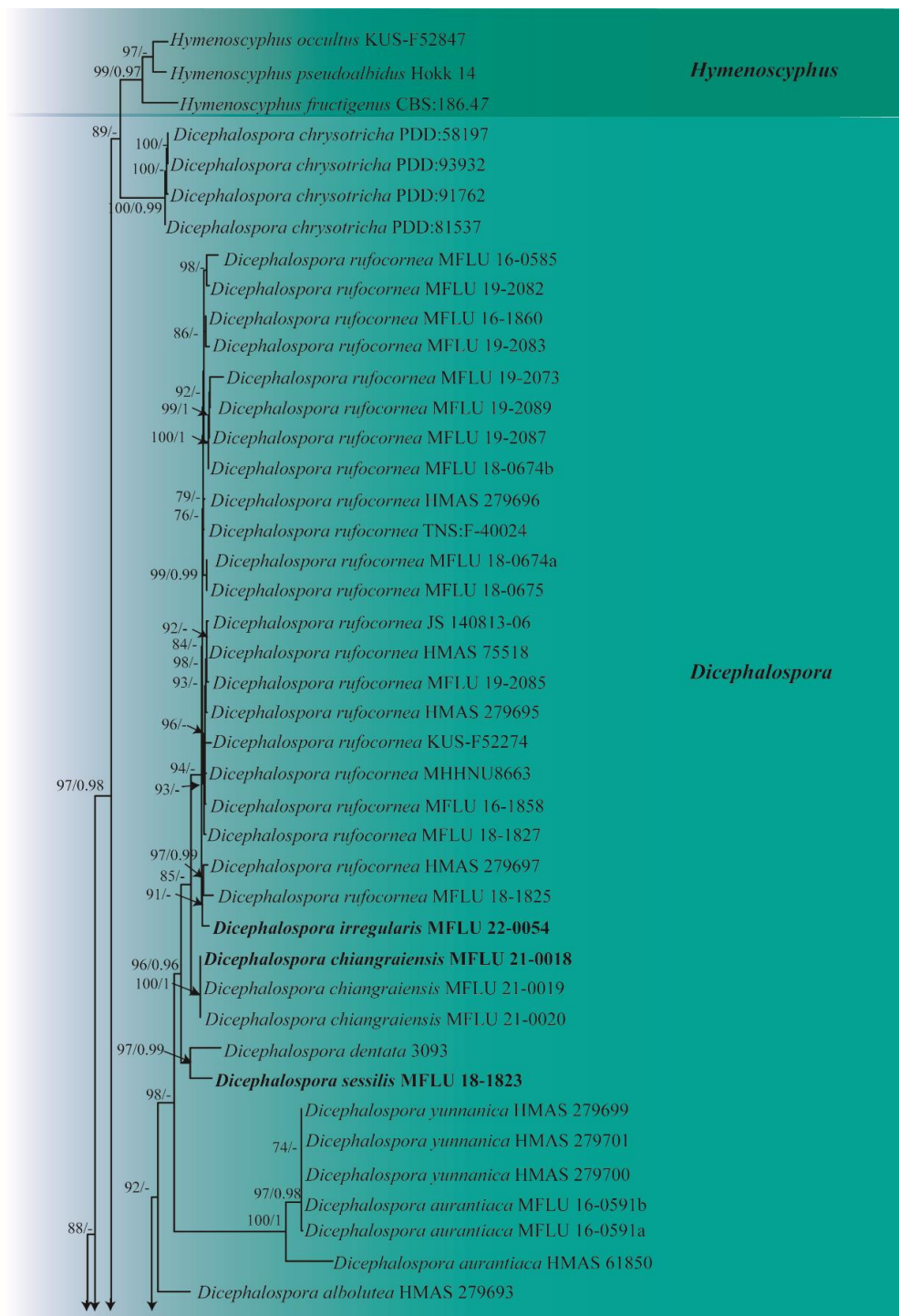


Figure 36 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, and LSU sequence data of *Helotiaceae* including *Cyathicula*. Eighty-seven strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAXML tree with a final likelihood value of -8931.242 is presented. The evolutionary model SYM+I+G is applied for all the genes. The matrix had 485 distinct alignment patterns, with 29.63% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.2204, C = 0.2223, G = 0.2794, T = 0.2523; substitution rates AC = 1.18800, AG = 2.05674, AT = 1.17804, CG = 0.51031, CT = 4.75697, GT = 1.00; gamma distribution shape parameter α = 0.576. Bootstrap support values for ML greater than 70% and

Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree is rooted with *Pleuroascus nicholsonii* (CBS 345.73) and *Connersia rilstonii* (CBS 537.74). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

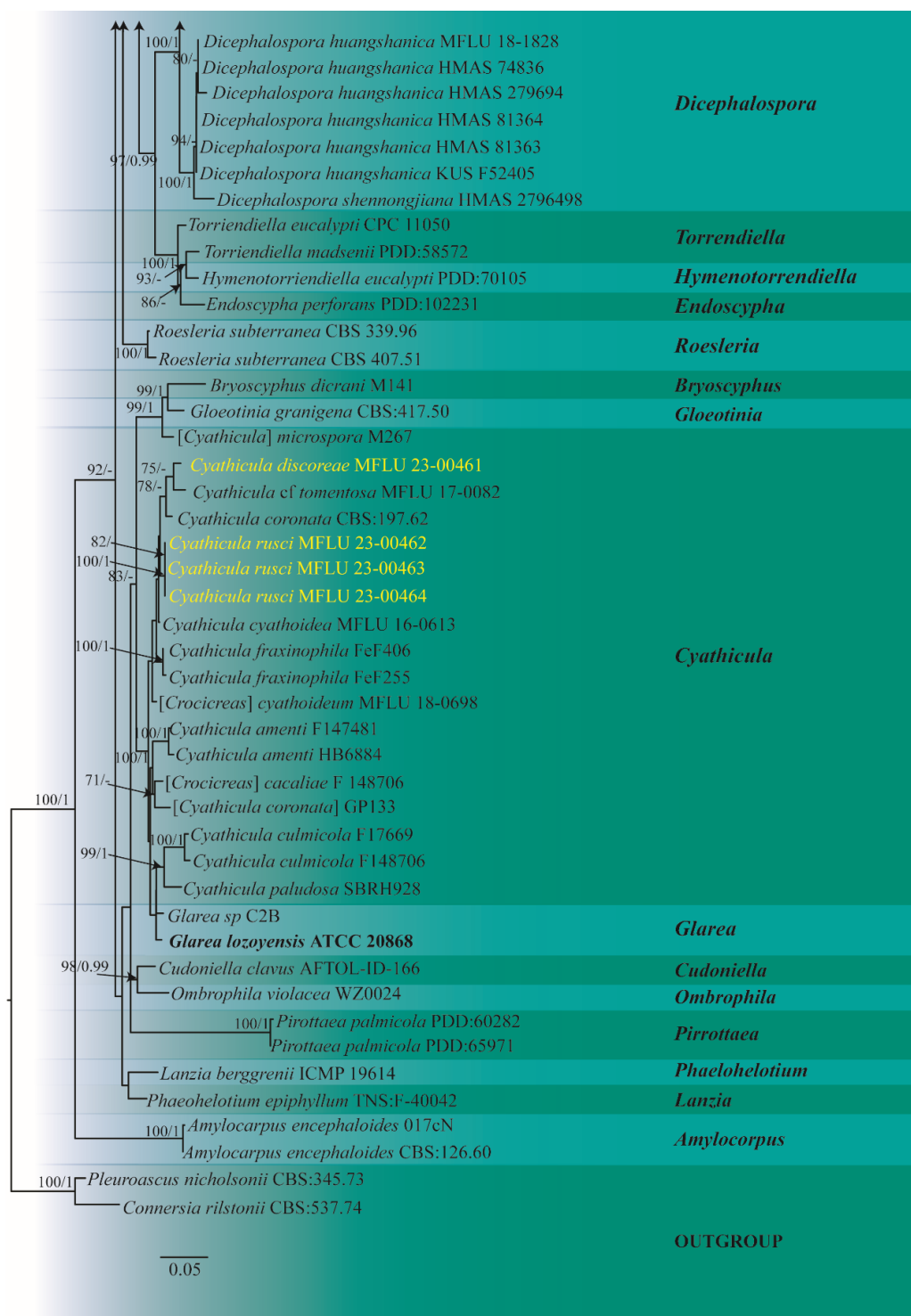


Figure 36 – Continued.

Material examined – Italy, Province of Perugia, near Valfabbrica, on a dead and aerial stem of *Dioscorea communis* (*Dioscoreaceae*), 20 November 2020, Erio Camporesi, IT 4757 (MFLU 23- 0461).

GenBank numbers – MFLU 23-0461: ITS: OR652408, LSU: OR652435.

Known distribution – Italy (this study)

Known hosts – *Dioscorea communis* (this study).

Notes – In the combined LSU and ITS phylogenetic analysis (Fig. 36), our strain (MFLU 23-0461) clustered with *C. cf tomentosa* (MFLU 17-0082) with 75% ML bootstrap support. The nucleotide differences between in ITS and LSU of our collection and *C. cf tomentosa* (MFLU 17-0082) are 2.2 % and 0.98 %, respectively (Table 1). These two collections exhibit distinct habits of apothecia, excipulum cells and asci. The apothecia of our collection (MFLU 23-0461) are greyish white with cupulate receptacle whereas *C. cf tomentosa* (MFLU 17-0082) is characterized by dark apothecia with mostly enclosed, goblet receptacles (Table 2). Excipulum cells of our collection is *textura porrecta* vs *textura oblita-prismatica* (*C. cf tomentosa*). Also, our collection (MFLU 23-0461) has smaller ($45\text{--}52 \times 4.9\text{--}6.3$ vs $50\text{--}65 \times 5.5\text{--}7$ μm) asci than *C. cf tomentosa* (Table 2). Hence, based on the morphological evidence with multi-gene phylogeny we introduce, *Cyathicula dioscoreae* as a new species (Fig. 37).

Table 1 Comparison of ITS and LSU sequences of closely related *Cyathicula* species with *C. dioscorea* (MFLU 23-00461).

Species	ITS (%)	LSU (%)
<i>Cyathicula cf tomentosa</i> (MFLU 17-0082)	2.2	0.98
<i>Cyathicula coronata</i> (CBS:197.62)	3.3	1.4
<i>Cyathicula rusci</i> (MFLU 23-0462)	2.9	1.1
<i>Cyathicula cyathoidea</i> (MFLU 16-0613)	3.7	0.86
<i>Cyathicula fraxinophila</i> (FeF255)	5.1	N/A
<i>Cyathicula fraxinophila</i> (FeF406)	4.6	N/A
[<i>Crocicreas</i>] <i>cyathoideum</i> (MFLU 18-0698)	4.4	1.2

Table 2 Morphological comparison of newly introduced *Cyathicula* species with phylogenetically closely related taxa.

Species	Apothecia	Excipulum cells	Paraphysis μm (	Asci μm (	Ascospore characters μm (	Reference(s)
<i>Cyathicula cf tomentosa</i> (MFLU 17-0082)	Black, stipitate with hair	Ectal: <i>textura oblita - prismatica</i> Medulary: <i>t. oblita - porrecta</i>	2–2.5; cylindrical	50–65 $\times$ 5.5–7; cylindrical with stipitate base, J+, conical to obtuse apex, arising from croziers	9–12 $\times$ 2–3.5; ellipsoid to fusoid, hyaline with guttules	Ekanayaka et al. (2019)
<i>Cyathicula coronata</i>	Cream with crown-like structure, stipitate	Ectal: <i>textura oblita</i> Medulary: <i>t. oblita - intricata</i>	3–3.3; filiform, septate	127–133 $\times$ 10–11; cylindrical, J+ (faintly), rounded apical, arising from croziers	20.5–24.2 $\times$ 4.5–5.9; fusoid with guttules, hyaline, 1-septate	Domínguez (2020)
<i>Cyathicula cf cyathoidea</i> (MFLU 16-0613)	Cream, stipitate	Ectal: <i>textura porrecta</i> Medulary: <i>textura oblita-intricata</i>	1.5–2; filiform	35–45 $\times$ 4–5.5; cylindrical, conical to rounded apex, J+, arising from simple septa	8–9 $\times$ 1.6–1.8; fusoid with rather flattened at one side, hyaline, smooth	Ekanayaka et al. (2019)

Table 2 Continued.

Species	Apothecia	Excipulum cells	Paraphysis μm (	Asci μm (	Ascospore characters μm (	Reference(s)
<i>Cyathicula dioscorea</i> (MFLU 23-0461)	Cream (dried state), stipitate	Ectal: <i>textura prismatica</i> Medulary: <i>textura intricata-oblita</i> .	2–3.1; filiform (with slight apically swollen at terminal cells) to cylindrical, branched	45–52 $\times$ 4.9–6.3; cylindrical with short pedicellate, J+, conical to rounded apical, arising from croziers	8.7–11 $\times$ 2.3–2.8; fusoid with rather flattened at one side, hyaline smooth	This study
<i>Cyathicula fraxinophila</i>	White, stipitate	Ectal: <i>textura porrecta</i> Medulary: <i>textura porrecta-oblita</i> .	3–3.5; cylindrical, septate	90–95 $\times$ 8–8.5; cylindrical, J+, conical to rounded apex, arising from croziers	46–48 $\times$ 2.5–3; fusoid, hyaline, 1-septate	Baral (1993)
<i>Cyathicula rusci</i>	Cream (dried state), stipitate	Ectal: <i>textura porrecta</i> Medulary: <i>textura porrecta-oblita</i> .	2.2–3.8; cylindrical	45–53 $\times$ 4.3–5; cylindric with pedicellate, J+, rounded apex, arising from croziers, 8 spored	5.4–8 $\times$ 2.3–3; fusoid with guttules, hyaline	This study

Cyathicula rusci Lestari, Camporesi & K.D. Hyde, sp. nov.

Fig. 38

Index Fungorum number: IF901455; Facesoffungi number: FoF15215

Etymology – The epithet represents the host genus name ‘*Ruscus*’

Holotype – MFLU 23-0462

Saprobic on dead aerial of stems of *Ruscus aculeatus*. Sexual morph: *Apothecia* 718–917 μm high $\times$ 526–736 μm diam. ($\bar{x}$ = 805 $\times$ 597 μm , n = 10), white to creamy, solitary or in small clusters, stipitate. *Disc* concave. *Ectal excipulum* 44–65 μm ($\bar{x}$ = 55.2 μm , n = 10) wide at the lower part, composed of golden, thick-walled cells of *textura porrecta*. *Medullary excipulum* 47–60 μm ($\bar{x}$ = 54.4 μm , n = 10) in lower parts, composed of thin-walled, hyaline cells of *textura porrecta*. *Paraphyses* 2.2–3.8 μm ($\bar{x}$ = 2.7 μm , n = 10) wide, numerous, filiform, sometimes guttulate, septate near the base, rounded at the apex, similar in length with the asci. *Asci* 45–53 $\times$ 4.3–5 μm ($\bar{x}$ = 49 $\times$ 4.7 μm , n = 10), 8-spored, unitunicate, cylindric, with pedicels, rounded at the apex, arising from croziers. *Ascospores* 5.4–8 $\times$ 2.3–3 μm ($\bar{x}$ = 7 $\times$ 2.6 μm , n = 10), 1–2-seriate, cylindrical-fusoid, hyaline, aseptate, smooth-walled, guttulate. Asexual morph: Undetermined.

Material examined – Italy, Province of Forlì-Cesena [FC], near Meldola, on a dead and aerial stem of *Ruscus aculeatus* (*Asparagaceae*), 18 February 2021, Erio Camporesi, IT 4684b (MFLU 23-0462, holotype); *ibid*, Forlì-Cesena, near Meldola, on a dead aerial stem of *R. aculeatus* (*Asparagaceae*), 20 November 2020, Erio Camporesi, IT 4684 (MFLU 23-0463, paratype); *ibid*, Forlì-Cesena, near Meldola, on a dead aerial stem of *R. aculeatus* (*Asparagaceae*), 20 November 2020, Erio Camporesi, IT 4684a (MFLU 23-0464).

GenBank numbers – MFLU 23-0462: ITS: OR652405, LSU: OR652432; MFLU 23-0463: ITS: OR652406, LSU: OR652433; MFLU: 23-0464: ITS: OR652407, LSU: OR652434.

Notes – According to the phylogenetic analysis, our strains of *Cyathicula rusci* (MFLU 23-0462, MFLU 23-0463, MFLU 23-0464) formed a distinct clade from the group consists of *C. coronata* (CBS 197.62), *C. dioscoreae* (MFLU 23-0461) and *C. tomentosa* (MFLU 17-0082)

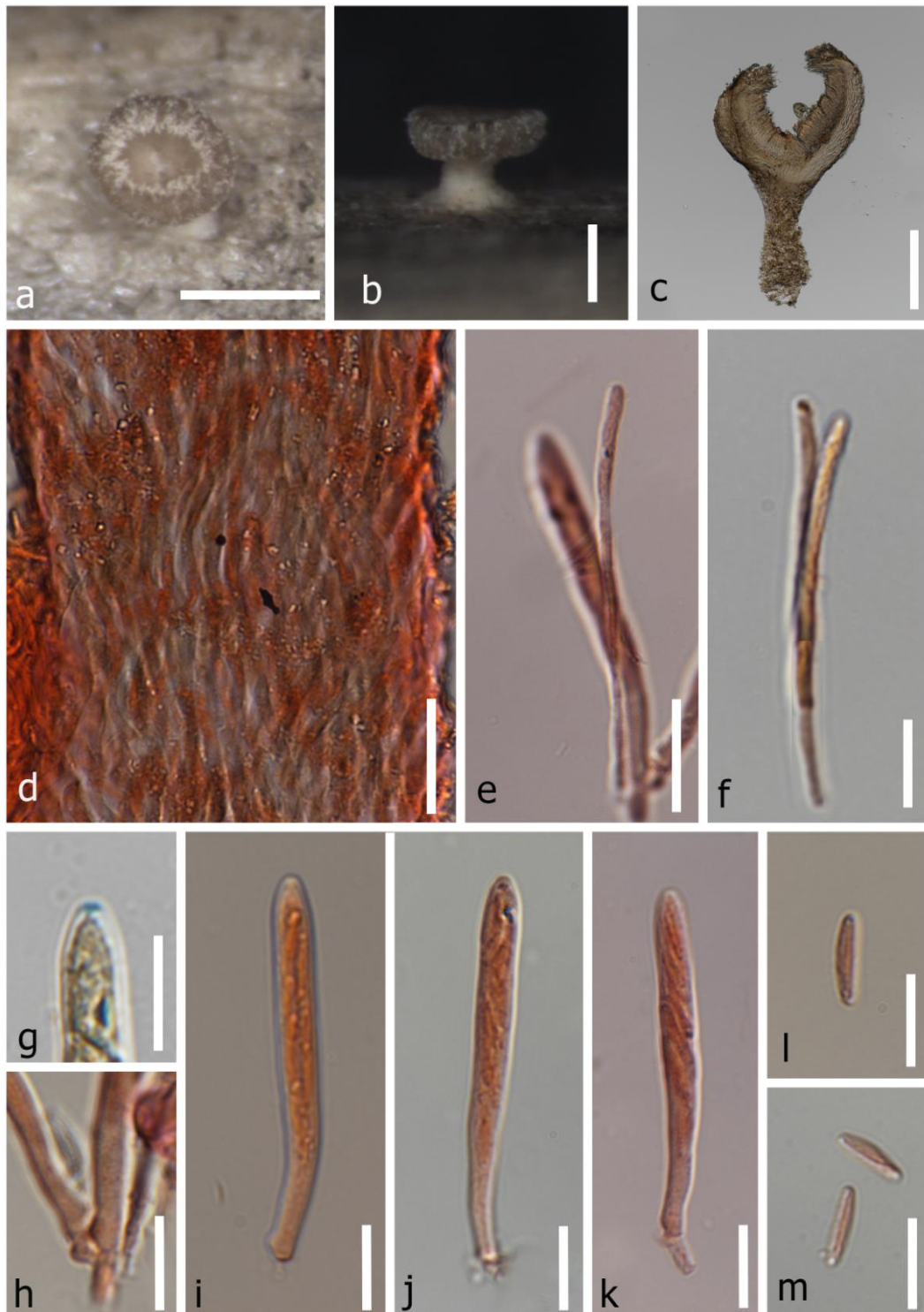


Figure 37 – Sexual morph of *Cyathicula dioscoreae* (MFLU 23-0461, holotype). a, b Appearance of apothecia on the host surface. c Close up section of an apothecium. d Medullary excipulum cells. e, f Paraphyses. g Ascus tip (mounted in Meltzer's agent without KOH). h A crozier at the base of asci (mounted in Congo red). i–k Asci (mounted in Congo red). l–m Ascospores (mounted in Congo red). Scale bars: a = 300 μ m, b, c = 200 μ m, d, e = 30 μ m, f–m = 10 μ m.

with 44% ML and 0.68 BYPP bootstrap support (Fig. 36). Also, *Cyathicula cyathoidea* (MFLU 16-0613) forms a separate lineage to our collections (MFLU 23-0462, MFLU 23-0463, MFLU 23-0464) with 45% ML and 0.66 BYPP bootstrap support (Fig. 36). The nucleotide differences in ITS and LSU sequences of our collection and phylogenetically closely related *Cyathicula* species are listed in Table 3. *Cyathicula rusci* differs from *C. tomentosa* by its apothecia appearance, asci and

ascospore size. The newly collected *Cyathicula* is characterized by creamy color apothecia while *C. cf tomentosa* has dark or black apothecia. In addition, *C. rusci* has smaller asci ($45\text{--}53 \times 4.3\text{--}5$ vs $50\text{--}65 \times 5.5\text{--}7 \mu\text{m}$) and ascospore size ($5.4\text{--}8 \times 2.3\text{--}3$ vs $9\text{--}12 \times 2\text{--}3.5 \mu\text{m}$) than *C. cf tomentosa*. Our collection differs from *C. cyathoidea* (MFLU 16-0613) in having wider paraphysis cells ($2.2\text{--}3.8$ vs $1.5\text{--}2 \mu\text{m}$), longer asci ($45\text{--}53$ vs $35\text{--}45 \mu\text{m}$) and smaller ascospores ($5.4\text{--}8 \times 2.3\text{--}3$ vs $8\text{--}9 \times 1.6\text{--}1.8 \mu\text{m}$) (Fig. 38, Table 2). *Cyathicula rusci* differs from *C. coronata* by lacking prominent teeth-like or crown-like structures on the apothecial disc, smaller asci ($45\text{--}53 \times 4.3\text{--}5$ vs $127\text{--}133 \times 10\text{--}11 \mu\text{m}$) and ascospores ($5.4\text{--}8 \times 2.3\text{--}3$ vs $20.5\text{--}24.2 \times 4.5\text{--}5.9 \mu\text{m}$) (Fig. 38, Table 2). Hence, the current study presents *C. rusci* as a new species on *Ruscus aculeatus*.

Table 3 Comparison of ITS and LSU sequences of closely related *Cyathicula* species with *C. rusci* (MFLU 23-00462).

Species	ITS (%)	LSU (%)
<i>Cyathicula cf tomentosa</i> (MFLU 17-0082)	3.4	1.9
<i>Cyathicula coronata</i> (CBS:197.62)	2.9	0.6
<i>Cyathicula cyathoidea</i> (MFLU 16-0613)	1.3	0.6
<i>Cyathicula fraxinophila</i> (FeF255)	3.1	N/A
<i>Cyathicula fraxinophila</i> (FeF406)	2.6	N/A
[<i>Crocicreas</i>] <i>cyathoideum</i> (MFLU 18-0698)	3.1	0.4

Tricladiaceae P.R. Johnst. & Baschien, Fungal Systematics and Evolution 6: 234 (2020)

Tricladium Ingold, Trans. Br. mycol. Soc. 25(4): 388 (1942) [1941]

Index Fungorum number: IF10306; Facesoffungi number: FoF14077

Tricladium was introduced by Ingold (1942) to accommodate *T. splendens* as the type species. *Tricladium*, the largest aquatic hyphomycetes genus, is polyphyletic in *Tricladiaceae* (Johnston & Baschien 2020). Even though members are known from both sexual and asexual morphs, most are described only from asexual morphs, characterized by dark colonies, various conidiogenesis, and long, sigmoid or arcuate conidia with septa. Some members have reported sexual morphs characterized by hymenoscypus-like apothecia and small ascospores as in *T. varicosporioides* and *Hymenoscypus splendens* (the asexual morph of *T. splendens*) (Ingold 1942, Sati & Tiwari 1992, Campbell et al. 2009, Gulis et al. 2012, Johnston & Baschien 2020). To date, there are 30 species listed in the Index Fungorum (2024) under this genus.

Tricladium terrestre D. Park, Trans. Br. mycol. Soc. 63(1): 180 (1974)

Fig. 40

Index Fungorum number: IF325017; Facesoffungi number: FoF15299

Saprobic on decayed wood. Sexual morph: *Apothecia* 0.8–1.6 mm wide $\times$ 0.6–1.1 mm high when dry, superficial, solitary or gregarious in groups, trumpet-shaped, sessile, rarely very short stipitate, glabrous. *Disc* flat to concave, pale yellow when young, pale orange, margin wavy and brownish-orange when mature. *Receptacle* pale yellow, glabrous. *Hymenium* 92–114 μm , hyaline with brownish-orange patches. *Subhymenium* 43–55 μm , hyaline, comprises hyphae of *textura intricata* mingled with *textura angularis* cells. *Excipulum* hyaline, composed of thin-walled *textura angularis* cells, divided into two layers with no clear demarcation, cells of inner layer reach to 18.4–28.4 μm ($\bar{x} = 22.7 \mu\text{m}$, $n = 15$) diam.; then becoming smaller in the outer layer, cells 7.6–17.2 μm ($\bar{x} = 11.6 \mu\text{m}$, $n = 50$) diam.; the outermost layer composed of *textura globulosa* cells, 5.2–11.2 μm ($\bar{x} = 7.8 \mu\text{m}$, $n = 70$) diam.; some marginal cells specialize to elongate to 2–3 times the diameter. *Paraphyses* 1.5–2.2 diam., filiform, filled with brownish-orange contents. *Asci* 71–100 $\mu\text{m} \times 7.5\text{--}12.2 \mu\text{m}$ ($\bar{x} = 85.4 \times 9.6 \mu\text{m}$, $n = 20$), 8-spored, unitunicate, clavate, rounded apex, shrinking down to a subtruncate base. *Ascospores* 8–14 $\times$ 2.6–4.5 μm ($\bar{x} = 10.6 \times 3.4 \mu\text{m}$, $n = 30$), $Q = 2.4\text{--}4.7 \mu\text{m}$, $Q_m = 3.1 \pm 0.3 \mu\text{m}$, overlapping, uniseriate, elongate to ellipsoidal, hyaline, slightly curved, with rounded ends, thin-walled, smooth, aseptate with 1–4 guttules. Asexual morph: Undetermined.

Material examined – China, Yunan Province, Kunming City, Kunming Botanical Garden, altitude 1900 m, on decayed wood, 11 October 2021, Cuijinyi Li, LCJY-348 (HKAS 128303).

GenBank numbers – HKAS 128303: ITS: OR437505

Known distribution (based on molecular data) – China (this study), Northern Ireland (Vu et al. 2019), Portugal (Campbell et al. 2009).



Figure 38 – Sexual morph of *Cyathicula rusci* (MFLU 23-0462, holotype). a A herbarium package. b Appearance of an apothecium on the host tissue. c A vertical section of an apothecium. d Close-up of excipulum cells. e–f Paraphyses. g Tip of an ascus (mounted in Meltzer’s reagent without KOH). h A crozier at the base of asci (mounted in Congo red). i–k Asci (mounted in Congo red). l–m Ascospores (mounted in Congo red). Scale bars: b = 500 mm, c = 350 μ m, d–k = 20 μ m, l–m = 10 μ m.

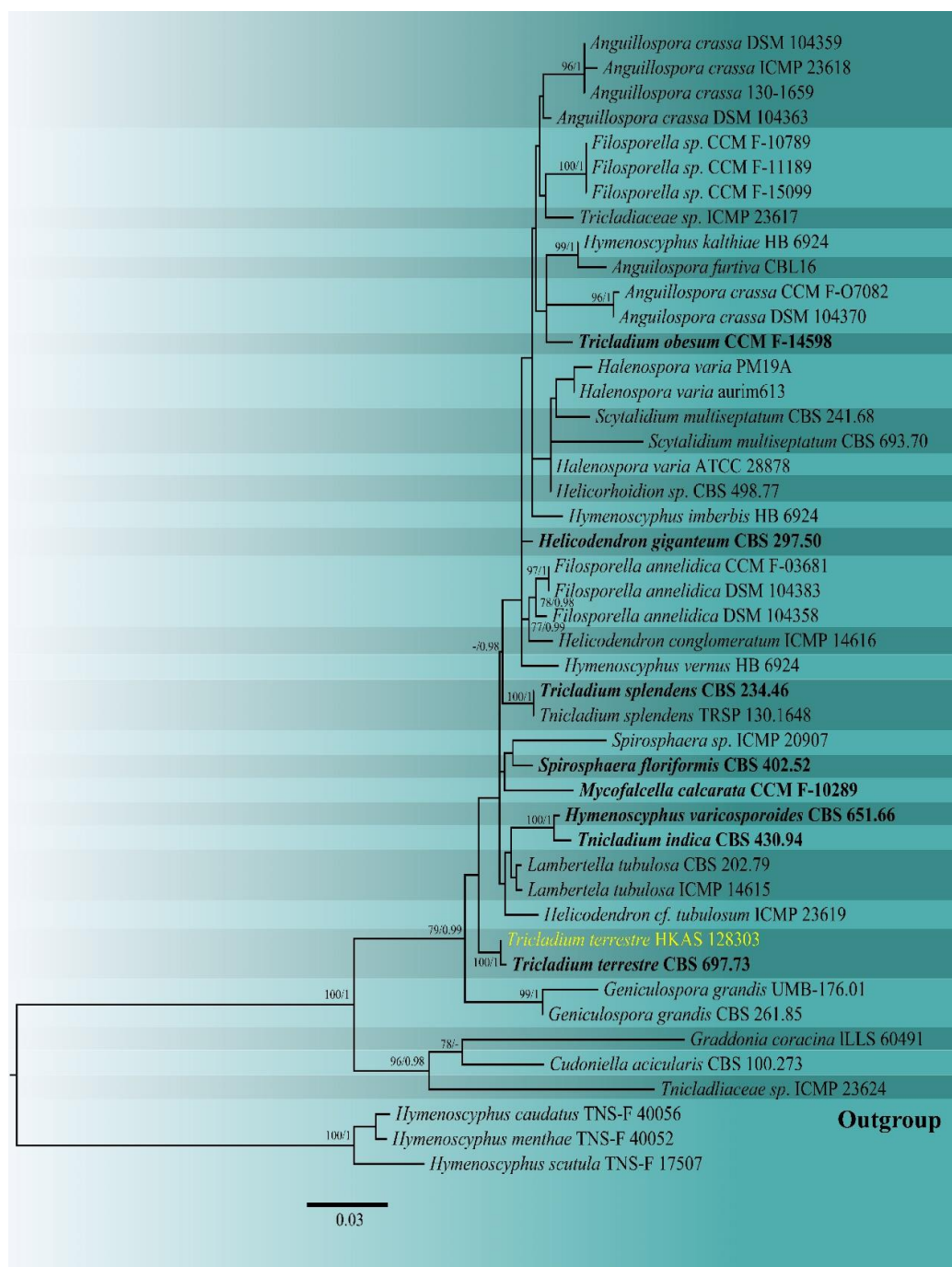


Figure 39 – Phylogram generated from the maximum likelihood analysis based on the ITS sequence data of *Tricladaceae*. Forty-six strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -3998.593462 is presented. The evolutionary model GTR+I+G is applied for the ITS gene. The matrix had 302 distinct alignment patterns, with 48.41% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.224995, C = 0.255721, G = 0.276096, T = 0.243188; substitution rates AC = 1.234678, AG = 2.044430, AT = 2.044430, CG = 0.372017, CT = 0.372017, GT = 1.000000; gamma distribution shape parameter α = 0.298088. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given on nodes. The tree was rooted with *Hymenoscyphus caudatus* (TNS-F 40056), *H. menthae* (TNS-F 40052) and *H. scutula* (TNS-F 17507). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Known hosts (based on molecular data) – *Quercus* sp. and *Prunus* sp. (Park 1974).

Notes – In the phylogenetic analysis, our collection (HKAS 128303) clustered with the type strain of *Tricladium terrestre* (CBS 697.73) with 100 % ML and 1.00 BYPP bootstrap support (Fig. 39). The sexual morph of *T. terrestre* resembles the *Hymenoscyphus splendens* and *Tricladium varicosporioides* by its light-colored hymenoscyphus-like apothecia, but differs from the glabrous surface, the indistinct inner layer of excipulum and aseptate ascospores (Tubaki 1966, Abdullah et al. 1981). This is the first sexual morph record of *T. terrestre* and also the first record in China.

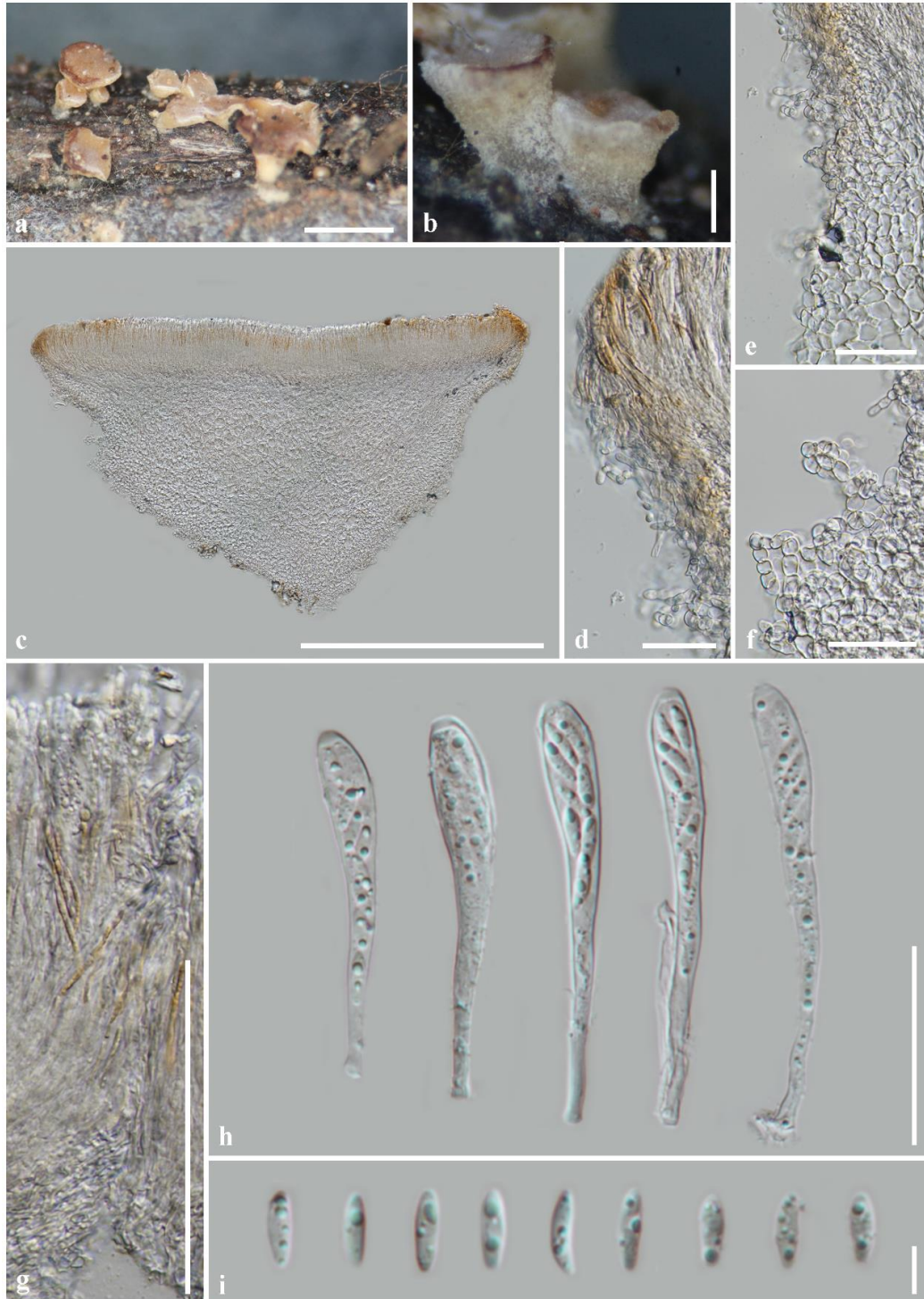


Figure 40 – Sexual morph of *Tricladium terrestre* (HKAS 128303, a new geographical record, first sexual morph). a, b Dried ascomata on the substrate. c Vertical section of an ascoma. d–f Excipulum. g Paraphyses. h Asci. i Ascospores. Scale bars: a = 1 mm, b = 150 μ m, c = 500 μ m, d = 25 μ m, e–f, h = 40 μ m, g = 80 μ m, i = 7 μ m.

Helotiales* order *incertae sedis

Caesiodiscus Holien & Suija, *Agarica* 42: 82 (2021)

Index Fungorum number: IF838686; Facesoffungi number: FoF16083

Caesiodiscus, is a monotypic genus introduced by Holien & Suija (2021) with *C. populicola* as the type species. *Caesiodiscus populicola* was found on the old trunks of living *Populus tremula* in a boreal rainforest, on *Fraxinus excelsior* and *Sambucus racemosa* in Norway (Holien & Suija 2021). *Caesiodiscus* has bluish-grey to greyish apothecial discs with pruina, a grey excipulum, 4-spored asci and eumuriform ascospores (Holien & Suija 2021). Based on the molecular phylogenetic evidence of ITS and LSU sequence data, the position of *Caesiodiscus* is still unclear in *Helotiales*. However, the placement is related to *Connersia rilstonei* and *Pleuroascus nicholsonii* based on LSU sequences. The eumuriform ascospores are very rare in *Leotiomyces* and only appear in *Mellitiosporium* (*Marthamycetaceae*, *Marthamycetales*) and *Triblidiaceae* (*Triblidiiales*) (Holien & Suija 2021). However, there is no phylogenetic evidence to prove the homology between *Caesiodiscus populicola* and *Triblidiaceae* within the order (Holien & Suija 2021). Even though the molecular evidence for *Mellitiosporium* is unavailable, the genus differs from *Caesiodiscus populicola* by having erumpent ascomata and non-amyloid asci (Holien & Suija 2021). To date, *Caesiodiscus* only accommodates a single species and is placed in *Helotiales* order *incertae sedis* (Holien & Suija 2021).

Caesiodiscus populicola Holien & Suija, *Agarica* 42: 82 (2021)

Fig. 42

Index Fungorum number: IF838687; Facesoffungi number: FoF15300

Saprobic on decayed wood. Sexual morph: *Apothecia* 1.25–3 mm wide when fresh, 1–3.9 mm wide × 0.2–0.4 mm high ($\bar{x}$ = 1.3 × 0.3 mm, n = 10), superficial, arising scattered or several apothecia gregarious in groups, sessile, rounded to irregular, greyish blue with pruina, glabrous. *Disc* flat to concave, pruinose, margin swollen, greyish blue. *Receptacle* disc-like, white, thick pruinose. *Hymenium* 220–250 μ m, hyaline, the uppermost part dark greenish. *Subhymenium* 28–36 μ m, composed of terra brown *textura intricata* hyphae. *Ectal excipulum* 40–90 μ m ($\bar{x}$ = 67 μ m, n = 20), composed of greyish and irregular cells of *textura angularis*, 4.7–9.3 diam. ($\bar{x}$ = 6.7 μ m, n = 40), hairs not observed, some cells slightly elongated and curved from the outermost layer. *Medullary excipulum* 105–160 μ m ($\bar{x}$ = 127 μ m, n = 30), composed of light yellowish-brown hyphae of *textura intricata*, 2.2–3.6 μ m diam. ($\bar{x}$ = 3 μ m, n = 20), non-gelatinous. *Paraphyses* 0.6–1 μ m ($\bar{x}$ = 0.8 μ m, n = 25) at the widest, filiform and soft, sometimes multiple septate and branched from apex to base, slightly exceeding asci. *Asci* 153–220 × 10–12 μ m ($\bar{x}$ = 187 × 11 μ m, n = 40), unitunicate, mostly 4-spored, rarely 6–8-spored, cylindrical to subclavate, apically thickened, I+ red, tapering to narrow subtruncate base. *Ascospores* 22–31 × 11–14 μ m ($\bar{x}$ = 26 × 12 μ m, n = 100), Q = 1.7–2.6 μ m, Q_m = 2.1 ± 0.06 μ m, uniseriate, eumuriform with multiple cells, sometimes slightly curved, hyaline, thin-walled. Asexual morph: Undetermined.

Material examined – China, Yunnan Province, Lijiang City, Naxi autonomous County, altitude 3800 m – 3900 m, on decayed wood, 23 July 2022, Cuijinyi Li, LCJY-965 (HKAS 128337).

GenBank numbers – HKAS 128337: LSU: OR398803

Known distribution (based on molecular data) – China (this study), Norway (Holien & Suija 2021).

Known hosts (based on molecular data) – *Fraxinus excelsior* (Holien & Suija 2021), *Populus tremula* (Holien & Suija 2021), *Sambucus racemosa* (Holien & Suija 2021).

Notes – Based on the phylogenetic analysis of LSU sequence data, our collection (HKAS 128337) clustered with the strains of *C. populicola* (RH-F-17665 and TU87471) with 100% ML and 1.00 BYPP bootstrap support (Fig. 41). Our collection shares very similar characters with *C. populicola* (RH-F-17665) by having bluish-grey to greyish apothecia, a pruinose disc and receptacle, a grey excipulum, 4-spored asci and eumuriform ascospores with multiple cells. However, the asci of our collection (HKAS 128337) are longer than the type species (153–220 μ m vs. 125–150 μ m), and the apical pores were not observed (Holien & Suija 2021). Based on

morphology and phylogenetic analysis, we conclude our collection is *C. populicola*. This study reports the first record of this species in China.

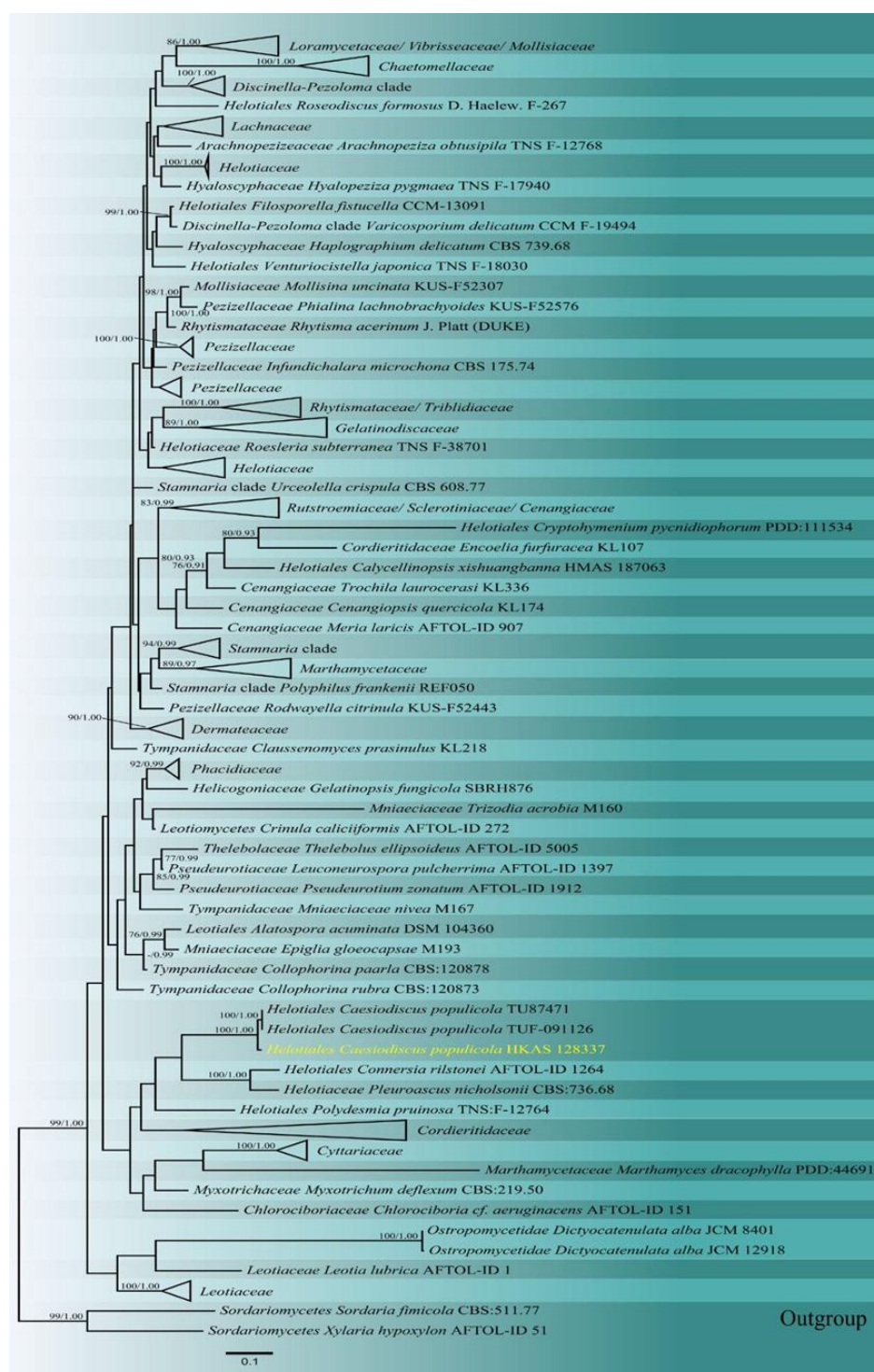


Figure 41 – Phylogram generated from the maximum likelihood analysis based on the LSU sequence data of *Helotiales*, *Leotiomyces*. One hundred and nine strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAXML tree with a final likelihood value of -21427.224769 is presented. The evolutionary model GTR+I+G is applied for the ITS gene. The matrix had 497 distinct alignment patterns, with 5.60% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.087127, C = 0.033474, G = 0.033474, T = 0.058542; substitution rates AC = 0.312229, AG = 2.081526, AT = 3.217693, CG = 0.095403, CT =

0.138768, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.320497$. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Sordaria fimicola* (CBS:511.77) and *Xylaria hypoxylon* (KUS-F52678) of *Sordariomycetes*. The newly generated sequences are indicated in yellow.



Figure 42 – *Caesiodiscus populicola* (HKAS 128337, a new geographical record). a, b Fresh ascomata on the substrate. c–e Dried ascomata on the substrate. f Vertical section of an ascoma. g–h Excipulum. i–j Paraphyses. k Asci. l Ascospores. Scale bars: c = 3.5 mm, d = 400 μm , e = 150 μm , f = 800 μm , g, j = 60 μm , h = 40 μm , i = 90 μm , k = 100 μm , l = 15 μm .

Rhytismatales M.E. Barr ex Minter, *Systema Ascomycetum* 5: 182 (1986)

Cudoniaceae P.F. Cannon, Ainsworth & Bisby's *Dictionary of the fungi*, Ed. 9: IX (2001)

Cudonia Fr., Summa vegetabilium Scandinaviae 2: 348 (1849)

Index Fungorum number: IF1353; Facesoffungi number: FoF16084

Cudonia was reported as a saprobic genus with *C. circinans* as the type species (Fries 1849, Ge et al. 2014). The relationship between *Cudonia* and *Spathularia* has been the focus of research for decades (Nannfeldt 1942, Gargas et al. 1995, Platt & Spatafora 2000, Gernandt et al. 2001, Lutzoni et al. 2001, Pfister & Kimbrough 2001, Wang et al. 2002, 2006, 2007, 2009, Ge et al. 2014). Both genera have hymenia covered by a stromatic membrane at the early stages of development, curved paraphyses, club-shaped asci lacking an amyloid pore, and long, thin, hyaline ascospores with gelatinous sheaths, hence were linked (Nannfeldt 1942, Wang et al. 2002, 2007, Ge et al. 2014, Yang 2023). However, the macro-morphology of *Cudonia* and *Spathularia* show significant differences. *Cudonia* species have rounded and club-shaped ascomata, whereas *Spathularia* species have flattened ascomata (Ge et al. 2014). Up to now, most *Cudonia* species have been recorded based on their sexual morphs and ten species have been reported (Kirk et al. 2008, Yang 2023). Here, we introduce two new species into the genus, *C. gracilistipitata* and *C. yunnanensis*, based on morphology and phylogenetic analysis (Fig. 43).

Cudonia gracilistipitata H.L. Su, K.D. Hyde & Q. Zhao, sp. nov.

Fig. 44

Index Fungorum number: IF902308; Facesoffungi number: FoF14759

Etymology – Referring to more elongated and thinner stipe of the species

Holotype – HKAS 129661

Saprobic on dead stems. Sexual morph: *Apothecia* 3–5 cm high, up to about 1 cm diam. when fresh, gregarious, scattered to subcaespitose, superficial, pileate, stipitate. *Pileus* up to about 1 cm diam., convex or nearly saddle-shaped, thinning out from center to the margin, fleshy when fresh, leathery when dry, smooth, greyish brown to yellowish, with some brown radiating projections on the back. *Margin* undulate, incurved or flat, pale. *Stipe* 3–4 cm long, attenuated upward, enlarged at the base, slightly rough, brown, deepened upward, often longitudinally striated especially at the upper part. *Hymenium* 110–130 μm ($\bar{x}$ = 117 μm , n = 10) thick, surface smooth, hyaline. *Medullary excipulum* 155–255 μm ($\bar{x}$ = 230 μm , n = 10) thick, with brownish, thin-walled *textura porrecta*, hyphae 3.9–6.1 μm ($\bar{x}$ = 4.5 μm , n = 45) diam. *Ectal excipulum* 90–125 μm ($\bar{x}$ = 103 μm , n = 10) thick, light brown, thick-walled *textura angularis*, 3.5–7.8 $\times$ 3.2–6.7 μm ($\bar{x}$ = 5.7 $\times$ 4.8 μm , n = 60). *Stipitipellis* 25–75 μm ($\bar{x}$ = 49 μm , n = 10) thick, uneven thickness, slightly thick-walled *textura epidermoidea*, 3.2–5.1 $\times$ 4.6–9.4 μm ($\bar{x}$ = 4.2 $\times$ 6.9 μm , n = 50). *Paraphyses* 1.3–2.1 μm ($\bar{x}$ = 1.6 μm , n = 57) diam., slightly higher than the asci, filiform, strongly curved or circinate above, branched and septate on the base, rounded ends, smooth, hyaline. *Asci* 90–132 $\times$ 8.5–13 μm ($\bar{x}$ = 107 $\times$ 10.4 μm , n = 50), 8-spored, inoperculate, pleurohynchous, prototunicate, clavate, narrow at the apex, swollen at the base, hyaline, inamyloid. *Ascospores* 51.3–72.5 $\times$ 1.8–2.7 μm ($\bar{x}$ = 62.4 $\times$ 2.2 μm , n = 72), uniseriate, hyaline, aseptate, clavate-filiform, slightly thick-walled, multi-guttulate, with overall gelatinous layer and prominent gelatinous caps, 2–3.9 μm ($\bar{x}$ = 3 μm , n = 30) thick, present at ends in the black ink. Asexual morph: Undetermined.

Material examined – China, Yunnan, Ailao Mountains, alt. 2398 m, on dead stems, 2 September 2021, Hongli Su, SHL110 (HKAS 129661, holotype); *ibid.*, alt. 2434 m, on dead stems, 1 September 2022, Hongli Su, SHL1248 (HKAS 129662, paratype).

GenBank numbers – HKAS 129661: ITS: OR500915; HKAS 129662: ITS: OR500916.

Notes – In our phylogenetic analysis, *Cudonia gracilistipitata* strains (HKAS 129661, HKAS 129662) formed a clade separated from strain *Cudonia* sp. 6 (Yang 5219) with 0.98 BYPP bootstrap support (Fig. 43). Sequence comparison for the ITS region between our strains (*C. gracilistipitata*) and *Cudonia* sp. 6 (Yang 5219) showed a 1.56% (7/446 bp, excluding gaps) base pair difference. *Cudonia gracilistipitata* exhibits remarkable similarities to other *Cudonia* species in macro- and ascospore morphologies and differs mainly in their pileus morphologies. *Cudonia gracilistipitata* has a saddle-shaped, grey pileus with a gradually thinning margin and elongated and thinner stipes, while most known *Cudonia* species have irregular clumps or spheres and a yellow pileus (Ge et al. 2014). *Cudonia gracilistipitata* and *C. yunnanensis* differ in morphologies by them

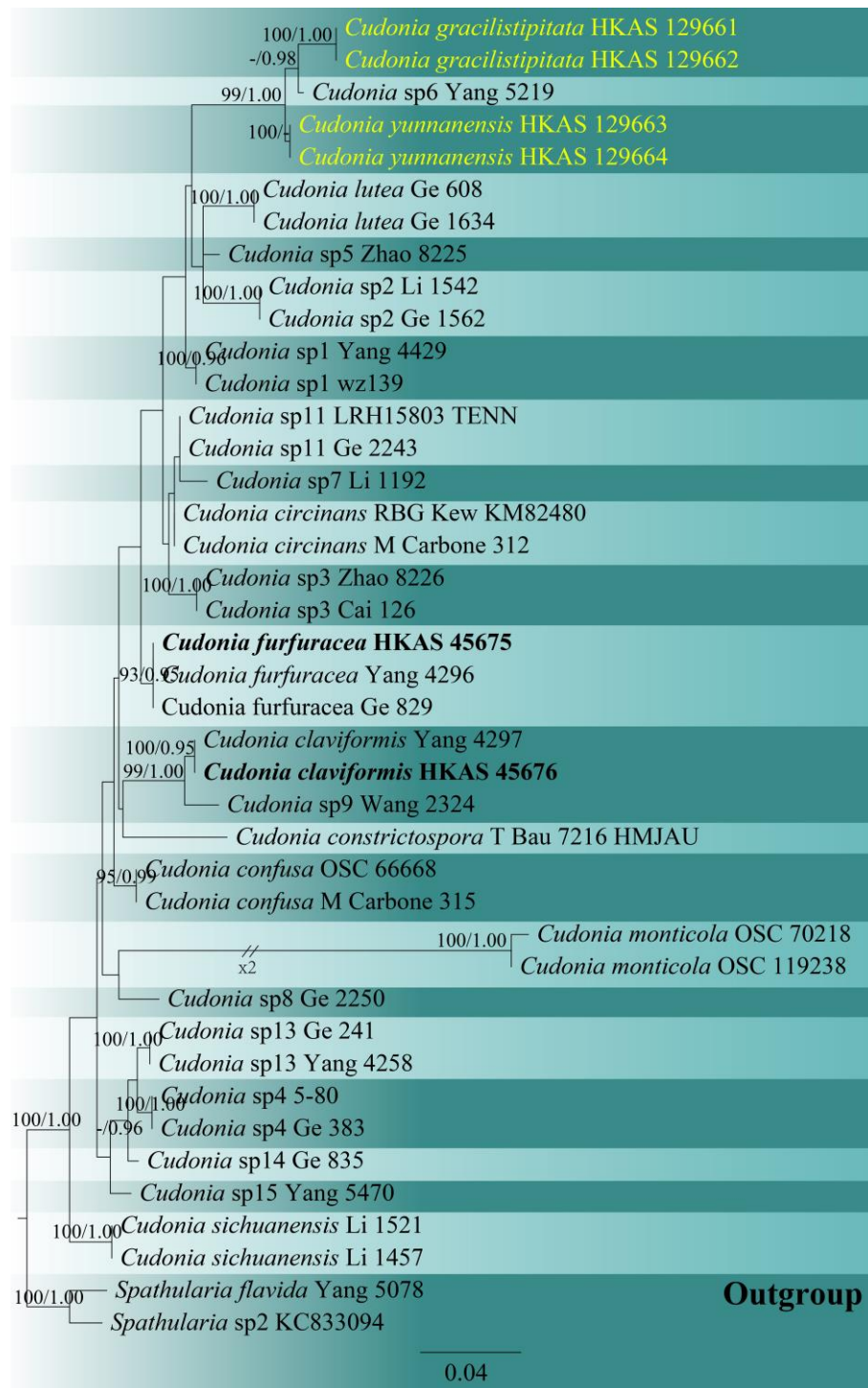


Figure 43 – Phylogram generated from the maximum likelihood analysis based on ITS sequences of *Cudonia*. Forty-one strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -2057.524101 is presented. The evolutionary model SYM+I+G is applied for all the genes. The matrix had 143 distinct alignment patterns, with 2.47% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.241330, C = 0.252125, G = 0.245287, T = 0.261258; substitution rates AC = 1.711138, AG = 2.236492, AT = 0.594875, CG = 0.167506, CT = 4.208565, GT = 1.000000; gamma distribution shape parameter α = 0.188772. Bootstrap support values for ML greater than 90% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Spathularia* sp. KC833094 and *Spathularia flavida* Yang 5078. Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

ectal excipulum, paraphyses and ascospores. *Cudonia gracilistipitata* has a light brown, branched ectal excipulum and septate paraphyses, whereas *C. yunnanensis* has a hyaline, unbranched ectal excipulum and aseptate paraphyses. Besides, *C. gracilistipitata* has slightly larger ascospores compared to *C. yunnanensis* ($51.3\text{--}72.5 \times 1.8\text{--}2.7 \mu\text{m}$ vs. $45\text{--}64 \times 1.4\text{--}2.7 \mu\text{m}$). However, it is difficult to compare the morphologies between our isolates and *Cudonia* sp. 6 as this isolate has not been published; hence, morphological characters are unavailable for us to compare *C. gracilistipitata* and *Cudonia* sp. 6. Based on the phylogenetic evidence we conclude our collection as a new species, *C. gracilistipitata*.

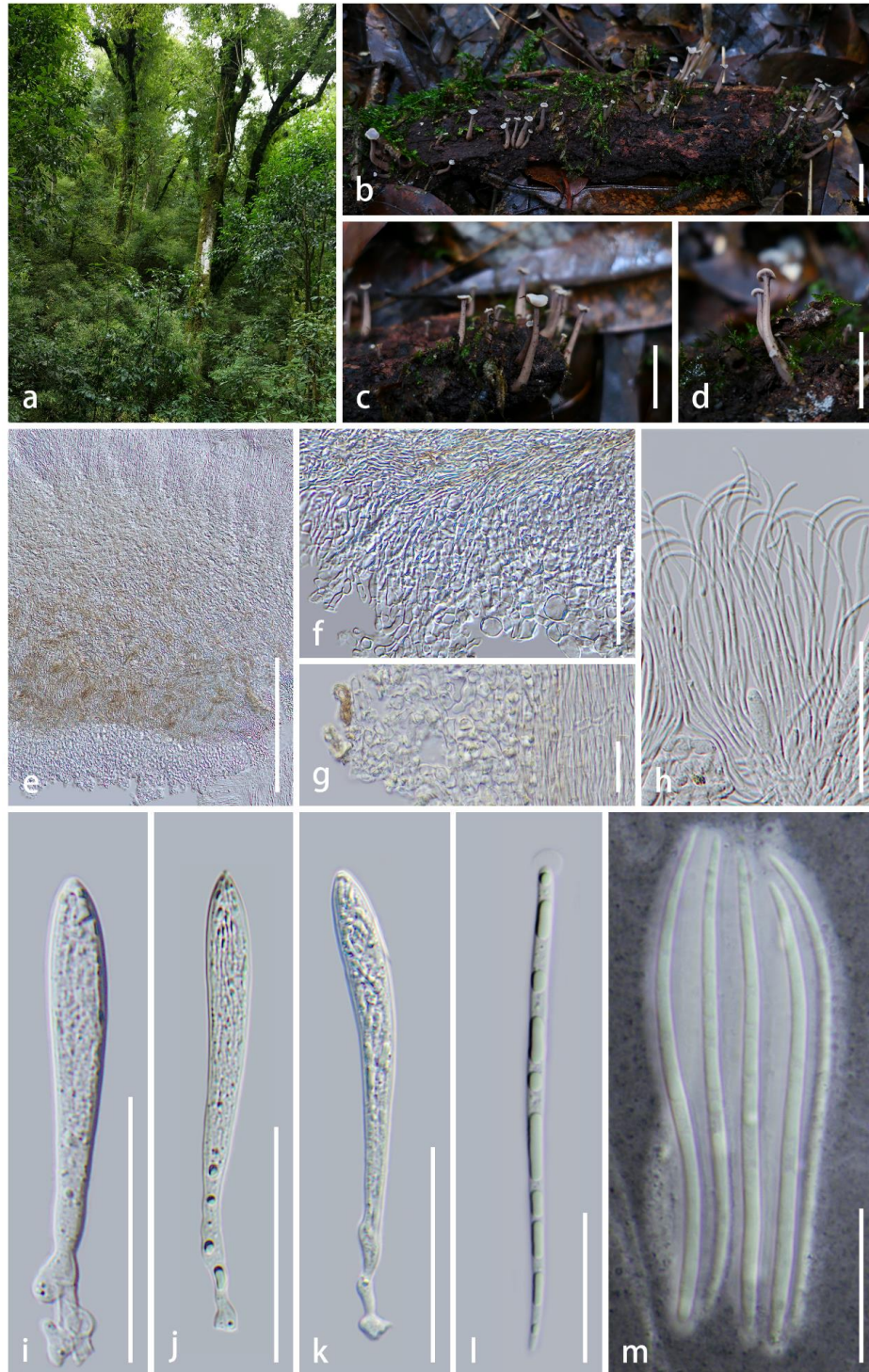


Figure 44 – Sexual morph of *Cudonia gracilistipitata* (HKAS 129661, holotype). a Habitat. b–d Fresh apothecia. e Vertical section of the pileus. f Ectal and medullary excipulum.

g Stipitipellis. h Paraphyses. i–k Asci. l Ascospore. m Ascospores stained in Indian ink. Scale bars: b = 5 cm, c–d = 2 cm, e = 200 μ m, f = 50 μ m, g = 20 μ m, h–k = 50 μ m, l, m = 20 μ m.

Cudonia yunnanensis H.L. Su, K.D. Hyde & Q. Zhao, sp. nov.

Fig. 45

Index Fungorum number: IF902309; Facesoffungi number: FoF14760

Etymology – Referring to the type locality of the species in Yunnan, China

Holotype – HKAS 129663

Saprobic on dead wood. Sexual morph: *Apothecia* 3–4 cm high, up to about 1 cm diam. when fresh, gregarious, solitary to caespitose, superficial, pileate, stipitate. *Pileus* up to about 1 cm diam., center slightly depressed, the outer slightly convex, and the margin involute or nearly saddle-shaped, thinning out from center to margin, fleshy when fresh, leathery when dry, smooth, grey-brown to pale. *Margin* undulate to flat, pale. *Stipe* 2.5–3 cm long, attenuated upward, swollen at the base, slightly rough, brown, deepened to dark brown upward, often longitudinally striated especially at the upper part. *Hymenium* 121–170 μ m ($\bar{x}$ = 154 μ m, n = 15) thick, surface smooth, hyaline. *Medullary excipulum* 150–560 μ m ($\bar{x}$ = 285 μ m, n = 15), thick, hyaline, thin-walled *textura porrecta*, hyphae 3.2–5.8 μ m ($\bar{x}$ = 4.3 μ m, n = 55) diam. *Ectal excipulum* 40–120 μ m ($\bar{x}$ = 67 μ m, n = 30) thick, hyaline, thick-walled, *textura angularis*, 5.8–19.7 $\times$ 4.1–11.9 μ m ($\bar{x}$ = 10.6 $\times$ 7.1 μ m, n = 45), outermost layer arranged closely subglobose to oblong hyphae. *Stipitipellis* 25–55 μ m ($\bar{x}$ = 36 μ m, n = 15) thick, uneven thickness, slightly thick-walled cells of *textura epidermoidea*, 3.5–13.7 $\times$ 3–6.5 μ m ($\bar{x}$ = 6.7 $\times$ 4.3 μ m, n = 32). *Paraphyses* 1.35–2.82 μ m ($\bar{x}$ = 2.1 μ m, n = 44) diam., slightly longer than the asci, stick-like, unbranched, aseptate, rounded ends, rough, smooth, hyaline, with a strongly curved apex. *Asci* 93–123 $\times$ 7.4–14.5 μ m ($\bar{x}$ = 112 $\times$ 10.8 μ m, n = 32), 8-spored, inoperculate, pleurorhynchous, prototunicate, clavate, narrow at the ends, hyaline, inamyloid. *Ascospores* 45–64 $\times$ 1.4–2.7 μ m ($\bar{x}$ = 55 $\times$ 2.2 μ m, n = 60), uniseriate, clavate-filiform, slightly thick-walled, hyaline, multi-guttulate, aseptate, with an overall gelatinous layer and prominent gelatinous caps, 0.7–2.4 μ m ($\bar{x}$ = 1.4 μ m, n = 25). *Ascoconidia* 0.71–1.45 $\times$ 0.68–1.22 μ m ($\bar{x}$ = 1.05 $\times$ 0.99 μ m, n = 33), subspherical or irregular ellipsoid, hyaline, sometimes replacing the ascospores and filling the asci. Asexual morph: Undetermined.

Material examined – China, Yunnan, Ailao Mountains, alt. 2410 m, on dead wood, 2 September 2021, Hongli Su, SHL139 (HKAS 129663, holotype); *ibid.*, alt. 2337 m, on dead wood, 2 September 2022, Hongli Su, SHL1281 (HKAS 129664, paratype).

GenBank numbers – HKAS 129663: ITS: OR500917; HKAS 129664: ITS: OR500918.

Notes – Our phylogenetic analysis showed that *Cudonia yunnanensis* strains (HKAS 129663, HKAS 129664) clustered separately from *C. gracilistipitata* (HKAS 129661, HKAS 129662) and *Cudonia* sp. 6 (Yang 5219) strains with 99% ML and 1.00 BYPP bootstrap support (Fig. 43). Sequence comparison for the ITS region between our strains (*C. yunnanensis*) with *Cudonia* sp. 6 (Yang 5219) and *C. gracilistipitata* (HKAS 129661, HKAS 129662) strains showed 0.89% (4/446 bp) and 179% (8/446 bp base pair differences, respectively (excluding gaps). *Cudonia yunnanensis* has different ectal excipulum, paraphyses and ascospore characters compared to *C. gracilistipitata*. Also, *C. yunnanensis* has a light brown ectal excipulum, thicker, unbranched, aseptate paraphyses and shorter ascospores (45–64 $\times$ 1.4–2.7 μ m vs. 51.3–72.5 $\times$ 1.8–2.7 μ m) compared to *C. gracilistipitata*. Additionally, *C. yunnanensis* differs from other published *Cudonia* species in their macro-morphologies; *C. yunnanensis* possesses a saddle-shaped pileus with a grey hymenium, while most *Cudonia* species have irregular clumps or spherical pileus with a yellow hymenium. Besides, *C. yunnanensis* has a significantly longer stipe than other *Cudonia* species (Ge et al. 2014). Based on morphology and phylogeny we introduce our collection as a new species, *C. yunnanensis*.

Pezizomycetes

Pezizales J. Schröt., Die Natürlichen Pflanzenfamilien nebst ihren Gattungen und wichtigeren Arten 1 (1): 173 (1894)

Sarcosomataceae Kobayasi, J. Jap. Bot.: 516 (1937)

Plectania Fuckel, Jahrb. Nassauischen Vereins Naturk. 23-24: 323 (1870)
 Index Fungorum number: IF4187; Facesoffungi number: FoF16085

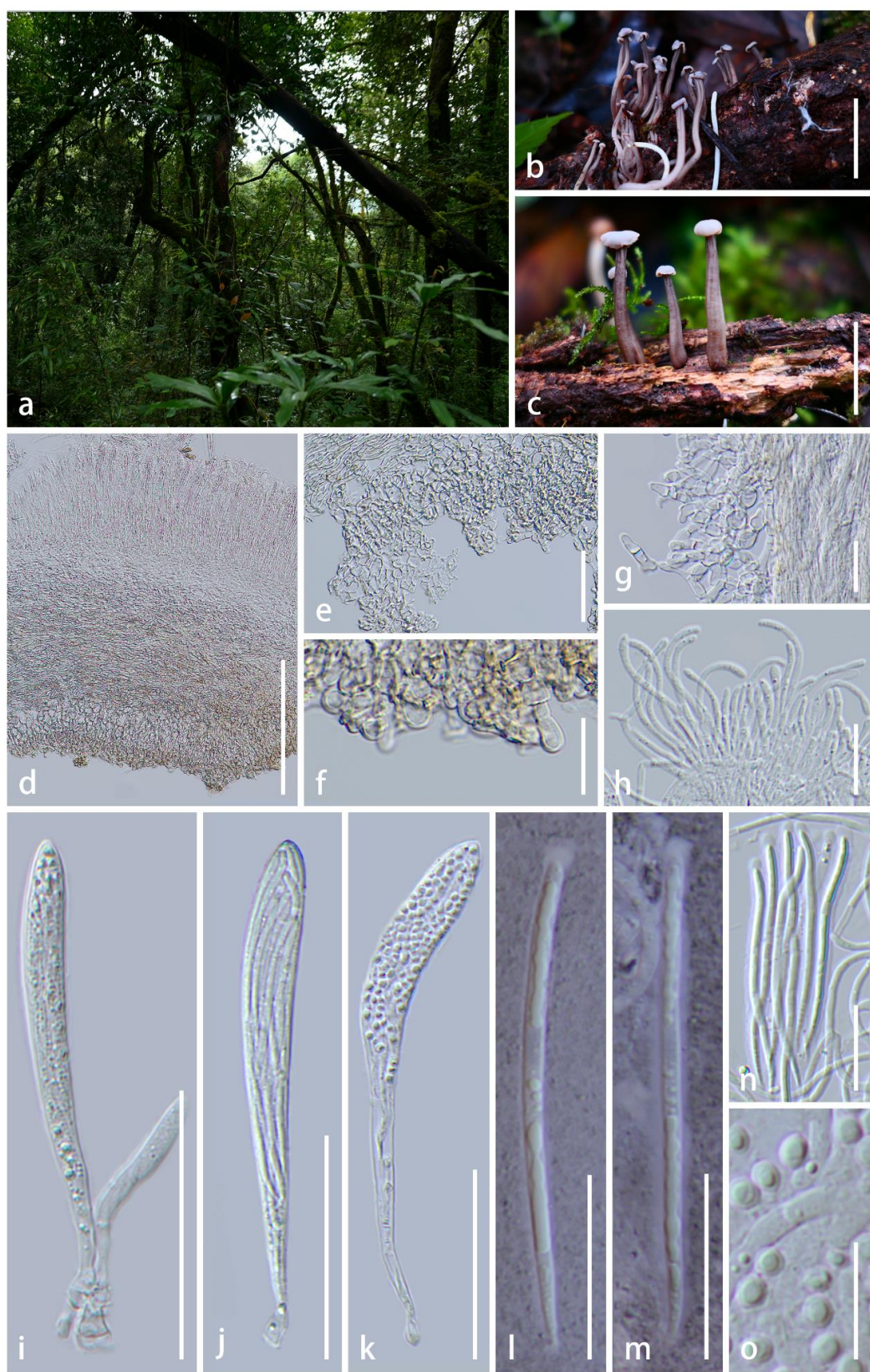


Figure 45 – Sexual morph of *Cudonia yunnanensis* (HKAS 129663, holotype). a Habitat. b, c Fresh apothecia. d Vertical section of the pileus. e, f Ectal excipulum. g Stipitipellis. h Paraphyses. i–k Asci. l–m Ascospores stained in Indian ink. Scale bars: b–c = 2 cm, d = 200 μ m, e = 50 μ m, f–h = 20 μ m, i–k = 50 μ m, l–n = 20 μ m, o = 10 μ m.

Plectania was reported as a saprobic genus with *P. melastoma* as the type species (Korf 1972, Zeng et al. 2021). *Plectania* is distinguished by its discoid to cupulate, substipitate to stipitate apothecia, ellipsoid to kidney-shaped ascospores with a smooth or transversally furrowed wall (Zhuang et al. 2004, Carbone et al. 2013, Ekanayaka et al. 2018, Zeng et al. 2021). *Plectania* is a polyphyletic genus and forms a clade with *Galiella* in the combined ITS and LSU phylogenetic studies (Zeng et al. 2021). However, *Plectania* differs from *Galiella* in having larger, lighter colored apothecia, and a much more extensive, gelatinous medullary excipulum (Korf 1957). Following recent publications, *Plectania* includes about 20 species (Zhuang et al. 2004, Wijayawardene et al. 2017, 2022, Carbone et al. 2021, Zeng et al. 2021). In the current study, we present the updated phylogeny for *Plectania* (Fig. 46), and introduce one new species *P. submilleri*, from China.

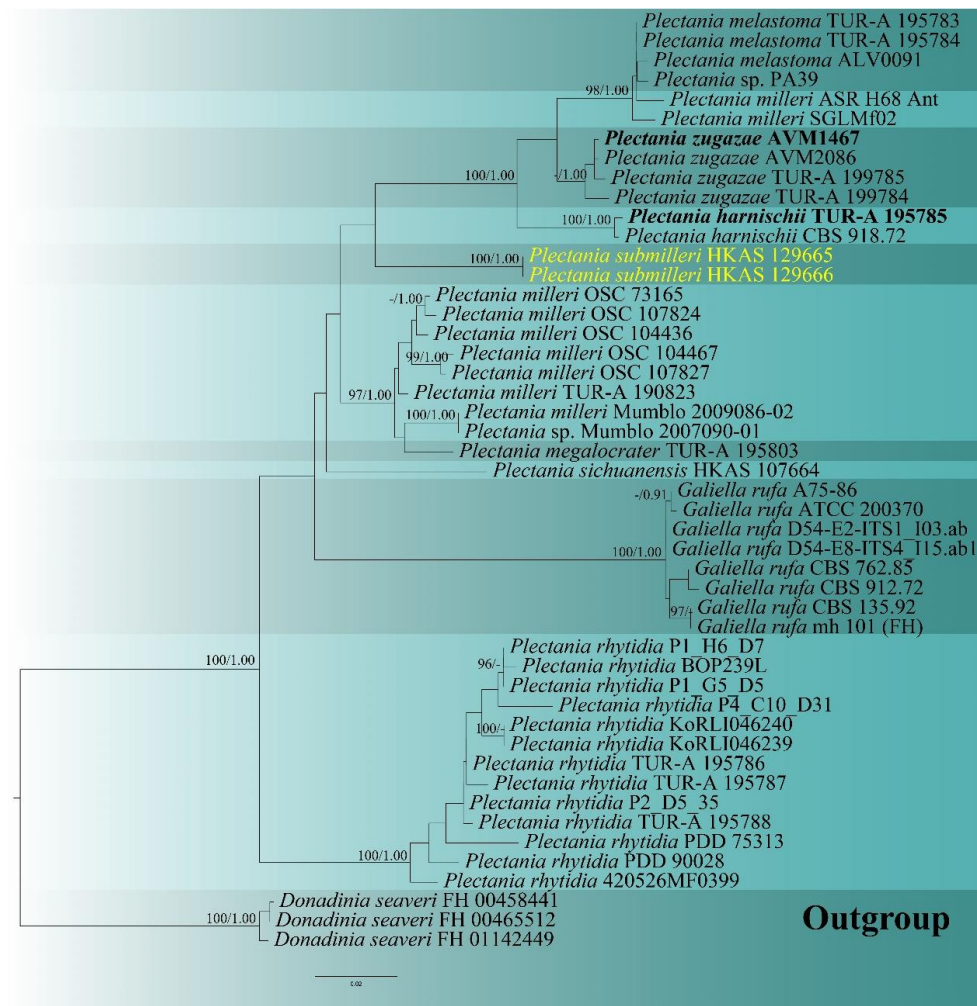


Figure 46 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and LSU sequence data of *Plectania* and *Galiella*. Forty-eight strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -4974.687777 is presented. Evolutionary model HKY+I+G is applied for ITS, GTR+I+G for LSU. The matrix had 348 distinct alignment patterns, with 27.85% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.249543, C = 0.213114, G = 0.271976, T = 0.265367; substitution rates AC = 1.698456, AG = 3.357672, AT = 1.555331, CG = 0.970697, CT = 4.930380, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.140037$. Bootstrap support values for ML greater than 90% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Donadinia seaveri* (FH 01142449, FH 00465512, and FH 00458441). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Plectania submilleri H.L. Su & Q. Zhao, sp. nov.

Fig. 47

Index Fungorum number: IF902310; Facesoffungi number: FoF14761

Etymology – Referring to the similarity with *Plectania milleri*

Holotype – HKAS 129665

Saprobic on dead pine needles. Sexual morph: *Apothecia* 0.3–0.5 cm high, 0.3–0.8 cm diam. when fresh, superficial, scattered, urceolate to cupulate, sessile, leathery. *Disc* dark rufous, slightly rough. *Receptacle* dark, slightly rough. *Margin* obviously involute, slightly fragile, gray. *Ectal excipulum* 60–150 μm ($\bar{x}$ = 95 μm , n = 5) thick, with two layers, brown to dark brown outer layer with carbonaceous, thick-walled cells of *textura globulosa*, 4.6–13.6 $\times$ 3.9–9.5 μm ($\bar{x}$ = 8.9 $\times$ 6.7 μm , n = 42), light brown to hyaline inner layer with thin-walled cells of *textura angularis*, 7.8–24.2 $\times$ 5.8–13.6 μm ($\bar{x}$ = 15.4 $\times$ 9 μm , n = 66). *Medullary excipulum* 180–255 μm ($\bar{x}$ = 187 μm , n = 5) thick, hyaline, with thin-walled cells of *textura intricate*, 2.4–5 μm ($\bar{x}$ = 3.6 μm , n = 67) diam. *Hymenium* 210–320 μm ($\bar{x}$ = 269 μm , n = 5) thick, hyaline. *Hairs* 4.4–7 μm ($\bar{x}$ = 5.5 μm , n = 45) diam., cylindrical, thick-walled, septate, brown. *Paraphyses* 1.7–2.6 μm ($\bar{x}$ = 2.2 μm , n = 20) diam., filiform, apically and middle branched, slightly rough, thin-walled, septate, hyaline. *Asci* 370–440 $\times$ 10.8–17.7 μm ($\bar{x}$ = 424 $\times$ 13.3 μm , n = 25), 8-spored, unitunicate, suboperculate, cylindrical, hyaline, with the narrow bases and truncated to obtuse apex, inamyloid. *Ascospores* 16–23.5 $\times$ 8.4–11 μm ($\bar{x}$ = 20.7 $\times$ 10 μm , n = 52), uniseriate, ellipsoid, hyaline, slightly rough, thin-walled, multi-guttulate. Asexual morph: Undetermined.

Material examined – China, Yunnan, Qujing, alt. 1933 m, on dead pine needles (*Pinaceae*), 10 July 2021, Hongli Su, SHL 13 (HKAS 129665, holotype); *ibid.*, alt. 1978 m, 11 July 2021, Hongli Su, SHL 35 (HKAS 129666, paratype).

GenBank numbers – HKAS 129665: ITS: OR500919, LSU: OR500933; HKAS 129666: ITS: OR500920, LSU: OR500934.

Notes – The phylogenetic analysis shows that our strains (HKAS 129665 and HKAS 129666) clustered within *Plectania* sister to the clade comprising *P. melastoma*, *P. milleri*, *P. zugazae* and *P. harnischii* strains (Fig. 46). Comparison of the base pair differences between *Plectania submilleri* and *P. melastoma* (TUR-A 195783), reveals 14.31%, 70/489 bp (with 11 gaps) in ITS and 1.95%, 16/817 bp in LSU, with *P. milleri* (SGLMf02 and ASR H68 Ant), show 19.73%, 119/603 bp (with 27 gaps), and 14.06%, 63/448 bp differences (with 9 gaps) in ITS, respectively. Also, the bp comparison between *P. submilleri* with *P. zugazae* (AVM1467) shows 12.29%, 60/488 bp difference (with 10 gaps) in ITS, and 1.83%, 15/816 bp difference in LSU, while with *P. harnischii* (TUR-A 195785) shows 14.72%, 72/489 bp difference (with 11 gaps) in ITS, and 1.71%, 14/816 bp difference in LSU. *Plectania submilleri* differs from *P. melastoma*, *P. zugazae* and *P. harnischii* by its macromorphology, while the last three species have orange or brownish granules or crystals covering the external surface of apothecia, *P. submilleri* lacks granules or crystals (Carbone et al. 2015, 2021, Zeng et al. 2021). *Plectania submilleri* shares similar characters to *P. milleri*. However, these two species differ in asci and external surface of apothecia. *Plectania submilleri* has shorter asci than *P. milleri* (370–440 $\times$ 10.8–17.7 μm vs. 380–600 $\times$ 13–14 μm) and a relatively smooth external surface without granules, crystals, pimples and bumps compared to the rough external surface with small pimples or bumps of *P. milleri*. Furthermore, *P. submilleri* and *P. milleri* have different distributions; *P. submilleri* was found in China (Asia), whereas *P. milleri* is distributed in Northwest America (Carbone 2011). Thus, based on morphology and multi-gene phylogeny we conclude our collection is a new species, *Plectania submilleri*.

Sordariomycetes O.E. Erikss. & Winka, Myconet 1(1): 10 (1997)

Subclass *Diaporthomycetidae* Senan., Maharachch. & K.D. Hyde 2015

Conlariales K.D. Hyde & Hongsanan, Fungal Diversity 107, 94 (2021)

Conlariaceae Huang Zhang, K.D. Hyde & Maharachch., Fungal Diversity 85, 90 (2017)

Conlarium F. Liu & L. Cai, Mycologia 104: 1180 (2012)

Index Fungorum number: IF564382; Facesoffungi number: FoF05074

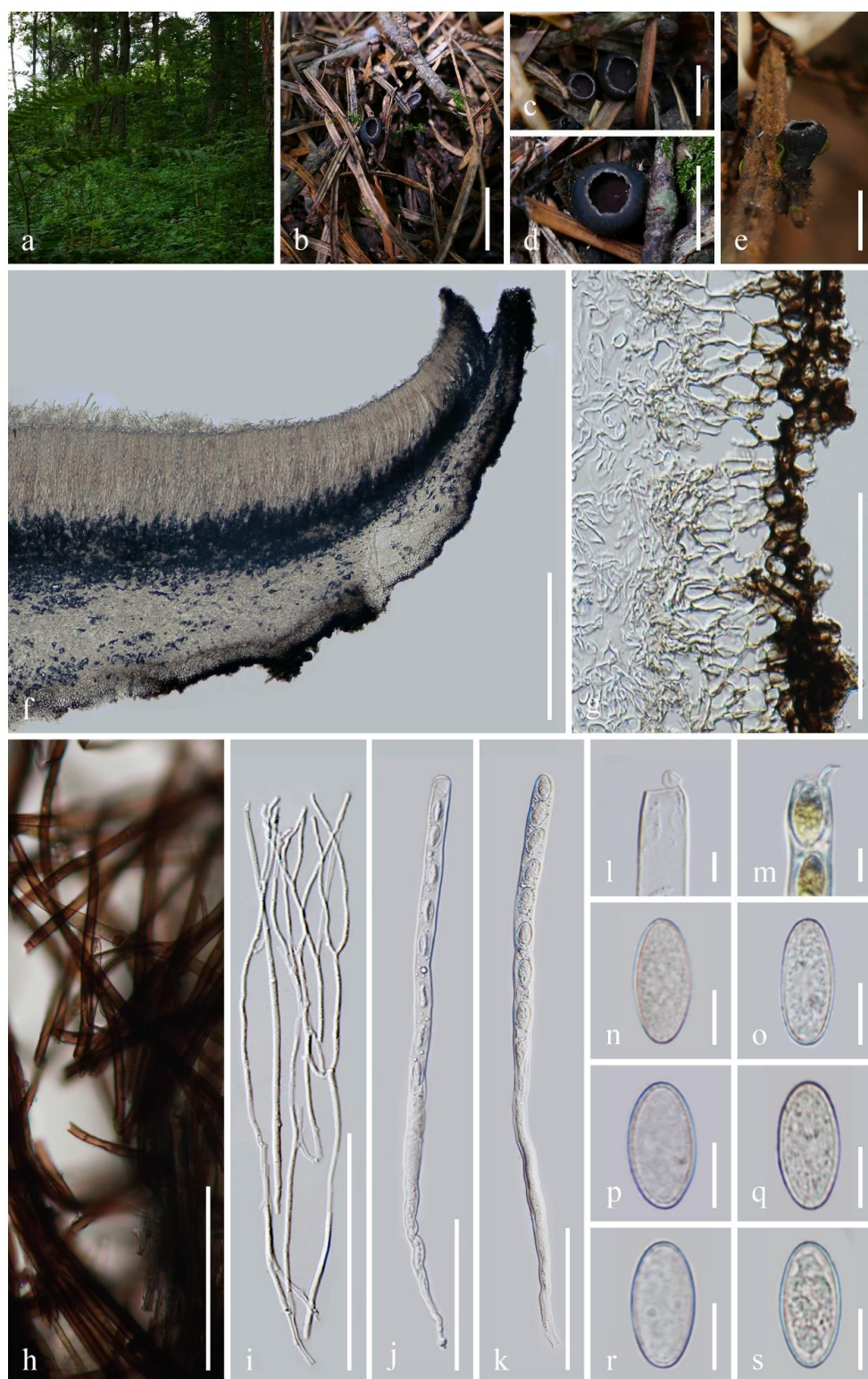


Figure 47 – Sexual morph of *Plectania submilleri* (HKAS 129665, holotype). a Habitat. b–e Fresh apothecia. f Vertical section of an apothecium. g Ectal and medullary excipulum. h Hairs. i Paraphyses. j, k Asci. l, m Apices of asci (m Apex of an ascus in Melzer's reagent). n–s Ascospores. Scale bars: b = 2 cm, c–e = 1 cm, f = 500 μ m, g–k = 100 μ m, l–s = 10 μ m.

Conlarium was introduced by Liu et al. (2012b) with *C. dupliciascosporum* (sexual morph) as the type species, which belongs to *Conlariaceae* (*Conlariales*, *Sordariomycetes*). *Conlarium* are mainly known by the asexual morph, which is characterized by muriform, irregularly globose or subglobose conidia (Liu et al. 2012b, Xie et al. 2019, Hyde et al. 2020b, Zhang et al. 2021a).

Currently, 13 species belong to this genus (including our two novel species), of which six species are from freshwater habitats, and seven species from terrestrial habitats (Zhang et al. 2021a, Hyde et al. 2020c, 2023, Yang et al. 2023b, this study). Here, we provide the updated phylogeny for the *Conlarium* taxa (Fig. 48).

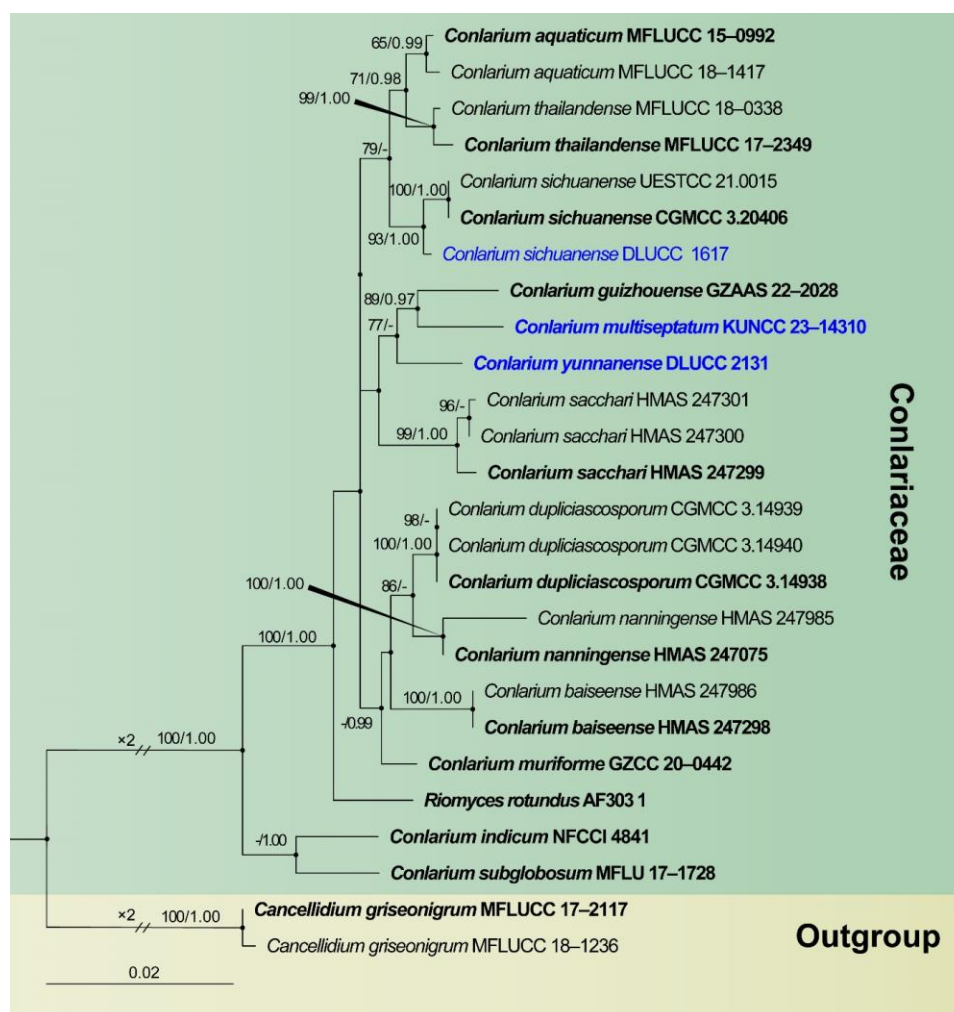


Figure 48 – Phylogram generated from the maximum likelihood analysis based on the combined LSU, ITS and SSU sequence data of *Conlarium*. Twenty-six strains are included in the combined analyses which comprise 2285 characters including gaps (829 characters for LSU, 501 characters for ITS, and 955 characters for SSU). The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -5366.591985 is presented. The evolutionary model GTR+I+G is applied for all the genes. The matrix had 236 distinct alignment patterns, with 14.40% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.255078, C = 0.221492, G = 0.275863, T = 0.247567; substitution rates AC = 1.883794, AG = 2.953060, AT = 3.130793, CG = 1.222701, CT = 10.634496, GT = 1.000000; gamma distribution shape parameter α = 0.020000. Bootstrap support values for ML greater than 65% and Bayesian posterior probabilities greater than 0.97 are given near nodes, respectively. The tree was rooted with *Cancellidium griseonigrum* (MFLUCC 17-2117 and MFLUCC 18-1236). Ex-type strains are in bold. The newly generated sequences are indicated in blue.

Conlarium multiseptatum H.W. Shen, Z.L. Luo & K.D. Hyde sp. nov.

Fig. 49

Index Fungorum number: IF571755; Facesoffungi number: FoF14879

Etymology – “multiseptatum” refers to multi-transversely-longitudinally septate conidia of this species.

Holotype – HKAS 130430

Saprobic on submerged decaying wood in a freshwater Lake. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate superficial, sporodochial, punctiform, gregarious, dark brown to black. *Mycelium* mostly immersed, comprises branched, pale brown to hyaline, smooth and thin-walled hyphae. *Conidiophores* absent or reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, holoblastic, integrated, determinate, doliiform, cylindrical, hyaline, smooth. *Conidia* 47–66(–76) × 40–52(–60) µm ($\bar{x}$ = 56 × 46 µm, n = 20), acrogenous, solitary, dry, muriform, irregular, subglobose to ellipsoidal, initially hyaline to pale brown, becoming brown to dark brown at maturity, multi-transversely-longitudinally septate, slightly constricted at the septa, smooth, thin-walled.

Material examined – China, Yunnan, Puer City, Dujuanhu Lake, 24°32'22.7634"N, 101°16.8482"E (2500m), on a submerged decaying wood, 24 February 2023, Hong-Wei Shen, FD 50–59–1 (HKAS 130430, holotype), ex-type living culture, KUNCC 23–14310.

GenBank numbers – KUNCC 23–14310: ITS: OR555906, LSU: OR619797, SSU: OR555910.

Notes – Our phylogenetic analysis showed that *Conlarium multiseptatum* (KUNCC 23–14310) forms a sister lineage with *C. guizhouense* (GZAAS 22–2028) with 89% ML and 0.97 BYPP bootstrap support (Fig. 48). *Conlarium multiseptatum*, *C. guizhouense*, and *C. yunnanense* (KUNCC 23–14310, GZAAS 22–2028, and DLUCC 2131, respectively) are clustered within the same clade, sister to the clade of *C. sacchari* (HMAS 247299, HMAS 247300 and HMAS 247301) (Fig. 48). A comparison of the ITS and LSU sequence data between *C. multiseptatum* (KUNCC 23–14310) and *C. guizhouense* (GZAAS 22–2028) showed 95.13% (488/513 bp, including four gaps) and 99.23% (811/819 bp) sequence similarity, respectively. Comparison of ITS and LSU sequence data between *C. multiseptatum* (KUNCC 23–14310) and *C. yunnanense* (DLUCC 2131) revealed 95.09% (484/509 bp, including four gaps) and 99.04% (1232/1244 bp) differences, respectively. *Conlarium multiseptatum* differs from *C. guizhouense* and *C. yunnanense* by its larger conidia (47–66(–76) × 40–52(–60) µm vs. 32–50(–67) × 20–33(–44.5) µm vs. (18–)26–38(–49) × 20–32(–43) µm) (Hyde et al. 2023, this study). Therefore, we identified *C. multiseptatum* and *C. yunnanense* as new species based on morphological and phylogenetic evidence, although further collections of this complex are needed.

Conlarium sichuanense Tian Zhang & Jian K. Liu, Phytotaxa 528(1): 4 (2021)

Fig. 49

Index Fungorum number: IF840499; Facesoffungi number: FoF14878

Saprobic on submerged decaying wood in Red River (Asia). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate superficial, sporodochial, punctiform, gregarious, dark brown to black. *Mycelium* mostly immersed, comprises branched, pale brown to hyaline, smooth and thin-walled hyphae. *Conidiophores* absent or reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, holoblastic, integrated, determinate, doliiform, cylindrical, hyaline to pale brown, smooth. *Conidia* (28–)36–54(–69) × (23–)31–44(–54) µm ($\bar{x}$ = 45 × 38 µm, n = 35), acrogenous, solitary, dry, muriform, irregular, subglobose to ellipsoidal, pale to dark brown, 3–6-transversely septate, 3–5-longitudinally septate, slightly constricted at the septa, smooth, thin-walled.

Material examined – China, Yunnan, Honghe City, a small tributary of the Red River, 102°17'39"E, 23°25'01"N (340m), on a submerged decaying wood, 23 February 2022, Hong-Wei Shen, YJ 23–79–3 (HKAS 130428), living culture, DLUCC 1617.

GenBank numbers – DLUCC 1617: ITS: OR555905, LSU: OR619796, SSU: OR555909.

Notes – Phylogenetic analysis showed that our new strain (DLUCC 1617) formed a sister clade with a terrestrial species, *C. sichuanense* (CGMCC 3.20406 and UESTCC 21.0015) with 93% ML and 1.00 BYPP bootstrap support (Fig. 48). A comparison of the ITS and LSU base pairs of our strain (DLUCC 1617) and *C. sichuanense* (ex-type, CGMCC 3.20406) revealed that 0.78% (506/510 bp, including one gap) and 2.90% (835/860 bp, including two gap) differences, respectively (Zhang et al. 2021a). The nucleotide differences between our new strain and

C. sichuanense (CGMCC 3.20406) are mainly in the 45bp at the end of the LSU gene of *C. sichuanense*. This may be a sequence that exceeds the effective read length, and the credibility of this part of the sequence is low. Morphologically, our new collection fits the generic concept of *Conlarium*, with muriform, subglobose to ellipsoidal, irregular, pale to dark brown conidia (Liu et al. 2012b, Xie et al. 2019, Hyde et al. 2020b, Zhang et al. 2021a). However, our new collection has larger conidia ((28–)36–54(–69) × (23–)31–44(–54) μm vs. 15.5–19.5 × 13.5–17 μm), more transverse septate (3–6 vs. 0–2), and longitudinal septate (3–5 vs. 1–3). If the sequence of *C. sichuanense* is correct, then our new collection may indeed be a novel species, as they have significant differences in conidia size. However, considering factors such as habitat and host influence, it is temporarily identified as *C. sichuanense*, which was first found in freshwater habitats.

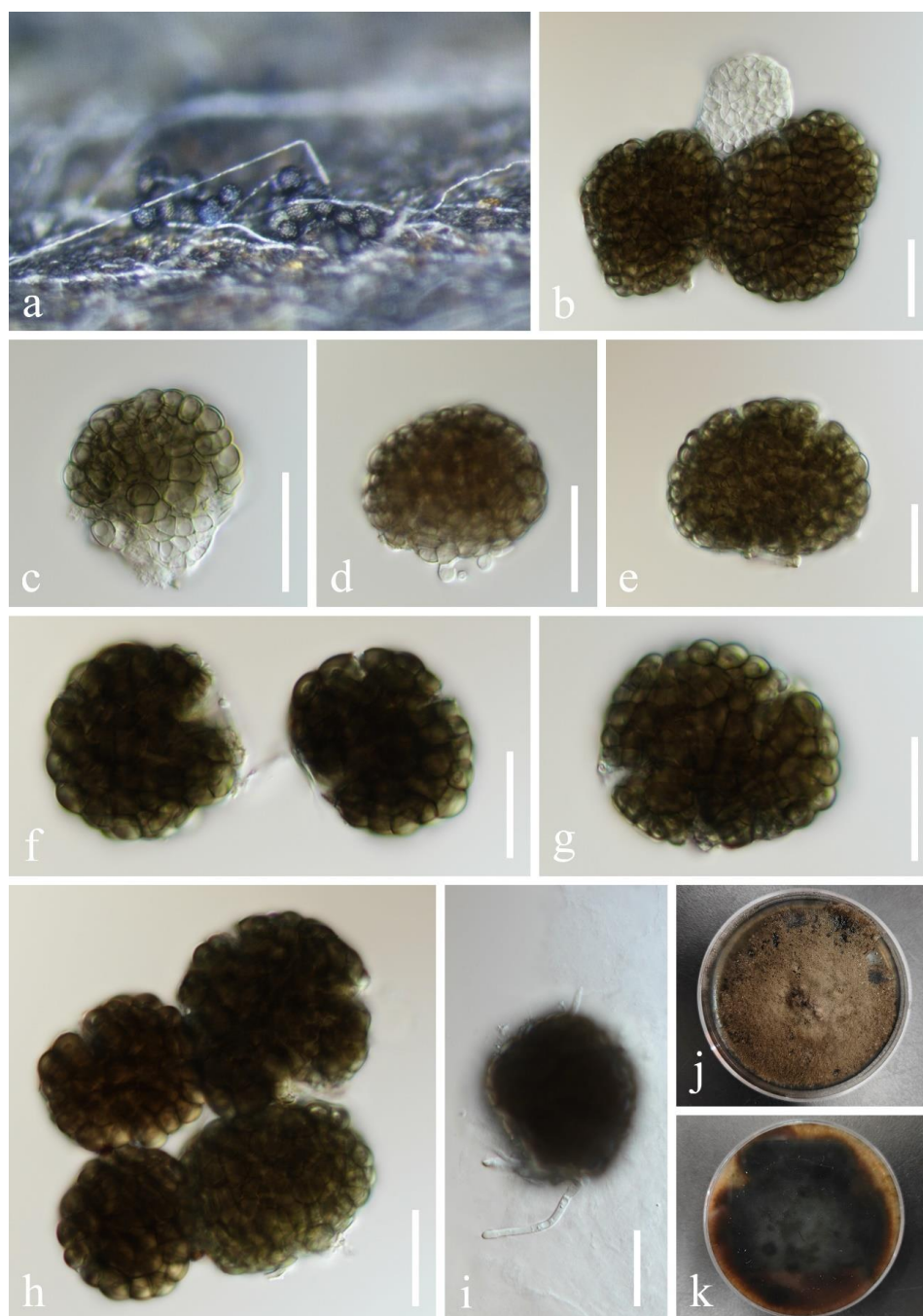


Figure 49 – *Conlarium multiseptatum* (HKAS 130430, holotype). a Colonies on the natural substrate. b–h Conidia. i A germinated conidium. j, k Colony on PDA from surface (j) and reverse (k). Scale bars: b–i = 30 μm.



Figure 50 – *Conlarium sichuanense* (HKAS 130428, a new record in freshwater habitat). a, b Colonies on the natural substrate. c–i Conidia. Scale bars: b–i = 30 μ m.

Conlarium yunnanense H.W. Shen, Z.L. Luo & K.D. Hyde sp. nov.

Fig. 51

Index Fungorum number: IF571756; Facesoffungi number: FoF14880

Etymology – “yunnanense” refers to the Yunnan Province, China, where the species was collected.

Holotype – HKAS 130429

Saprobic on submerged decaying wood in a freshwater Lake. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate superficial, sporodochial, punctiform, gregarious, dark brown to black. *Mycelium* mostly immersed, comprises branched, pale brown to hyaline, smooth and thin-walled hyphae. *Conidiophores* absent or reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, holoblastic, integrated, determinate,

doliiform, cylindrical, hyaline to pale brown, smooth. *Conidia* (18–)26–38(–49) × 20–32(–43) μm ($\bar{x}$ = 32 × 26 μm, n = 35), acrogenous, solitary, dry, muriform, irregular, subglobose to ellipsoidal, pale brown to dark brown, 3–5-transversely septate, 2–4-longitudinally septate, slightly constricted at the septa, smooth, thin-walled.

Material examined – China, Yunnan, Puer City, Djuanh Lake, 24°32'30.4443"N, 101°1'39.5087"E (2500m), on a submerged decaying wood, 24 February 2023, Hong-Wei Shen, FD 48–14–2 (HKAS 130429, holotype), ex-type living culture, DLUCC 2131.

GenBank numbers – DLUCC 2131: ITS: OR555907, LSU: OR619798, SSU: OR555911.

Notes – Refer to the “Notes” of *Conlarium multiseptatum* (this study).

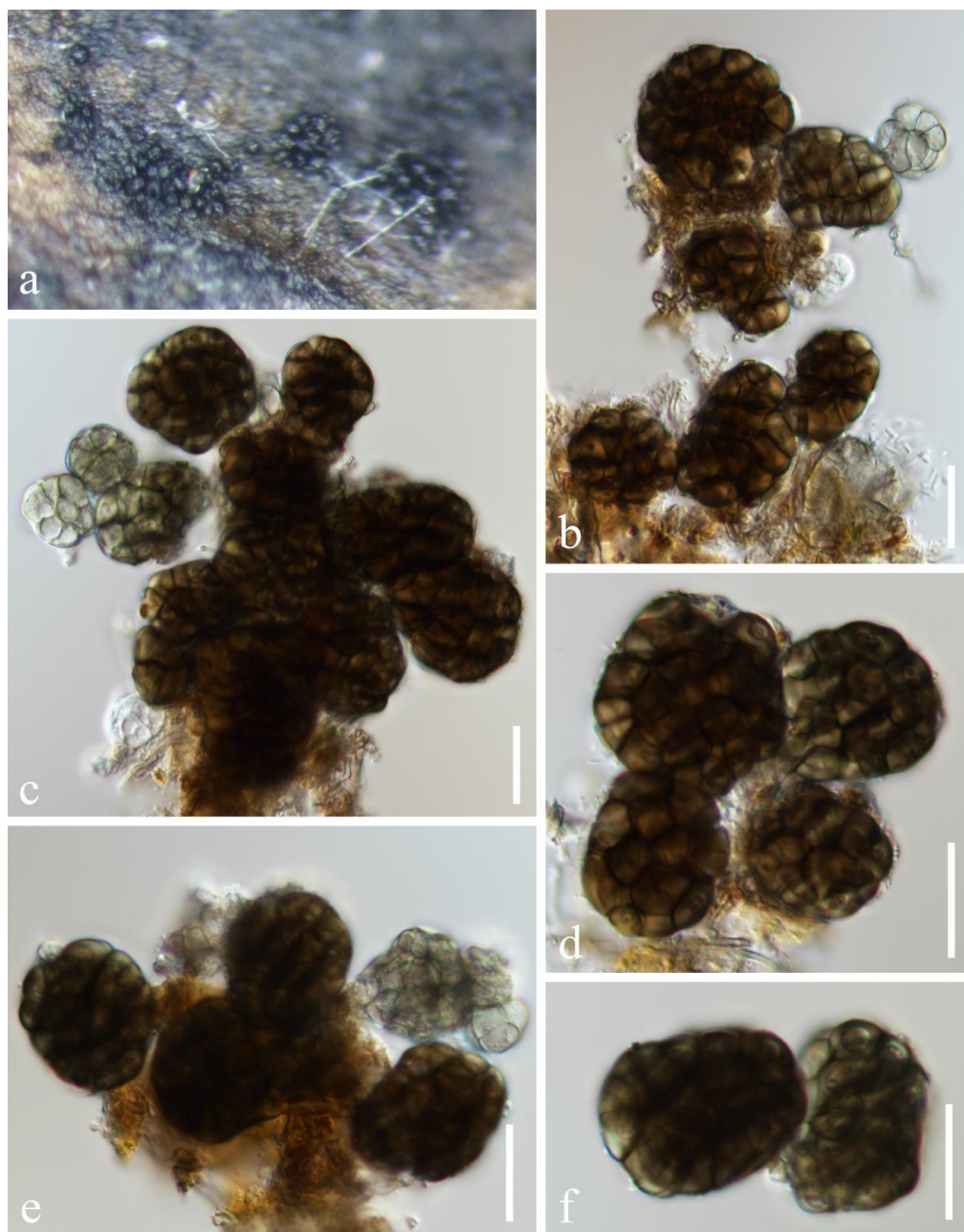


Figure 51 – *Conlarium yunnanense* (HKAS 130430, holotype). a Colonies on the natural substrate. b–f Conidia (immature to mature). Scale bars: b–i = 20 μm.

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

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

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

Index Fungorum number: IF551833; Facesoffungi number: FoF01755

Distoseptispora, a sporidesmium-like genus was introduced by Su et al. (2016) with *D. fluminicola* as the type species. Members of *Distoseptispora* have been reported as saprobes, and commonly known from asexual morph characterized by effuse, hairy colonies, macronematous, mononematous, unbranched, olive-green to brown, cylindrical conidiophores; monoblastic or polyblastic, integrated, terminal, cylindrical or clavate conidiogenous cells; and acrogenous, mostly cylindrical to obclavate, rostrate, olivaceous, brown or yellowish-brown conidia (Su et al. 2016, Li et al. 2017b, Luo et al. 2019, Shen et al. 2021, Yang et al. 2021, Ma et al. 2022, Zhai et al. 2022, Liu et al. 2023). The generic concept of *Distoseptispora* was broadened by Yang et al. (2021) who reported the first sexual morph of *Distoseptispora hyalina*, which is similar to *Sporidesmium thailandense*. Currently, 79 epithets are listed in Index Fungorum (2024) under *Distoseptispora*. In this study, the new records (host, habitats, and geographical) of *Distoseptispora crassispora*, *D. dehongensis*, *D. nonrostrata*, *D. suoluensis*, and *D. thysanolaenae* are described based on morphology and updated phylogeny (Fig. 52).

Distoseptispora crassispora R. Zhu & Huang Zhang, Journal of Fungi 8 (10, no. 1063): 14 (2022)
Fig. 53

Index Fungorum number: IF559920; Facesoffungi number: FoF12577

Saprobic on decaying wood in terrestrial habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the substrate superficial, effuse, gregarious, smooth, septate, hairy, brown to dark brown. *Mycelium* mostly immersed, composed of branched, septate, smooth, pale brown to brown hyphae. *Conidiophores* 28–58 × 5–9 µm ($\bar{x}$ = 40 × 7 µm, n = 20), macronematous, mononematous, cylindrical, erect, simple, straight or flexuous, unbranched, solitary, brown to dark brown, smooth, thick-walled. *Conidiogenous cells* 3.5–9 × 4–6 µm ($\bar{x}$ = 6 × 5 µm, n = 20), holoblastic, monoblastic, terminal, integrated, cylindrical, pale brown or brown, smooth. *Conidia* 84–166 × 10–17 µm ($\bar{x}$ = 126 × 13 µm, n = 20), acrogenous, solitary, multi-distoseptate, obclavate, rostrate, straight or curved, verrucose, pale brown or dark brown, rounded at apex, with a truncate base, guttulate, thick-walled, smooth-walled.

Material examined – China, Guizhou Province, Qiannan Buyi and Miao Autonomous Prefecture, Libo County, on decaying wood in terrestrial habitat, 17 January 2021, Jian Ma, XQK3 (GZAAS 23-0608), living culture, GZCC 23-0606.

GenBank numbers – GZCC 23-0606: ITS: ITS: OR514699, LSU: OR514708, *tef1-α*: OR513900, *rpb2*: OR513897.

Known distribution (based on molecular data) – China (Zhang et al. 2022b, this study).

Known hosts (based on molecular data) – On decaying wood from freshwater and terrestrial habitats (Zhang et al. 2022b, this study).

Notes – In the multi-gene phylogeny, our newly isolated strain (GZCC 23-0606) clustered with *Distoseptispora crassispora* (KUNCC 12-10726) with 100% ML and 1.00 BYPP bootstrap support (Fig. 52). Zhang et al. (2022a) introduced *D. crassispora* from the dead wood in a freshwater habitat. Our new collection shares similar morphological characteristics with the holotype (HKAS 122181) of *D. crassispora*. However, our collection (GZAAS 23-0608) has larger conidiophores ($\bar{x}$ = 28 × 58 µm) than those of the holotype ($\bar{x}$ = 14 × 27 µm) (Zhang et al. 2022b). Therefore, we identified our new isolate as *D. crassispora* based on molecular data and morphological characteristics. This is the first report of *D. crassispora* in terrestrial habitats.

Distoseptispora dehongensis W. Dong, H. Zhang & K.D. Hyde, Fungal Diversity 96, 145 (2019)
Fig. 54

Index Fungorum number: IF555406; Facesoffungi number: FoF05057

Saprobic on dead bamboo culms in terrestrial habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the substrate surficial, scattered or in small groups, dark brown to black. *Mycelium* partly immersed, partly superficial, composed of septate, smooth-walled,

pale brown to brown hyphae. *Conidiophores* 72–105 × 3–4 μm ($\bar{x}$ = 84 × 3.5 μm, n = 15),

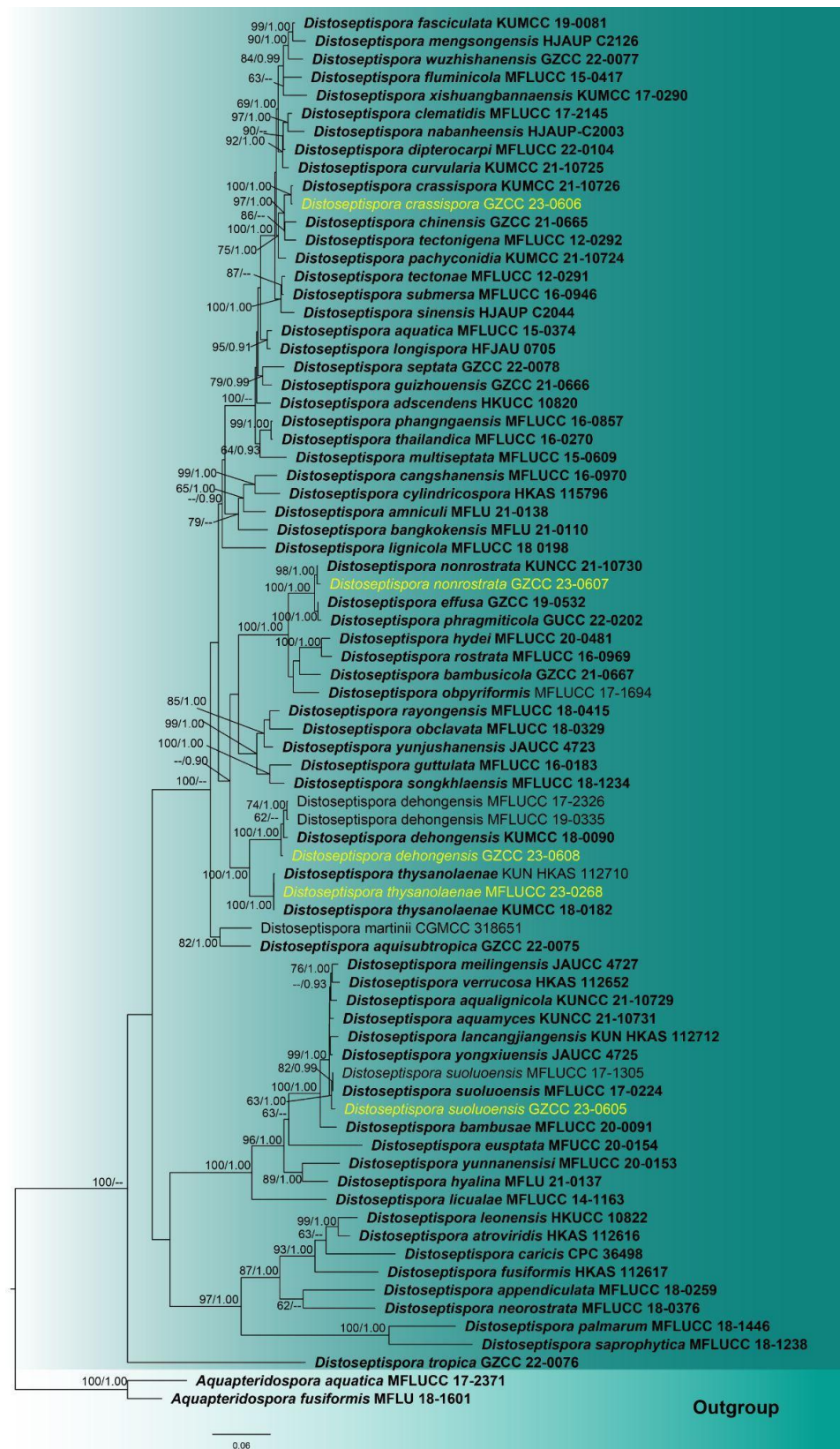


Figure 52 – Phylogram generated from the maximum likelihood analysis based on the combined LSU, ITS, *tef1-α* and *rpb2* sequence data of *Distoseptispora*. Seventy-seven strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAXML tree with a final likelihood value of -28779.838588 is presented. The evolutionary model GTR+GAMMA is applied for all the genes. The matrix had

1497 distinct alignment patterns, with 27.99% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.238830, C = 0.265303, G = 0.282576, T = 0.213291; substitution rates AC = 1.471026, AG = 3.715831, AT = 1.329884, CG = 0.917160, CT = 7.403858, GT = 1.000000; gamma distribution shape parameter α = 0.227725. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Aquapteridospora aquatica* (MFLUCC 17-2371) and *A. fusiformis* (MFLU 18-1601). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.



Figure 53 – Asexual morph of *Distoseptispora crassispora* (GZAAS 23-0608, a new record in terrestrial habitat). a, b Colonies on the host surface. c–f Conidiophores and conidiogenous cells bearing conidia. g–i Conidia. j A germinating conidium. Scale bars: c–j = 20 μm.

macronematous, mononematous, erect, solitary or caespitose, 5–7-septate, slightly constricted at septa, straight or flexuous, cylindrical, rounded at the apex, smooth-walled, unbranched, grayish brown. *Conidiogenous cells* (6–)12.5–20 × 3–5 µm ($\bar{x}$ = 16 × 3.8 µm, n = 15), monoblastic, integrated, terminal, determinate, cylindrical, pale brown. *Conidia* 24–41 × (6.5–)7.5–9.5 µm ($\bar{x}$ = 31.5 × 8.5 µm, n = 20), acrogenous or intercalary, solitary or catenate, obclavate, broad cylindrical, pale olivaceous to brown, mostly 5-septate, smooth-walled, truncate at the base.

Culture characteristics – conidia germinating on PDA within 15 h. Colonies growing on PDA, reaching 16 mm after 15 days at 25 °C, circular, grey, white from above, in reverse dark brown with thin, grey-white margin.

Material examined – China, Guizhou Province, Suiyang County, on a dead stem of bamboo (*Poaceae*), in a distributed forest from land habitat, 15 March 2023, Jing-Yi Zhang, SY5 (GZAAS 23-0610), living culture, GZCC 23-0608.

GenBank numbers – ITS: OR826536, LSU: OR826539.

Known distribution (based on molecular data) – China (Hyde et al. 2019, this study), Thailand (Zhang et al. 2022b).

Known hosts (based on molecular data) – Bamboo in the terrestrial habitat (this study), and submerged decaying wood in freshwater habitat (Hyde et al. 2019, Zhang et al. 2022b).

Notes – The phylogenetic analysis confirmed that our strain (GZCC 23-0608) grouped with *Distoseptispora dehongensis* strains (MFLUCC 17-2326, MFLUCC 19-0335 and KUMCC 18-0090) with 100% ML and 1.00 BYPP bootstrap support (Fig. 52). Hyde et al. (2019) introduced *D. dehongensis* from aquatic habitats in China. Later, Zhang et al. (2022a) reported *D. dehongensis* in Thailand. Our collection fits well with the holotype of *D. dehongensis* (HKAS 101738), except for the longer conidiophores (72–105 µm vs. 45–80 µm) and conidia (24–41 µm vs. 17–30 µm) in our collection. However, the sizes of conidiophores and conidia match well with the description *D. dehongensis* (MFLU 17-1671) (Zhang et al. 2022b). Based on morphology and multi-gene phylogeny, we identified our isolate as *D. dehongensis*. This is a new host record of *D. dehongensis* on dead bamboo culms and the first report from terrestrial habitats.

Distoseptispora nonrostrata Y. Qing & Huang Zhang, Journal of Fungi 8 (10, no. 1063): 20 (2022)
Fig. 55

Index Fungorum number: IF559923; Facesoffungi number: FoF12580

Saprobic on dead wood in terrestrial habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the substrate, effuse, scattered or in small groups, gregarious, hairy, smooth, brown to dark brown. *Mycelium* mostly immersed, composed of branched, septate, smooth, brown to dark brown hyphae. *Conidiophores* 98–119 × 6.5–7.5 µm ($\bar{x}$ = 108 × 7 µm, n = 20), macronematous, mononematous, cylindrical, erect, straight or slightly flexuous, unbranched, brown to yellowish brown, smooth, thick-walled. *Conidiogenous cells* 12.5–20 × 4.5–5.5 µm ($\bar{x}$ = 16.5 × 5 µm, n = 20), holoblastic, monoblastic, terminal, integrated, cylindrical, brown, smooth. *Conidia* 120–175 × 9–12 µm ($\bar{x}$ = 157 × 10 µm, n = 30), solitary, acrogenous, cylindric-obclavate, rostrate, straight, or slightly curved, guttulate, thick-walled, smooth-walled, green-brown or brown, up to 26-distoseptate, with a truncate base.

Material examined – China, Guizhou province, Xishui county, Xishui Reserve, on decaying wood in terrestrial habitat, 7 September 2020, Yong-Zhong Lu, XSX3 (GZAAS 23-0609), living culture, GZCC 23-0607.

GenBank numbers – GZCC 23-0607: ITS: OR514700, LSU: OR514709, *rpb2*: OR513898.

Known distribution (based on molecular data) – China (Zhang et al. 2022b, this study).

Known hosts (based on molecular data) – *Bamboo* (Zhang et al. 2022b, this study), on decaying wood from terrestrial habitat (this study).

Notes – In the phylogenetic analysis, our strain (GZCC 23-0607) clustered with *Distoseptispora nonrostrata* with 100% ML and 1.00 BYPP bootstrap support (Fig. 52), which indicates that they are conspecific. However, our collection (GZAAS 23-0609) has larger conidia ($\bar{x}$ = 120 × 175 µm) than those of the holotype ($\bar{x}$ = 22 × 51 µm) (Zhang et al. 2022b). Based on

morphology and multi-gene phylogeny, we identify our new collection is *D. nonrostrata*. This is a new record of the species from terrestrial habitats.



Figure 54 – *Distoseptispora dehongensis* (GZAAS 23-0610, a new host record and a new record from terrestrial habitat). a, b Colonies on natural substrate. c–g Conidiophores with conidiogenous cell. h–l conidia. m, n Colonies on PDA from above (m) and reverse (n). Scale bars: c–f, i = 30 μ m, g, h, j–l = 20 μ m.

Distoseptispora suoluoensis J. Yang, Maharachch. & K.D. Hyde, Mycological Progress 17 (5): 609 (2017) Fig. 56

Index Fungorum number: IF512048; Facesoffungi number: FoF00168



Figure 55 – Asexual morph of *Distoseptispora nonrostrata* (GZAAS 23-0609, a new record in terrestrial habitat). a–c Colonies on the host surface. d Conidiophores and conidia. e, h Conidiophores and conidiogenous cells. f Conidiogenous cells bearing conidia. g A germinating conidium. i Conidia. j, k Colonies on PDA, (j) above, (k) below. Scale bars: d–i = 20 μm.

Saprobic on decaying wood in freshwater habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the substrate effuse, brown, hairy, glistening. *Mycelium*

partly superficial, partly immersed in the substratum, composed of hyaline to pale brown, septate, branched hyphae. *Conidiophores* 70–187 × 5.5–6.5 µm ($\bar{x}$ = 127 × 6 µm, n = 20), macronematous, mononematous, solitary or aggregated at the base, cylindrical, straight or slightly flexuous, septate, brown to dark brown, rounded and paler at the apex. *Conidiogenous cells* 18–31 × 5–6 µm ($\bar{x}$ = 22 × 5.5 µm, n = 20), integrated, terminal, monoblastic, cylindrical, brown. *Conidia* 61–109 × 10–13 µm ($\bar{x}$ = 90 × 11 µm, n = 20), acrogenous, solitary, narrowly obclavate or obspatulate, rostrate, 4–6-septate, yellowish brown or dark olivaceous, becoming paler or hyaline towards the apex, guttulate, verrucose, smooth.

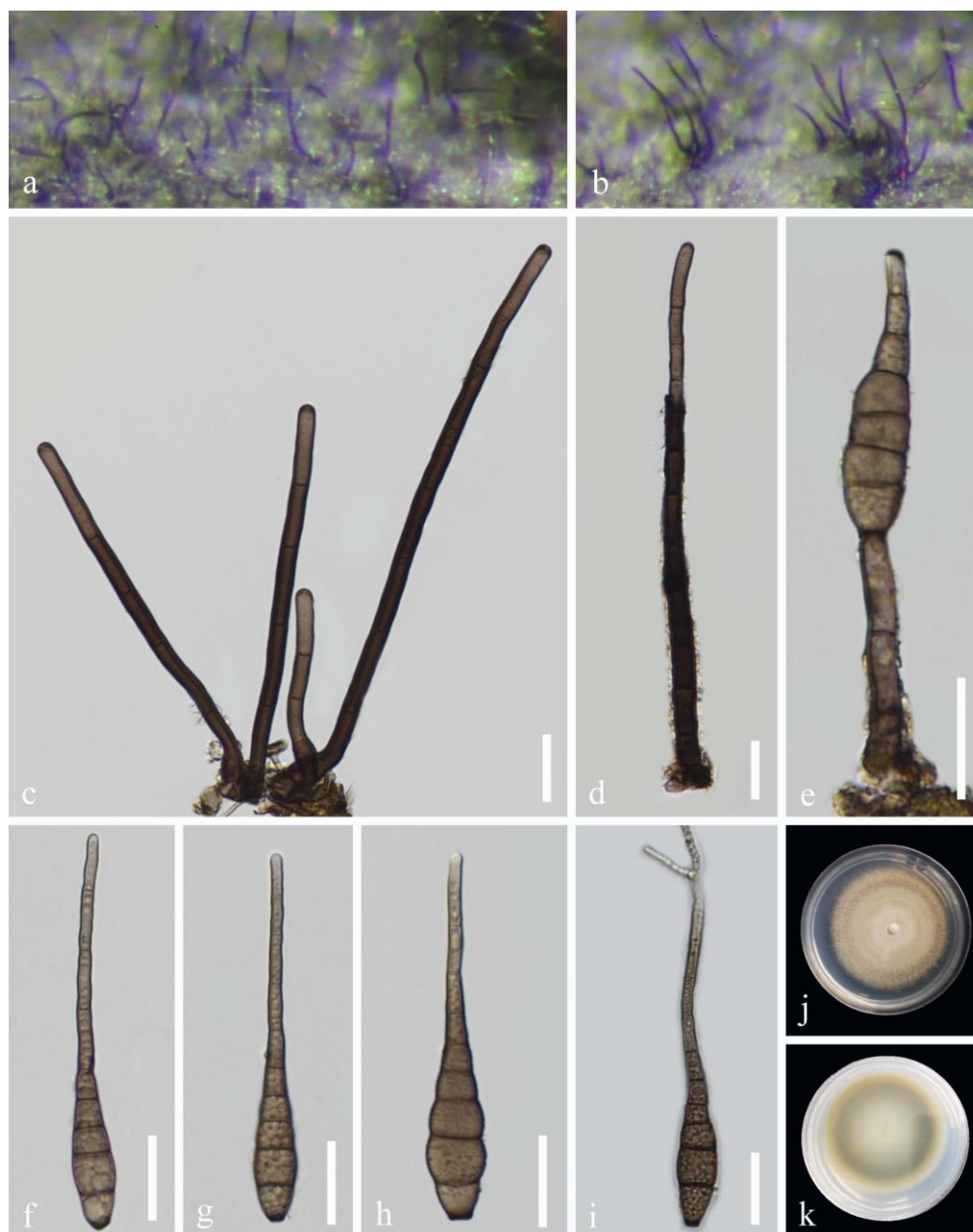


Figure 56 – Asexual morph of *Distoseptispora suoluensis* (GZAAS 23-0607, a new host record). a, b Colonies on the host surface. c–e Conidiophores and conidiogenous cells bearing conidia. f–h Conidia. i A germinating conidium. j, k Colonies on PDA, (j) from above, (k) from below. Scale bars: c–i = 20 µm.

Material examined – China, Guangxi Zhuang Autonomous Region, Liuzhou City, Luzhai County, on decaying wood in a freshwater stream, 4 May 2021, Jian Ma, LZ6 (GZAAS 23-0607), living culture, GZCC 23-0605.

GenBank numbers – GZCC 23-0605: ITS: OR514701, LSU: OR514710, *tef1-α*: OR513902, *rpb2*: OR513899.

Known distribution (based on molecular data) – China (Yang et al. 2018, this study).

Known hosts (based on molecular data) – *Bamboo* (this study), on decaying submerged wood of unidentified plants (Yang et al. 2018).

Notes – In the multi-gene phylogeny, our strain (GZCC 23-0605) clustered with *Distoseptispora suoluoensis* (MFLUCC 17-0224) with 100% ML and 1.00 BYPP bootstrap support (Fig. 52). Yang et al. (2018) introduced *D. suoluoensis*, isolated from a freshwater habitat in China. Our collection shares similar morphological characteristics with the holotype (MFLU 17-0853) of *D. suoluoensis*. Thus, we identified our new isolate as *D. suoluoensis*. This is the first report of this species from culms of bamboo in China.

Distoseptispora thysanolaenae Goonas., Dayar., Phookamsak & K.D. Hyde, Fungal Diversity 95: 126 (2019) Fig. 57

Index Fungorum Number: IF555408; Facesoffungi Number: FoF05011

Saprobic on unidentified wood in terrestrial habitats. Sexual morph: Undetermined. Asexual morph: *Colonies* on the substrate, superficial, effuse, erect, hairy, scattered or in small groups, olivaceous, glistening. *Mycelium* partly immersed, partly superficial, composed of septate, smooth-walled, brown hyphae. *Conidiophores* 26–62 × 3.5–5.5 μm ($\bar{x}$ = 40 × 4.5 μm, n = 20), macronematous, mononematous, erect, solitary or in groups, straight or slightly flexuous, cylindrical, rounded at the apex, smooth-walled, 2–4-septate, unbranched, brown. *Conidiogenous cells* (9–)14–18.5 × 4–5 μm ($\bar{x}$ = 16 × 4.5 μm, n = 15), monoblastic, terminal, integrated, determinate, cylindrical or ellipse rarely, pale brown or brown. *Conidia* 76–129 × 8–10 μm ($\bar{x}$ = 108 × 8.8 μm, n = 20), acrogenous, solitary, obclavate, elongated, straight, or slightly curved, olivaceous brown to light brown, paler towards the apex, 6–14-septate, smooth-walled, truncate and darkened scar at the base.

Culture characteristics – Conidia germinating on WA within 12 h and germ tubes produced from the ends of conidia. Colonies growing on PDA reaching 16 mm after 15 days at 25 °C in natural light, circular, entire margin with flat surface, with fluffy, dense, gray-brown mycelium on the surface, in reverse dark olivaceous with sparser, white margin, and not producing pigmentation in the culture.

Material examined – Thailand, Chiangmai Province, Mushroom Research Center (MRC), on a dead stem of bamboo, 11 September 2020, Hong-Wei Shen, Y217 (MFLU 23-0466); living culture, MFLUCC 23-0268.

GenBank numbers – ITS: OR826535, LSU: OR826538.

Known distribution (based on molecular data) – China (Phookamsak et al. 2019, Shen et al. 2021), Thailand (this study).

Known hosts (based on molecular data) – Bamboo in the terrestrial habitat (this study), *Thysanolaena maxima* (Phookamsak et al. 2019), unidentified wood (Shen et al. 2021).

Notes – A BLASTn search of the LSU and ITS sequence data indicated that our newly isolated strain (MFLUCC 23-0268) is closely related to *Distoseptispora thysanolaenae* (KUN-HKAS 102247) with 99.88% and 99.43% similarity, respectively. In the multi-gene phylogeny, our strain (MFLUCC 23-0268) clustered with *D. thysanolaenae* (KUMCC 18-0182 and KUN-HKAS 102247) with 100% ML and 1.00 BYPP bootstrap support (Fig. 52). The morphology of our collection and *D. thysanolaenae* (KUN-HKAS 102247; the holotype) are indistinguishable, except that the obviously longer conidia was observed in our collection (76–129 vs. 21.5–80 μm). However, the long conidia also can be found from the sporulation on PDA media, of *D. thysanolaenae* (KUMCC 18-0182). Thus, based on morphology and multi-gene phylogeny, we conclude our new collection is *D. thysanolaenae*, and it is a new record found on bamboo from Thailand.

Hypocreomycetidae O.E. Erikss. & Winka

Glomerellales Chadef. ex Réblová, W. Gams & Seifert, Stud. Mycol. 68: 170 (2011)
Glomerellaceae Locq., Mycol. gén. struct. (Paris): 175 (1984)
Colletotrichum Corda, in Sturm, Deutschl. Fl., 3 Abt. (Pilze Deutschl.) 3(12): 41 (1831)
 Index Fungorum number: IF7737; Facesoffungi number: FoF00144



Figure 57 – *Distoseptispora thysanolaenae* (MFLU23-0466, a new host and a geographical record). a, b Colonies on natural substrate. c–f Conidiophores, conidiogenous cell and conidia. g, h Conidia. i A germinating conidium. j, k Colonies on PDA, from (j) above and (k) reverse. Scale bars: a = 300 µm, b = 100 µm, c–i = 50 µm.

Colletotrichum was introduced by Corda (1831) with *C. lineola* as the type species. Species of this genus have been recorded as endophytes, pathogens and saprobes (Than et al. 2008, Huang et al. 2013, Hyde et al. 2020b, Jayawardena et al. 2021, Chethana et al. 2023). Recent studies have reported *Colletotrichum* species from medicinal plants (Zhang et al. 2023a), ornamental plants (Zhang et al. 2023b) and tea (Peng et al. 2023). Most of the species of *Colletotrichum* are reported by their asexual morph (Jayawardena et al. 2021, Talhinas & Baroncelli 2021). The identification of *Colletotrichum* species using molecular phylogenetics and morphology is fairly well-established (Chen et al. 2022, Abeywickrama et al. 2023). Liu et al. (2022) accepted 280 species comprising 16

species complexes in this genus. Since then, 25 new species have been introduced in *Colletotrichum* based on polyphasic taxonomic approaches. Here, we provide the updated phylogeny for the species in the *Colletotrichum dematium* species complex (Fig. 58).

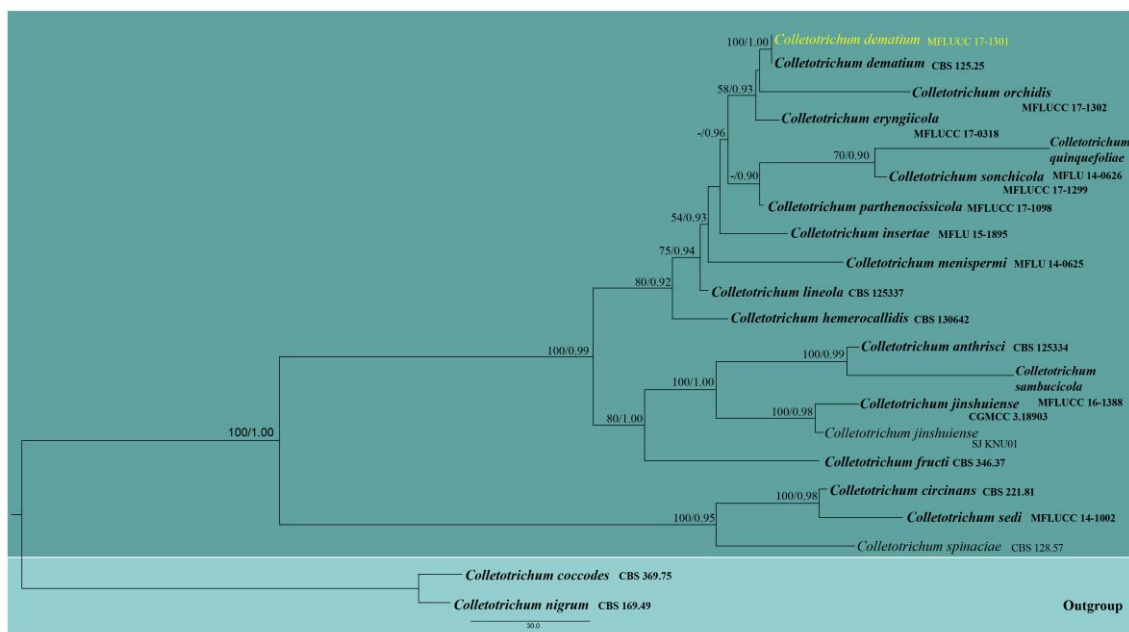


Figure 58 – Phylogram generated from the maximum parsimony analysis based on the combined ITS, *gapdh*, *chs-1*, *act* and *tub2* sequence data of *Colletotrichum dematium* species complex. Twenty-one strains are included in the combined analyses. The tree topology of the maximum parsimonious analysis is similar to the Bayesian analysis. Constant characters were 1249. Parsimony-informative characters and parsimony-uninformative characters were 420 and 134 respectively. Bootstrap support values for MP greater than 75% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Colletotrichum coccodes* (CBS 369.75) and *C. nigrum* (CBS 169.49). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Colletotrichum dematium (Pers.) Grove, J. Bot., Lond. 56: 341 (1918)

Fig. 59

Index Fungorum number: IF120313; Facesoffungi number: FoF03598

Saprobic on dead and aerial stem of *Galega officinalis*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 130–380 µm ($\bar{x}$ = 260 µm, n = 10) diam., acervulus, oval, solitary, gregarious, black, consisting of dark brown, cylindrical to sub-cylindrical cells where setae and conidiophores originate. *Setae* straight or $\pm$ bent, dark brown, becoming paler towards the apex, opaque, smooth-walled, 3–6-septate, 36–135 µm long, base cylindrical, slightly inflated, 7–11 µm diam., smooth, with acute to rounded tip. *Conidiophores* 20 µm long, simple, hyaline to pale brown, septate. *Conidiogenous cells* 4–14 × 2–4 µm ($\bar{x}$ = 10 × 3 µm, n = 20), enteroblastic, hyaline, smooth-walled, cylindrical, slightly inflated, opening 0.5–1 µm wide, collarette or periclinal thickening not observed. *Conidia* 18–23 × 3–4 µm ($\bar{x}$ = 21 × 4 µm, n = 15), L/W = 5, hyaline, smooth or verruculose, aseptate, curved, both sides gradually tapering towards the round to slightly acute apex, base truncate, guttulate, form a septum while germinating. *Appressoria* on PDA 3–10 × 3–7 µm ($\bar{x}$ = 7 × 4 µm, n = 15), L/W = 1.8, solitary, elliptical to clavate, brown, smooth-walled, aseptate.

Cultural characteristics – Colonies on PDA, reaching 40–55 mm in 7 days at 25 °C, flat with entire margin, aerial mycelium sparse, short, pale olivaceous-grey, colony surface buff, some sectors dark grey-olivaceous to dark olivaceous-grey, iron-grey acervuli observed mainly on the edge of the colony. Reverse olivaceous-green, concentric rings are clearly observed.

Material examined – Italy, Province of Forlì-Cesena [FC], Riofreddo – Bagno di Romagna, on a dead and aerial stem of *Galega officinalis* (Fabaceae), 2 October 2016, Camporesi Erio, IT3117 (MFLU 16-2541), living culture MFLUCC 17-1301.

GenBank numbers – MFLUCC 17-1301: ITS: OR984747, *chs*: OR997965, *gapdh*: OR997966, *tub2*: OR997967, *act*: OR997968.

Known distribution (based on molecular data) – Australia, Cuba, Czech Republic, France, South Africa, Venezuela, and West Indies (Damm et al. 2009), Russia (Jayawardena et al. 2018a), Japan (Sato et al. 2012), China (Guan et al. 2016, Liu et al. 2016b), India (Rather et al. 2018), Italy (Karimi et al. 2016, this study)

Known hosts (based on molecular data) – *Bidens pilosa*, *Eryngium campestre*, *Genista tinctoria*, *Solanum tuberosum*, *Vitis vinifera* (Damm et al. 2009, Jayawardena et al. 2018a), *Armeria maritima* (Sato et al. 2012), *Polygonatum odoratum* (Karimi et al. 2016), *Asparagus racemosus*, *Hemidesmus indicus* (Rather et al. 2018), *Lycopus lucidus*, *Polygonum aviculare* (Guan et al. 2016, Liu et al. 2016b), *Galega officinalis* (this study).

Notes – According to the phylogenetic analysis, our strain (MFLUCC 17-1301) clustered with strains of *C. dematium* (CBS 122055, MFLUCC 17-0334, MFLUCC 17-0339) with 100% ML and 1.00 BYPP bootstrap support (Fig. 58). *Colletotrichum dematium* in the *dematium* species complex is mainly characterized by having curved conidia (Damm et al. 2009, Jayawardena et al. 2016). It has been reported as a pathogen, saprobe or an endophyte (Jayawardena et al. 2021) of various hosts (Talhinhas & Baroncelli 2023). Valenzuela-Lopez et al. (2018) and Bucha et al. (2019) reported *C. dematium* as an opportunistic pathogen in humans. The morphologies of both our collection and the type collection share similar characteristics (Damm et al. 2009). Based on morphology and molecular phylogeny, we conclude our collection is *C. dematium*. The current study presents a new host record of the species on *Galega officinalis* in Italy.

Hypocreales Lindau, Nat. Pflanzenfam., Teil. I (Leipzig) 1(1): 343 (1897)

Nectriaceae Tul. & C. Tul., Select. fung. carpol. (Paris) 3: 3 (1865)

Nectria (Fr.) Fr., Summa veg. Scand., Sectio Post. (Stockholm): 387 (1849)

Index Fungorum number: IF3431; Facesoffungi number: FoF02122

Nectria was previously accepted as *Hypocrea* sect., and later Fries (1849) accepted it as a separate genus. Clements & Shear (1931) designated *Nectria cinnabarina* as the lectotype (Rossman et al. 1999). Both sexual and asexual morphs have been reported for this genus (Perera et al. 2023). The sexual morph is characterized by globose to subglobose ascomata, red to bay to sienna, seated on or slightly or completely immersed in a stroma, asci are clavate to narrowly clavate or cylindrical, ascospore are up to 4-septate, ellipsoidal, oblong, fusiform, pyriform or allantoid and hyaline (Rossman et al. 1999). The asexual morph is characterized by sporodochia which are superficial on stroma, cerebriform or tuberculoid, stipitate, pustulate, discoid or cylindric-capitate, white to whitish yellow, sometimes orange, conidiophores arising from hymenium, hyaline, straight or curved, conidia 0–1-septate, ellipsoidal, oblong, cylindrical to allantoid or subglobose to ellipsoidal, straight to slightly curved, rounded at ends, hyaline (adapted from Lombard et al. 2015, Maharachchikumbura et al. 2016). *Nectria* species have been reported as saprobic or weakly parasitic on plants in both terrestrial and marine habitats. Over a thousand species are listed in this genus (Wijayawardene et al. 2022, Index Fungorum 2024). Here, we provide the updated phylogeny for *Nectria* (Fig. 60) with a new host record of *N. asiatica* (Fig. 61).

Nectria asiatica Hirooka, Rossman & P. Chaverri, Stud. Mycol. 68: 35-56. (2011)

Fig. 61

Index Fungorum number: IF516721; Facesoffungi number: FoF15218

Saprobic on dead twig of *Pinus massoniana*. Sexual morph: Not observed. Asexual morph: *Stromata* erumpent through epidermis, light brown to black. *Conidiomata* 300–1100 × 380–920 µm ($\bar{x}$ = 719 × 744 µm; n = 15), sporodochial, stipitate, superficial on well-developed stromata, smooth, scattered, solitary or groups of 2–5, cerebriform or tuberculate. *Stipe* 420–780 µm ($\bar{x}$ = 669 µm; n = 15), continuous with stroma, composed of brown to dark brown cells of *textura angularis*.

Hymenium 240–690 µm ($\bar{x}$ = 482 µm; n = 15) long, 2–6 µm ($\bar{x}$ = 4.2 µm; n = 30) wide cells, forming with the cells of *textura prismatica*, elongating with *textura angularis* cells, curved at margin. *Conidiophores* growing from hymenium, monoverticillate or rarely bi-verticillate, septate, strongly coiled, hyaline to pale brown, smooth-walled. *Conidiogenous cells* phialidic, intercalary, occurring below each septum, rarely terminal; *intercalary phialides* 4.9–7.2 µm ($\bar{x}$ = 6.2 µm; n = 50), monophialidic; *terminal cells* monophialidic, sometimes sterile, without collarettes. *Conidia* 6–9 × 2–3 µm ($\bar{x}$ = 7.4 × 2.4 µm; n = 50) hyaline, narrowly long ellipsoidal to cylindrical, obtuse at both ends straight, slightly curved, aseptate, smooth-walled.

Material examined – China, Yunnan province, Yuanmou county (25°53' N 101°42'E), on a dead twig of *Pinus massoniana* (Pinaceae), 14 January 2023, SS02 (MHZU 23-0235), living cultures ZHKUCC 23-0959, ZHKUCC 23-0962.

GenBank numbers – ITS: OR690744, LSU: OR690773, *tef1-α*: OR818431; *tub2*: OR818433; *rpb2*: OR818429 (ZHKUCC 23-0959); ITS: OR690745, LSU: OR690774, *tef1-α*: OR818432; *tub2*: OR818434; *rpb2*: OR818430 (ZHKUCC 23-0962)



Figure 59 – *Colletotrichum dematium* (MFLU 16-2541, a new host record). a Acervuli on the host tissue. b Acervulus. c, d Conidiophores and setae arising from dark brown, cylindrical to sub-cylindrical cells. e A seta with septa. f Conidiophores. g A tip of a seta. h–k Appressoria. l–n Conidia. Scale bars: a = 50 µm, b = 100 µm, c, e, f = 20 µm, d, h–k, l–n = 10 µm.

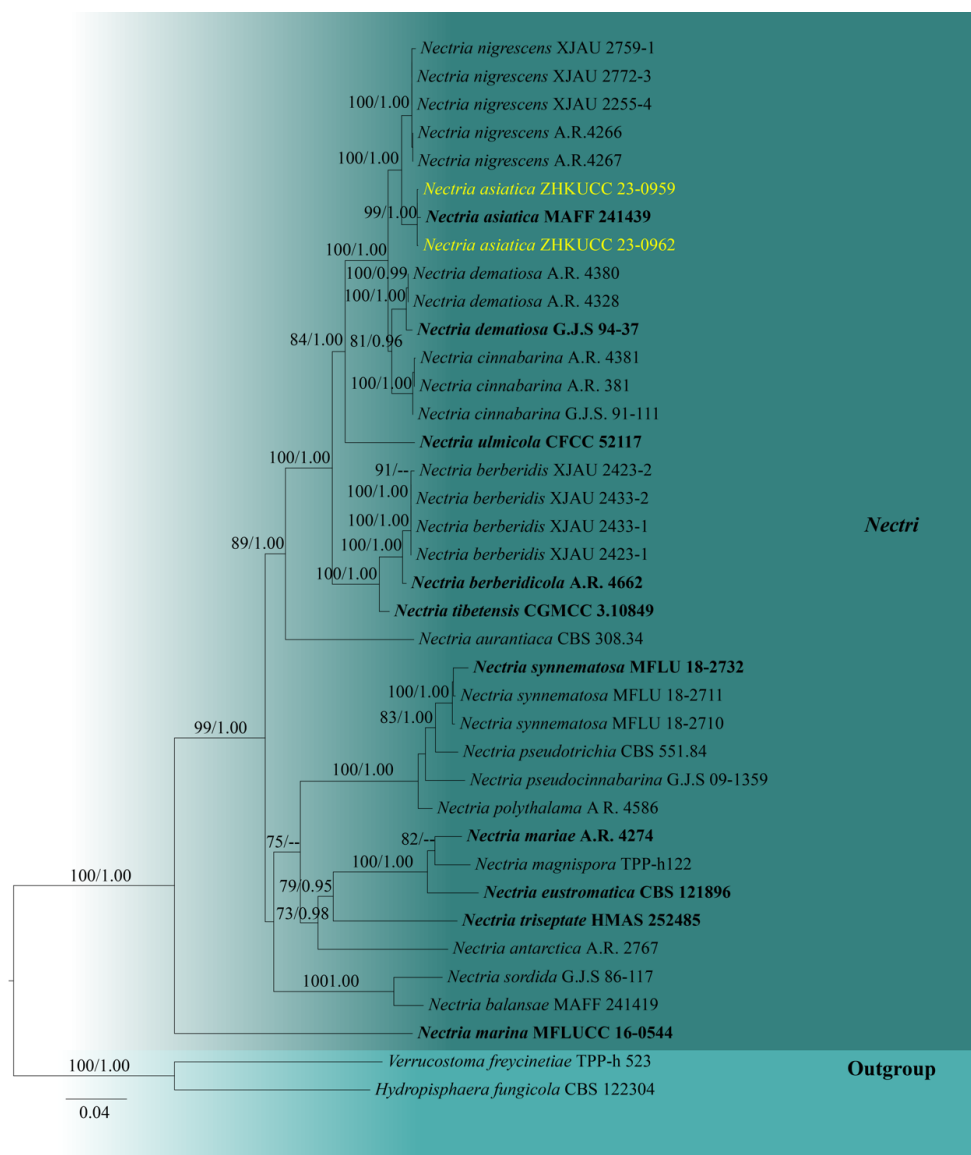


Figure 60 – Phylogram generated from the maximum likelihood analysis based on the combined ACT, ITS, LSU, *tef1- α* and *tub2* sequence data of *Nectria*. Thirty-eight strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of - 17913.226293 is presented. The evolutionary model GTR+GAMMA is applied for all the genes. The matrix had 1240 distinct alignment patterns, with 17.99% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.220838, C = 0.280337, G = 0.261368, T = 0.237457; substitution rates AC = 0.701394, AG = 1.891411, AT = 1.286301, CG = 0.758222, CT = 4.804870, GT = 1.000000; gamma distribution shape parameter α = 0.542067. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Hydropisphaera fungicola* (CBS 122304) and *Verrucostoma freycinetiae* (TPP h 523). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Known distribution (based on molecular data) – China, Japan (Hirooka et al. 2011, this study).

Known hosts (based on molecular data) – *Acer* sp., *Betula lutea*, *Prunus* sp., *Sorbus commixta*, *Zelkova serrata*, *Mangifera indica* (Hirooka et al. 2011), and *Pinus massoniana* (this study).

Notes – In the phylogenetic analysis, our strains ZHKUCC 23-0959, ZHKUCC 23-0962) grouped with the *Nectria asiatica* (MAFF 241439, ex-type) with 99% ML and 0.99 BYPP bootstrap support (Fig. 60). *Nectria asiatica* was reported by Hirooka et al. (2011). Morphologically, our collection shares similar characteristics with *N. asiatica* (MAFF 241439) by sporodochial, stipitate, cerebriform or tuberculate conidiomata; strongly coiled, conidiophores developing acropleurogenously for several levels; and hyaline, narrowly long ellipsoidal to cylindrical, aseptate conidia (Hirooka et al. 2011). However, our collection has light brown to black stromata, smaller sporodochial conidiomata ($300\text{--}1100 \times 380\text{--}920 \mu\text{m}$ vs. $250\text{--}800 \times 300\text{--}2000 \mu\text{m}$), and narrower stipe ($420\text{--}780 \mu\text{m}$ vs. $440\text{--}610 \mu\text{m}$) than MAFF 241439 (Hirooka et al. 2011). Based on these evidences, we conclude our collection is *N. asiatica*, and is a new host record on *Pinus massoniana* from Yunnan Province, China.

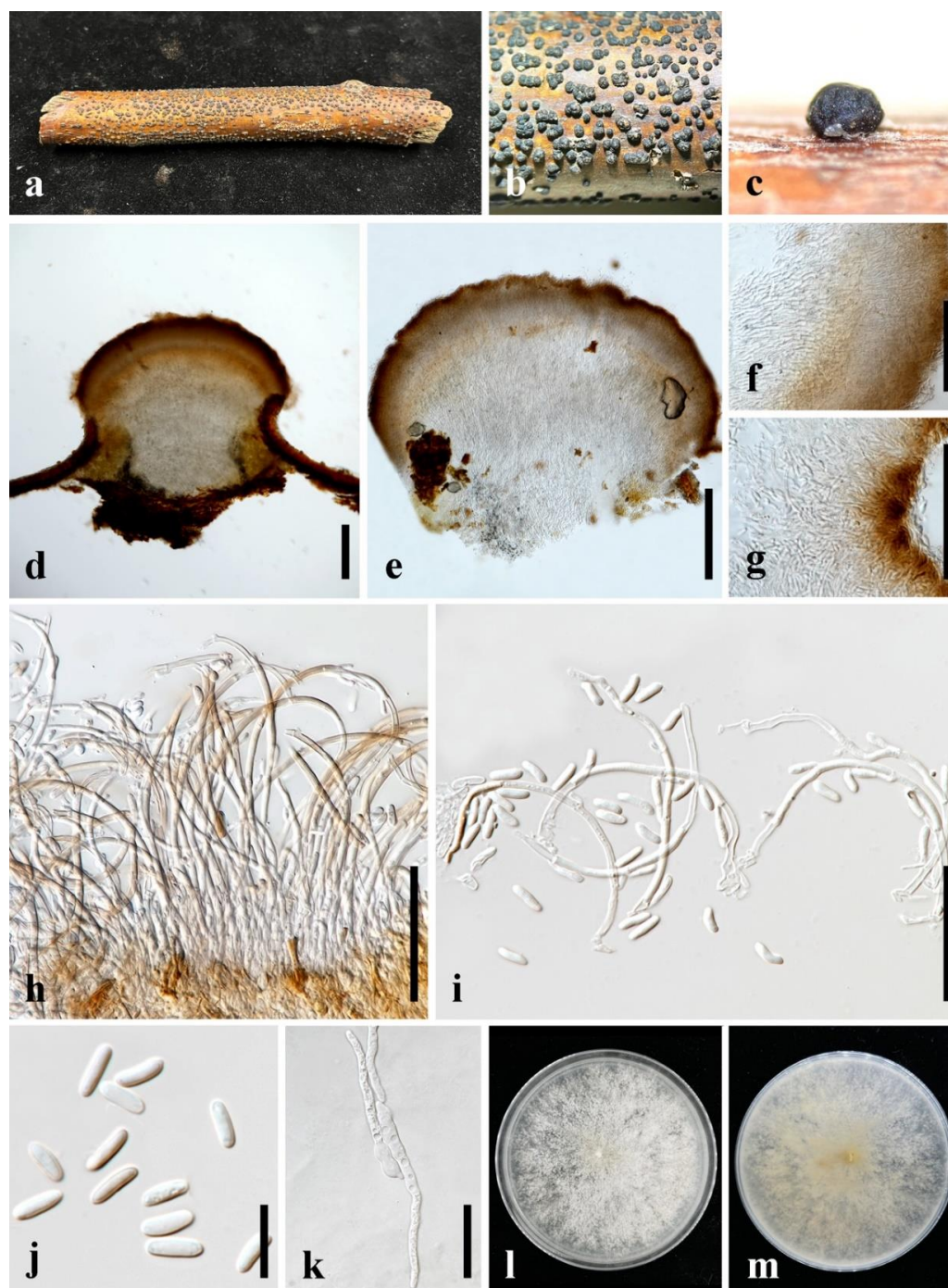


Figure 61 – *Nectria asiatica* (MHZU 23-0235, a new host record). a–c Appearance of sporodochia on host surface. d, e Sections through sporodochium. f, g Edges of a sporodochium.

h, i Conidiophores, conidiogenous cells, and conidia. J Conidia. k Germinating conidia. l, m Colonies on PDA, (l) above view, (m) reverse view. Scale bars: d–f = 200 μ m, g–i = 50 μ m, j, k = 10 μ m.

Microascales Luttr. ex Benny & Kimbr., Mycotaxon 12 (1): 40 (1980)

Microascales* family *incertae sedis

Parasporendocladia W.P. Wu & Y.Z. Diao, Fungal Diversity 116: 333 (2022)

Index Fungorum number: IF 841540; Facesoffungi number: FoF 13655

Parasporendocladia was introduced by Wu & Diao (2022) to accommodate *Parasporendocladia bactrospora* ($\equiv$ *Phialocephala bactrospora*, = *Sporendocladia bactrospora*) as the type species, which was initially placed in a separate family from the type species (Jacobs et al. 2003). The morphology of *Phialocephala* and *Sporendocladia* is remarkably similar, making it difficult to differentiate these genera without molecular evidence (Jacobs et al. 2001, 2003, Wu & Diao 2022). Based on the phylogenetic studies, the type species of *Phialocephala* (*Ph. dimorphospora*), belongs to *Mollisiaceae* within *Helotiales*, and the type species of *Sporendocladia* (*S. fumosa*) belongs to *Chaetosphaeriaceae*. However, *S. bactrospora* is a member of the *Microascales* (Wingfield et al. 1987, Mouton & Wingfield 1993, Jacobs et al. 2001, 2003, Day et al. 2012, Wu & Diao 2022). Only one species belongs to this genus (Index Fungorum 2024). Here, we provide a new host record of *P. bactrospora* on *Carpinus betulus* from Iran (Figs 62, 63).

Parasporendocladia bactrospora (W.B. Kendr.) W.P. Wu & Y.Z. Diao, Fungal Diversity 116: 333 (2022) Fig. 63

Index Fungorum number: IF841745; Facesoffungi number: FoF14762

Saprobic on a dead wood of *Carpinus betulus*. Sexual-morph: Undetermined. Asexual morph: Hyphomycetous. *Mycelium* superficial to immersed. *Conidiophores* 625–1250 μ m long ($\bar{x}$ = 976.8 μ m, n = 25), macronematous, mononematous, solitary to aggregated, erect, branched at the apex, smooth, septate, brown, 4–6 μ m wide ($\bar{x}$ = 4.8 μ m, n = 25) at the base, conidiogenous head at the apex, branched with 3–8 series of terminal phialides. *Conidiogenous cells* 20–25 $\times$ 3–3.5 μ m ($\bar{x}$ = 22.5 $\times$ 4 μ m, n = 30), monophialidic, discrete, determinate, ampulliform, subulate with well-defined collarettes. *Conidia* 4–8 $\times$ 1.5–2 μ m ($\bar{x}$ = 1.5 $\times$ 6.5 μ m, n = 30), arranged in long chains, bacilliform, hyaline, smooth, aseptate, and truncated at both ends.

Culture characteristics – Colonies growing on PDA, completely covering the petri dish after 14 days (reaching 55 mm in diameter), at 25°C under dark conditions, circular, entire margin, dense at the center, dark brown to grey, mycelium mostly superficial to immersed, sporulating at the center after 14 days.

Material examined – Iran, Mazandaran, Sari, Pol sefid, Sangdeh forest, on dead *Carpinus betulus* (*Betulaceae*), 6 October 2017, Omid Karimi, FUM 20-015.

GenBank numbers – ITS: MG602683.

Known distribution – Brazil (Barbosa et al. 2009, Barreto et al. 2022), Canada (Kendrick 1961, Ginns 1986, Grünig et al. 2002), Cuba (Camino-Vilaro et al. 2019), England (Kendrick 1961), Iran (this study, Sohrabi & Mohammadi 2023), Japan (Jacobs et al. 2003), Norway (Roux et al. 2014), South Korea (Lee et al. 2017), Spain (Luque et al. 2000), Sweden (Roux et al. 2014).

Known hosts – *Abies balsamea* (Ginns 1986), *Carpinus betulus* (this study), *Clusia melchiorii* (Barbosa et al. 2009), *Eucalyptus urophylla* (Barreto et al. 2022), *Juglans regia* (Sohrabi & Mohammadi 2023), *Populus trichocarpa* and *P. tremuloides* (Grünig et al. 2002), *Quercus suber* (Luque et al. 2000), *Quercus variabilis* (Lee et al. 2017), *Syzygium jambos* (Camino-Vilaro et al. 2019), *Tilia* sp. (Kendrick 1961).

Notes – The phylogenetic analysis of ITS and LSU sequence data revealed that our strain (FUM 20-015) clustered with *Parasporendocladia bactrospora* strains (CBS 299.62 and IRNMSX3) with 96% ML and 0.95 BYPP bootstrap support (Fig. 62). Our collection resembles *P. bactrospora* in having macronematous, mononematous, solitary conidiophores, phialidic conidiogenous cells, and deep, cylindrical collarette, catenate, bacilliform, hyaline, smooth,

aseptate conidia (Kendrick 1961, Wingfield et al. 1987). Based on morphology and multi-gene phylogeny we conclude our collection is *P. bactrospora*. This study reports a new host record of *P. bactrospora* on *Carpinus betulus* in Iran.

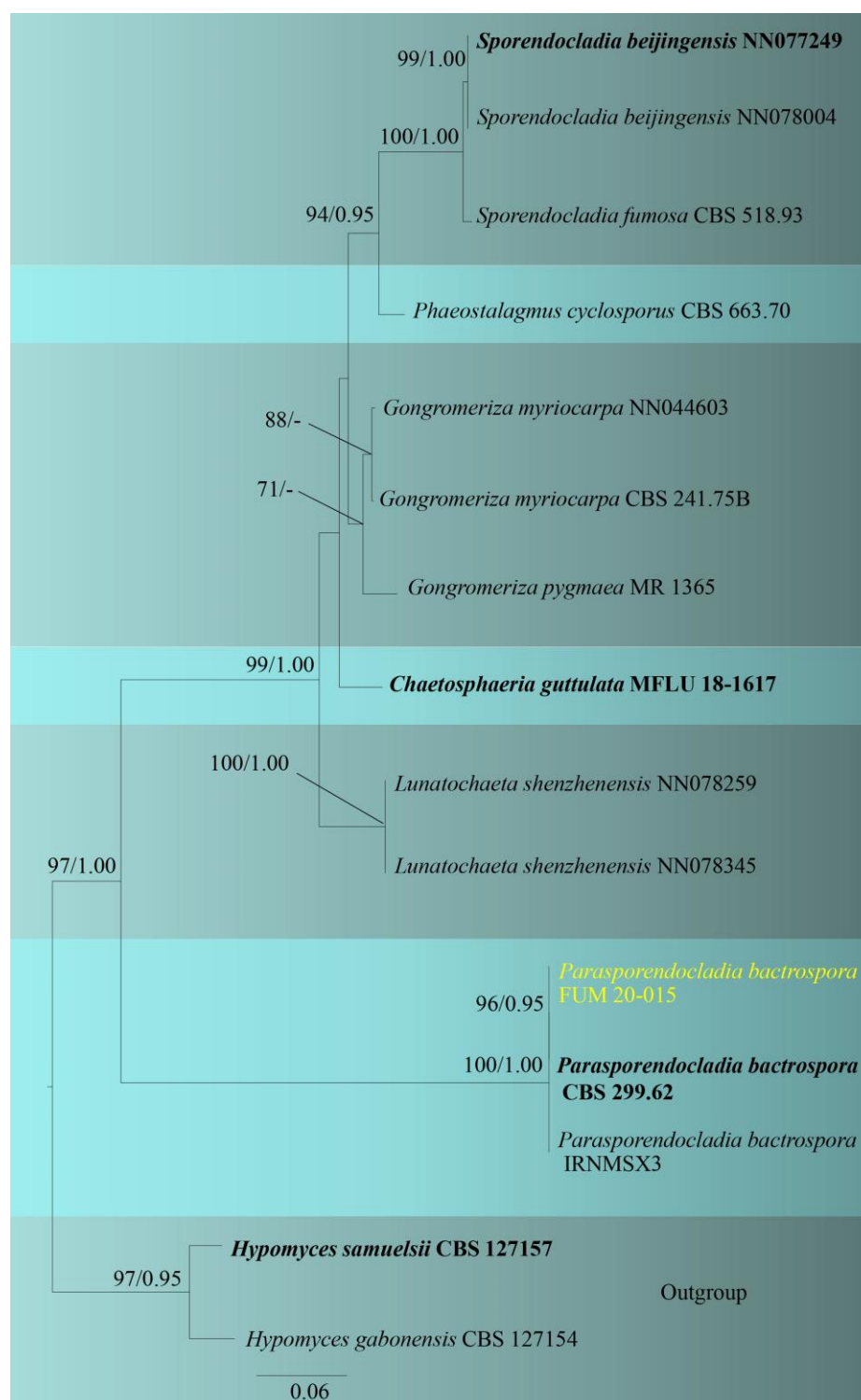


Figure 62 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of *Microascales*. Fifteen strains are included in the combined analyses. Maximum likelihood bootstrap support values greater than or equal to 70% and Bayesian posterior probabilities greater than or equal to 0.95 are given near nodes. The best-scoring RAXML tree with a final likelihood value of -4904.120808 is presented. Estimated base frequencies were as follows: A = 0.235851, C = 0.271895, G = 0.294902, T = 0.197352; substitution rates AC = 1.783255, AG = 1.816030, AT = 1.632304, CG = 0.797477, CT = 6.742133, GT = 1.000000; gamma distribution

shape parameter $\alpha = 0.282300$. The tree was rooted with *Hypomyces samuelsii* (CBS 127157) and *Hypomyces gabonensis* (CBS 127154). The newly generated sequence is indicated in yellow. All the type specimens are in bold.

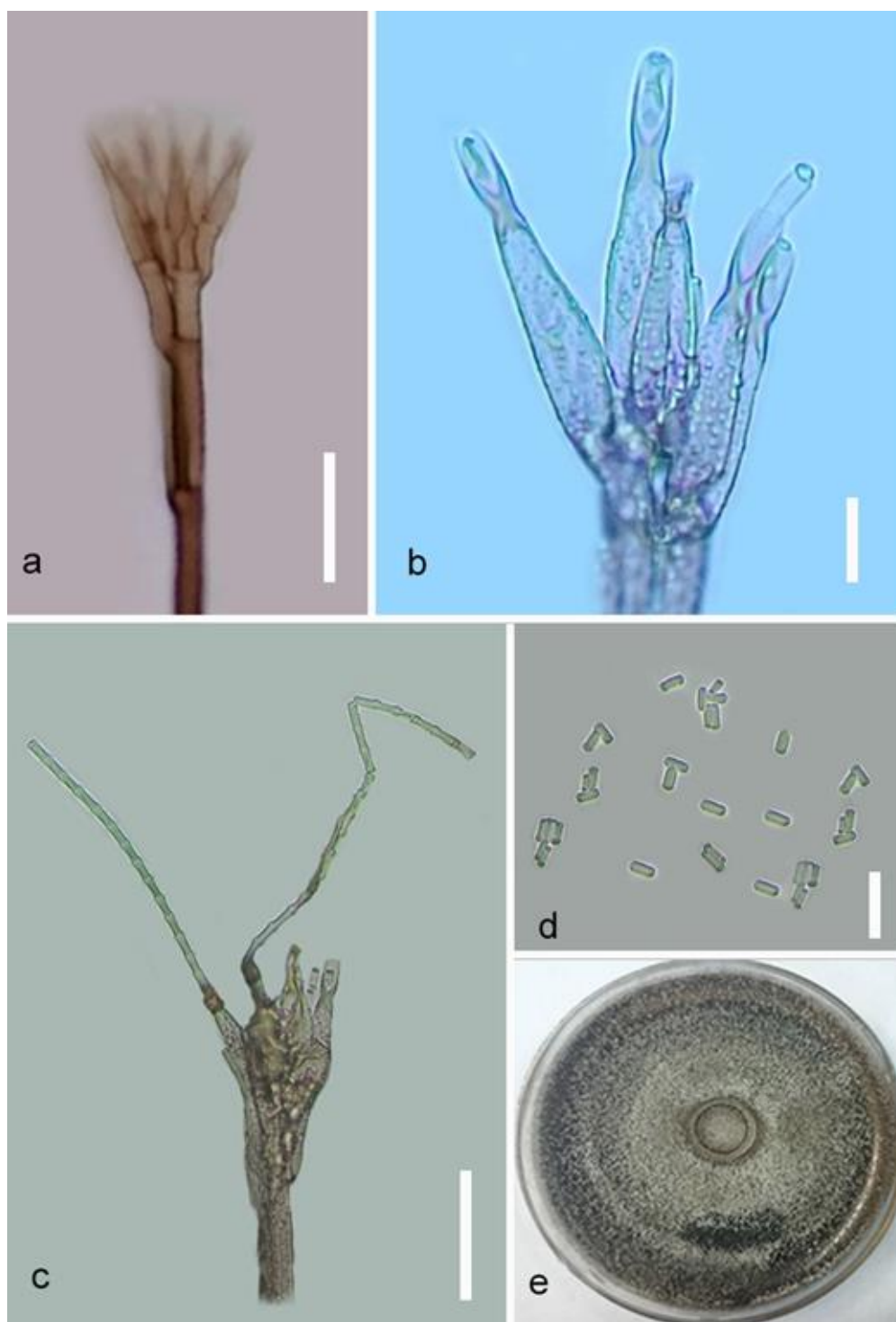


Figure 63 – Asexual morph of *Parasporendocladia bactrospora* (FUM 20-015, a new host record). a Conidiophore. b Conidiogenous cells in Lactophenol cotton blue (LPCB). d Conidial chains and conidia e Colony on PDA (upper view). Scale bars: a = 20 μm , b, d = 5 μm , e = 10 μm .

Phomatosporales Senan., Maharachch. & K.D. Hyde, Mycosphere 7 (5): 631 (2016)

Phomatosporaceae Senan. & K.D. Hyde, Mycosphere 7 (5): 633 (2016)

Phomatospora Sacc., Grevillea 4 (29): 22 (1875)

Index Fungorum number: IF4015; Facesoffungi number: FoF024488

Phomatospora was introduced to accommodate *P. berkeleyi* (= *Sphaeria phomatospora*) (Fournier & Lechat 2010). *Phomatospora* species have been reported as endophytes or saprobes in aquatic, terrestrial and marine habitats (Senanayake et al. 2016, Phukhamsakda et al. 2020). The sexual morph of the genus is characterized by immersed, globose or subglobose ascomata, small pseudoparenchymatous-celled peridium with cells of *textura angularis* to *textura prismatica*, unitunicate, cylindrical or oblong-fusiform, short pedicellate asci with J- apical ring, and ellipsoidal to fusiform, hyaline, aseptate to multi-septate ascospores with a rounded bipolar gelatinous cap. The asexual morphs are sporothrix-like and reported from culture (Fallah & Shearer 1998, Fournier & Lechat 2010). *Phomatospora* comprises 121 epithets in Index Fungorum (2024).

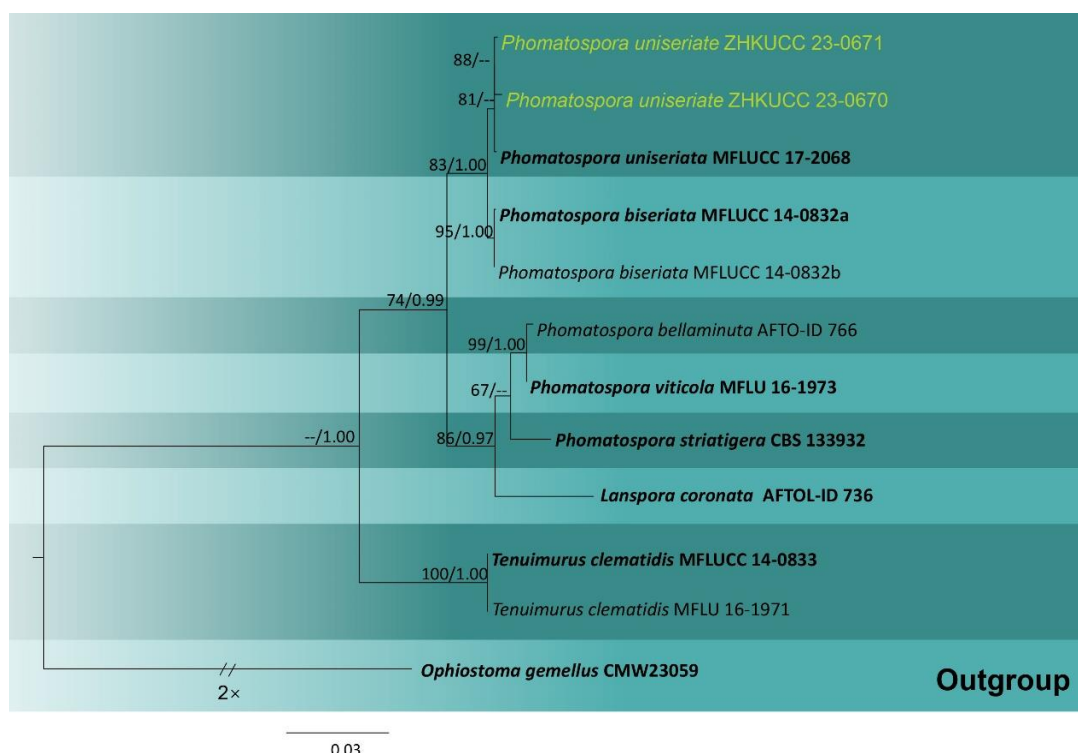


Figure 64 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU and SSU sequence data. Twelve strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -5202.333152 is presented. The evolutionary model GTR+I+G is applied for all the genes. The matrix had 236 distinct alignment patterns, with 25.15% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.253779, C = 0.237853, G = 0.293100, T = 0.215269; substitution rates AC = 2.741547, AG = 3.406331, AT = 1.541980, CG = 2.280569, CT = 9.129893, GT = 1.000000; gamma distribution shape parameter α = 0.191795. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Ophiostoma gemellus* (CMW23059). All type strains are in bold. The newly generated sequences are indicated in yellow.

Phomatospora uniseriata Phukhams., M.V. de Bult & K.D. Hyde, Fungal Diversity 102: 167 (2020) Fig. 65

Index Fungorum number: IF557302; Facesoffungi number: FoF06577

Saprobic on dead twigs of *Coffea* sp. Sexual morph: Ascomata 140–200×160–200 μ m ($\bar{x}$ = 162 × 180 μ m, n = 10), solitary to aggregated, immersed, becoming erumpent with age, globose to subglobose, coriaceous, brown to dark brown, heavily pigmented at the apex, ostiolate. Ostioles 40–60 × 40–55 μ m ($\bar{x}$ = 46×43 μ m, n = 5), papillate, central or eccentric, broadly conical, filled with periphyses. Peridium 8–15 μ m wide ($\bar{x}$ = 12 μ m, n = 10), from outer towards inner layers

comprising brown to hyaline, 4–6 thin-walled cells of *textura prismatica* and *textura angularis*. *Hamathecium* comprises 4–10 μm ($\bar{x}$ = 6 μm , n = 20), sparse, hypha-like, thin-walled, septate paraphyses, constricted at septa, tapering at the apex, shorter than asci. Asci 70–150 $\times$ 3–5 μm ($\bar{x}$ = 96 $\times$ 4 μm , n = 20), 8-spored, unitunicate, cylindrical, thin-walled, sometimes with long stipes, with a refractive, normally with a J-, apical ring, occasionally with a J+, apical ring. Ascospores 6–8 $\times$ 2.5–3.5 μm ($\bar{x}$ = 7.2 $\times$ 3 μm , n = 30), overlapping, uniseriate, oblong or ellipsoidal, hyaline, aseptate, bi-guttulate at the maturity, guttules located at both ends, with longitudinally striate. Asexual morph: Not observed.

Material examined – China, Yunnan Province, Pu'er City, on dead twigs of *Coffea* sp. (*Rubiaceae*), 16 September 2021, Li Lu, Puer 3-1 (MFLU 23-0080), living culture ZHKUCC 23-0670 = ZHKUCC 23-0671.

Culture characters – Ascospores germinating on PDA within 12 hours. Colonies on PDA reaching 30 mm within 4 weeks at 25 °C. Culture from above, cream, margin undulate, flat, medium dense, and covered with spare white aerial mycelium; reverse white radiating outwardly.

GenBank numbers – ZHKUCC 23-0670: ITS: OR826585, LSU: OR836017, SSU: OR836023; ZHKUCC 23-0671: ITS: OR826586, LSU: OR836018, SSU: OR836024.

Known distribution (based on molecular data) – China (this study), Thailand (Phukhamsakda et al. 2020).

Known hosts (based on molecular data) – dead twigs of *Coffea* sp. (this study), dead stems of *Clematis subumbellata* (Phukhamsakda et al. 2020).

Notes – According to multi-gene phylogenetic analysis of ITS, LSU and SSU sequence data, our strains (ZHKUCC 23-0670, ZHKUCC 23-0671) nested with *Phomatospora uniseriata* (MFLUCC 17-2068, ex-type strain) with 85% ML bootstrap support (Fig. 64). The ITS of *Phomatospora uniseriata* (MFLUCC 17-2068) contains only 344 bp (ITS1: 1–13, 5.8S: 14–171, ITS2: 172–344). Our collection shares similar morphology with the holotype, *P. uniseriata* in having a peridium with the cells of *textura prismatica* mixed with *textura angularis*, and oblong-ellipsoidal, hyaline, aseptate ascospores (Phukhamsakda et al. 2020). *Phomatospora uniseriata* have been reported from dead stems of *Clematis subumbellata* in Thailand (Phukhamsakda et al. 2020). Based on morphology and phylogenetic evidence, we conclude our collection is *P. uniseriata*. This is the first record of *P. uniseriata* collected from *Coffea* sp., as well as in China.

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

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

Codinaea Maire, Publ. Inst. Bot. Barcelona 3(no. 4): 15 (1937)

Index Fungorum number: IF7720; Facesoffungi number: FoF06287

Codinaea represents one of the largest genera within *Chaetosphaeriaceae*. The genus was established by Maire (1937) and is typified by *C. aristata*. However, Gamundi et al. (1977) erroneously synonymized *Codinaea* under *Dictyochaeta*, due to a misidentification of *D. fuegiana*, the type species of *Dictyochaeta*. Nonetheless, a morphological reassessment of *D. fuegiana* conducted by Réblová et al. (2004), revealed the differentiation between *Codinaea* and *Dictyochaeta* as distinct genera within *Chaetosphaeriaceae*. Subsequent research further supported this reclassification (Xia et al. 2015, Lin et al. 2019, Réblová et al. 2020, 2021). Currently, a total of 79 epithets attributed to *Codinaea* are found in Index Fungorum (2024). This study identifies two novel collections affiliated with *Codinaea*, found on submerged wood in northern Thailand. These species are designated as *C. aseptata* and *C. fertilis*, based on morphology and phylogenetic evidence (Fig. 66).

Codinaea aseptata J.Y. Zhang and Y.Z. Lu, Journal of Fungi 8 (6, no. 643): 13 (2022) Fig. 67

Index Fungorum number: IF559697; Facesoffungi number: FoF11038

Saprobic on decaying wood in freshwater habitats. Sexual morph: Unknown. Asexual morph: Hyphomycetous. *Colony* on natural substrate superficial, effuse, glitter, hairy. *Mycelium* mostly immersed, composed of branched, septate, smooth, brown hyphae. *Setae* 216–368 $\times$ 5–6 μm ($\bar{x}$ =

312 × 5, n = 10), erect, dark brown to subhyaline, 8–10-septate, unbranched, smooth, rarely fertilizable. *Conidiophores* 37–87 × 3–5 µm ($\bar{x}$ = 72 × 3, n = 15), macronematous, mononematous, unbranched, single or 2–3 groups from the mycelial knots associated with the bases of setae, shorter than setae, straight or slightly flexuous, short, cylindrical, 3–5-septate, pale brown to subhyaline. *Conidiogenous cells* monophialidic, integrated, determinate, terminal, cylindrical to cylindrical-lageniform, subhyaline to hyaline towards the apex, with flared collarettes, funnel-shaped. *Conidia* 12–16 × 2–3 µm ($\bar{x}$ = 14 × 3, n = 30), acrogenous, solitary, aseptate, cylindrical or long fusiform, curved, with hair-like and 8–10 µm-long appendages at both ends, hyaline, smooth-walled, guttulate.



Figure 65 – *Phomatospora uniseriata* (MFLU 23-0080, a new host and a geographical record). a, b Appearance of ascomata on host surface. c A section through ascoma. d Peridium. e Paraphyses. f A geminated ascospore. g Colony on PDA from above and reverse. h–k Asci stained with Melzer's reagent (arrows indicate J+ apical ring bluing). l Ascus in water. m–o Ascospores. Scale bars: c = 50 µm, d, e, h–l = 20 µm, f = 10 µm, m–o = 5 µm.

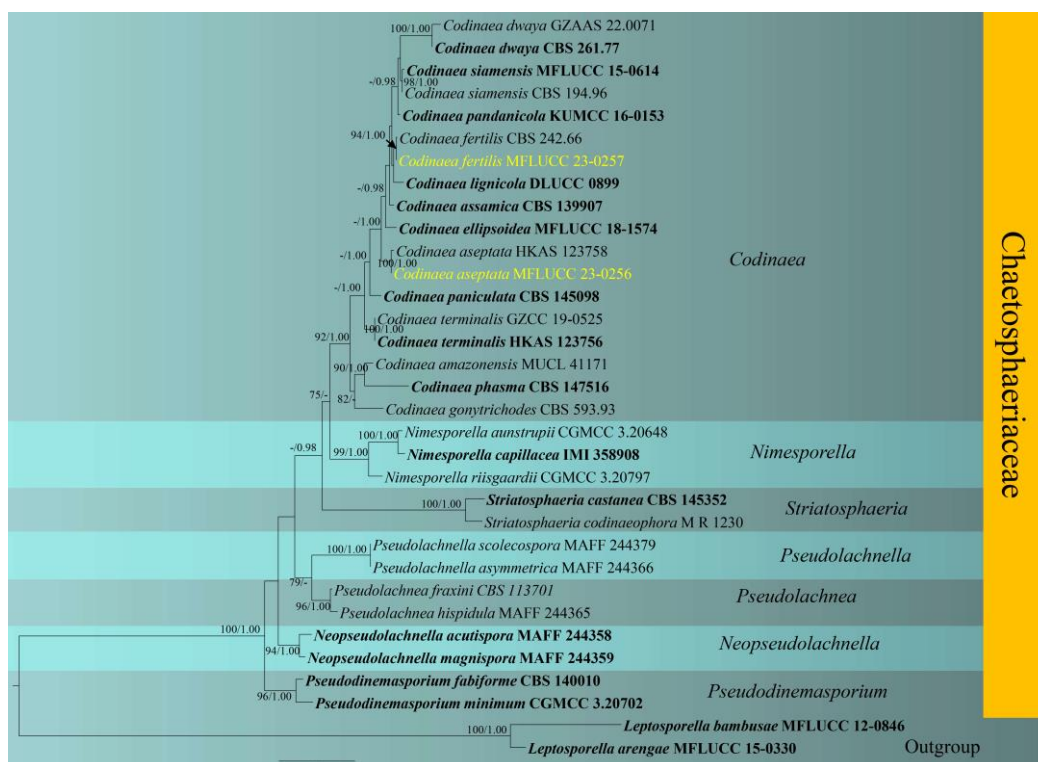


Figure 66 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and LSU sequence data of *Codinaea*. Thirty-three strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of - 6272.080083 is presented. Evolutionary model GTR+I+G is applied for all the genes. The matrix had 372 distinct alignment patterns, with 6.58% of undetermined characters or gaps. The estimated base frequencies were A = 0.218629, C = 0.279512, G = 0.305643, T = 0.196216; substitution rates AC = 2.856482, AG = 3.268000, AT = 2.499862, CG = 0.985437, CT = 11.826344, GT = 1.000000; gamma distribution shape parameter α = 0.181234. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Leptospora bambusae* MFLUCC 12-0846 and *Leptospora arengae* MFLUCC 15-0330. Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Material examined – Thailand, Chiang Rai Province, Nang Lae, Mueang, saprobic on decaying wood submerged in a freshwater stream, 18 July 2020, R. J. Xu, MD-89 (MFLU 23-0448), living culture, MFLUCC 23-0256.

GenBank numbers – MFLUCC 23-0256: ITS: OR826591, LSU: OR826596.

Known distribution (based on molecular data) – China (Zhang et al. 2022c), Thailand (this study).

Known hosts (based on molecular data) – submerged decaying wood (this study).

Notes – In the phylogenetic analysis, our strain (MFLUCC 23-0256) clustered with the ex-type strain of *C. aseptata* (GZCC 22-0081) with 100% ML and 1.00 BYPP bootstrap support (Fig. 66). *Codinaea aseptata* was introduced by Zhang et al. (2022b), which is isolated from submerged decaying wood in Hainan Province, China. Our collection largely overlaps by conidial size with the holotype (12–16 × 2–3 μ m vs. 13.4–16.2 × 2.1–3 μ m), except for slightly shorter conidiophores (37–87 × 3–5 μ m vs. 41.6–105.1 × 2–3.74 μ m) (Zhang et al. 2022c). Based on morphology and multi-gene phylogeny we identified our collection is *C. aseptata*, and this is a new record of *C. aseptata* in Thailand.

Codinaea fertilis S. Hughes & W.B. Kendr., N.Z. J. Bot. 6: 347 (1968)

Index Fungorum number: IF328555; Facesoffungi number: FoF15310

Fig. 68

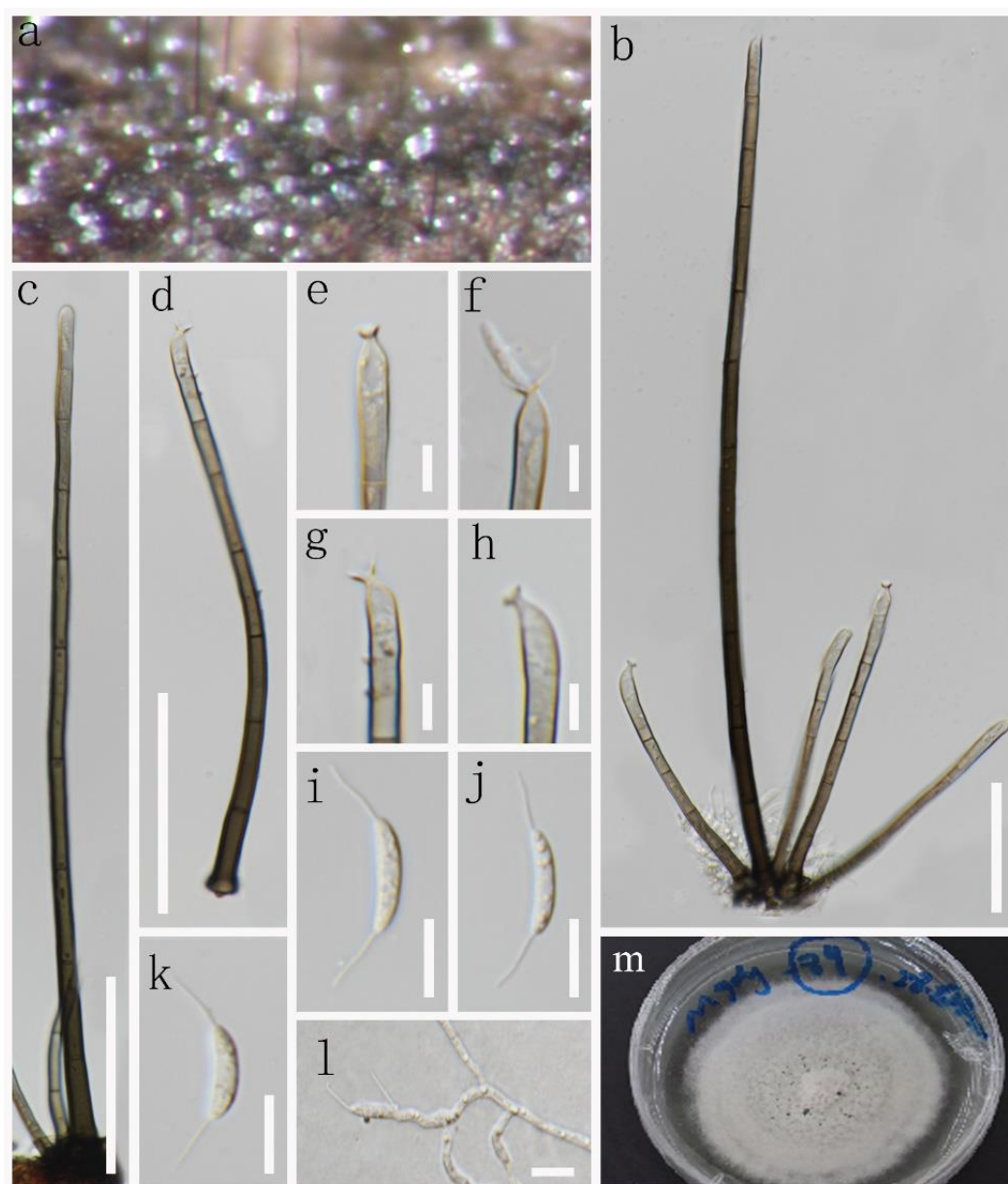


Figure 67 – *Codinaea aseptata* (MFLU 23-0448, a new geographical record). a Colonies on nature substrate. b–d Conidiophores with setae and conidiogenous cells. e–h Conidiogenous cells with developmental conidia. i–k Conidia. l A germinated conidium. m Colony on PDA (upper view). Scale bars: b–d = 50 μ m, e–h = 20 μ m, i–l = 10 μ m.

Saprobic on a decaying wood in freshwater habitats. Sexual morph: Unknown. Asexual morph: Hyphomycetous. *Colony* on natural substrate superficial, effuse, glitter, hairy, dark brown. *Mycelium* mostly immersed, composed of branched, septate, smooth, brown hyphae. *Setae* 198–275 $\times$ 5–7 μ m ($\bar{x}$ = 252 $\times$ 6, n = 10), arise solitary or in group of 2–3 from dark brown stromatic cells, erect, dark brown to subhyaline, septate, unbranched, smooth, fertilizable, with a terminal phialidic opening. *Conidiophores* 77–138 $\times$ 3–5 μ m ($\bar{x}$ = 101 $\times$ 4, n = 20), macronematous, mononematous, unbranched, single or 2–3 groups from the mycelial knots associated with the bases of setae, shorter than setae, straight or slightly flexuous, short, cylindrical, 3–5-septate, pale brown to subhyaline. *Conidiogenous cells* monophialidic, integrated, determinate, terminal, subcylindrical, lageniform, pale brown, subhyaline at the apex. *Conidia* 8–14 $\times$ 3–5 μ m ($\bar{x}$ = 11 $\times$ 4, n = 30), acrogenous, solitary, aseptate, falcate to ellipsoidal-fusiform, curved, with hair-like and 4–9 μ m-long appendages at both ends, hyaline, smooth-walled, sometimes with a large oil droplet in the central cell.

Material examined – Thailand, Chiang Rai Province, Nang Lae, Mueang, saprobic on decaying wood submerged in a freshwater stream, 14 August 2020, R. J. Xu, MD-103 (MFLU 23-0449), living culture, MFLUCC 23-0257.

GenBank numbers – MFLUCC 23-0257: ITS: OR826592, LSU: OR826597.

Known distribution (based on molecular data) – Africa, Australasia, Europe, South and North America, and Southeast Asia, Brazil, Brunei, Canada, Czech Republic, China, Ivory Coast, Malaysia, New Zealand, The Netherlands, Philippines, Slovak Republic, USA and Thailand (Réblová et al. 2021, this study).

Known hosts (based on molecular data) – on decaying leaves, petioles, palm fronds, bark, wood, woody fruits and roots of *Alchornea cordifolia*, *Calathea stromata*, *Carya ovata*, *Cedrela odorata*, *Ctenanthe oppenheimiana*, *Euterpe oleracea*, *Fraxinus excelsior*, *Freycinetia* sp., *Maranta bicolor*, *Nothofagus menziesii*, *Pandanus tectorius*, *Pandanus* sp., *Quercus ilex*, *Q. robur*, *Quercus* sp., *Rhopalostylis sapida*, and *Stromanthe sanguinea* (Réblová et al. 2021).



Figure 68 – *Codinaea fertilis* (MFLU 23-0449, a new geographical record). a, b Colonies on nature substrate. c–f Conidiophores with setae. g–j Conidiogenous cells with developmental conidia. k–n Conidia. o Germinated conidium. p Culture from PDA. Scale bars: c–f = 50 μ m, g–j = 10 μ m, k–o = 5 μ m.

Notes – In the phylogenetic analysis, our strain (MFLUCC 23-0257) clustered with *C. fertilis* (CBS 242.66) with 100% ML and 1.00 BYPP bootstrap support (Fig. 66). *Codinaea fertilis* was isolated from dead leaves of *Phopalostylidis sapidae* in New Zealand by Hughes & Kendrick

(1968). Our collection share similar characteristics with *C. fertilis* by having macronematous, straight or slightly flexuous, septate conidiophores, integrated, terminal, subcylindrical conidiogenous cells, and conidia that are falcate to ellipsoidal-fusiform, with hair-like appendages at each end. Based on morphology and multi-gene phylogeny we identified our collection as *C. fertilis*. This is a new record of *C. fertilis* in Thailand.

Xylariomycetidae O.E. Erikss. & Winka, Myconet 1(1), 12 (1997).

Amphisphaeriales D. Hawksw. & O.E. Erikss., Syst. Ascom. 5(1): 177 (1986)

Amphisphaeriaceae G. Winter, Rabenh. Krypt.-Fl., Edn 2 (Leipzig) 1.2: 259 (1885)

Amphisphaeria Ces. & De Not., Comm. Soc. crittog. Ital. 1(fasc. 4): 223 (1863)

Index Fungorum number: IF173; Facesoffungi number: FoF02099

Amphisphaeria was introduced by Cesati & De Notaris (1863) and Winter (1885) accommodated it as the type genus of *Amphisphaeriaceae*. The genus consists of 90 species (Wijayawardene et al. 2022, Wang et al. 2023, Zhang et al. 2023c). *Amphisphaeria* species are known as saprobes and endophytes on woody materials in marine, mangrove, and terrestrial habitats distributed from Asia, Australia, Europe and North America (Dissanayake et al. 2020b, Samarakoon et al. 2020, Wang et al. 2023). The sexual morph of *Amphisphaeria* is characterized by immersed clypeate ascomata and, cylindrical J⁻ asci, and 1-septate, ellipsoid brown ascospores. The coelomycetous asexual morph is characterized by solitary or aggregated, globose conidiomata, septate, branched, hyaline conidiophores, elongated, conical, septate, hyaline, annellidic conidiogenous cells and hyaline, elongate-fusiform, 1-celled, smooth-walled conidia. Often *Lepteutypa* is confused with *Amphisphaeria* with its similar morphological characteristics except for eutypoid stromata and multi-septate ascospores (Samarakoon et al. 2020). Based on phylogenetic analysis, morphological characteristics are of secondary importance compared to molecular studies and *Lepteutypa* is synonymized with *Amphisphaeria* (Samarakoon et al. 2020, Wang et al. 2023, Zhang et al. 2023c). In this study, we provide a new host and a country record of *Amphisphaeria uniseptata* from Thailand.

Amphisphaeria uniseptata (C.K.M. Tsui, K.D. Hyde & Hodgkiss) Samarak., Maharachch. & K.D. Hyde 2020 Fig. 70

≡ *Clypeosphaeria uniseptata* C.K.M. Tsui, K.D. Hyde & Hodgkiss

Index Fungorum number: IF836132; Facesoffungi number: FoF08763

Saprobic on a dead twig of *Nephelium lappaceum*. Sexual morph: *Ascomata* 150–200 × 400–430 µm ($\bar{x}$ = 185 × 418 µm, n = 5) except neck, lignicolous, solitary, coriaceous, flattened, ostiolate. *Ostioles* 65–90 × 40–65 µm, central canal with periphyses, composed of oil globules. *Peridium* 16–20 µm, comprising thin walled, brown cells of *textura angularis* and *textura prismatica*, slightly thick at the middle lateral end. *Hamathecium* comprises basal loosely connected cells with paraphysis, sparsely present aseptate, unbranched numerous oil globules. *Paraphyses* up to 5.5 µm wide, filamentous, sparsely present, longer than asci. *Asci* (80) 84–115 × 6.2–8.5 µm ($\bar{x}$ = 106 × 7.5 µm, n = 30), unitunicate, 8-spored, cylindrical, apically rounded, with J⁻ apical ring, short pedicellate. *Ascospores* 11–17 × 4.8–6.8 µm ($\bar{x}$ = 13.8 × 5.6 µm, n = 30), uniseriate, oblong, 1-septate, slightly constricted at the central septa, initially hyaline, becoming pale brown at the maturity, with symmetrical obtuse end, smooth walled. Asexual morph: Undetermined.

Material examined – Thailand, Chiang Mai Province, Mae Taeng, Pa Pae, 50150. 19°07'25.6"N 98°44'18.9"E, on decaying twigs of *Nephelium lappaceum*. 04 May 2023, Mekala Niranjana, 2348 (MFLU 24-0022), living culture (MFLUCC 23-0654).

Culture characteristics – Ascospores germinated on PDA within 24 h at 28 °C. Colony circular, opaque, two-dimensional growth spanning 30 mm diam after 2 weeks at 28 °C, central hyaline umbonate elevation, depressed and raised gray zone and becoming white cottony. Filamentous margin, rough surface, partly glistening due to chemical exudates near the colony origin and non-pigmentation. Background black to pale brown at center and hyaline margin.

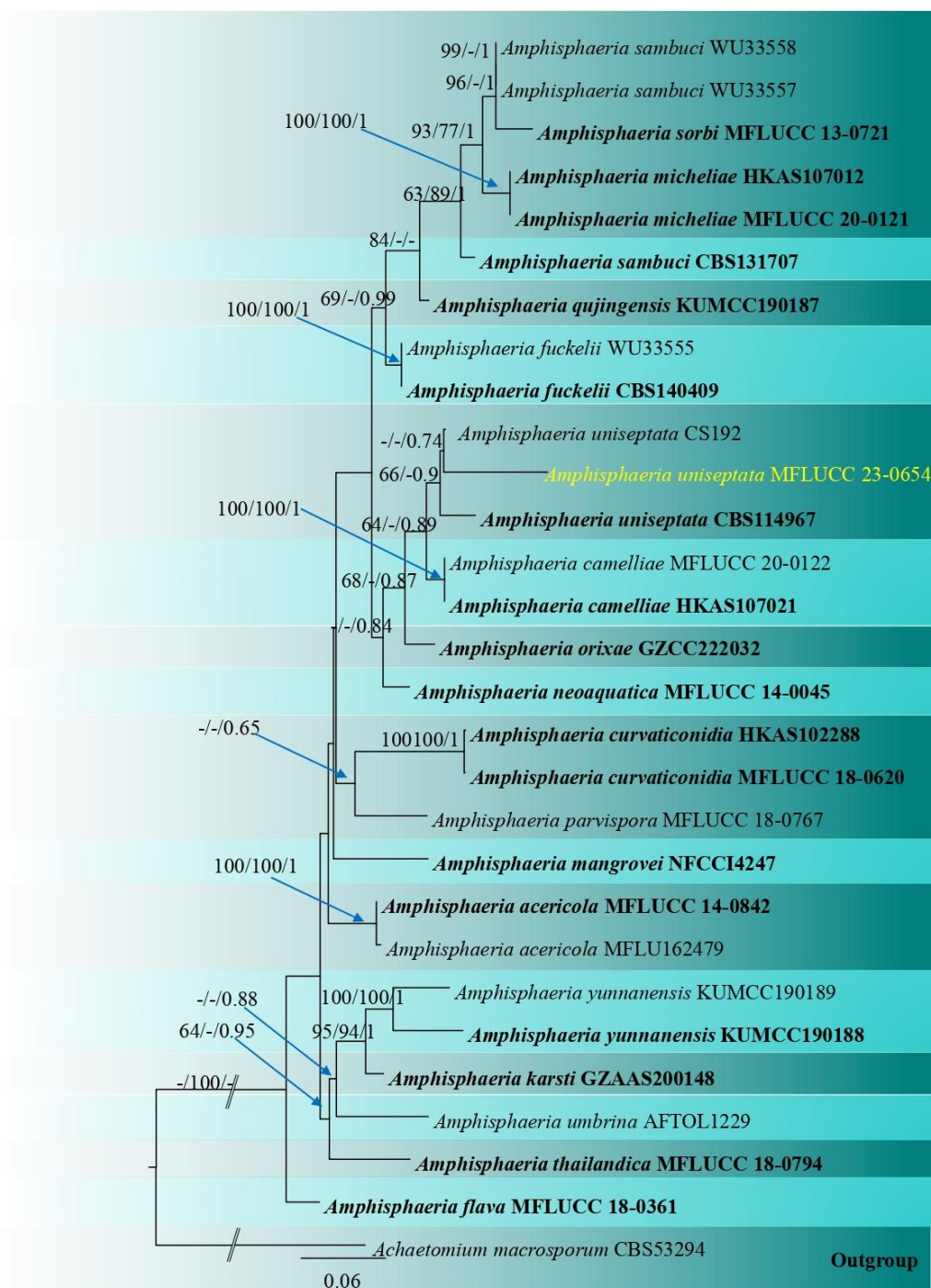


Figure 69 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU and *rpb2* sequence data of *Amphisphaeria*. Twenty-nine strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -11510.02 is presented. The evolutionary model GTR+I+G was applied to all the genes. The matrix had 884 distinct alignment patterns, with 26.14% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.255176, C = 0.228601, G = 0.267805, T = 0.248419; substitution rates AC = 0.801395, AG = 2.810360, AT = 1.018730, CG = 1.238822, CT = 5.488092, GT = 1.000000; gamma distribution shape parameter α = 0.627471. Bootstrap support values for ML, MP, and BI greater than 60% and 0.90 are given near nodes. In the multigene dataset, *A. uniseptata* (CS192) lack of *rpb2* sequence therefore it clades separately from type. The tree was rooted with

Achaetomium macrosporum (CBS 53294). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Known distribution (based on molecular data) – Hong Kong, China (Liu et al. 2019) and Thailand (this study).

Known hosts (based on molecular data) – Undermined wood (Liu et al. 2019) and *Nephelium lappaceum* (this study).

Notes – Based on the phylogenetic analyses of LSU, ITS and *rpb2* sequence data, our strain (MFLUCC 23-0654) grouped with *Amphisphaeria uniseptata* strains (CS 192 and CBS 114967) with 66% ML and 0.90 BYPP bootstrap support (Fig. 69). The three strains do not cluster together with strong support and according to the guidelines of Maharachchikumbura et al. (2021), may represent more than a single species. However, the morphology of our collection is similar to the holotype of *A. uniseptata* in terms of ascomata, peridium and paraphyses (Tsui et al. 2001). However, there are slight differences in asci size ($84\text{--}115 \times 6.2\text{--}8.5 \mu\text{m}$ vs. $120\text{--}160 \times 6\text{--}8 \mu\text{m}$) and ascospores size ($11\text{--}17 \times 4.8\text{--}6.8 \mu\text{m}$ vs. $14\text{--}19 \times 5\text{--}7 \mu\text{m}$). This might depend on different environmental conditions of freshwater and terrestrial habitats and the substrates. The holotype, *A. uniseptata* was found on submerged wood, in Hong Kong (China) as *Clypeosphaeria uniseptata* by Tsui et al. (2001), based on morphology. Later it was transferred to *Lepteutypa* based on the morphological similarity (Jaklitsch et al. 2016). Later, Samarakoon et al. (2020) provided a new combination for the species as *Amphisphaeria uniseptata*. Based on morphology and multigene phylogeny we conclude our collection as *A. uniseptata*. Therefore, this study presents a new host, geographical and habitat record of *A. uniseptata*.

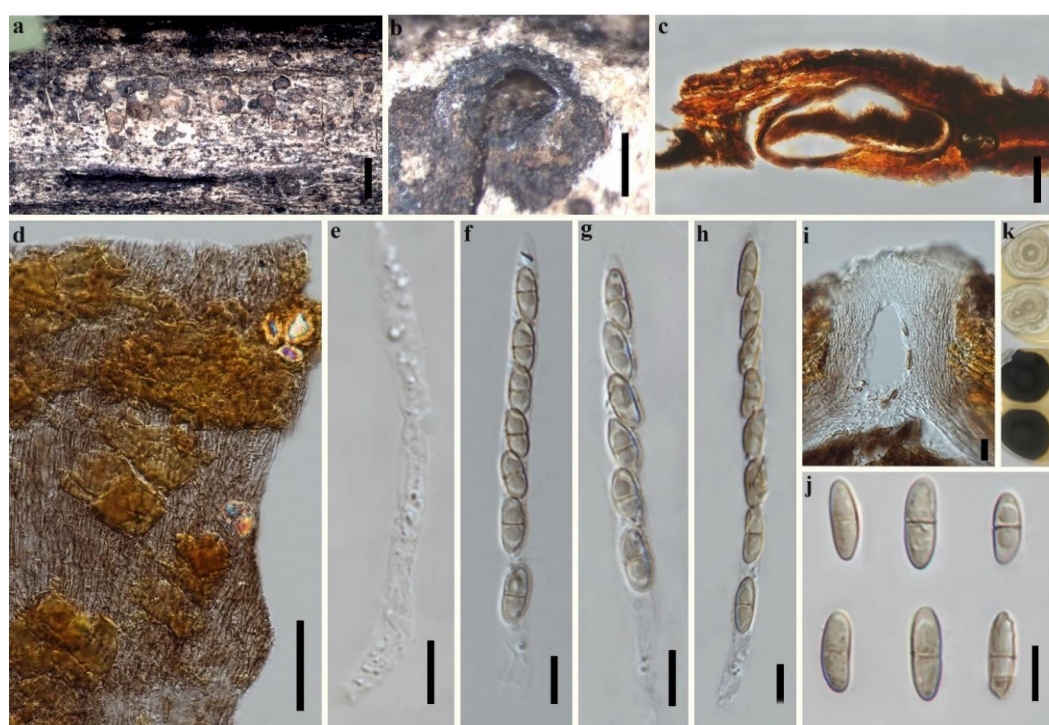


Figure 70 – *Amphisphaeria uniseptata* (MFLU 24-0022, a new host, geographical and habitat record). a, b Ascomata on host surface. c Vertical section of an ascoma. d Peridium. e Paraphysis. f–h Asci. i Ostiolar neck filled with paraphyses. j Ascospores. k Colonies on PDA; upper and reverse. Scale bars: a = 500 μm , b = 200 μm , c = 100, d = 50, f = 200 μm , e–j = 10 μm .

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr, in Hyde, Fröhlich & Taylor, Sydowia 50(1): 23 (1998).

Apiospora Sacc., Atti Soc. Veneto-Trent. Sci. Nat., Padova, Sér. 44: 85 (1875)

Index Fungorum number: IF264; Facesoffungi number: FoF06785

Apiospora was introduced by Saccardo (1875) with *A. montagnei* as the type species. *Apiospora* shares morphological similarities with *Arthrimum* and *Nigrospora*, however, its phylogenetic placement results in distinct clades (Pintos & Alvarado 2021). The sexual morph of the genus is characterized by immersed, dark brown to black, dome-shaped ascostromata, unitunicate, broadly clavate to cylindric-clavate asci, and hyaline ascospores surrounded by a thick gelatinous sheath (Pintos et al. 2019). *Apiospora* species have been reported as endophytes, pathogens on plants or opportunistic pathogens on humans, and saprobes (Phukhamsakda et al. 2022). They exhibit a wide host distribution with various host substrates in both aquatic and terrestrial environments (Crous & Groenewald 2013, Pintos & Alvarado 2021, Phukhamsakda et al. 2022). Currently, 139 species are listed in Index Fungorum (2024). Here, we provide an updated phylogeny for the *Apiospora* taxa (Fig. 71) and present new host records of *A. guizhouensis* and *A. phyllostachydis* on *Wurfbainia villosa* in China.

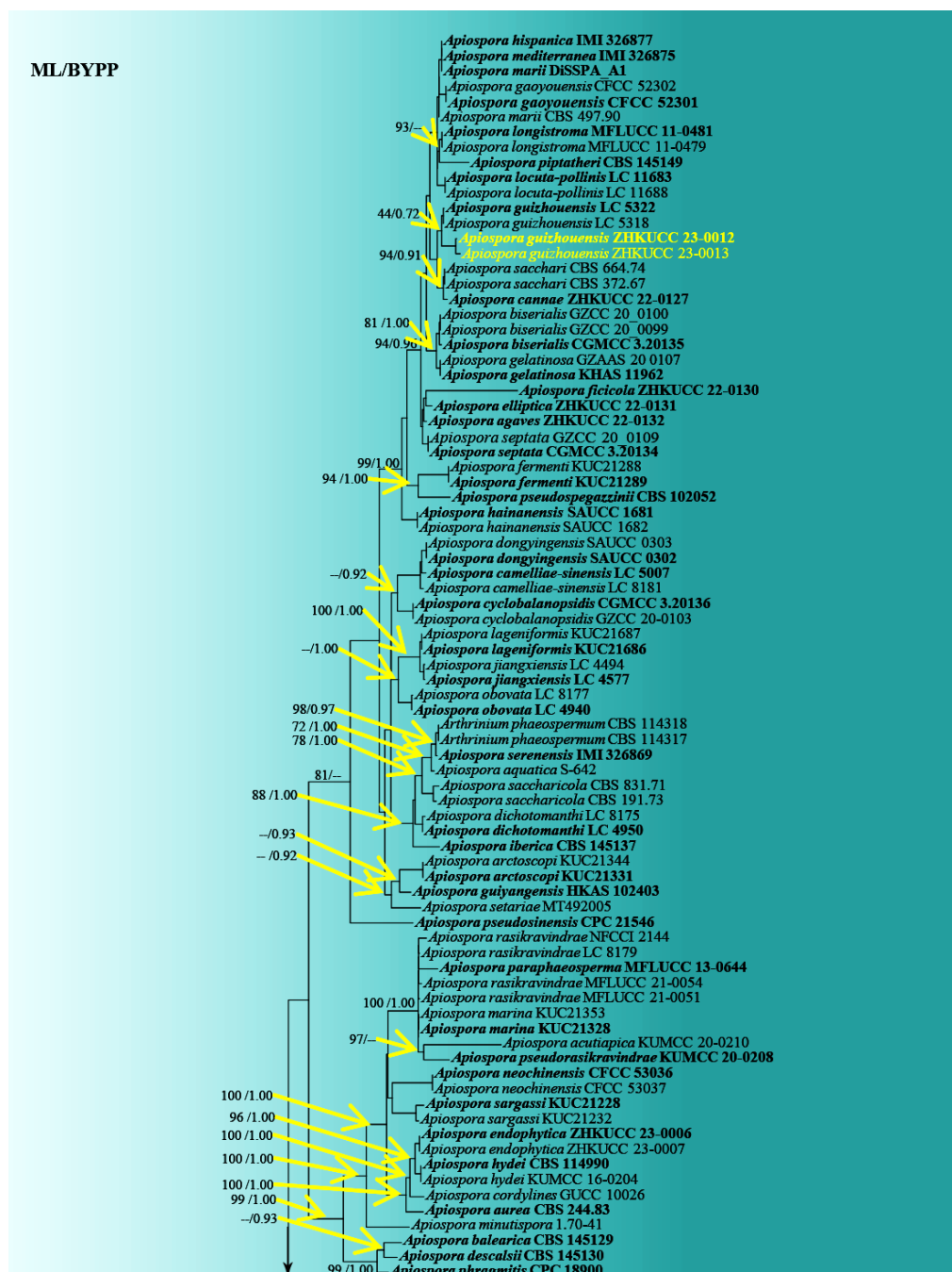


Figure 71 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, *tef1-α* and *tub2* sequence data of *Apiospora*. One hundred ninety-one strains are

included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -36321.892470 is presented. The evolutionary model GTR+I+G is applied for all loci. The matrix had 1805 distinct alignment patterns, with 38.08% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.208057, C = 0.296775, G = 0.242495, T = 0.252673; substitution rates AC = 1.090339, AG = 3.411914, AT = 1.286700, CG = 0.887072, CT = 4.062650, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.777262$. Bootstrap support values for ML greater than 75% and 0.90 BYPP, respectively. The tree was rooted with *Sporocadus trimorphus* strains (CFCC 55171) and (ROC 113). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

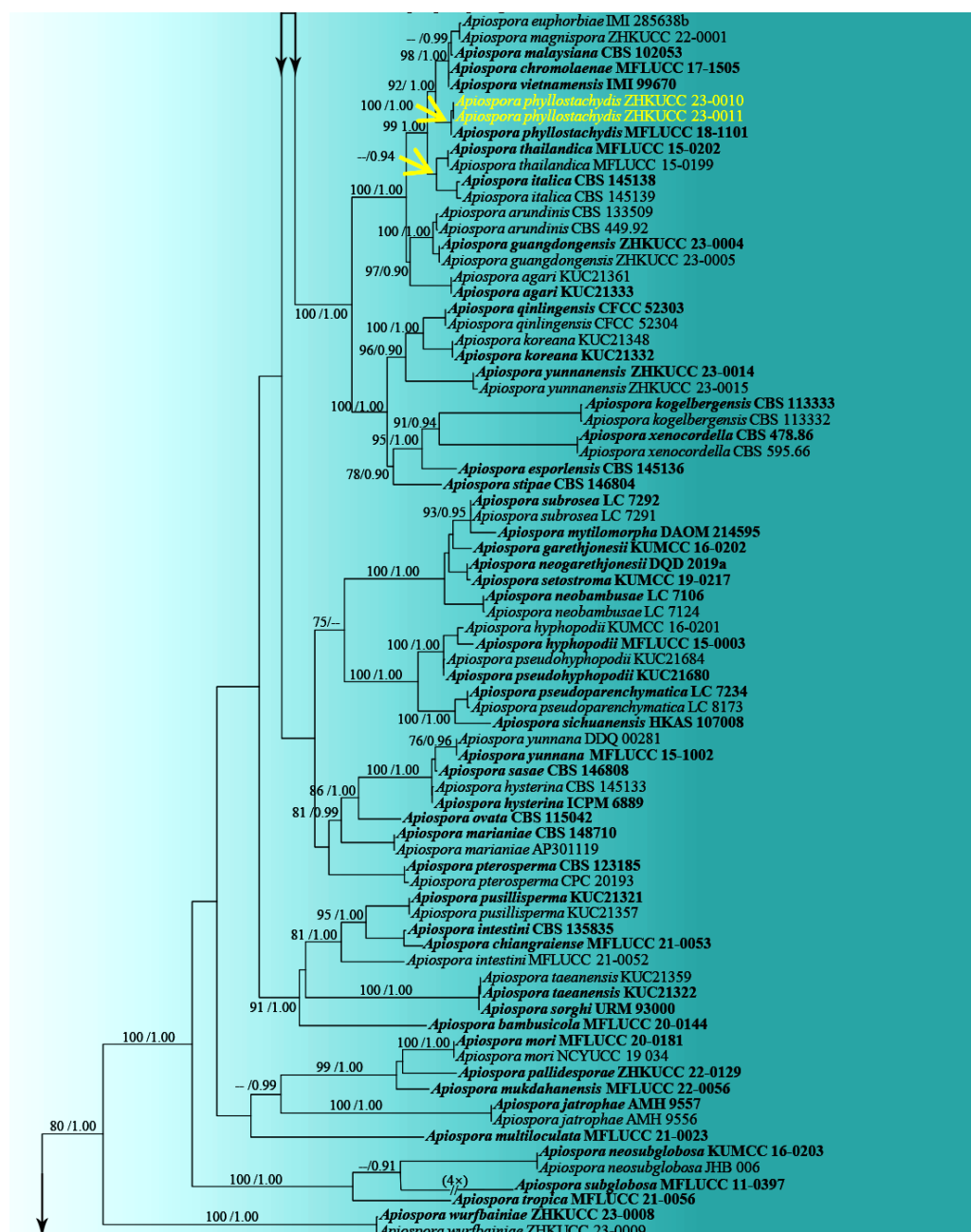


Figure 71 – Continued.

Apiospora guizhouensis (M. Wang & L. Cai) Pintos & P. Alvarado. Fungal Systematics and Evolution. 7: 205 (2021) Fig. 72

Index Fungorum number: IF837673; Facesoffungi number: FoF15219

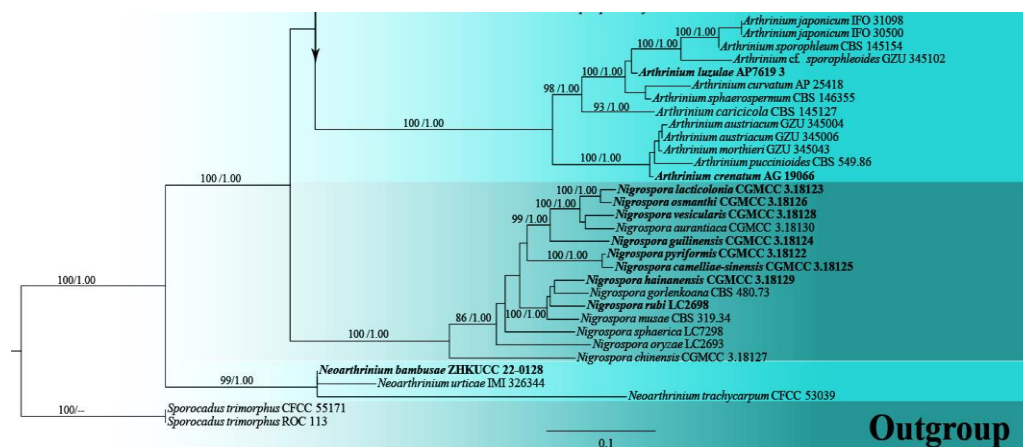


Figure 71 – Continued.

Endophytic from asymptomatic leaves of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Sporulated on PDA after one month, spore mass visible as black, scattered on white colonies. *Hyphae* 1–6 µm diam. ($\bar{x}$ = 3 µm, n = 30), branched, hyaline to pale brown, septate, with minute guttulate, smooth-walled. *Conidiophores* 16–166 × 2–6 µm ($\bar{x}$ = 89 × 4 µm, n = 20), hyaline to pale brown, erect, clavate, branched, septate, constricted at the septa, smooth-walled. *Conidiogenous cells* 3–13 × 2–6 µm ($\bar{x}$ = 6.5 × 4 µm, n = 15), hyaline, clavate, ovate or cylindrical, aggregated in clusters or solitary. *Conidia* in the face view 6–10 × 5–8 µm ($\bar{x}$ = 7 × 6 µm, n = 30), in the side view 5–8 × 3–6 µm ($\bar{x}$ = 6 × 4 µm, n = 30), initially hyaline, becoming pale brown to dark brown at the maturity, globose, subglobose to oval in the face view, lenticular with equatorial germ-slit in the side view, with smaller guttules, smooth-walled. *Sterile cells* 10–40 × 2–20 µm ($\bar{x}$ = 21 × 10.5 µm, n = 15), dark brown, straight or curved, cylindrical.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District, on living leaves of *Wurfbainia villosa* (*Zingiberaceae*), 1 October 2021, Chunfang Liao, AML30E-1 (MHZU 23-0009, dried culture), living culture ZHKUCC 23-0012; *ibid.*, living culture ZHKUCC 23-0013.

GenBank numbers – ZHKUCC 23-0012, ITS: OQ588002, LSU: OQ587990, *tub2*: OQ586068, *tef1-α*: OQ586081; ZHKUCC 23-0013, ITS: OQ588003, LSU: OQ587991, *tub2*: OQ586069, *tef1-α*: OQ586082.

Known distribution (based on molecular data) – China (Wang et al. 2018, this study).

Known hosts (based on molecular data) – air in karst cave (Wang et al. 2018), *Wurfbainia villosa* (this study).

Notes – In the phylogenetic analyses, our strains (ZHKUCC 23-0011, ZHKUCC 23-0012) clustered with *Apiospora guizhouensis* (LC5322; ex-type, LC5318) (Fig. 71). The base pair comparison of ITS and *tef1-α* sequence data between our strains and *A. guizhouensis* (LC 5322; ex-type) revealed a base pair difference of 1.38% (8/577 bp) and 0.99% (4/404 bp), respectively. No differences were observed in LSU and *tub2* sequence data. Our collection has larger conidiogenous cells than those of *A. guizhouensis* (3–13 × 2–6 µm vs. 3.5–8 × 3–4.5 µm). Based on morphology and multi-gene phylogeny, we identified our collection as *A. guizhouensis*, and this is the first report of *A. guizhouensis* from *Wurfbainia villosa*.

Apiospora phyllostachydis (C.L. Yang, X.L. Xu & K.D. Hyde) Pintos & P. Alvarado. Fungal Systematics and Evolution. 7: 206 (2021) Fig. 73

Index Fungorum number: IF837729; Facesoffungi number: FoF81935

Endophytic from asymptomatic leaves of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Sporulated on PDA after two months, spore mass visible as black, scattered on

colonies. *Hyphae* 2–4 μm diam. ($\bar{x}$ = 3 μm , n = 30), branched, hyaline to pale brown, septate, smooth-walled. *Conidiophores* mostly reduce to conidiogenous cells. *Conidiogenous cells* 3–21 $\times$ 3–5 μm ($\bar{x}$ = 11 $\times$ 4 μm , n = 10), hyaline, oblong to obpyriform, aggregated in clusters. *Conidia* in the face view 5–9 $\times$ 4–8 μm ($\bar{x}$ = 7 $\times$ 6 μm , n = 30), in the side view 5–7 $\times$ 4–5 μm ($\bar{x}$ = 6 $\times$ 4.5 μm , n = 30), initially hyaline, becoming pale brown to dark brown at maturity, guttulate, globose to subglobose in the face view, lenticular with pale equatorial slit in the side view, aseptate, smooth-walled. *Sterile cells* 8–20 $\times$ 2–6 μm ($\bar{x}$ = 12 $\times$ 5 μm , n = 15), brown to dark brown, pyriform to cylindrical, vase-shaped.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District, in living leaves of *Wurfbainia villosa* (*Zingiberaceae*), 1 October 2021, Chunfang Liao, AML12A-2 (MHZU 23-0010, dried culture), living culture ZHKUCC 23-0010; *ibid.*, living culture ZHKUCC 23-0011.

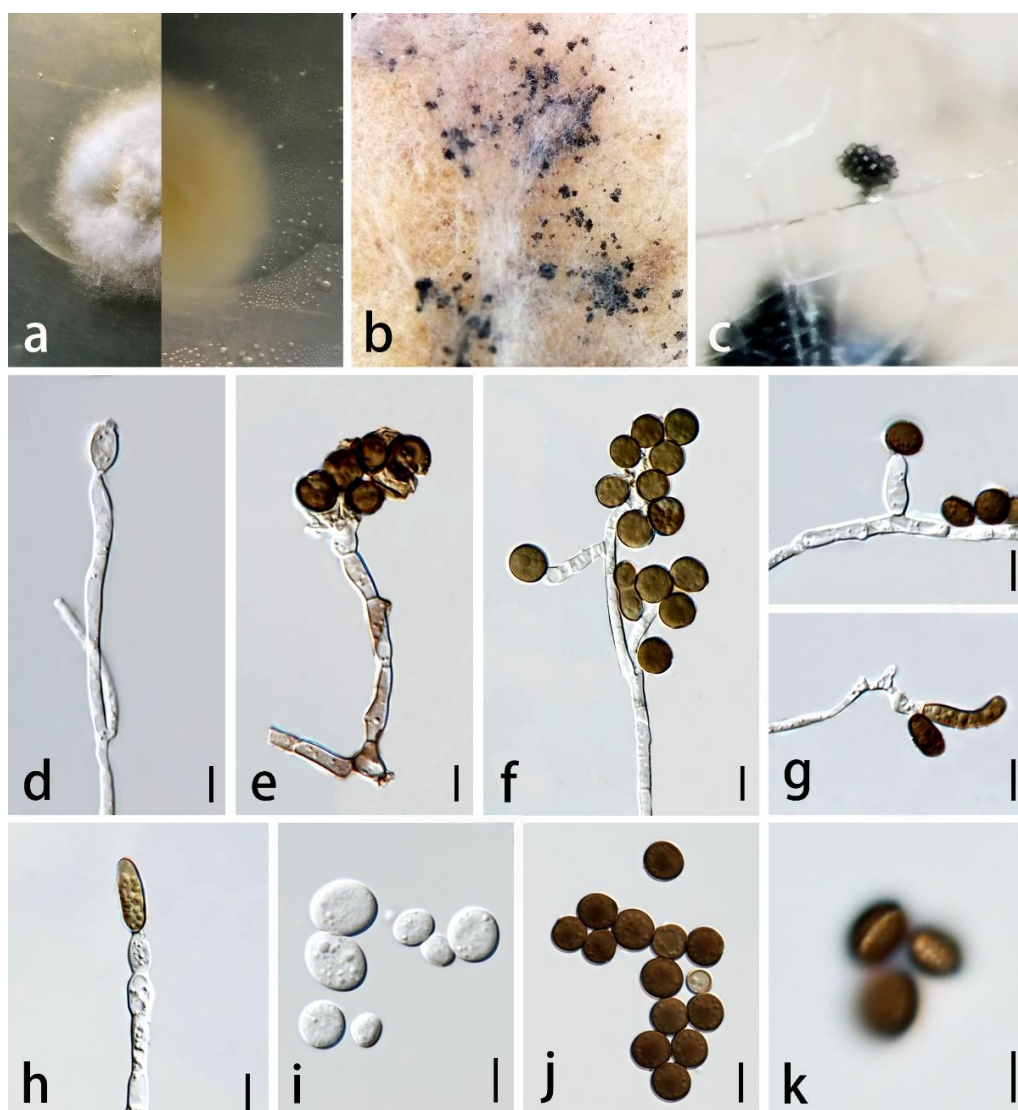


Figure 72 – *Apiospora guizhouensis* (MHZU 23-0009, a new host record). a Colony on PDA; (a) upper and (b) reverse views. b, c Conidia on aerial mycelia on PDA. d–h Conidiophores with conidiogenous cells. i, j Conidia. k Conidia with germ-slit. Scale bars: d–k = 10 μm .

GenBank numbers – ZHKUCC 23-0010, ITS: OQ588000, LSU: OQ587988, *tef1- α* : OQ586079, *tub2*: OQ586066; ZHKUCC 23-0011, ITS: OQ588001, LSU: OQ587989, *tef1- α* : OQ586080, *tub2*: OQ586067.

Known distribution (based on molecular data) – China (Yang et al. 2019, this study),

Known hosts (based on molecular data) – *Phyllostachys heteroclada* (Yang et al. 2019), *Wurfbainia villosa* (this study).

Notes – In the phylogenetic analysis, our strains (ZHKUCC 23-0010, ZHKUCC 23-0011) clustered with *A. phyllostachydis* strains (MFLUCC 18-1101; ex-type) with 100% ML and 1.00 BYPP bootstrap support (Fig. 71). The base pair comparison of ITS, LSU, *tef1-α*, and *tub2* sequence data between our strains and MFLUCC 18-1101 are identical. Our collection differs from *A. phyllostachydis* (MFLUCC 18-1101) in having shorter and wider conidiogenous cells ($3\text{--}21 \times 3\text{--}5\ \mu\text{m}$ vs. $20\text{--}55 \times 1.5\text{--}2.5\ \mu\text{m}$) (Yang et al. 2019). We conclude that our collection is *A. phyllostachydis* based on molecular evidence, despite the minor differences in conidia and conidiogenous cell size being negligible. This is the first report of *A. phyllostachydis* from *Wurfbainia villosa*.

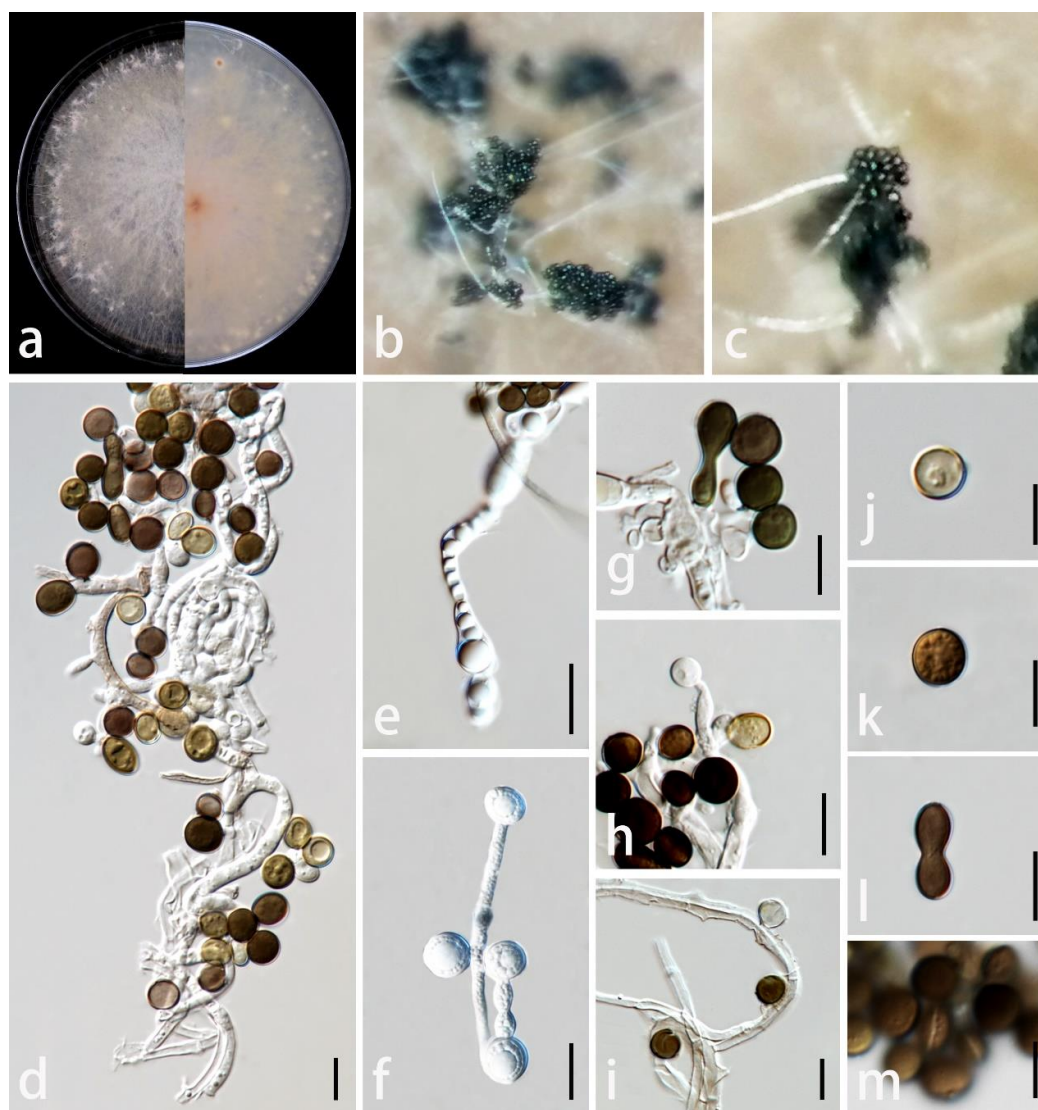


Figure 73 – *Apiospora phyllostachydis* (MHZU 23-0010, a new host record). a Colony on PDA; (a) upper and (b) reverse views. b, c Conidia on aerial mycelia on PDA. d, g–i Conidiophores with conidiogenous cells. e, f Chlamydoconidia. j, k Conidia. l Elongated conidium (sterile cell). m Conidia with germ-slit. Scale bars: d–m = 10 μm .

Nigrospora Zimm., Centbl. Bakt. ParasitKde, Abt. II 8: 220 (1902)

Index Fungorum number: IF9124; Facesoffungi number: FoF14273

Nigrospora was introduced by Zimmermann (1902) including *N. panici* as the type species. *Nigrospora* shares morphological similarities with *Apiospora* and *Arthrinium*, however, their

phylogenetic placement results in distinct clades (Wang et al. 2017). The asexual morph of the genus is characterized by branched, micronematous or semi-macronematous conidiophores, black, monoblastic conidiogenous cells, and shiny, aseptate conidia. Sexual morphs have perithecial ascomata, short-stalked asci with 2-seriate ascospores (Wang et al. 2017). *Nigrospora* species have a wide host distribution, are found as endophytes, and saprobes, and are commonly known as plant pathogens worldwide, which cause leaf spots, leaf blight and squirter disease in plants. Additionally, they cause onychomycosis, hay fever, and respiratory, and allergic diseases in humans (Wang et al. 2017, Raza et al. 2019, Chethana et al. 2023). Currently, 43 species are listed in Index Fungorum (2024). Here, we provide an updated phylogeny for *Nigrospora* (Fig. 74), and present a new host record of *N. macaranga* (Fig. 75) and *N. oryzae* (Fig. 76) on *Kaempferia elegans*, as well as a new geographical record of *N. sphaerica* (Fig. 77) on *Wurfbainia villosa* in China.

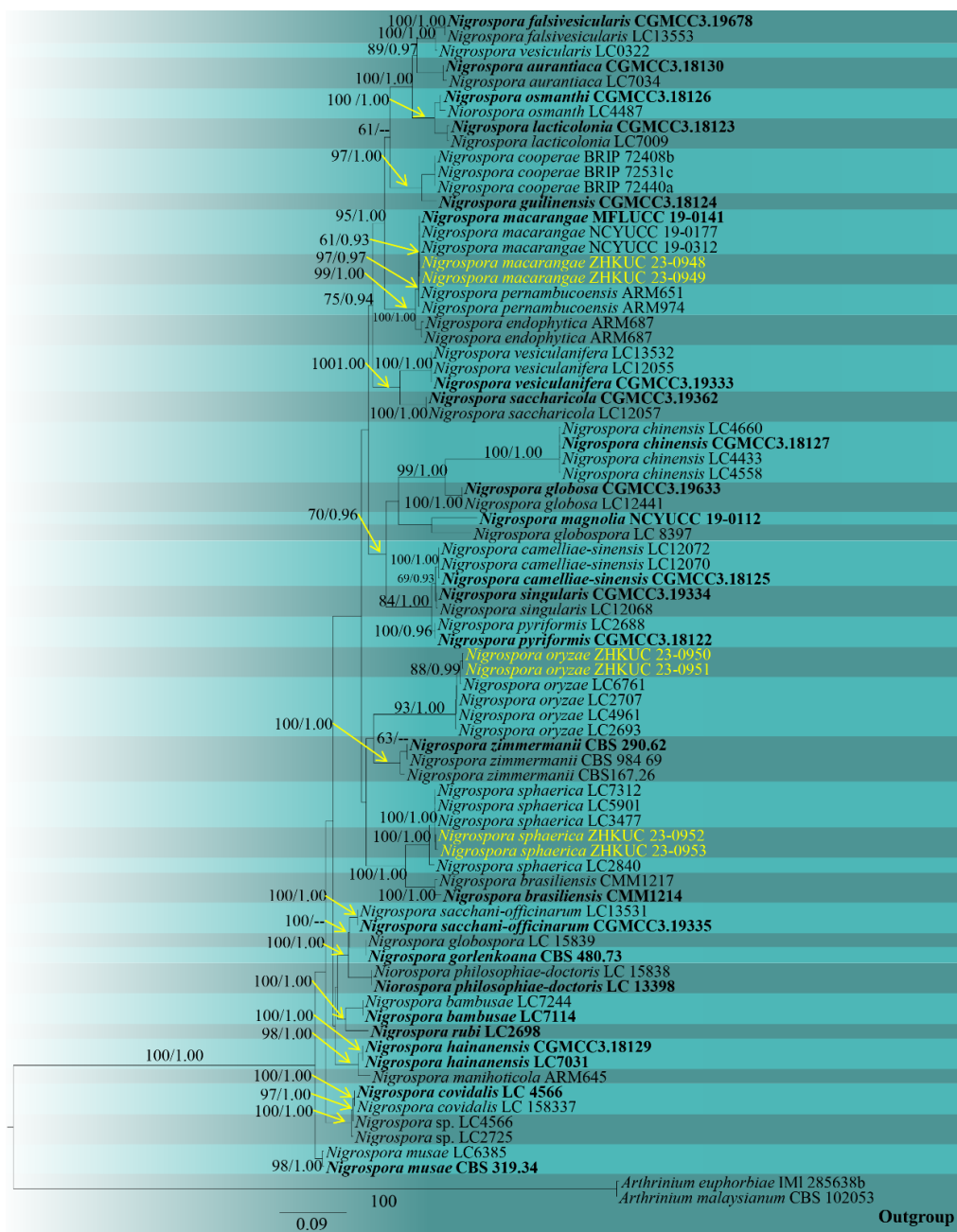


Figure 74 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, *tef1-α* and *tub2* sequence data of *Nigrospora*. Seventy-nine strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian

analysis. The best RAxML tree with a final likelihood value of -11260.567850 is presented. The evolutionary model GTR+I+G is applied for all loci. The matrix had 763 distinct alignment patterns, with 15.64% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.212768, C = 0.304366, G = 0.243583, T = 0.239283; substitution rates AC = 1.091302, AG = 3.196978, AT = 1.123868, CG = 0.994435, CT = 4.716342, GT = 1.000000; gamma distribution shape parameter α = 0.214460. Bootstrap support values for ML greater than 60% and 0.90 BYPP, respectively. The tree was rooted with *Arthrinium euphorbiae* (IMI 285638b) and *A. malaysianum* (CBS 102053). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Nigrospora macarangae Tennakoon, C.H. Kuo & K.D. Hyde (2020)

Fig. 75

Index Fungorum number: IF555454; Facesoffungi number: FoF09343

Endophytic from fresh leaves of *Kaempferia elegans*. Sexual morph: Undetermined. Asexual morph: *Hyphae* 2.5–4 μm wide ($\bar{x}$ = 3.3 μm , n = 30), smooth, hyaline to pale brown, septate, branched with thick walls. *Conidiophores* mostly reduced to conidiogenous cells. *Conidiogenous cells* 5–11 $\times$ 3–8 μm ($\bar{x}$ = 8 $\times$ 6 μm , n = 30), aggregated in clusters or single on hyphae, monoblastic, cylindrical or ampulliform, ellipsoidal or subglobose, straight or curved, smooth, hyaline to pale brown. *Conidia* 12–19 $\times$ 11–18 μm ($\bar{x}$ = 15.5 $\times$ 15 μm , n = 30), solitary, subglobose to globose, aseptate, initially hyaline, becoming pale brown to black at the maturity.

Material examined – China, Guangdong Province, Guangzhou City, South China Botanical Garden, in living leaves of *Kaempferia elegans* (*Zingiberaceae*), 16 June 2021, Chunfang Liao, SN03B (MHZU 23-0228), living culture ZHKUCC 23-0948; *ibid.*, living culture ZHKUCC 23-0949.

GenBank numbers – ZHKUCC 23-0948, ITS: OR984154, *tef1- α* : OR992766, *tub2*: OR992760; ZHKUCC 23-0949, ITS: OR984155, *tef1- α* : OR992767, *tub2*: OR992761.

Known distribution (based on molecular data) – China (Tennakoon et al. 2021, this study).

Known hosts (based on molecular data) – *Kaempferia elegans* (this study), *Macaranga tanarius* (Tennakoon et al. 2021).

Notes – According to the phylogenetic analysis, our strains (ZHKUCC 23-0948, ZHKUCC 23-0949) clustered with *N. macarangae* strains (MFLUCC 19-0141, NCYUCC 19-0177, NCYUCC 19-0312) with 61% ML and 0.93 BYPP bootstrap support (Fig. 74). The morphology of asexual morph of our collection shares similar characteristics to other *Nigrospora* species (e.g., *N. macarangae* and *N. pernambucoensis*) in having conidiophores mostly reduced to conidiogenous cells, and subglobose to globose, aseptate conidia. Also, our collection has smaller conidiogenous cells (5–11 $\times$ 3–8 μm vs. 5–22.5 μm $\times$ 5–12.5 μm) than *N. pernambucoensis* (de Queiroz Brito et al. 2023). However, our collection has narrower conidiogenous cells (3–8 μm) compared to those of *N. macarangae* (11–14 μm). The comparison of ITS sequence data from our isolates (ZHKUCC 23-0948 and ZHKUCC 23-0949) and the type sequences of *N. macarangae* reveals they are identical. However, the comparison with the *tef1- α* and *tub2* sequences is not possible due to their unavailability. The ITS, *tef1- α* and *tub2* sequences of our strains are similar to *N. pernambucoensis*.

Introducing this collection as a new species is questionable, because of its placement in the phylogenetic tree and the weak support for identification as a single species. This uncertainty of the phylogenetic placement may be because, only the ITS sequence is available for *N. macarangae*, whereas standard sequences are available for *N. pernambucoensis*. These collections share similar morphologies. However, Queiroz Brito et al. (2023) designated *N. pernambucoensis* as a novel species, while omitting *N. macarangae* in the phylogenetic analysis. Therefore, we speculate that the phylogeny of this clade is complex. Further studies are essential to validate the placement of this species. Based on the available information, including morphology and multi-gene phylogeny we conservatively identify our collection as *N. macarangae*. Therefore, the current study presents a tentative new host record of *N. macarangae* on *Kaempferia elegans* in China.

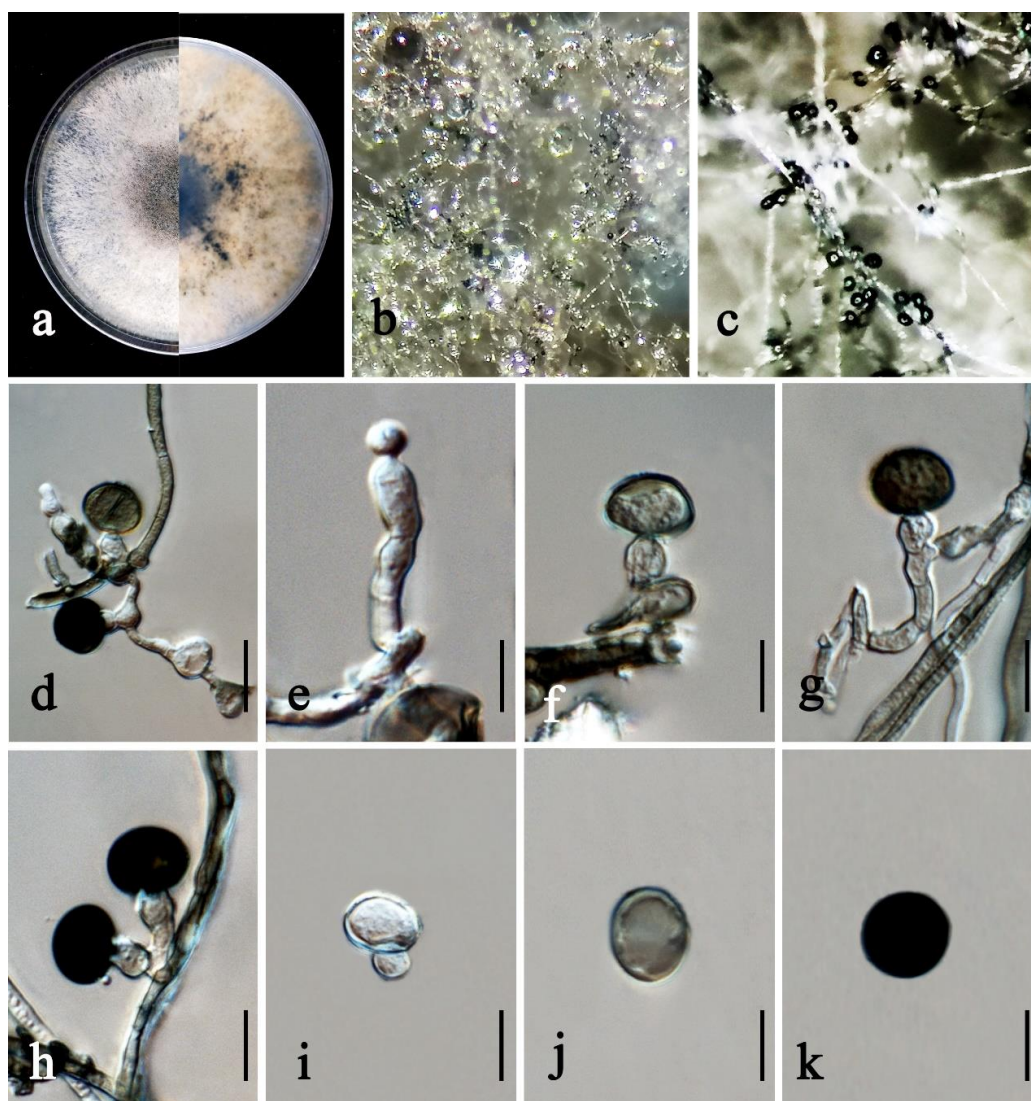


Figure 75 – *Nigrospora macarangae* (MHZU 23-0228, a new host record). a Colony on PDA; upper and reverse views. b, c Conidia on aerial mycelia on PDA. d–g Conidia with conidiogenous cells. h–k Conidia. Scale bars: d–k = 10 µm.

Nigrospora oryzae (Berk. & Broome) Petch, J. Indian Bot. Soc. 4:24 (1924)

Fig. 76

Index Fungorum number: IF253729; Facesoffungi number: FoF06596

Endophytic from healthy leaf of *Kaempferia elegans*. Sexual morph: Undetermined. Asexual morph: *Hyphae* 3–7 µm wide ($\bar{x}$ = 4 µm, n = 30), smooth, hyaline, branched, septate. *Conidiophores* mostly reduced to conidiogenous cells. *Conidiogenous cells* 5–13 × 5–9 µm ($\bar{x}$ = 8 × 6 µm, n = 30), aggregated in clusters on hyphae, monoblastic, ampulliform to ellipsoidal, straight or curved, smooth, hyaline. *Conidia* 3.5–9 × 9.5–13 µm ($\bar{x}$ = 7 × 10.5 µm, n = 30), solitary, subglobose to oblate, aseptate, pale brown to black.

Material examined – China, Guangdong Province, Guangzhou City, South China Botanical Garden, in living leaves of *Kaempferia elegans* (*Zingiberaceae*), 16 June 2021, Chunfang Liao, SNJ04A (MHZU 23-0229), living culture ZHKUCC 23-0950; *ibid.*, living culture ZHKUCC 23-0951.

GenBank numbers – ZHKUCC 23-0950, ITS: OR984156, *tef1-α*: OR992768, *tub2*: OR992762; ZHKUCC 23-0951, ITS: OR984157, *tef1-α*: OR992769, *tub2*: OR992763.

Known distribution (based on molecular data) – Canada (Zheng et al. 2012), China (Zhang et al. 2012a, Zhai et al. 2013, Wu et al. 2014, Li et al. 2018a, Hao et al. 2020, Han et al. 2021, Liu et al. 2021, this study), Sri Lanka (Berk & Broome 1873).

Known hosts (based on molecular data) – *Aloe vera* (Zhai et al. 2013), cotton (Zhang et al. 2012a), *Dendrobium candidum* (Wu et al. 2014), *Hibiscus mutabilis* (Han et al. 2021), *Kaempferia elegans* (this study), *Kentucky bluegrass* (Zheng et al. 2012), Kiwifruit (Li et al. 2018a), *Oryza sativa* (Berk & Broome 1873, Liu et al. 2021), *Scirpus* sp. (Hao et al. 2020).

Notes – According to the phylogenetic analysis, our strains (ZHKUCC 23-0950 and ZHKUCC 23-0951) clustered with *N. oryzae* strains (LC6761, LC2707, LC4961, and LC2693) with 88% ML and 0.99 BYPP bootstrap support (Fig. 74). The asexual morph characters of our fungal collections are similar to the holotype of *N. oryzae* isolated from dead leaf of rice (Berkeley & Broome 1873). However, our collection has smaller conidia ($3.5\text{--}9 \times 9.5\text{--}13\ \mu\text{m}$) compared to those of *N. oryzae* ($12.5\text{--}16$; mostly $12\text{--}14\ \mu\text{m}$). Based on morphology and multi-gene phylogeny we identified our collection as *N. oryzae*. The current study presents a new host record of *N. oryzae* on *Kaempferia elegans* in China.

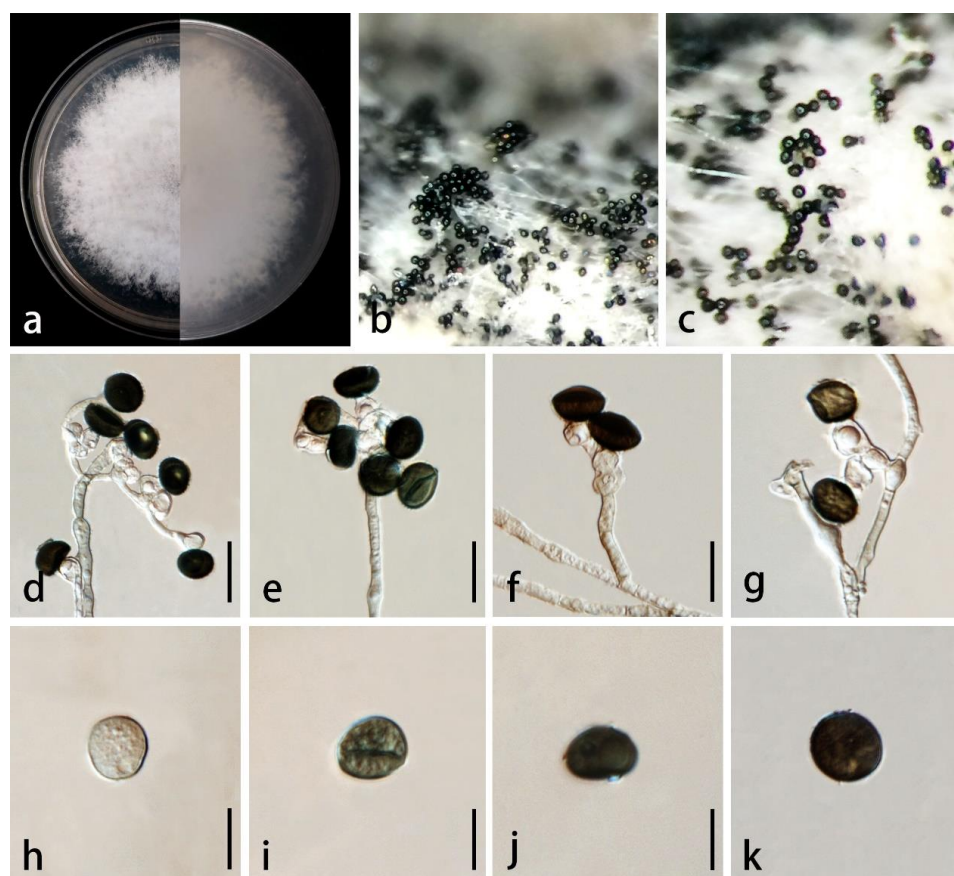


Figure 76 – *Nigrospora oryzae* (MHZU 23-0229, a new host record). a Colony on PDA; a upper (left) and reverse (right) views. b, c Conidia on aerial mycelia on PDA. d–g Conidia with conidiogenous cells. h–k Conidia. Scale bars: d–k = $10\ \mu\text{m}$.

Nigrospora sphaerica (Sacc.) E.W. Mason, Trans. Br. mycol. Soc. 12(2-3): 158 (1927) Fig. 77
Index Fungorum number: IF254776; Facesoffungi number: FoF06599

Endophytic from fresh leaves of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Hyphae* $2\text{--}6\ \mu\text{m}$ wide ($\bar{x} = 4\ \mu\text{m}$, $n = 30$), smooth, hyaline to pale brown, septate, branched. *Conidiophores* mostly reduced to conidiogenous cells. *Conidiogenous cells* $9\text{--}20 \times 8\text{--}15\ \mu\text{m}$ ($\bar{x} = 13.5 \times 11\ \mu\text{m}$, $n = 30$), aggregated in clusters on hyphae, monoblastic, ampulliform, subspherical, unbranched, smooth, hyaline to pale brown. *Conidia* $16\text{--}22\ \mu\text{m}$ diam. ($\bar{x} = 18.5\ \mu\text{m}$, $n = 30$), solitary, globose, aseptate, black.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District, in living leaves of *Wurfbainia villosa* (*Zingiberaceae*), 1 October 2021, Chunfang Liao, AMR13A-1 (MHZU 23-0230), living culture ZHKUCC 23-0952; *ibid.*, living culture ZHKUCC 23-0953.

GenBank numbers – ZHKUCC 23-0952, ITS: OR984158, *tef1-α*: OR992770, *tub2*: OR992764; ZHKUCC 23-0953, ITS: OR984159, *tef1-α*: OR992771, *tub2*: OR992765.

Known distribution (based on molecular data) – Argentina (Wright et al. 2008), China (Liu et al. 2016a, Wang et al. 2017, Chen et al. 2018, Hong et al. 2021, this study), India (Dutta et al. 2015, Arunakumar et al. 2019, Deepika et al. 2021), Malaysia (Kee et al. 2019), Pakistan (Rehman et al. 2022).

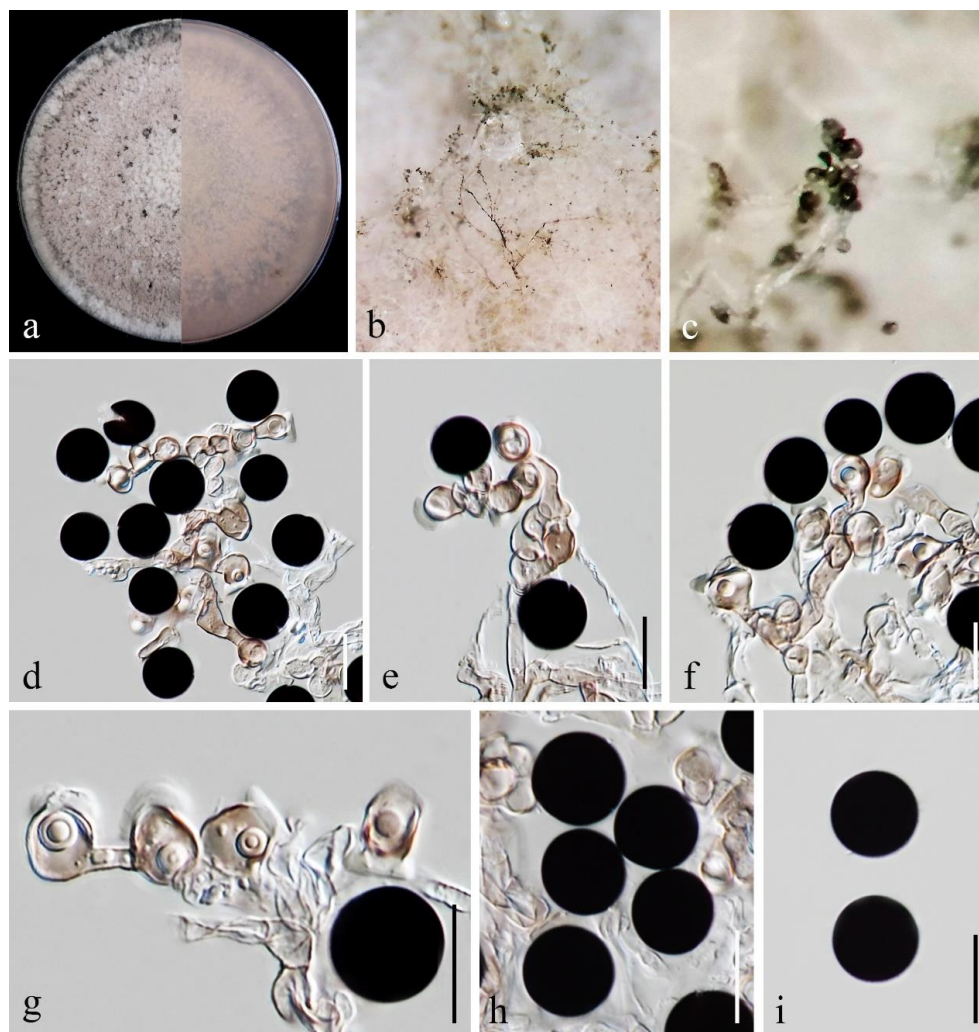


Figure 77 – *Nigrospora sphaerica* (MHZU 23-0230, a new host record). a Colony on PDA; upper (left) and reverse (right) views. b, c Conidia on aerial mycelia on PDA. d–g Conidia with conidiogenous cells. h, i Conidia. Scale bars: d–i = 10 μm.

Known hosts (based on molecular data) – *Akebia trifoliata* (Hong et al. 2021), Blueberry (Wright et al. 2008), *Camellia sinensis* (Liu et al. 2016c), *Castanopsis* sp., *Cephalotaxus sinensis*, *Citrus reticulata*, *Cleyera japonica* (Wang et al. 2017), Cowpea (Deepika et al. 2021), *Daphniphyllum macropodum*, *D. oldhamii*, dragon fruit (Kee et al. 2019), *Hamamelis mollis*, Mulberry (Chen et al. 2018, Arunakumar et al. 2019), *Musa paradisiacal*, *Nelumbo* sp., *Osmanthus* sp., *Pentactina rupicola*, Pitaya (Liu et al. 2016a), *Pittosporum illicioides*, *Rhododendron* sp., *Rhododendron* sp., *Rubus reflexus*, Sesame (Rehman et al. 2022), *Symplocos zizyphoides*, Tea (Dutta et al. 2015), *Ternstroemia* sp., *Tutcheria macrocarpa*, *Wurfbainia villosa* (this study).

Notes – According to the phylogenetic analysis, our strains (ZHKUCC 23-0952 and ZHKUCC 23-0953) clustered with *N. sphaerica* strains (LC 7312, LC 5901, and LC 3477) with 100% ML and 1.00 BYPP bootstrap support (Fig. 74). The morphology of asexual morphs of our collection shares similar characteristics to the holotype of *N. sphaerica*. However, our collection

has larger conidiogenous cells ($3.5\text{--}9\text{--}20 \times 8\text{--}15 \mu\text{m}$ vs. $6\text{--}12 \mu\text{m}$ diam. compared to those of *N. sphaerica*. Based on morphology and multi-gene phylogeny, we identified our collection is *N. sphaerica*. This study presents a new host record of *N. sphaerica* on *Wurfbainia villosa* in China.

Xylariomycetidae O.E. Erikss & Winka, Myconet 1: 12 (1997)

Amphisphaeriales Hawksw. & O.E. Erikss., Syst. Ascom. 5(1): 177 (1986)

Sporocadaceae Corda, Icon. fung. (Prague) 5: 34 (1842)

Neopestalotiopsis Maharachch., K.D. Hyde & Crous, Stud. Mycol. 79: 135 (2014)

Index Fungorum number: IF809759; Facesoffungi number: FoF01545

Neopestalotiopsis are appendage-bearing asexual coelomycetes (Jayawardena et al. 2016) and the genus was introduced by Maharachchikumbura et al. (2014) including *N. protearum* as its type species. Maharachchikumbura et al. (2014) separated *Sporocadaceae* into three genera namely *Neopestalotiopsis*, *Pestalotiopsis*, and *Pseudopestalotiopsis*. *Neopestalotiopsis* can be distinguished from *Pseudopestalotiopsis* and *Pestalotiopsis* by the versicolorous (two upper median cells darker than the lowest median cell) median cells and indistinct conidiophores, while *Pseudopestalotiopsis* differs from *Pestalotiopsis* by darker-colored concolorous (equally pigmented median cells) of conidia. Members of *Neopestalotiopsis* are important plant pathogens and are roughly ubiquitous in agricultural settings, causing several diseases and losses on various hosts worldwide (Maharachchikumbura et al. 2014, Jayawardena et al. 2016, Norphanphoun et al. 2019, Chethana et al. 2021b, Sun et al. 2022, Farr & Rossman 2023). Also, several species have been reported as saprobes and endophytes (Chethana et al. 2021b). There are 76 listed species of *Neopestalotiopsis* based on morpho-molecular data (Sun et al. 2022, Species Fungorum 2024). There are 91 species epithets of *Neopestalotiopsis* based on morpho-molecular data listed in the Species Fungorum (2024).

Neopestalotiopsis neomaricae Aumentado, Jayawardena & K.D. Hyde sp. nov.

Fig. 79

Index Fungorum number: IF901464; Facesoffungi number: FoF15226

Etymology – The specific epithet “*neomaricae*” is named after the host genus *Neomarica* from which the taxon was isolated.

Holotype – MFLU23-0455

Pathogenic on *Neomarica longifolia* leaves. Symptoms of brown necrotic lesions surrounded with yellowish margin starting from the tip of the leaves, and conidiomata appear on the leaf surface. Sexual morph: Undetermined. Asexual morph: *Conidiomata* pycnidial, solitary, globose to subglobose, black, semi-immersed on the leaf surface. *Conidiophores* on PDA indistinct. *Conidiogenous cells* lageniform to fusoid, hyaline, smooth- and thin-walled, collarette present. *Conidia* $15.95\text{--}22.42 \mu\text{m} \times 6.25\text{--}9.32 \mu\text{m}$ ($\bar{x} = 19.08 \mu\text{m} \pm 1.18 \times 7.64 \mu\text{m} \pm 0.94$, $n = 30$), fusiform to clavate, straight to slightly curved, 4-septate, apical cell conical, $2.19\text{--}3.91 \mu\text{m}$ long ($\bar{x} = 2.95 \mu\text{m} \pm 0.43$, $n = 30$), hyaline, with two to three appendages $8.56\text{--}27.21 \mu\text{m}$ long ($\bar{x} = 8.56 \mu\text{m} \pm 4.53$, $n = 40$), basal cell obconic, with a truncate base, $2.07\text{--}4.62 \mu\text{m}$ long ($\bar{x} = 3.23 \mu\text{m} \pm 0.52$, $n = 30$), hyaline or sometimes pale brown, thin- and smooth-walled, three median cells brown, $10.14\text{--}14.06 \mu\text{m}$ long ($\bar{x} = 12.16 \mu\text{m} \pm 1.26$, $n = 30$), second cell from base pale brown, $2.97\text{--}4.88 \mu\text{m}$ long ($\bar{x} = 4.24 \mu\text{m} \pm 0.58$, $n = 30$), third cell brown, $3.09\text{--}5.02 \mu\text{m}$ long ($\bar{x} = 4.01 \mu\text{m} \pm 0.63$, $n = 30$), fourth cell brown, $3.67\text{--}5.14 \mu\text{m}$ long ($\bar{x} = 4.19 \mu\text{m} \pm 0.42$, $n = 30$), septa and periclinal walls darker than rest of the cell, versicolored, wall rugose, and with one appendage $2.23\text{--}4.53 \mu\text{m}$ long ($\bar{x} = 3.21 \mu\text{m} \pm 0.63$, $n = 20$).

Culture Characteristics – Colonies on PDA produced white, cottony, round, and filamentous mycelium with filiform margin. The reverse is initially white and becomes off-white to yellowish with time. It measures 30.08 mm diameter on PDA at 2 days after incubation (dai) at room temperatures ($28 \pm 2^\circ\text{C}$), reaching the edge of the plate at 7 dai.

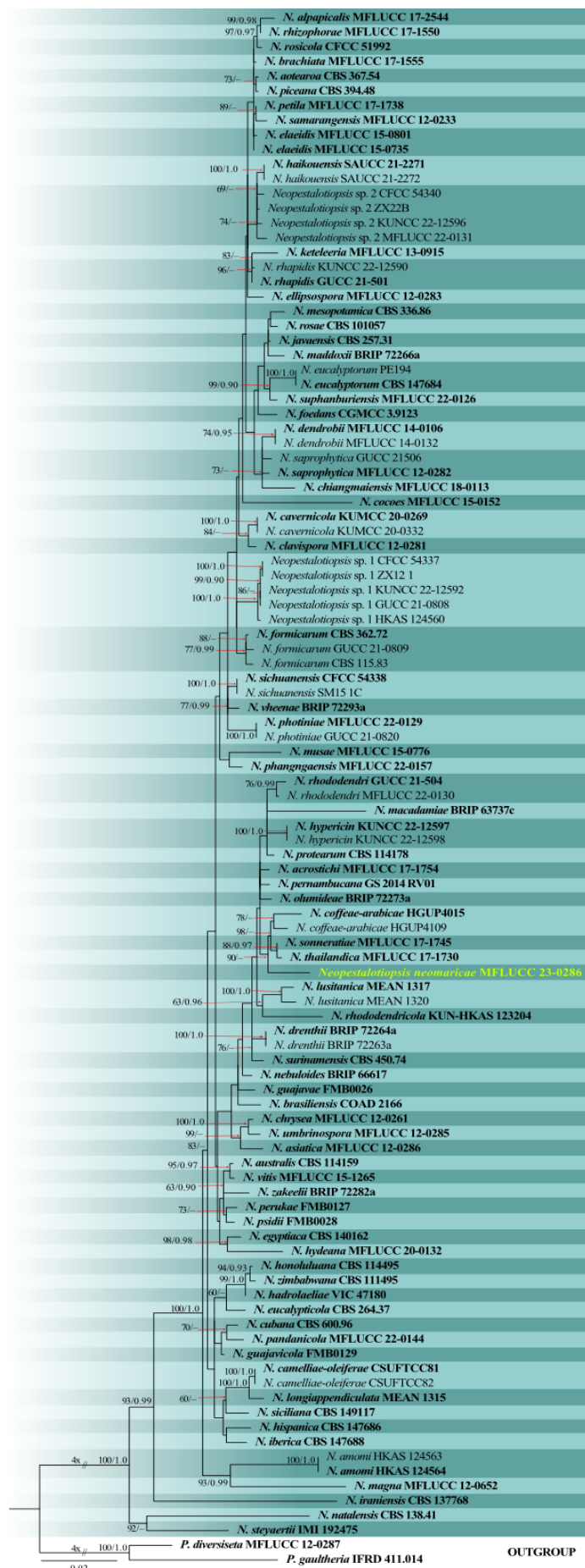


Figure 78 – Phylogenetic tree obtained from maximum likelihood analyses of a combined ITS, *tub2*, and *tef1-α* sequence dataset representing the species of *Neopestalotiopsis*. The best RAXML

tree with a final likelihood value of -9536.740637 is presented. The evolutionary model GTR+GAMMA is applied to all the genes. One hundred six strains were included in the combined analyses, which comprised 2023 characters of which had 697 distinct patterns, 352 parsimony-informative, 182 singleton sites, and 1489 constant sites. Estimated base frequencies were as follows: A = 0.234367, C = 0.270090, G = 0.219399, T = 0.276145; substitution rates AC = 0.929330, AG = 3.213023, AT = 1.339739, CG = 0.706325, CT = 4.936948, GT = 1.000000; gamma distribution shape parameter α = 0.244463. Bootstrap support values for maximum likelihood (ML) $\geq 60\%$ and Bayesian Posterior Probabilities (PP) ≥ 0.90 are indicated at the nodes as ML/PP. The tree is rooted to *Pestalotiopsis diversiseta* (MFLUCC 12-0287) and *P. gaultheria* (IFRD 411.014). The ex-type strains are in bold, and the new isolate of this study is in yellow. Bar = 0.02 represents the estimated number of nucleotide substitutions of site per branch. The new species described in Cui et al. (2024) were not included in the tree, as they are not closely related to the new species described herein and have also not yet been released in MycoBank.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, Mae Fah Luang University, on symptomatic leaf of *Neomarica longifolia* (*Iridaceae*), 13 Jan 2023, Herbert Dustin Aumentado, PD006 (MFLU 23-0455, holotype), ex-type living culture, MFLUCC 23-0286, dried culture permanently preserved in a metabolically inactive state, holotype, MFLU 23-0455.

GenBank numbers – MFLU 23-0455: ITS: OR853052, *tub2*: OR886388, *tef1*- α : OR886389.

Known distribution (based on molecular data) – Thailand (this study).

Known hosts (based on molecular data) – *Neomarica longifolia* (this study).

Notes – Based on multi-gene phylogenetic analysis, *Neopestalotiopsis neomaricae* MFLUCC 23-0286 formed a separate lineage sister to *N. thailandica* (MFLUCC 17-1730), *N. sonnerati* (MFLUCC 17-1744), and *N. coffeae-arabicae* (HGUP4015) strains with 90% ML bootstrap support (Fig. 78). A single gene comparison of ITS, *tef1*- α , and *tub2* of our strain MFLUCC 23-0286 with the type strains of closely related taxa revealed base pair differences: *N. thailandica* MFLUCC 17-1730 [1/474 (0.21%), 4/868 (0.46%), 10/681 (1.45%)], *N. coffeae-arabicae* HGUP4015 [0/474 (0%), 3/868 (0.34%), 15/681 (2.20%)], and *N. sonnerati* MFLUCC 17-1745 [0/474 (0%), 4/868 (0.46%), 9/681 (1.32%)], respectively. Additionally, the PHI test indicated that there is no significant recombination ($\Phi_w = 0.1587$) between *N. neomaricae* (MFLUCC 23-0286) and closely related taxa (Fig. 80). The morphological characteristics and differences of these species are summarized in Table 4. Thus, based on morphology (Fig. 79), multi-gene phylogeny, and GCPSR analyses, we conclude that our collection *Neopestalotiopsis neomaricae* MFLUCC 23-0286 is a novel species.

This fungus is weakly pathogenic in wounded and non-wounded *N. longifolia* leaves and produced relatively similar lesion symptoms from the disease sample (Fig. 81). Symptoms incited in mycelium plug inoculation were brown necrotic lesions with white abundant mycelium. An identical isolate was isolated from the infected inoculation sites thus Koch's postulate was established. No infection was observed on *N. longifolia* non-wounded leaves and fruits and controls. *Neopestalotiopsis neomaricae* (MFLUCC 23-0286) was isolated from *Neomarica longifolia* in Thailand. The current study presents a new species and pathogenicity of *N. neomaricae* in Thailand.

Sporocadaceae Corda [as 'Sporocadeae'], Icon. fung. (Prague) 5, 34 (1842).

Pestalotiopsis Steyaert, Bull. Jard. bot. État Brux. 19, 300 (1949).

Index Fungorum number: IF9272; Facesoffungi number: FoF00458

Pestalotiopsis was erected by Steyaert (1949) and is typified by *P. guepinii*. *Pestalotiopsis* is a species-rich asexual genus with appendage-bearing conidia in the family *Amphisphaeriaceae* (Lee et al. 2006, Maharachchikumbura et al. 2014, Dong et al. 2023). The genus is mainly characterized by 5-celled conidia, with three concolorous median cells, hyaline terminal cells, and simple or unbranched appendages arising from the apex of the apical and basal cells (Steyaert 1949, Maharachchikumbura et al. 2014). *Pestalotiopsis* species are widely distributed throughout tropical

and temperate regions (Bate-Smith & Metcalfe 1957, Maharachchikumbura et al. 2014). The genus includes commonly isolated pathogens and endophytes, and many of them persist as saprobes (Hu et al. 2007, Maharachchikumbura et al. 2012, 2014, Chethana et al. 2021b). Pathogens cause many diseases, including canker lesions, fruit rots, grey blight, leaf spots, needle blight, scabby canker, severe chlorosis, shoot dieback, tip blight and various post-harvest diseases (Xu et al. 1999, Hu et al. 2007, Crous et al. 2011, Maharachchikumbura et al. 2012, 2013a, b, c, Ismail et al. 2013, Zhang et al. 2012c, Maharachchikumbura et al. 2014). Currently, more than 370 species belong to this genus (Wijayawardene et al. 2022, Dong et al. 2023, Index Fungorum 2024). Here, we provide the multi-gene phylogeny for *Pestalotiopsis* taxa (Fig. 82).



Figure 79 – *Neopestalotiopsis neomaricae* (MFLU 23-0455, holotype). a, b Symptoms on *Neomarica longifolia* leaves. c Conidiomata submerged on the leaf surface. d Conidial attachments and conidiophores. e, f Conidiophores with conidia g, h Conidiogenous cells and conidial attachments. i–n Conidia. o–q Germinating conidia. r, s Colony on PDA at 1-month post-incubation (obverse, reverse). Scale bars: d–h = 20 μ m, i–n = 5 μ m, o–q = 10 μ m.

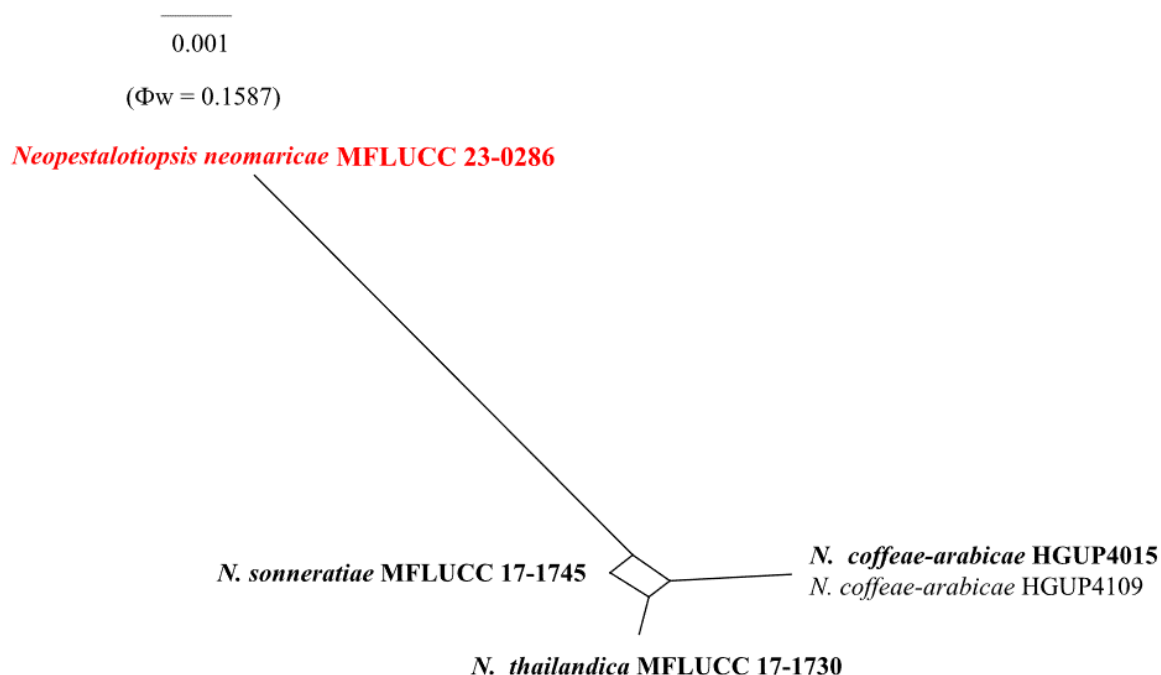


Figure 80 – Split graphs showing the results of the PHI test of *Neopestalotiopsis neomaricae* MFLUCC 23-0286 and closely related taxa using LogDet transformation and splits decomposition. PHI test results $\Phi_w \geq 0.05$ indicates that there is significant recombination within the dataset. The new taxon is shown in red.

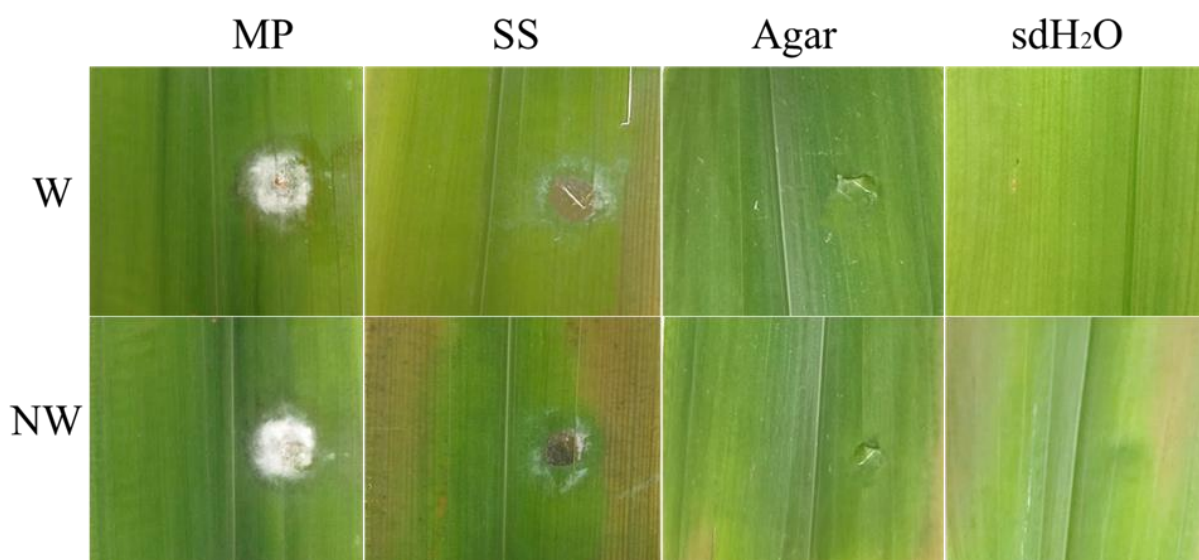


Figure 81 – Pathogenicity testing on *Neomarica longifolia* leaves. Symptoms at 14 days post-inoculation. Pathogen inoculations using mycelial plug (MP) and spore suspension (SS). W: Wounded, NW: Non-wounded. Control inoculations were done using blank agar and sterile distilled water (sdH₂O).

Pestalotiopsis trachicarpicola Y. M. Zhang & K.D. Hyde in Zhang, Maharachchikumbura, McKenzie and Hyde, *Cryptogamie Mycologie* (2012). Fig. 83

Index Fungorum number: IF631319; Facesoffungi number: FoF15296

Isolated from soil in a cave habitat. Sexual morph: Undetermined. Asexual morph: *Colony* on PDA, *Vegetative hyphae* 1.5–5 μm wide, hyaline, septate, branched, thin-walled, aerial mycelia

abundant. *Conidiomata* on PDA up to 200 µm diam., pycnidial, semi-immersed, scattered or aggregated, globose to clavate, dark brown to black, exuding dark brown to black conidial masses. *Conidiophores* up to 50 µm long, septate, simple, rarely branched at the base, subcylindrical, hyaline to subhyaline. *Conidiogenous cells* 4.5–16.5 × 1.5–8 µm ($\bar{x}$ = 8.50 × 4.55 µm, n = 60), discrete, holoblastic, cylindrical, hyaline to pale brown, smooth-walled. *Conidia* 16–26 × 5–8.5 µm ($\bar{x}$ = 22.20 × 6.81 µm, n = 60), fusiform, ellipsoid, straight to slightly curved, 4-septate, constricted at the septum, granulate, basal cell conic to obconic, with a truncated base, hyaline, thin-walled, 3–5.5 µm long ($\bar{x}$ = 4.49 µm, n = 30); three median cells 10–14.5 µm long ($\bar{x}$ = 12.53 µm, n = 30), doliiform, smooth-walled, yellow-brown to brown, septa darker than the rest of the cell, second cell from the base 2–4.5 µm long, pale brown; third cell 3–5 µm long, yellow-brown; fourth cell 2.5–5.5 µm long, brown; apical cell 3–7 µm long ($\bar{x}$ = 4.83 µm, n = 30), hyaline, subcylindrical, rugose, thin- and smooth-walled; with 2–4 tubular apical appendages (mostly 3, rarely 2 and 4), 6–31 µm ($\bar{x}$ = 13.78 µm, n = 60), arising from the apical crest, unbranched, filiform; basal appendage 3.5–12.5 µm long ($\bar{x}$ = 7.99 µm, n = 30) single, filiform, tubular, unbranched, centric.

Culture characteristics – Colonies on PDA attaining 3 cm after 7 days at room temperature (20–25 °C), with undulate edge, white, sparse aerial mycelium on the surface; reverse pale yellow. Sporulating conidiomata on PDA with black conidial mass after 50 days.

Material examined – China, Yunnan Province, Kunming, Fuming County, Gem Cave (N 25°17'31.49", E 102°40'08.59"), 21 May 2020, Samantha C. Karunarathna, A3-A (ZHKU 23-0278), living culture ZHKUCC 23-1026; *ibid.* A3-B, living culture ZHKUCC 23-1027.

GenBank numbers – ZHKUCC 23-1026: ITS: PP029403; *tef1-α*: PP061780, *tub2*: PP077038; ZHKUCC 23-1027: ITS: PP029404; *tef1-α*: PP061781, *tub2*: PP077039.

Known distribution – China (Maharachchikumbura et al. 2012, Zhang et al. 2012c, Jayawardena et al. 2015, Liu et al. 2017, Li et al. 2018b, Shu et al. 2020, this study).

Known hosts or substrate – *Camellia sinensis* (Liu et al. 2017), cave substrata (this study), *Chrysophyllum* sp. (Maharachchikumbura et al. 2014), *Eucommia ulmoides* (Li et al. 2018b), *Gentiana rhodantha* (Zhang et al. 2021b), *Mangifera indica* (Shu et al. 2020), *Panax notoginseng* (Lin et al. 2023b), *Pinus bungeana* (Qi et al. 2021), *Podocarpus macrophyllus* (Maharachchikumbura et al. 2014), *Schima* sp. (Maharachchikumbura et al. 2014), *Symplocos* sp. (Maharachchikumbura et al. 2014), *Trachycarpus fortunei* (Maharachchikumbura et al. 2012, Zhang et al. 2012c), *Vitis vinifera* (Jayawardena et al. 2015).

Table 4 Comparison of conidial morphology of *Neopestalotiopsis neomaricae* (PD006, MFLUCC 23-0286) to type collections of closely related *Neopestalotiopsis* species.

Species	Strain	Conidial size (µm)	Apical appendages		Basal appendage Length (µm)	Reference(s)
			Number	Length (µm)		
<i>Neopestalotiopsis neomaricae</i> sp. nov.	MFLUCC 23-0286	15.95–22.42 × 6.25–9.32 ($\bar{x}$ = 19.08 ± 1.18 × 7.64 ± 0.94, n = 30)	2–3	8.56–27.21 ($\bar{x}$ = 17.18 ± 4.53, n = 40)	2.23–4.53 ($\bar{x}$ = 3.21 ± 0.63, n = 20)	This study
<i>N. thailandica</i>	MFLUCC 17-1730	(20–)21–25(–25.5) × (5.7–)6–7(–7.3)	1–2	(30–)32.5–38(–40)	(3–)6–9(–10)	Norphanphoun et al. (2019)
<i>N. sonneratae</i>	MFLUCC 17-1744	(21.6–)24–26(–28.2) × (6.8–)7–7.5(–8.1)	1–3	(5.3–)7–8(–13.8)	(2.5–)3–4(–4.7)	Norphanphoun et al. (2019)
<i>N. coffeae-arabicae</i>	HGUP4015	16–20 × 5–7	2–4	11–16	3–5	Song et al. (2013), Fiorenza et al. (2022)

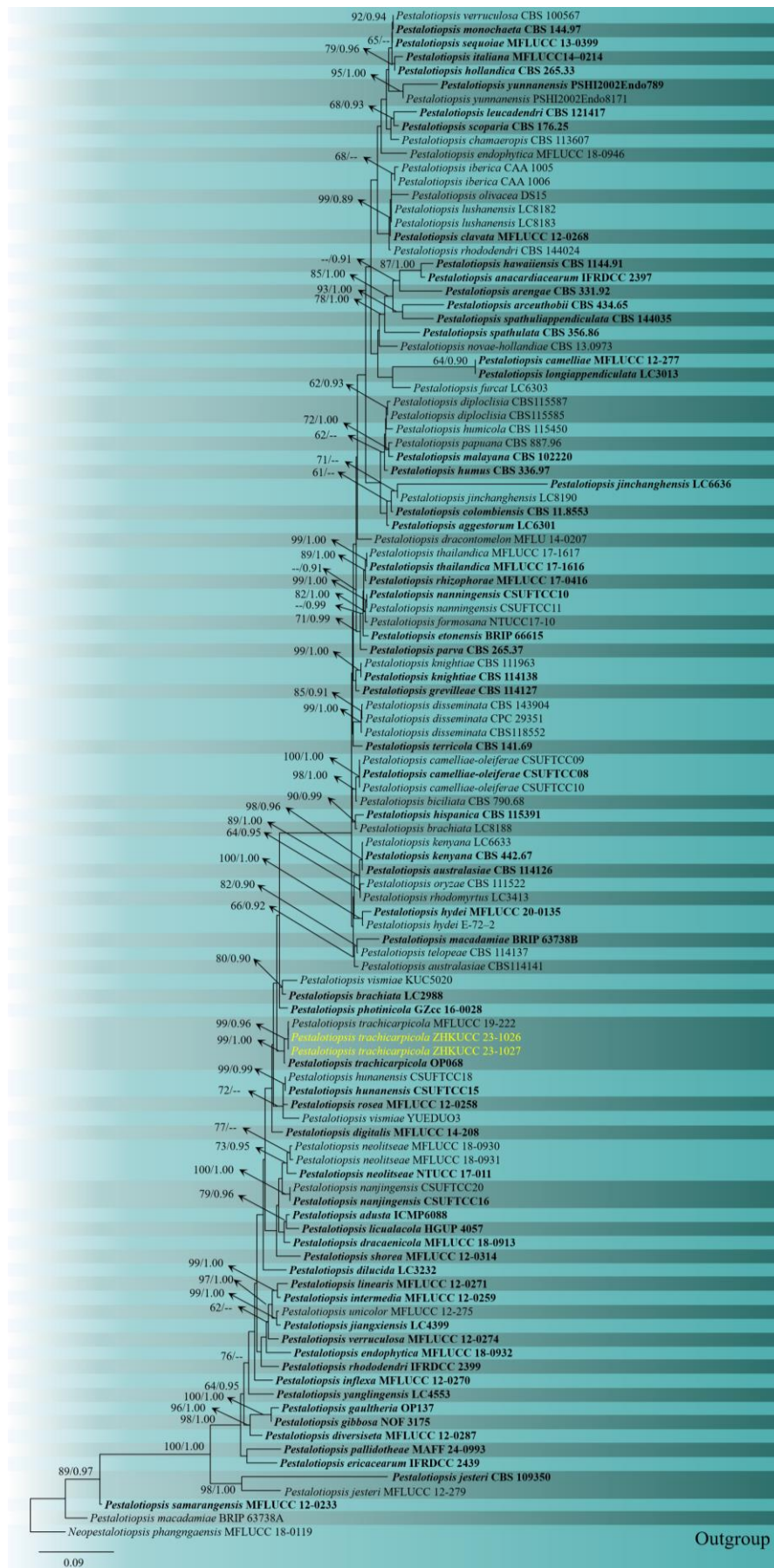


Figure 82 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, *tef1-α* and *tub2* sequence data of *Pestalotiopsis*. One hundred and eleven strains are included

in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -18377.016877 is presented. The evolutionary model GTR+I+G is applied to all the genes. The matrix had 1085 distinct alignment patterns, with 21.86% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.238295, C = 0.292231, G = 0.216332, T = 0.253142; substitution rates AC = 1.108308, AG = 3.054483, AT = 1.088802, CG = 0.955134, CT = 0.955134, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.628987$. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Neopestalotiopsis phangngaensis* (MFLUCC 18-0119). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

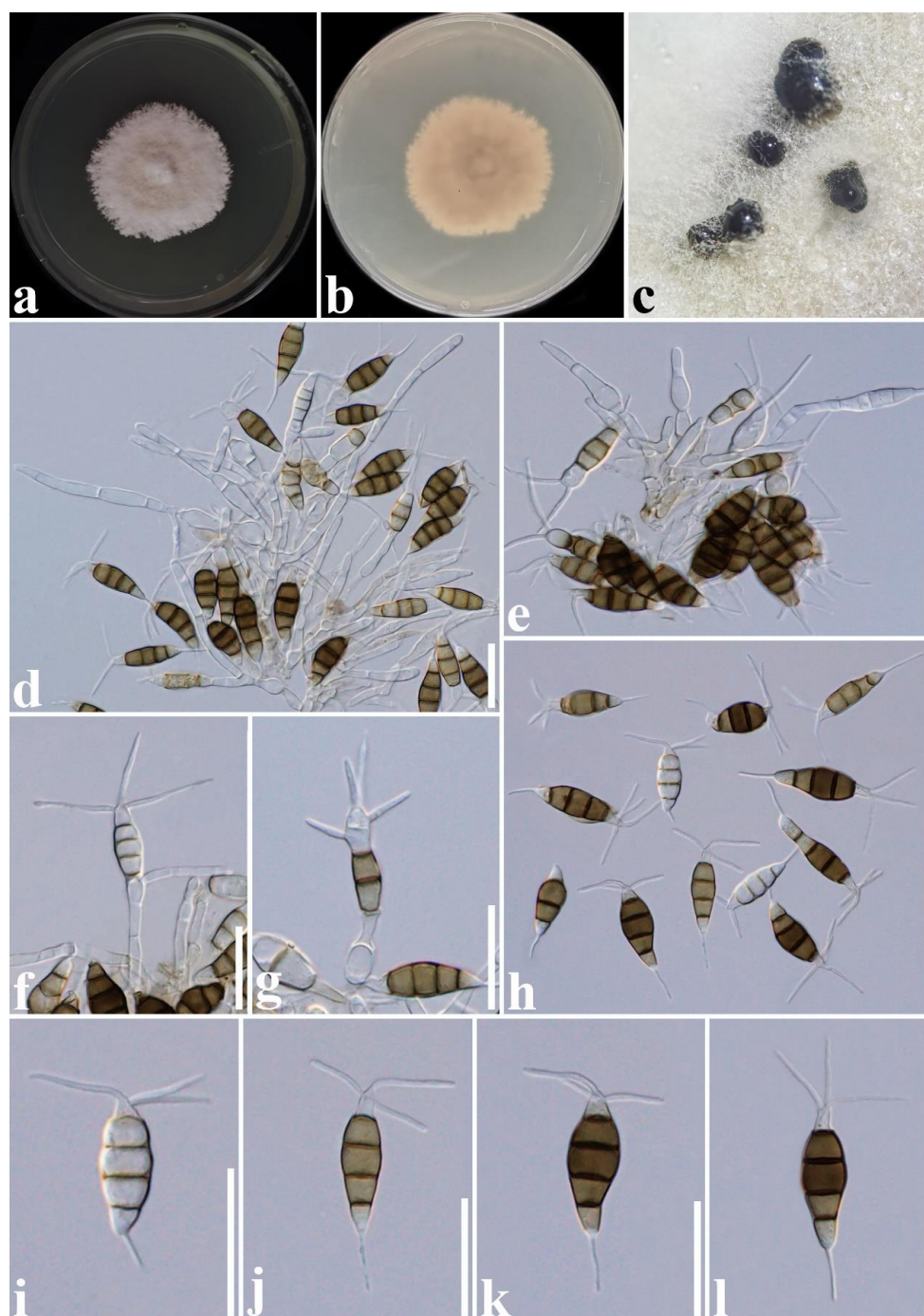


Figure 83 – *Pestalotiopsis trachicarpicola* (ZHKU 23-0278, a new record in cave habitat). a, b Colony on PDA (a-above and b-below). c Sporulating conidiomata on PDA (50 days old)

culture). d–g Conidiophores, conidiogenous cells with conidia. h–l Conidia with appendages. Scale bars: d–l = 20 μ m.

Notes – In multi-locus phylogenetic analysis of ITS, *tef1- α* and *tub2* sequence data, our strains (ZHKUCC 23-1026 and ZHKUCC 23-1027) clustered with *P. trachicarpicola* (OP068; type strain, and MFLUCC 19-222) strains with 99% ML and 1.00 BYPP bootstrap support (Fig. 82). *Pestalotiopsis trachicarpicola* was introduced by Zhang et al. (2012c) and isolated from leaf spots on *Trachycarpus fortunei* with both sexual and asexual morphs. Our new collection (KUMCC 21-0426) shares similar characteristics to *P. trachicarpicola* (OP068) by pale yellowish to brown, straight to slightly curved, 4-septate conidia, with 2–4 (mostly 3, rarely 2 and 4) tubular apical appendages, and one basal appendage (Zhang et al. 2012c). Based on morphology and phylogenetic evidence, the new isolates are identified as *P. trachicarpicola*. *Pestalotiopsis trachicarpicola* has been reported as saprobes, pathogens causing the leaf spots on *Eucommia ulmoides*, *Gentiana rhodantha*, *Mangifera indica*, *Podocarpus macrophyllus*, and *Trachycarpus fortunei* (Maharachchikumbura et al. 2014, Li et al. 2018b, Shu et al. 2020, Zhang et al. 2021b), and endophytes on living leaves of *Chrysophyllum* sp. and *Schima* sp. (Maharachchikumbura et al. 2014). This is the first report of *P. trachicarpicola* from a cave habitat.

Xylariales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 66 (1932)

Diatrypaceae Nitschke [as ‘Diatrypeae’], Verh. naturh. Ver. preuss. Rheinl. 26: 73 (1869)

Allocryptovalsa Senwanna, Phookamsak & K.D. Hyde, in Senwanna, Phookamsak, Doilom, Hyde & Cheewangkoon, Mycosphere 8(10): 1839 (2017)

Index Fungorum number: IF553857; Facesoffungi number: FoF12954

Allocryptovalsa was introduced by Senwanna et al. (2017) with *A. polyspora* as the type species. The genus is characterized by immersed perithecia, ostiole with periphyses, polysporous asci and oblong to allantoid ascospores. The asexual morph exhibits hyaline and elongate-allantoid conidia (Senwanna et al. 2017, Zhu et al. 2021, Chethana et al. 2023). Currently, 11 species are listed in Index Fungorum (2024) under this genus. Here, we provide the updated phylogeny for the *Allocryptovalsa* taxa (Fig. 84).

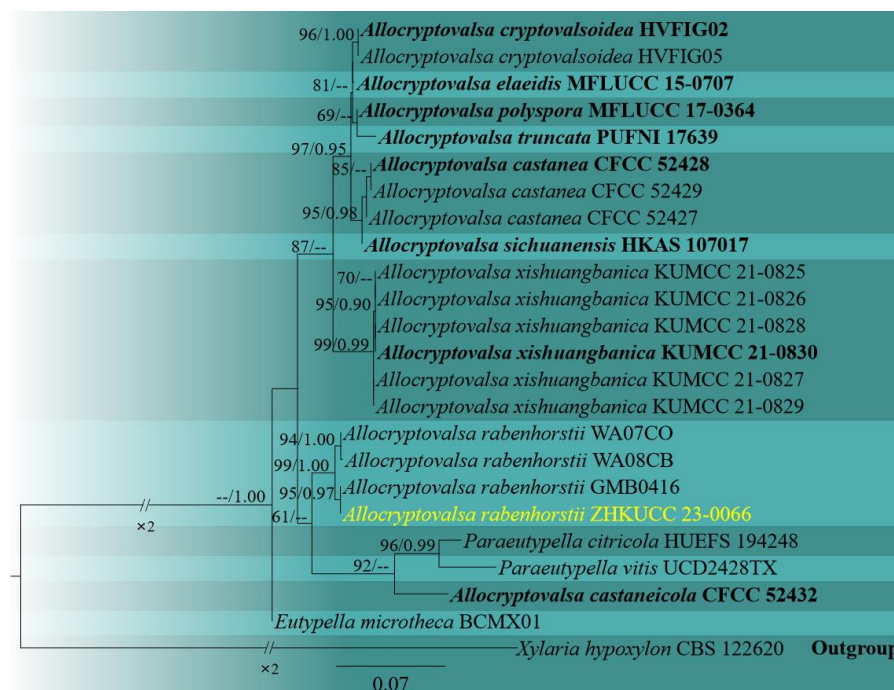


Figure 84 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and *tub2* sequence data of *Allocryptovalsa*. Twenty-four strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis.

The best RAxML tree with a final likelihood value of -3018.431511 is presented. Evolutionary model GTR+I+G is applied for all the genes. The matrix had 253 distinct alignment patterns, with 14.31% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.231703, C = 0.261144, G = 0.235751, T = 0.271402; substitution rates AC = 1.118383, AG = 4.073791, AT = 1.536942, CG = 0.998554, CT = 6.893615, GT = 1.000000; gamma distribution shape parameter α = 0.510715. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Xylaria hypoxylon* (CBS 122620). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Allocryptovalsa rabenhorstii (Nitschke) C. Senwanna, Phookamsak & K.D. Hyde, in Senwanna, Phookamsak, Doilom, Hyde & Cheewangkoon, *Mycosphere* 8(10): 1841 (2017) Fig. 85

Index Fungorum number: IF553864; Facesoffungi number: FoF14962

Saprobic on a dead branch of *Aquilaria* sp. Sexual morph: *Ascostromata* poorly developed, scattered or gregarious, 1–4-loculate, immersed through the substrate, inconspicuous, only the ostioles exposed to the surface. *Ascomata* 250–500 μm high $\times$ 300–600 μm diam. ($\bar{x}$ = 375 $\times$ 400 μm , n = 10) (excluding neck), perithecial, solitary or gregarious, immersed, ampuliform, brown to dark brown, not wrapped in white entostroma, the surrounding tissue is light yellow after section, ostiolate. *Ostiole* 200–350 μm high $\times$ 60–200 μm diam. ($\bar{x}$ = 280 $\times$ 140 μm , n = 10), central, slightly cylindrical, straight, not protruding or protruding slightly from the substrate, the upper part is wider than the lower part, dark brown to black, periphysate. *Peridium* 30–85 μm wide, composed of several layers, from outer toward inner layers with thick-walled, pale brown to thin-walled, hyaline to cells of *textura angularis* to *textura prismatica*. *Hamathecium* comprising 3–9 μm wide, filamentous, unbranched, hyaline, granular, septate paraphyses, slightly constricted at the septa, enlarged base, gradually tapers towards the tip. *Asci* (150–)155–175(–180) $\times$ (12.5–)14–15.5(–17) μm ($\bar{x}$ = 165.5 $\times$ 15 μm , n = 30), spore-bearing part (60–)65–85(–90) μm length ($\bar{x}$ = 75.5 μm , n = 30), unitunicate, thin-walled, polysporous, clavate, with J⁺ apical ring, 70–100 μm long pedicellate, some pedicel with subglobose structure, apically rounded, narrowing towards lower region. *Ascospores* (9.5–)11–14(–16) $\times$ 3–4.5 μm ($\bar{x}$ = 13 $\times$ 3.8 μm , n = 30), crowded, sub-allantoid, initially hyaline, turning pale yellow at the maturity, aseptate, curved, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h at 28 °C and germ tubes were produced from both ends. Colonies on PDA reached 6 cm diam. after one week at 28 °C. Colonies obverse: flat, circular, flossy, filiform margin, and white to cream, smooth in reverse.

Material examined – China, Yunnan Province, Xishuangbanna, Menghai City, Agarwood plantation, on a dead branch of *Aquilaria* sp. (*Thymeleaceae*), 15 September 2021, T.Y. Du, YNA22 (MHZU 23-0030, living culture ZHKUCC 23-0066).

GenBank numbers – ZHKUCC 23-0066: ITS: OR835565, *tub2*: OR853756.

Known distribution – Australia (Trouillas et al. 2011, Jayawardena et al. 2018b), China (this study), England (Mejia et al. 2011), Iran (Mehrabi et al. 2019), Japan (Kobayashi 2007), Pakistan (Ahmad 1969), South Africa (Moyo et al. 2019), United States of America (Trouillas et al. 2011), Ukraine (Dudka et al. 2004).

Known hosts – *Acacia farnesiana* (Ahmad 1969), *Aquilaria* sp. (this study), *Betula* sp. (Mejia et al. 2011), *Citrus* sp. (Mehrabi et al. 2019), *Dalbergia sissoo* (Ahmad 1969), *Echinops echinatus* (Ahmad 1978), *Morus alba* (Ahmad 1978), *Morus* sp. (Kobayashi 2007), *Robinia pseudoacacia* (Dudka et al. 2004), *Sambucus nigra* (Trouillas et al. 2011), *Viburnum* sp. (Ahmad 1978), *Vitis* sp. (Jayawardena et al. 2018b), *Vitis vinifera* (Trouillas et al. 2011).

Notes – According to the phylogenetic analyses, our strain (ZHKUCC 23-0066) clustered with *A. rabenhorstii* strains (WA07CO, WA08CB and GMB0416) with 99% ML and 1.00 BYPP bootstrap support (Fig. 84). Our fungal collection share similar morphology to *A. rabenhorstii* in color, shape, and size of asci and ascospores (Trouillas et al. 2011). Our collection has thinner 14–15.5 μm wide vs. 18–22 μm wide) pedicels of asci than *A. rabenhorstii* (WA07CO) (Trouillas et al.

2011). This might depend on different environmental factors and host plants. Based on morphology and multi-gene phylogeny we identified our collection as *A. rabenhorstii*. This is the first report of *Allocryptovalsa* species on *Aquilaria* plants, and it is reported for the first time in China. Therefore, this study presents a new host and geographical record of *A. rabenhorstii*.

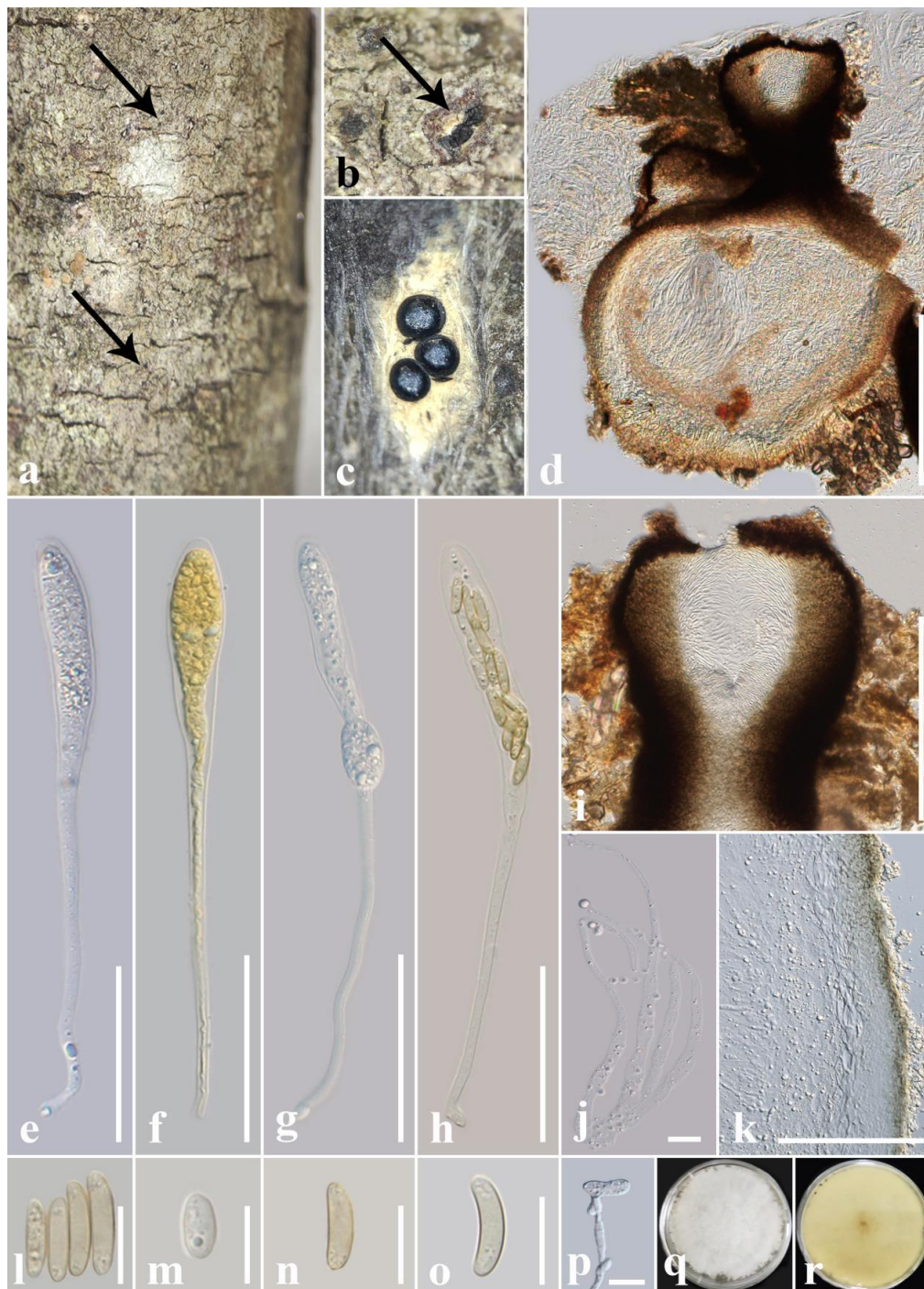


Figure 85 – *Allocryptovalsa rabenhorstii* (MHZU 23-0030, a new host and a geographical record). a, b Appearance of ascostromata on the host. c Transverse section of an ascostroma. d Section through an ascoma. e–h Asci (f is an ascus stained with Melzer's reagent). i Ostiole with periphyses. j Paraphyses. k Peridium. l–o Ascospores. p A germinating ascospore. q, r Colonies on PDA (q) obverse and (r) reverse view (two weeks). Scale bars: d = 300 μ m, e–h = 50 μ m, i = 200 μ m, j = 10 μ m, k = 50 μ m, l–p = 10 μ m.

Peroneutypa Berl., Icon. fung. (Abellini) 3(3-4): 80 (1902)

Index Fungorum number: IF3834; Facesoffungi number: FoF13145

Peroneutypa, was introduced by Berlese (1902) to accommodate three species including *P. bellula*, *P. corniculata* and *P. heteracantha*. The genus was typified with *P. bellula* by Rappaz (1987). Later, eight species were transferred to *Peroneutypa* based on the ITS phylogenetic analyses by Acero et al. (2004) and morphological evidence by Carmarán et al. (2006). The genus is shown to be monophyletic based on phylogenetic analyses (Carmarán et al. 2006, Shang et al. 2017, 2018, Senwanna et al. 2017, Phukhamsakda et al. 2022, Samarakoon et al. 2022). *Peroneutypa* is characterized by poorly developed, valsoid ascostromata, long, prominent perithecial necks, almost sessile, clavate asci, and allantoid, hyaline or yellowish ascospores (Du et al. 2022, Senwanna et al. 2017). Members of *Peroneutypa* are distributed worldwide including Africa, America, Asia and Europe (Du et al. 2022). They have been reported different life modes such as saprobic or pathogenic in terrestrial and marine habitats, as well as arbor plants, mainly on *Arthrocnemum fruticosum*, *Aquilaria sinensis*, and *Coffea robusta* hosts (Du et al. 2022). To date, 37 species are accommodated in *Peroneutypa* (Index Fungorum 2024).

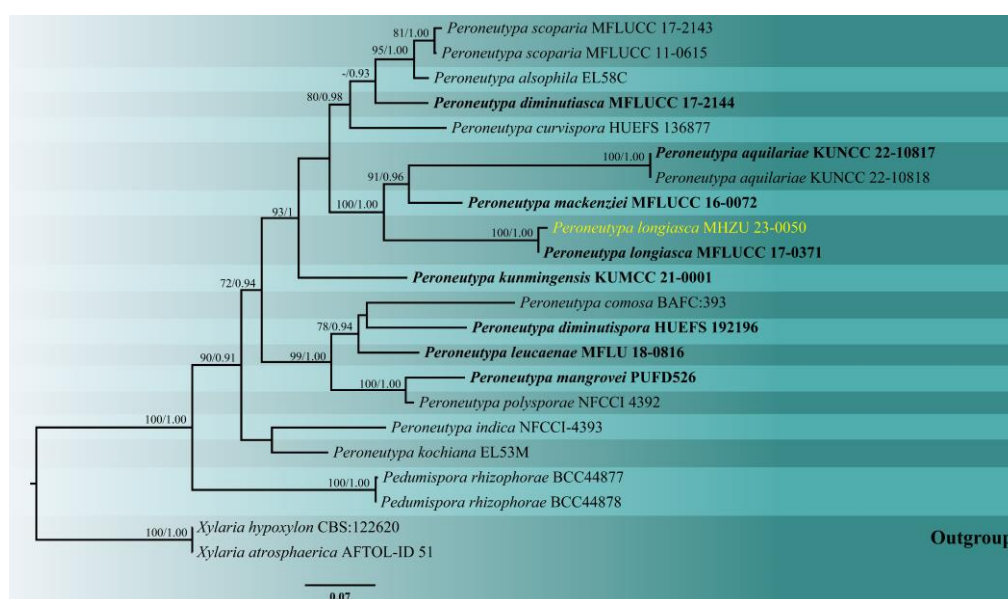


Figure 86 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and *tub2* sequence data of *Peroneutypa*. Twenty-two strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -11166.72321 is presented. The evolutionary model SYM+G is applied for the ITS gene and GTR+G. The matrix had 923 distinct alignment patterns, with 55.99 % of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.212972, C = 0.286568, G = 0.237565, T = 0.262896; substitution rates AC = 0.699287, AG = 2.261813, AT = 2.261813, CG = 2.261813, CT = 3.069423, GT = 1.000000; gamma distribution shape parameter α = 0.480123. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Xylaria hypoxylon* (CBS 122620) and *X. atrophaeria* (AFTOL-ID 51). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Peroneutypa longiasca Senwanna, Phookamsak & K.D. Hyde, in Senwanna, Phookamsak, Doilom, Hyde & Cheewangkoon, Mycosphere 8(10): 1848 (2017) Fig. 87

Index Fungorum number: IF553860; Facesoffungi number: FoF03776

Saprobic on dead twigs of *Acer palmatum*. Sexual morph: *Ascostromata* with well-developed interior, solitary to gregarious, immersed, erumpent with long necks, brownish-black to black, irregularly shaped. *Ascomata* 315–652 μ m high, 270–455 μ m diam., perithecial, single or aggregated, immersed on the substrate except for the ostiolar canal, irregular globose to globose,

dark brown to black. *Ostiolar canal* 20–55 μm wide, 260–350 μm long, cylindrical, long and straight necks, dark-brown to black. *Peridium* 17–48 μm thick, outer layer composed of 4–8 layers, dark brown, thick-walled *textura angularis* cells, inner layer composed of 2–4 layers, hyaline, thin-walled *textura prismatica* cells, sometimes ends rounded. *Paraphyses* not observed. *Asci* 15–19.1 $\times$ 3.6–6.2 μm ($\bar{x}$ = 16.8 $\times$ 5 μm , n = 50), unitunicate, 8-spored, cylindrical to elongated oval, short or long pedicellate, apex rounded, J-. *Ascospores* 5–7 $\times$ 1.4–1.9 μm ($\bar{x}$ = 5.9 $\times$ 1.6 μm , n = 80), overlapping, 2–3-seriate, allantoid, slightly curved, aseptate, hyaline to pale yellow, smooth-walled with a smaller guttule at each end. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h and germ tubes produced from one or both ends of the ascospore. Colonies covered the whole PDA medium in two weeks at 23–28 °C, irregular, flat or umbonate elevation, surface and margin rough with aerial mycelium, white with the black bulge in the center, reverse side white at the margin, greenish black to black in the center, no pigmentation on the PDA medium.

Material examined – China, Yunnan Province, Kunming City, Changchong Mountain, on decayed wood of *Acer palmatum* (*Sapindaceae*), 12 July 2021, Tianye Du, KMD17 (MHZU 23-0050), living cultures (ZHKUCC 23-0101, ZHKUCC 23-0113).

GenBank numbers – MHZU 23-0050 - ITS: OR405002

Known distribution (based on molecular data) – China (this study), Thailand (Senwanna et al. 2017).

Known hosts (based on molecular data) – *Acer palmatum* (this study), *Arthrocnemum fruticosum* (Acero et al. 2004, Carmarán et al. 2006), *Aquilaria sinensis* (Du et al. 2022), *Celtis tala* (Carmarán et al. 2006, Grassi et al. 2014), *Coffea robusta* (Saccas 1981), *Ficus racemosa*, *Macaranga tanarius*, *Streblus asper* (Rehm 1913), *Prunus melanocarpa* (Rappaz 1987, Arhipova et al. 2012).

Notes – Based on the phylogenetic analysis of ITS and *tub2* sequence data, our strain (MHZU 23-0050) clustered with *P. longiasca* (MFLUCC 17-0371 – ex-type strain) with 100% ML and 1.00 BYPP (Fig. 86). Our collection (MHZU 23-0050) shares very similar morphological characteristics with *P. longiasca* (MFLUCC 17-0371) by having brownish-black to black, multiple perithecia with long necks, 4–8 layers of thick-walled *textura angularis* cells, 2–4 layers of thin-walled *textura prismatica* cells in the peridium, short to long pedicellate asci, no paraphyses and allantoid ascospores with a single guttule at each end (Senwanna et al. 2017). The measurements of asci were not provided in the original description, and we provide the values in this study. Based on available morphology and multi-gene phylogeny we identified our collection as *P. longiasca*. This is the first record of this species growing on *Acer palmatum* and the first report in China.

***Junewangia* W.A. Baker & Morgan-Jones**

Index Fungorum number: IF28602; Facesoffungi number: FoF06603

Junewangia was established by Baker et al. (2002) to accommodate *J. sphaerospora* as the type species and four other *Acrodictys* species, with a newly described *J. sphaerospora*. Xia et al. (2017), established a new family *Junewangiaceae* to accommodate the genus, based on multigene phylogenetic analysis. Up to now, there are six species accepted in *Junewangia* (Delgado 2009, Xia et al. 2017, Song et al. 2018, Dong et al. 2021).

***Junewangia lamma* (Whitton, McKenzie & K.D. Hyde) W.A. Baker & Morgan-Jones, Mycotaxon 81: 310 (2002)**

Fig. 89

Index Fungorum number: IF484790; Facesoffungi number: FoF11038

Saprobic on decaying, submerged wood in freshwater habitats. Sexual morph: Undetermined. Asexual morph: Colonies effuse, consists with scattered, singly or small grouped conidiophores on the substrate. *Mycelia* immersed to superficial, superficial hyphae branched, cylindrical, septate, pale brown. *Conidiophores* 27–48 $\times$ 3–4 μm ($\bar{x}$ = 40 $\times$ 4, n = 25), macronematous, mononematous, cylindrical, erect, straight or slightly flexuous, short, 2–3-septae, smooth, pale brown at the apex. *Conidiogenous cells* holoblastic, monoblastic, integrated into the apex of the conidiophores,

terminal, smooth, cylindrical, pale brown, truncate. *Conidia* $10\text{--}23 \times 10\text{--}23 \mu\text{m}$ ($\bar{x} = 18 \times 18$, $n = 30$), solitary, dry, globose to elliptical, terminal, pale brown, 1-2 transverse septa and some longitudinal or oblique septa, with persistent basal cell protruding, basal cell pale brown, cylindrical.

Material examined – Thailand, Chiang Rai Province, Nang Lae, Mueang, on a decaying, submerged wood in a freshwater stream, 17 July 2020, R. J. Xu, (MFLU 23-0450), living culture, MFLUCC 23-0258. *ibid.*, 18 July 2020, R.J. Xu, MD-62-3 (MFLU 23-0451).

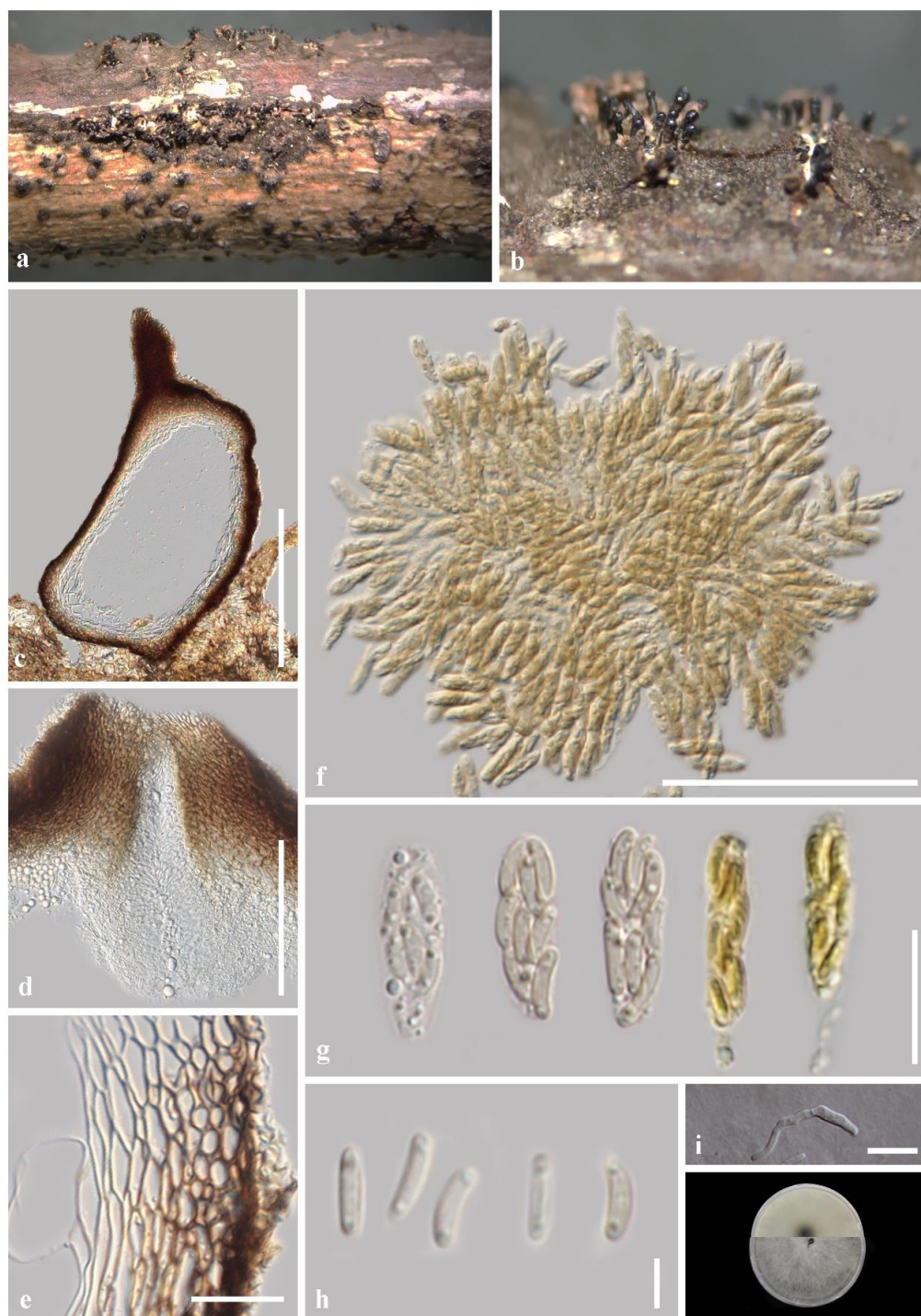


Figure 87 – *Peroneutypa longiasca* (MHZU 23-0050, a new host and a geographical record). a, b Fresh ascomata on the substrate. c Vertical section of an ascoma. d Ostiole. e Peridium. f–g Asci. h Ascospores. i A germinating ascospore. j. Colonies on PDA upper and reverse. Scale bars: c = 250 μm , d = 100 μm , e = 20 μm , f = 70 μm , g = 10 μm , h = 3 μm , i = 5 μm .

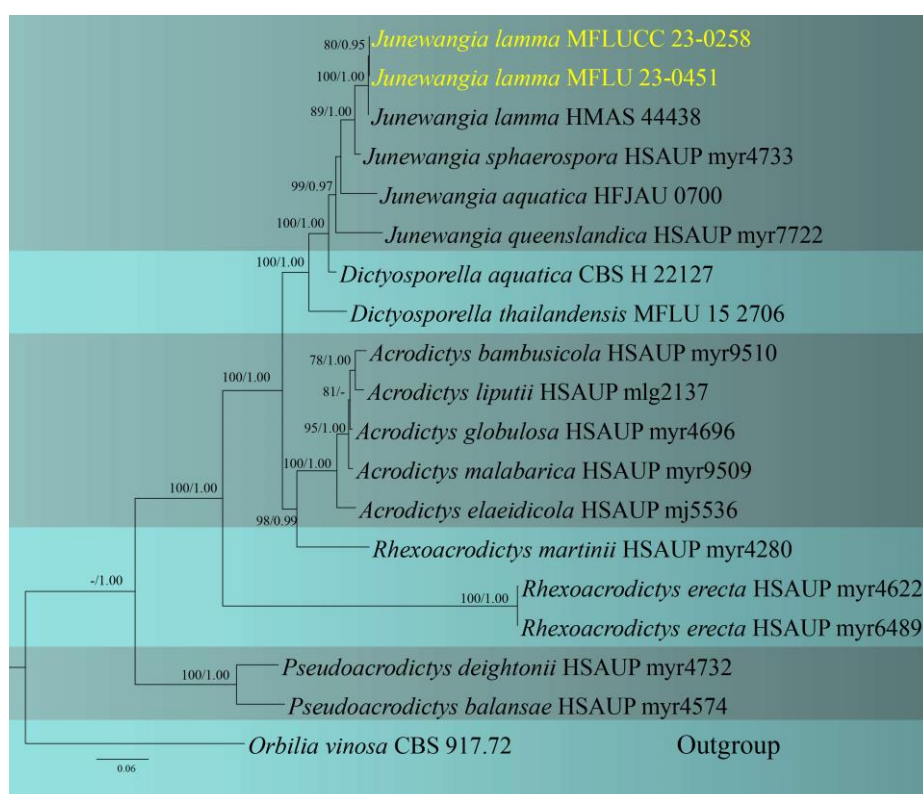


Figure 88 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU and SSU sequence data of *Junewangia*. Nineteen strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -8840.872322 is presented. The evolutionary model GTR +G is applied for all the genes. The matrix had 596 distinct alignment patterns, with 7.55% of undetermined characters or gaps. The estimated base frequencies were A = 0.237547, C = 0.231823, G = 0.287390, T = 0.243240; substitution rates AC = 1.016010, AG = 2.117608, AT = 1.067132, CG = 0.735253, CT = 5.648290, GT = 1.000000; gamma distribution shape parameter α = 0.273173. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Orbilia vinosa* CBS 917.72. Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

GenBank numbers – MFLUCC 23-0258: ITS: OR826589, LSU: OR826594, SSU: OR826600.

Known distribution (based on molecular data) – China (Hernández et al. 2000, Baker et al. 2002), Thailand (this study).

Known hosts (based on molecular data) – *Pandanus tectorius* (Hernández et al. 2000), submerged wood (this study).

Notes – In phylogenetic analysis, our strains (MFLUCC 23-0258 and MFLU 23-0451) clustered together with *J. lamma* (HMAS 44438) strain with 100% ML and 1.00 BYPP bootstrap support (Fig. 88). *Acrodictys lamma* was introduced by Hernández et al. (2000) and found on decaying leaves of *Pandanus tectorius* in Hong Kong, China. Later, Baker et al. (2002) synonymized *A. lamma* under *Junewangia lamma* based on morphological evidence. Xia et al. (2017) expanded the distribution of this species in Yunnan and Guizhou provinces, China whereas our collection is from Chiang Rai Province, Thailand. Morphological characters indicate that our collection is indistinguishable from *J. lamma*. Therefore, we describe here a new record for *J. lamma* in Thailand including new molecular data and illustration.



Figure 89 – *Junewangia lamma* (MFLU 23-0450, a new host record). a, b Colonies on natural substrate. c–h Conidiophores, conidiogenous cell and conidia of different development stages. i–k Conidia. l A germinating conidium. m, n Colonies on PDA (m) upper, (n) reverse. Scale bars: c–h = 20 µm; i–l = 5 µm.

Ascomycota genera incertae sedis

Pseudoacrodictys W.A. Baker & Morgan-Jones, Mycotaxon 85: 373 (2003)

Index Fungorum number: IF28723; Facesoffungi number: FoF06601

Pseudoacrodictys was introduced by Baker & Morgan-Jones (2003) to accommodate seven species of *Acrodictys*, including *P. eickeri* as the type species. The genus is characterized by solitary, acrogenous, subglobose, broadly pyriform to turbinate, brown conidia that are somewhat irregular, with brown undulate appendages (Gao et al. 2016). Currently, 14 species belong to this genus (Wijayawardene et al. 2022); however, molecular data in GenBank (<https://www.ncbi.nlm.nih.gov/>) is only available for two species (*P. balansae* and *P. deightonii*). Here, we provide an updated phylogeny for the *Pseudoacrodictys* taxa (Fig. 90).

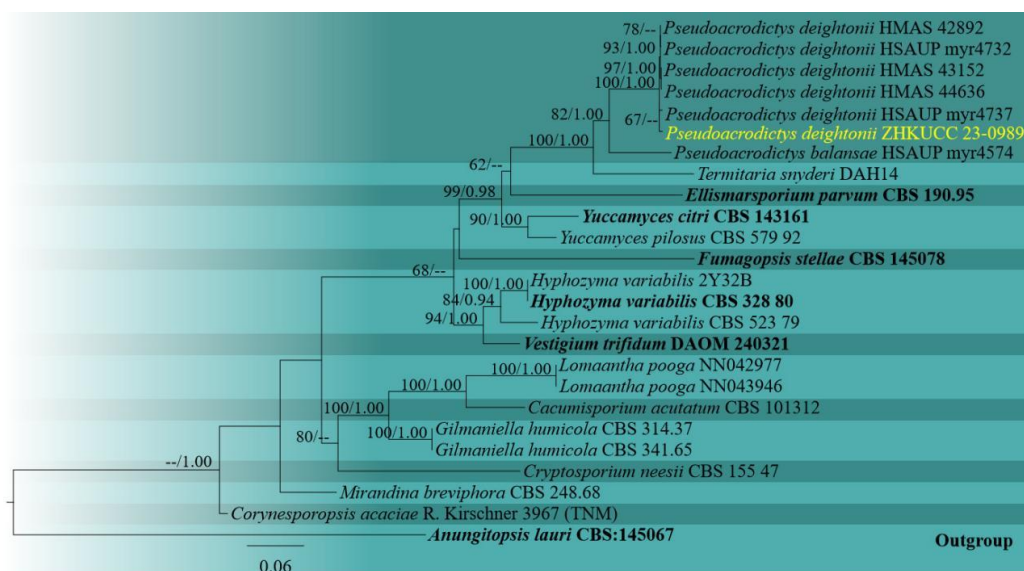


Figure 90 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, SSU and *tub2* sequence data of *Pseudoacrodictys*. Twenty-five strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -11371.407915 is presented. Evolutionary model GTR+I+G is applied for all the genes. The matrix had 731 distinct alignment patterns, with 46.33% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.259351, C = 0.212818, G = 0.303420, T = 0.224410; substitution rates AC = 0.735395, AG = 2.435768, AT = 1.079070, CG = 0.959961, CT = 6.710573, GT = 1.000000; gamma distribution shape parameter α = 0.526276. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. The tree was rooted with *Anungitopsis lauri* (CBS:145067). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

***Pseudoacrodictys deightonii* (M.B. Ellis) W.A. Baker & Morgan-Jones 2003**

Fig. 91

Index Fungorum number: IF373226; Facesoffungi number: FoF15260

Saprobic on dead branch of *Aquilaria* sp. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown. *Mycelium* partly superficial to immersed, composed of septate, branched, brown hyphae. *Conidiophores* 150–250 × 7–14(–17.5) μ m, macronematous, mononematous, erect, straight or slightly curved, septate, thick-walled, dark brown. *Conidiogenous cells* integrated, terminal, monoblastic, indeterminate, cylindrical, smooth, dark brown, truncate at the apex after schizolytic conidial secession. *Conidia* 40–120 × 50–130 μ m, acrogenous, solitary, subglobose or irregular, brown, dictyoseptate, with numerous obscure oblique septa, thick-walled, dry, sometimes cracking.

Culture characteristics – Conidia germinated on PDA within 48 h at 28 °C and germ tubes were produced from each cell. Colonies on PDA reached 2 cm diam. after two weeks at 28 °C. Colonies obverse: flat, irregular, floccose, white to pale grey, medium dense, irregular margin, and dark brown in reverse pale, edge is brown.

Material examined – China, Yunnan Province, Xishuangbanna, Menghai City, Agarwood plantation, on a dead branch of *Aquilaria* sp. (*Thymeleaceae*), 15 September 2021, T.Y. Du, YNA01 (GZAAS 23-0616, living culture ZHKUCC 23-0989).

GenBank numbers – ZHKUCC 23-0989: ITS: OR900221, LSU: OR898402, SSU: OR900226, *tub2*: OR914211.

Known distribution – China (Zhao et al. 2011, this study), Sierra Leone (Ellis 1961).

Known hosts – *Aquilaria* sp. (this study), *Cassia fruticosa* (Ellis 1961), *Gardenia nitida* (Ellis 1961), *Rauwolfia vomitoria* (Ellis 1961).

Notes – According to the phylogenetic analyses, our fungal strain (ZHKUCC 23-0989) clustered with *P. deightonii* strains (HMAS 42892, HMAS 43152, HMAS 44636, HSAUP myr4732 and HSAUP myr4737) with 100% ML and 1.00 BYPP bootstrap support (Fig. 90). Our fungal collection shares morphology with *P. deightonii* in having similar conidiophores, conidiogenous cells and conidial characteristics (Zhao et al. 2011). This collection has longer conidiophores and larger conidia (conidiophores: 150–250 μm ; conidia: 40–120 $\times$ 50–130 μm) than those of *P. deightonii* (HMAS 90312) (conidiophores: 40–120 μm ; conidia: 30–61 $\times$ 25–55 μm) (Zhao et al. 2011). This may depend on different environmental factors and host plants. This study is the first *Pseudoacrodictys* species found on *Aquilaria* species. Therefore, our fungal collection is identified as *P. deightonii* and we introduced a new host record based on morphological and phylogenetic analyses.



Figure 91 – *Pseudoacrodictys deightonii* (GZAAS 23-0616, a new host record). a, b Colonies on natural host substrate. c-i Conidiophores, conidiogenous cells and developing conidia.

j A germinating conidium. l–o Conidia. k, p Colonies on PDA from (k) above and (p) below (two weeks old). Scale bars: c–h = 100 μ m, i, j, l–o = 50 μ m.

Basidiomycota Whittaker ex R.T. Moore, Bot. Mar. 23 (6): 371 (1980)

Agaricomycetes Doweld, Prosyllabus Tracheophytorum, Tentamen systematis plantarum vascularium (Tracheophyta): LXXVII (2001)

Agaricales Underw., Moulds, mildews and mushrooms: 97 (1899)

Physalacriaceae Corner, Beihefte zur Nova Hedwigia 33: 10 (1970)

Mycotribulus Nag Raj & W.B. Kendr., Can. J. Bot. 48(12): 2219 (1970)

Index Fungorum number: IF9037; Facesoffungi number: FoF07459

Mycotribulus was introduced as a coelomycetous genus by Nag Raj & Kendrick (1970), and is typified by *M. mirabilis* collected from leaf litter of *Eucalyptus* spp. Phylogenetically, *Mycotribulus* is monophyletic, and morphologically related to *Ajrekarella*, *Dinemasporium* and *Polynema* due to conidial characteristics being hyaline, fusiform to navicular or ellipsoid with appendages (Li et al. 2020). However, they can be distinct based on the characteristics of conidiomata and paraphyses (Li et al. 2020). Index Fungorum (2024) listed two epithets under *Mycotribulus*, all of which have molecular data (Rungjindamai et al. 2008, Crous et al. 2014, Crous et al. 2015). Here, an updated phylogenetic tree for the *Mycotribulus* taxa is provided (Fig. 92).

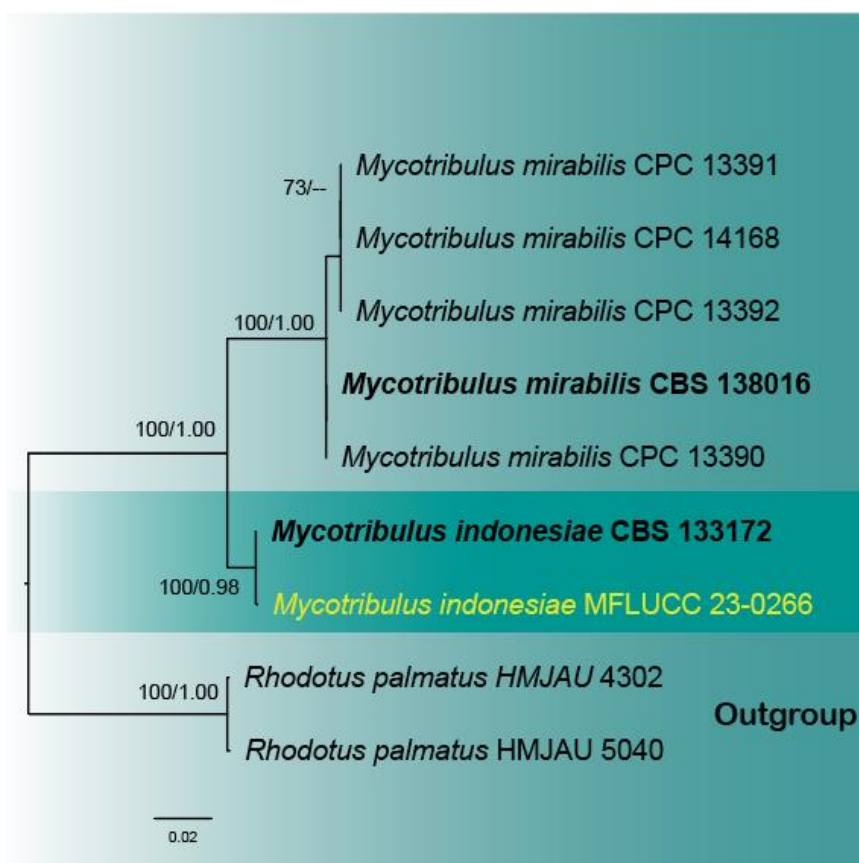


Figure 92 – Phylogram generated from the maximum likelihood analysis based on the combined LSU and ITS sequence data of *Mycotribulus*. Nine strains are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAXML tree with a final likelihood value of -3308.950200 is presented. The evolutionary model GTRGAMMA is applied for all the genes. The matrix had 97 distinct alignment patterns, with 3.28% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.248487, C = 0.198276, G = 0.264013, T = 0.289224; substitution rates AC = 1.483017, AG = 2.128947, AT = 2.457376, CG = 0.328246, CT = 6.166100, GT = 1.000000; gamma distribution shape parameter α = 0.244904. Bootstrap support values for ML greater than 70% and Bayesian

posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree was rooted with *Rhodotus palmatu* (HMJAU 5040 and HMJAU 4302). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Mycotribulus indonesiae Crous, Sydowia 67: 105 (2015)

Index Fungorum number: IF809685; Facesoffungi number: FoF14872

Fig. 93

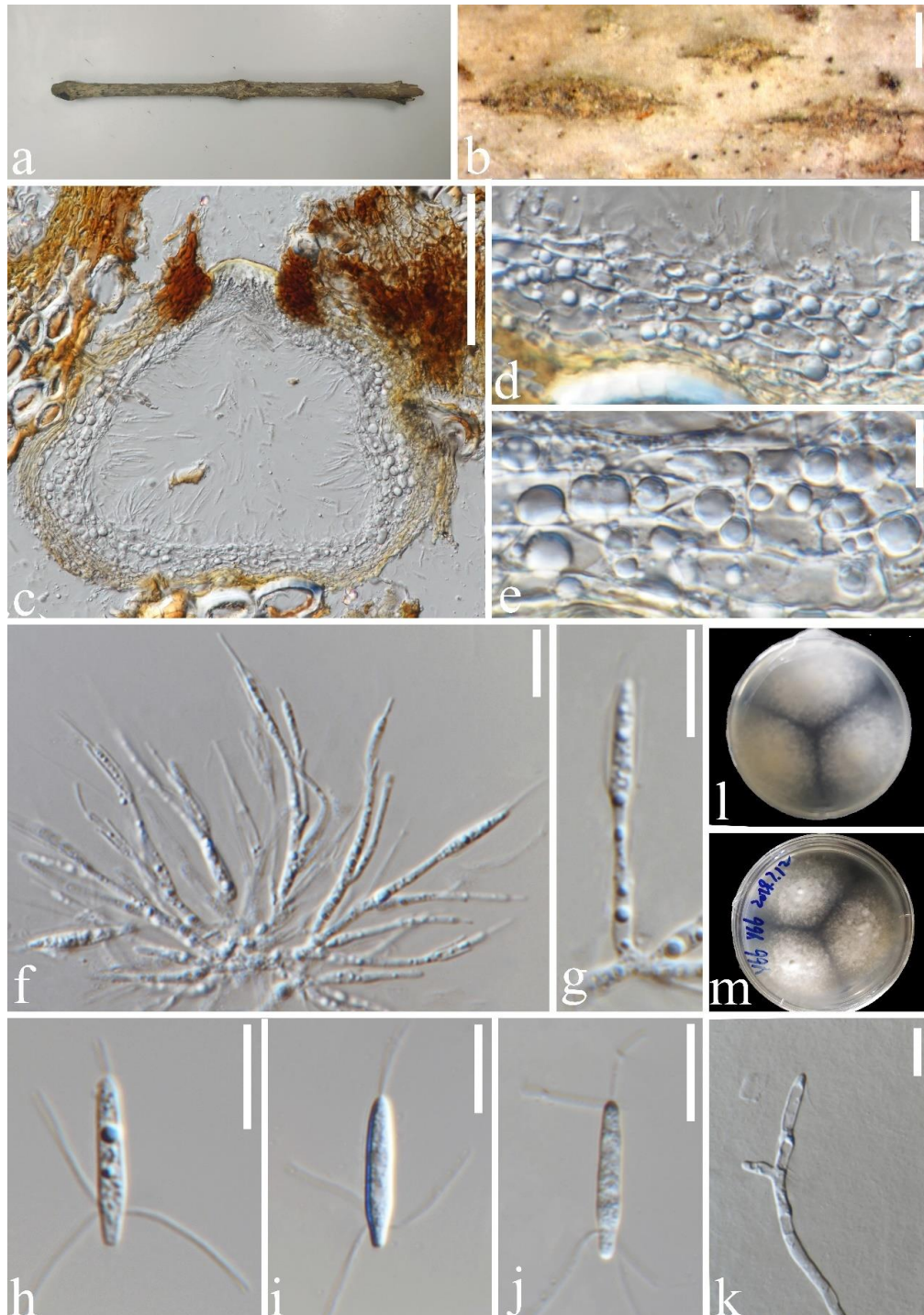


Figure 93 – *Mycotribulus indonesiae* (MFLU23-0467, a new geographical record). a Host. b Appearance of conidiomata on host surface. c Vertical section of a conidioma. d, e Sections through peridium. f, g Developing conidia attached to conidiogenous cells. h–j Conidia. k A germinating conidia l, m Colonies on PDA (m) from above and (l) below. Scale bars: b = 500 µm, c = 100 µm, d–k = 10 µm.

Saprobic on dead twig of unidentified wood. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 226–281 µm high × (214–)264–355 µm diam. ($\bar{x}$ = 257 × 316 µm, n = 10), pycnidial, mostly solitary, occasionally gregarious, immersed, subepidermal, subglobose to conical, thick-walled, glabrous, ostiolate, light brown. *Conidiomata wall* 25–56 µm wide, composed of thick-walled, hyaline cells of *textura angularis* to *textura globulosa*, with abundant guttules inside, lateral wall adjacent to host tissue composed of thick-walled, hyaline to yellowish cells of *textura prismatica*. *Conidiophores* 12–23 × 1.3–3 µm ($\bar{x}$ = 19 × 1.8 µm, n = 15), hyaline, branched, intermingled with paraphyses, cylindrical to subcylindrical, swollen at the base. *Conidiogenous cells* 6–17 × 1.2–1.9 µm ($\bar{x}$ = 11.5 × 1.5 µm, n = 20), holoblastic, terminal to lateral, cylindrical to subcylindrical, hyaline. *Conidia* 14.5–18 × 2.5–3 µm ($\bar{x}$ = 15 × 2.7 µm; n = 30), fusiform to naviculate, aseptate, smooth, guttulate, tapering to acutely rounded at both ends, hyaline, with hair-like, straight or slightly flexuous, 7.5–13.5 µm long ($\bar{x}$ = 11.5 µm, n = 30) appendages at both ends; apical appendage, polar, unbranched; basal appendages 2–3 laterally slightly above the truncate base, unbranched, divergent.

Culture characteristics – Conidia germinating on PDA within 15 h. Colonies growing on PDA, reaching 35 mm after 14 days at 25 °C, white, flattened, dense, radial, slightly cottony with aerial mycelium on the surface, with rounded margins, reverse white.

Material examined – Thailand, Kanchanaburi Province, Thong Pha Phum District, Pilok, on a dead twig of unidentified wood in a forest, 28 June 2019, Jing-Yi Zhang, Y66 (MFLU 23-0467), living culture, MFLUCC 23-0266.

GenBank numbers – ITS: OR826537 LSU: OR826540.

Known distribution (based on molecular data) – Indonesia (Crous et al. 2015), Thailand (this study).

Known hosts (based on molecular data) – *Eucalyptus pellita* and *E. brassiana* (Crous et al. 2015), unidentified wood (this study)

Notes – In the phylogenetic analyses, our strain (MFLUCC 23-0266) clustered with *M. indonesiae* (strain CBS 133172) with 100% ML and 0.98 BYPP bootstrap support (Fig. 92). *Mycotribulus indonesiae* was introduced by Crous et al. (2015), isolated from leaves of *Eucalyptus pellita* and *E. brassiana* (*Myrtaceae*) in Indonesia. Our collection matches the original diagnosis of *M. indonesiae* (Crous et al. 2015). Comparison of base pairs in LSU and ITS sequences revealed 99.50% (595/598, including 2 gaps) and 100% (890/890) similarities, respectively. Therefore, we identified our new collection as *M. indonesiae* and report a new geographical record of this species in Thailand.

Finally, we compiled a list of all 351 genera (including one family) discussed in Mycosphere notes 1–520 (Table 5).

Table 5 Genera in Mycosphere Notes 1–520.

Genus	Mycosphere note number	Reference(s)	Volume and page numbers
<i>Acarella</i>	292	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Achorella</i>	293	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Acrocallymma</i>	414, 415	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Acrodictys</i>	387	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Acrogenospora</i>	388	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Acrospermum</i>	198	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Actidium</i>	238	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Actinomucor</i>	154	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Alascospora</i>	294	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Albifimbria</i>	148, 149	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Alfaria</i>	215	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Alfaria</i>	150, 151	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Alfaria</i>	376	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557

Table 5 Continued.

Genus	Mycosphere note number	Reference(s)	Volume and page numbers
<i>Alina</i>	51	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Allocryptovalsa</i>	516	This study	This study
<i>Allophaeosphaeria</i>	18	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Alternaria</i>	119, 120, 121	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Alternaria</i>	38, 39, 40, 41, 42	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Amphisphaeria</i>	508	This study	This study
<i>Angatia</i>	274	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Anguillosporella</i>	295	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Angustimassarina</i>	112	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Angustimassarina</i>	416	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Aphanostigme</i>	76	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Apiospora</i>	509, 510	This study	This study
<i>Arthrinium</i>	221	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Ascitendus</i>	207	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Aspergillus</i>	158, 159	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Asterina</i>	199	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Asterinema</i>	296	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Asteromassaria</i>	297	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Asteromella</i>	298	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Asteronia</i>	290	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Aureobasidium</i>	389	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Aureobasidium</i>	111	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Aureobasidium</i>	347	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Austropleospora</i>	423	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Bactrodesmium</i>	299	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Bahusakala</i>	324	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Bahusutrabeeja</i>	320	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Balladyna</i>	52	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Balladynocallia</i>	53	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Balladynopsis</i>	54	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Bambusicola</i>	1	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Barbatosphaeria</i>	266	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Barbatosphaeria</i>	212	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Barriopsis</i>	469	This study	This study
<i>Belizeana</i>	279	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Bertiella</i>	178	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Bipolaris</i>	122	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Bonaria</i>	289	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Botryochora</i>	278	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Botryohypoxylon</i>	321	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Botryosphaeria</i>	102	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Botryostroma</i>	300	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Botrytis</i>	153	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Brevicollum</i>	183	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Bryorella</i>	301	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Byssocallis</i>	291	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Byssolophis</i>	283	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Byssosphaeria</i>	179	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Byssothecium</i>	281	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Caesiodiscus</i>	490	This study	This study
<i>Camarosporidiella</i>	171	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Cantharellus</i>	341	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Ceratosphaeria</i>	377	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Cerodothis</i>	302	Pem et al. (2019)	Mycosphere 10(1): 1115–1246

Table 5 Continued.

Genus	Mycosphere note number	Reference(s)	Volume and page numbers
<i>Cerothallia</i>	203	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Chaetomium</i>	130	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Chaetoplea</i>	247	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Chaetoscutula</i>	78	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Chaetosphaeria</i>	216	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Chaetosticta</i>	303	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Chevalieropsis</i>	74	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Chionomyces</i>	304	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Chuppia</i>	305	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Cladosporium</i>	228	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Cladosporium</i>	108, 109	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Cleistosphaera</i>	57	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Clonostachys</i>	462	Dong et al. (2023)	Mycosphere 14(1): 2208–2262
<i>Clypeococcum</i>	256	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Coccodothis</i>	306	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Coccoidella</i>	58	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Codinaea</i>	506, 507	This study	This study
<i>Colletotrichum</i>	136, 137, 138, 139, 140, 141	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Colletotrichum</i>	372, 373, 374, 375	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Colletotrichum</i>	502	This study	This study
<i>Collybiopsis</i>	382, 383	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Comoclathris</i>	357	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Comoclathris</i>	43, 44, 45	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Conicotenuis</i>	463, 464	Dong et al. (2023)	Mycosphere 14(1): 2208–2262
<i>Coniella</i>	135	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Coniochaeta</i>	370	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Coniothyrium</i>	2	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Conlarium</i>	390	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Conlarium</i>	494, 495, 496	This study	This study
<i>Corynespora</i>	418	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Crassiparies</i>	435	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Cronartium</i>	342	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Cryptophiale</i>	217	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Cryptovalsa</i>	142	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Cudonia</i>	491, 492	This study	This study
<i>Cyathicula</i>	487, 488	This study	This study
<i>Cytospora</i>	208, 209	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Cytospora</i>	371	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Dactylellina</i>	391	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Dendryphiella</i>	172	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Dendryphiella</i>	173	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Dermatodothis</i>	307	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Diamantinia</i>	267	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Dianesea</i>	308	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Diaporthe</i>	201, 211	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Diaporthe</i>	392	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Diaporthe</i>	132, 133, 134	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Dibaeis</i>	393	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Dictyocephalos</i>	339	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Dictyonella</i>	237	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Dictyospora</i>	394	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Didymella</i>	174	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Didymella</i>	113, 114	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114

Table 5 Continued.

Genus	Mycosphere note number	Reference(s)	Volume and page numbers
<i>Didymella</i>	3	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Didymocyrtidium</i>	309	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Dilophospora</i>	322	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Dimeriella</i>	88	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Dimerium</i>	59	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Diplodia</i>	200	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Diplodia</i>	103	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Discosia</i>	222	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Distoseptispora</i>	395	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Distoseptispora</i>	497, 498, 499, 500, 501	This study	This study
<i>Distoseptispora</i>	334, 335	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Dothichiza</i>	310	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Dothidasteromella</i>	275	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Dothiorella</i>	104, 105	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Dothiorella</i>	345	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Dothiorella</i>	470	This study	This study
<i>Dothivalsaria</i>	311	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Dubujiana</i>	286	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Dyfrolomyces</i>	201	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Dysrhynchis</i>	60	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Endosporium</i>	287	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Englerodothis</i>	285	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Eopyrenula</i>	241	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Epibelonium</i>	262	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Epibryon</i>	97	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Epicoccum</i>	175	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Epicoccum</i>	115	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Epicoccum</i>	4, 5, 6	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Episphaerella</i>	64	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Eudimeriolum</i>	80	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Eumela</i>	90	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Eumela</i>	277	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Excipulariopsis</i>	312	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Fasciatispora</i>	265	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Flabellascoma</i>	427	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Floricola</i>	123	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Fusarium</i>	396	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Fusarium</i>	146, 147	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Galiicola</i>	19	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Gibbago</i>	282	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Gibberidea</i>	276	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Gilletiella</i>	313	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Gliocladiopsis</i>	213	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Gloniopsis</i>	233	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Gloniopsis</i>	474	This study	This study
<i>Glonium</i>	232	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Gymnopus</i>	384, 385	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Halobyssothecium</i>	326	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Harknessiella</i>	314	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Hassea</i>	323	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Heliocybe</i>	386	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Helminthosporium</i>	397, 398	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Helminthosporium</i>	478	This study	This study
<i>Herpotrichia</i>	330	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156

Table 5 Continued.

Genus	Mycosphere note number	Reference(s)	Volume and page numbers
<i>Homostegia</i>	284	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Homostegia</i>	254	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Hyalomeliolina</i>	61	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Hymenoplella</i>	337	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Hypobryon</i>	315	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Hypsostroma</i>	325	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Hysterium</i>	348	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Hysterobrevium</i>	349	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Hysterocarina</i>	234	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Hysteroglonium</i>	235	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Hysterographium</i>	197	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Immotthia</i>	250	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Inocyclus</i>	71	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Irregularispora</i>	467, 468	Dong et al. (2023)	Mycosphere 14(1): 2208–2262
<i>Jarxia</i>	258	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Johansonia</i>	229	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Junewangia</i>	518	This study	This study
<i>Kalmusia</i>	352	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Kalmusibambusa</i>	7, 8	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Keratosphaera</i>	100	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Kirschsteiniotelia</i>	202	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Kirschsteiniotelia</i>	475	This study	This study
<i>Kirschsteiniotelia</i>	399	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Koordersiella</i>	280	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Kullhemia</i>	319	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Lasiodiplodia</i>	471	This study	This study
<i>Lasiostemma</i>	81	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Lepidosphaeria</i>	251	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Leptogium</i>	204	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Leptomeliola</i>	91	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Leptorhaphis</i>	259	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Leptospora</i>	355	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Letendraea</i>	351	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Letendraea</i>	476	This study	This study
<i>Leucoagaricus</i>	379, 380	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Leveillina</i>	92	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Lignosphaeria</i>	316	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Limaciniopsis</i>	317	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Lindgomyces</i>	248	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Linopeltis</i>	318	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Lizonia</i>	62	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Loculosulcatispora</i>	445, 446	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Lophiostoma</i>	117	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Lophiostoma</i>	426	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Lophiostoma</i>	430, 431, 432	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Lophiotrema</i>	424, 425	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Lophodermium</i>	206	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Macrovalsaria</i>	288	Pem et al. (2019)	Mycosphere 10(1): 1115–1246
<i>Macroventuria</i>	244	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Massarioramusclicola</i>	477	This study	This study
<i>Mazosia</i>	225	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Medicopsis</i>	184	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Melomastia</i>	400	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Melomastia</i>	473	This study	This study
<i>Melomastia</i>	449, 450, 451	Dong et al. (2023)	Mycosphere 14(1): 2208–2262

Table 5 Continued.

Genus	Mycosphere note number	Reference(s)	Volume and page numbers
<i>Microtheliopsis</i>	226	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Minimedusa</i>	166	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Minimispora</i>	465, 466	Dong et al. (2023)	Mycosphere 14(1): 2208–2262
<i>Monascostroma</i>	245	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Monascostroma</i>	246	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Montagnula</i>	401	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Montagnula</i>	420, 421	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Montagnula</i>	455	Dong et al. (2023)	Mycosphere 14(1): 2208–2262
<i>Mucidula</i>	381	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Mucor</i>	155, 156	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Mucor</i>	343, 344	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Muyocopron</i>	413	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Mycopcepon</i>	240	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Mycotribulus</i>	520	This study	This study
<i>Myxophora</i>	56	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Nectria</i>	503	This study	This study
<i>Nematostigma</i>	67	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Nematostoma</i>	82	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Nematothecium</i>	66	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Neoanthostomella</i>	152	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Neobrevicollum</i>	436	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Neocamarosporium</i>	182	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Neocoleroa</i>	89	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Neocucurbitaria</i>	419	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Neodendryphiella</i>	452	Dong et al. (2023)	Mycosphere 14(1): 2208–2262
<i>Neodidymelliopsis</i>	176	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Neofusicoccum</i>	106, 107	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Neokalmusia</i>	422	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Neokalmusia</i>	9,10	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Neolentithecia</i>	327	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Neolentithecia</i>	328	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Neoleptospora</i>	361	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Neomassaria</i>	118	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Neomassarina</i>	195	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Neooctidibambusa</i>	186	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Neoostropa</i>	486	This study	This study
<i>Neoparodia</i>	69	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Neopestalotiopsis</i>	124, 125	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Neopestalotiopsis</i>	514	This study	This study
<i>Neophaeosphaeria</i>	185	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Neophaeosphaeriopsis</i>	402, 403	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Neopyrenochaeta</i>	354	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Neoramichloridium</i>	15,16	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Neorousoella</i>	404	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Neosetophoma</i>	192, 193, 194	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Neosetophoma</i>	20	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Neospadicoides</i>	336	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Neostagonospora</i>	21,22	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Neotestudina</i>	252	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Neovaginatipora</i>	428	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Nigrograna</i>	405	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Nigrograna</i>	437, 438, 439, 440, 441, 442, 443	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Nigrograna</i>	482	This study	This study

Table 5 Continued.

Genus	Mycosphere note number	Reference(s)	Volume and page numbers
<i>Nigrospora</i>	511, 512, 513	This study	This study
<i>Oleaginea</i>	429	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Opeggrapha</i>	70	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Ophiocordyceps</i>	214	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Ophioparodia</i>	68	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Ophiosphaerella</i>	23	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Ostreichnion</i>	236	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Otidea</i>	205	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Otthia</i>	263	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Palmiascoma</i>	417	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Paraleptospora</i>	356	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Paramicrosphaeropsis</i>	454	Dong et al. (2023)	Mycosphere 14(1): 2208–2262
<i>Paramonodictys</i>	444	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Paraphaeosphaeria</i>	11	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Parasporendocladia</i>	504	This study	This study
<i>Parastagonospora</i>	24, 25, 26	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Parodiellina</i>	72	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Penicillium</i>	160, 161, 162	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Peniophora</i>	167	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Periconia</i>	187, 188, 189	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Periconia</i>	17	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Perisporiopsis</i>	73	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Peroneutypa</i>	517	This study	This study
<i>Pestalotiopsis</i>	406	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Pestalotiopsis</i>	126, 127	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Pestalotiopsis</i>	515	This study	This study
<i>Pestalotiopsis</i>	459, 460, 461	Dong et al. (2023)	Mycosphere 14(1): 2208–2262
<i>Phaeodimeriella</i>	75	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Phaeoisaria</i>	218	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Phaeopoacea</i>	27, 28, 29	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>*Phaeoseptaceae</i>	190	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Phaeoseptum</i>	191	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Phaeostigme</i>	93, 94	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Phellorinia</i>	340	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Phialemoniopsis</i>	269	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Phomatospora</i>	505	This study	This study
<i>Phragmeriella</i>	99	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Phragmocephala</i>	331	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Phycorella</i>	264	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Phyllosticta</i>	346	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Pilgeriella</i>	55	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Placocrea</i>	86	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Platystomum</i>	249	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Plectania</i>	493	This study	This study
<i>Plenodomus</i>	480, 481	This study	This study
<i>Pleospora</i>	46	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Pleostigma</i>	98	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Pleurotheciella</i>	219, 220	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Pleurothecium</i>	407	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Poaceascoma</i>	177	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Poaceicola</i>	30, 31, 32, 33	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Pododimeria</i>	77	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Polyclypeolina</i>	79	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Polycoccum</i>	257	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Pseudoacrodictys</i>	519	This study	This study

Table 5 Continued.

Genus	Mycosphere note number	Reference(s)	Volume and page numbers
<i>Pseudobyssosphaeria</i>	180, 181	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Pseudocamarosporium</i>	116	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Pseudocapulatispora</i>	329	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Pseudocercospora</i>	110	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Pseudochaetosphaeronema</i>	433, 434	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Pseudocoleophoma</i>	453	Dong et al. (2023)	Mycosphere 14(1): 2208–2262
<i>Pseudofusicoccum</i>	472	This study	This study
<i>Pseudolachnea</i>	131	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Pseudonitschkia</i>	243	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Pseudopaucispora</i>	456	Dong et al. (2023)	Mycosphere 14(1): 2208–2262
<i>Pseudopestalotiopsis</i>	128	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Pseudophialocephala</i>	362, 363, 364, 365, 366, 367, 368	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Pseudothyridariella</i>	447	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Pteridiospora</i>	170	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Pycnocarpon</i>	227	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Pyrenidium</i>	242	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Pyrenophora</i>	47	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Pythium</i>	168	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Quasiconcha</i>	239	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Raciborskiomyces</i>	101	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Rhizophila</i>	270	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Rhizopus</i>	157	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Rhodoveronaea</i>	408	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Rhytidhysterion</i>	350	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Rivilata</i>	230	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Robillarda</i>	359	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Roussoella</i>	196	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Roussoella</i>	409	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Roussoella</i>	48, 49	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Saccardia</i>	271	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Savoryella</i>	378	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Schizothyrium</i>	83	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Scolionema</i>	95	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Seimatosporium</i>	223	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Seimatosporium</i>	129	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Semifissispora</i>	63	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Septoriella</i>	34, 35	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Setophoma</i>	36	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Sparticola</i>	50	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Spegazzinia</i>	12	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Sporocadus</i>	360	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Stagonospora</i>	13, 14	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Stomatogene</i>	84, 85	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Strangospora</i>	272	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Stuartella</i>	96	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Synnemapestaloides</i>	338	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Syrropeltis</i>	261	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Talaromyces</i>	163, 164, 165	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Talaromyces</i>	485	This study	This study
<i>Tarzettia</i>	332, 333	Hyde et al. (2021)	Mycosphere 12(1): 1101–1156
<i>Thelenidia</i>	273	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Thozetella</i>	369	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Thyridaria</i>	483	This study	This study

Table 5 Continued.

Genus	Mycosphere note number	Reference(s)	Volume and page numbers
<i>Tomasellia</i>	260	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Toroo</i>	87	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Torula</i>	457, 458	Dong et al. (2023)	Mycosphere 14(1): 2208–2262
<i>Torula</i>	410	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Torula</i>	358	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Torula</i>	484	This study	This study
<i>Trichoderma</i>	143, 144, 145	Jayawardena et al. (2018a)	Mycosphere 9(1): 1–114
<i>Trichoglossum</i>	411	Hyde et al. (2023)	Mycosphere 14(1): 663–744
<i>Tricladium</i>	489	This study	This study
<i>Truncatella</i>	224	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Uleodothis</i>	169	Hyde et al. (2018)	Mycosphere 9(2): 271–430
<i>Uleomyces</i>	65	Boonmee et al. (2017)	Mycosphere 8(10): 1695–1801
<i>Ulospora</i>	253	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Urupe</i>	268	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Vagicola</i>	37	Thambugala et al. (2017)	Mycosphere 8(4): 697–796
<i>Vaginatisspora</i>	353	Manawasinghe et al. (2022)	Mycosphere 13(1): 454–557
<i>Vaginatisspora</i>	479	This study	This study
<i>Valsaria</i>	448	Li et al. (2023a)	Mycosphere 14(1): 1436–1529
<i>Venturia</i>	255	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Vonarxella</i>	231	Doilom et al. (2018)	Mycosphere 9(4): 647–754
<i>Zeloasperisporium</i>	412	Hyde et al. (2023)	Mycosphere 14(1): 663–744

* Note for a family

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